JOINT MEETING OF ICHTHYOLOGISTS AND HERPETOLOGISTS

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The Joint Meeting of
ASIH SSAR HL
Ichthyologists & Herpetologists

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ABSTRACTS

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

Curtis Abney, Glenn Tattersall and Anne Yagi

Brock University, St. Catharines, Ontario, Canada

Thermal Preference and Habitat Selection of *Thamnophis sirtalis sirtalis* in a Southern Ontario Peatland

Gartersnakes represent the most widespread reptile in North America. Despite occupying vastly different biogeoclimatic zones across their range, evidence suggests that the thermal preferenda (T_{set}) of gartersnakes has not diverged significantly between populations or different *Thamnophis* species. The reason behind gartersnake success could lie in their flexible thermoregulatory behaviours and habitat selection. We aimed to investigate this relationship by first identifying the T_{set} of a common gartersnake species (*Thamnophis sirtalis sirtalis*) via a thermal gradient. We then used this T_{set} parameter as a baseline for calculating the thermal quality of an open, mixed, and forested habitat all used by the species. We measured the thermal profiles of these habitats by installing a series of temperature-recording analogues that mimicked the reflectance and morphology of living gartersnakes and recorded environmental temperatures as living snakes experience them. Lastly, we used coverboards to survey the current habitat usage of *T. s. sirtalis*. Of the three habitats, we found that the open habitat offered the highest thermal quality throughout the snake's active season. In contrast, we recorded the greatest number of snakes using the mixed habitat which had considerably lower thermal quality. Although the open habitat offered the greatest thermal quality, we regularly recorded temperatures exceeding the upper range of the animals' thermal preference. Therefore, the open habitat may have been less thermally attractive to *T. s. sirtalis* than the more buffered mixed shrub. Our data shows *T. s. sirtalis* may select more thermally stable habitats over habitats that present them with temperature extremes.

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

Cory Adams and Daniel Saenz

USDA Forest Service, Southern Research Station, Nacogdoches, Texas, USA

Calling Ecology of the Introduced Rio Grande Chirping Frog (*Eleutherodactylus cystignathoides*)

The Rio Grande Chirping Frog (*Eleutherodactylus cystignathoides*) is a small direct developing frog species in the family Leptodactylidae. Their native range extends from northeastern Mexico to extreme southern Texas; however, it has been rapidly expanding into other parts of Texas presumably by way of accidental human transport. Little information is known about this species across most of its introduced range. The purpose of this study was to determine the

calling ecology of the introduced Rio Grande Chirping Frog. We surveyed for calling Rio Grande Chirping Frogs at two sites within their introduced range, in eastern Texas, using automated recording devices set to record for the first minute of every hour, each day. We detected Rio Grande Chirping frogs calling every month, with calling mainly occurring during the warmer months. Calling activity was significantly positively associated with daily minimum temperature, day length, humidity and cumulative rainfall. The mild climate of eastern Texas appears to be suitable to support an established population of Rio Grande Chirping Frogs.

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460 Herpetology Physiology, Highland C, Saturday 14 July 2018

Joseph Agugliaro[1], Craig Lind[2] and Terence Farrell[3]

Fairleigh Dickinson University, Madison, NJ, USA. [2]Stockton University, Galloway, NJ, USA. [3]Stetson University, DeLand, FL, USA

Snake Fungal Disease Increases Resting Metabolic Rate and Total Evaporative Water Loss Rate in a Winter-active Snake (*Sistrurus miliarius*)

Despite increased monitoring efforts to assess the prevalence of snake fungal disease (SFD) in free-ranging snakes, little is known regarding its sublethal physiological consequences, including the energetic and hydric costs of infection. We sampled a population of winter-active Pygmy Rattlesnakes (*Sistrurus miliarius*) in central Florida known to exhibit SFD. Recent work in this population has suggested that SFD infection may incur a substantial energetic cost during winter when energy intake is limited, which we predicted would be manifested as an increase in resting metabolic rate (RMR) of SFD-infected snakes. Furthermore, given that *Ophidiomyces ophiodiicola* is a keratinophilic fungus that preferentially invades the epidermis, we predicted that SFD infection would also increase total evaporative water loss rate (EWL). To test these hypotheses, we measured RMR (CO_2 production rate) and EWL of 27 field-acclimatized *S. miliarius* as a function of SFD infection status (infected [n = 9], uninfected [n = 18]) and acute temperature (17, 25, 32°C) via open-flow respirometry. SFD infection status was assigned based on presence/absence of clinical signs of SFD and confirmed via detection of *O. ophiodiicola* DNA using qPCR of skin swabs. Both mean RMR and EWL were significantly higher in SFD-infected snakes across all temperatures, with mean RMR of SFD-infected snakes exceeding that of uninfected snakes by more than 30%. We also present results of modeling exercises that predict daily resting energy expenditure by free-ranging SFD-infected *S. miliarius* in winter, using simulated hourly body temperature profiles and incorporating presumptive effects of behavioral fever.

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

Daniel Akin and Aaron Geheber

University of Central Missouri, Warrensburg, Missouri, USA

Minnows be Dammed: Rapid Morphological Change Induced by Alteration of Stream Flow

Cyprinella lutrensis is historically a stream dwelling minnow species (Family Cyprinidae) native to Missouri. Now, via damming, *C. lutrensis* occurs in both streams and reservoirs, including those of the Osage River drainage. The construction of Truman Dam (completed in 1979) has resulted in relatively high abundances of *C. lutrensis* within the reservoir and its surrounding tributaries. The widespread distribution of this species across the reservoir and connected streams provided an optimal study system for testing the effects of habitat alteration (through stream impoundment) on fish populations. Specifically, we were interested in the effects of flow alteration on *C. lutrensis* body shape. We hypothesized that populations in systems with no flow (i.e., reservoirs) would have reduced body shape streamlining. This was predicted due to the known importance of fish body form as it relates to locomotion in differing environment types. Here, we assumed that body streamlining would be beneficial for swimming in flowing environments. Analyses of morphology comparing *C. lutrensis* samples taken from Truman reservoir to samples taken from surrounding streams in the Osage River watershed showed significant differences in body shape between reservoir and stream populations, which indicated greater streamlining in stream populations. One possible mechanism of change (flow induced phenotypic plasticity) was tested in the lab using stream flow mesocosm units. This experiment also yielded significant results in support of the original hypothesis, and displays rapid phenotypic change dictated by environmental factors. Methods used, result implications, and future directions of study will be discussed.

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

Maria Akopyan[1], Aryn Wilder[2] and Nina Therkildsen[1]

[1]*Cornell University, Ithaca, NY, USA.* [2]*San Diego Zoo, San Diego, CA, USA*

Characterizing the Genomic Basis of Local Adaptation in the Atlantic Silverside (*Menidia menidia*)

Linking phenotype to genotype remains a central biological pursuit, and is a powerful approach for discovering the factors driving adaptive divergence in nature. Here, we explore the genomic basis of local adaptation in the Atlantic silverside (*Menidia menidia*), an estuarine fish distributed along the world's steepest thermal cline along the east coast of North America. Prior work has demonstrated that the silverside shows pronounced signatures of local adaptation in various physiological and morphological traits despite ongoing gene flow across their distribution range, but the genomic basis for this divergence remains unknown. Using a QTL mapping approach, we dissect the genomic basis of key physiological traits by testing for statistical associations between variation in these traits and particular alleles within individuals. We test

the hypotheses that a) locally adapted traits map to genomic regions that also show signatures of divergent selection along the environmental cline and b) correlated locally adapted traits are genetically linked because they are controlled either by the same or linked genomic regions. By measuring phenotypic trait values and genotyping wild-caught parental populations and F2 intercrossed hybrids, we can understand the genomic patterns underlying adaptive trait divergence and evaluate how genomic trait architectures enable or constrain selection to overcome gene flow.

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

Rachel Alenius and Dean Williams

Texas Christian University, Fort Worth, Texas, USA

Can Specialists Generalize? Diets of Texas Horned Lizards (*Phrynosoma cornutum*) in Small Texas Towns.

The Texas horned lizard (*Phrynosoma cornutum*) is considered a threatened species in Texas and Oklahoma, due to substantial range declines over the past several decades. Horned lizards are believed to be highly vulnerable to habitat alterations, due to extreme specialization on ants, particularly harvester ants (*Pogonomyrmex* spp.). I analyzed diets of Texas horned lizards from two small towns of south Texas by identifying exoskeletons of prey items found in 133 fecal pellets. In contrast to previous studies, small-bodied big-headed ants (*Pheidole* spp.) were the most commonly consumed prey (40%), followed by harvester termites (*Tenuirostritermes cinereus*; 34%), and harvester ants (8%). The consumption of harvester ants varied between study sites and was related to the number of available harvester ant mounds per horned lizard. We also found evidence of harvester termite consumption at nearby ranches, suggesting these termites may serve as a comparable dietary alternative to harvester ants for horned lizards in southern Texas. These results contribute to increasing evidence that Texas horned lizards are not necessarily dependent on harvester ants when alternative high-quality prey are available.

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175 General Herpetology III, Highland B, Sunday 15 July 2018

Matthew Allender[1], Sarah Baker[2], Megan Britton[1] and Angela Kent[1]

[1]*University of Illinois, Urbana, IL, USA.* [2]*Illinois Natural History Survey, Champaign, IL, USA*

Snake Fungal Disease Reduces Skin Bacterial and Fungal Diversity in an Endangered Rattlesnake

Snake Fungal Disease (SFD), caused by *Ophidiomyces ophiodiicola*, is the most recently described fungal disease afflicting snake populations across North America and Europe. It has been proposed as a significant conservation threat and yet much about its ecology is unknown. To document ongoing prevalence and assess differences in microbial assemblages between positive and negative individuals, we collected 144 skin swabs from Eastern Massasaugas (*Sistrurus catenatus*) in 2015 and 2016. There was a significant depletion of bacterial and fungal diversity in

SFD-positive snakes. *Ophidiomyces* was present on the skin of affected animals, even on body sites distant to lesions indicating that the microbiome on entire surface of the skin is altered. *Ophidiomyces* was not detected in any SFD-negative snake. This is the first study to determine the impact that this fungal pathogen has on the skin microbiome.

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36 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Highland D, Thursday 12 July 2018

Kayla Anatone and Barry Chernoff

Wesleyan University, Middletown, Connecticut, USA

The Evolutionary Consequences of Living in a Historically Metal Polluted River: the Genetic Variation of Blacknose Dace (*Rhinichthys atratulus*)

Environmental stressors, such as pollutants, can shift selection pressures exerted on natural populations of freshwater fishes. Previous studies have observed that pollutants alter the genetic variation and genetic diversity of organisms. The loss of genetic variation within a population due to anthropogenic stress is primarily due to increased mortality. Studies have shown that mortality can be random or can be associated with particular genotypes. Pollutants can also act as a barrier to gene flow by limiting the migration of new genes into the affected population. The objective of this study is to evaluate the genetic diversity of populations of the freshwater fish, Eastern Blacknose Dace, *Rhinichthys atratulus*, inhabiting a mercury-contaminated river, the Still River, CT. Although, the release of mercury into the Still River from the hatting industry ceased in 1943, preliminary results show that high levels of mercury are currently found in the water column and in the muscle tissues of *R. atratulus*. We combine mercury measurement data with microsatellite genetic diversity data to decipher the microevolutionary processes that shape the genetic variation of *R. atratulus* Still River populations. This study will advance our knowledge on the pollutant-induced evolutionary processes that shape the genetic diversity of organisms inhabiting contaminated environments.

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

Corey Anderson[1], Colleen McDonough[1], Namrata Bhandari[1], Gregory Lee[2] and J. Mitchell Lockhardt[1]

[1]Valdosta State University, Valdosta, GA, USA. [2]Moody AFB Environmental Element, Moody Air Force Base, GA, USA

Spatial Distribution and Co-distribution of Burrows in a Syntopic Population of Nine-banded Armadillo (*Dasypus novemcinctus*) and Gopher Tortoise (*Gopherus polyphemus*)

The gopher tortoise (*Gopherus polyphemus*) and the nine-banded armadillo (*Dasypus

novemcinctus) now cohabit pine forests in the southeastern United States, but no studies have examined the co-distribution of burrows in a stand to determine whether they are segregating. We sampled all (163 gopher tortoise and 245 armadillo) burrow locations (after a prescribed burn) within a 13.35 ha plot of managed pine forest on Moody Air Force Base (near Valdosta, GA) and used point pattern analysis (coupled with GPS- and LiDAR-derived structural data) to examine intensity of burrowing and proximity between burrow types. Gopher tortoise burrows exhibited evidence of weak clustering at intermediate to long distances, but such clustering could be explained by slight inhomogeneity in the intensity of burrowing driven by covariates such as the distance to the edge of the stand. Similarly, apparent clustering of armadillo burrows could be partly explained by local variation in burrowing intensity, which was more extreme for the armadillo and appeared to be driven by locations of man-made berms, where burrowing intensity was significantly higher. At short distances, the processes driving the co-distribution of gopher tortoise and armadillo burrows exhibited evidence of independence, but results varied for longer distances contingent upon how the intensity function was estimated. Ongoing work focuses on modeling the effect of other potential covariates and on accounting for the effect of burrow cooptation by armadillos.

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

Thomas Anderson[1], Brittany Ousterhoust[2], Dana Drake[3], Jacob Burkart[4], Freya Rowland[4], William Peterman[5] and Jon Davenport[1]

[1]Southeast Missouri State University, Cape Girardeau, MO, USA. [2]National Great Rivers Research and Education Center, Alton, IL, USA. [3]University of Connecticut, Storrs, CT, USA. [4]University of Missouri, Columbia, MO, USA. [5]The Ohio State University, Columbus, OH, USA

The impact of climate variability on body size variation of larval salamanders

One expected consequence of environmental change is increasing variability in climatic conditions. For organisms that depend on suitable climatic conditions for certain life history events, such increases in climate variability may alter ontogenetic patterns, with subsequent ramifications to population and community dynamics. Altered breeding phenology in pond-breeding amphibians has already been demonstrated for numerous taxa, though typically only shifts in the mean or median date. We tested whether greater variability in temperature and rainfall patterns, expected proxies for greater variation in breeding phenology, resulted in increased body size variability of larval ringed (*Ambystoma annulatum*), marbled (*A. opacum*) and spotted salamanders (*A. maculatum*). We collected data on body size of each species from 162 ponds over a 5-yr period (2012-2016) at Fort Leonard Wood, MO. We estimated variability in body size, precipitation and temperature as the coefficient of variation. Rainfall variability in September–November has significantly increased over the study period, with the number of rainfall events greater than 10 mm significantly decreasing. The average minimum and maximum temperatures have also each increased by approximately 3 degrees Celsius, but not changed in variability. However, we found no significant relationship between climate and body size variability for any of our three species. Thus, increasing climatic variability has not resulted in greater body size variability. Numerous processes, including cannibalism, winter environmental stress, or compensatory growth, could be affecting body size, thus eliminating

our expectations of greater size structure with increasing variability in rainfall.

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

Thomas Anderson[1], Brittany Ousterhout[2], Freya Rowland[3], Jacob Burkart[3], Dana Drake[4] and William Peterman[5]

[1]Southeast Missouri State University, Cape Girardeau, MO, USA. [2]National Great Rivers Research and Education Center, Alton, IL, USA. [3]University of Missouri, Columbia, MO, USA. [4]University of Connecticut, Storrs, CT, USA. [5]The Ohio State University, Columbus, OH, USA

Direct effects influence larval salamander size more than indirect effects

Direct and indirect effects both influence population and community dynamics. The relative strengths of these two pathways are often tested for and disentangled using experimental approaches. Empirical evidence of direct vs indirect effects from observational studies is less understood, and thus such studies are needed to understand their *in situ* impacts. We examined how direct and indirect effects influenced patterns of larval body size of sympatric ringed (*Ambystoma annulatum*) and marbled salamanders (*A. opacum*). We recorded larval salamander density and size in 166 ponds surveyed from 2012–2014, along with biotic and abiotic features at each pond including densities of other food web members, habitat complexity, percent canopy cover and hydroperiod. We then determined the relative strength of direct and indirect pathways using structural equation models and path analysis. We found that ringed salamander body size was directly and negatively related to marbled salamander and leech densities, while red-spotted newts (*Notophthalmus viridescens*) and pond substrate amount had positive and negative indirect effects via their influence on marbled salamanders. There were also significant indirect effects of hydroperiod and canopy via their effect on leeches, which were much weaker in strength than the direct effects. Aeshnid dragonflies had a strong positive direct effect on marbled salamander body size, and there was a marginally significant and weaker indirect effect of hydroperiod via aeshnids on size. Overall, we found that a combination of direct and indirect effects were important in a species-specific manner, but that the relative strength of direct effects were typically greater.

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

A.Z. Andis

Yale University, School of Forestry, New Haven, Connecticut, USA

A New, Noninvasive Method of Batch-marking Amphibians Across Developmental Stages

Organisms that undergo complex morphological change like many amphibian species pose a particular challenge for marking individuals with labels that persist across ontogeny. I evaluate a method for non-invasive, inter-stage, mass marking of wood frog (*Rana* [*Lithobates*] *sylvatica*) larvae with calcein, a fluorochrome that binds to calcified tissue. I tested short- and long-term, inter- and intra-stage probability of detecting calcein labelled individuals via non-lethal observation. I compared the utility of two methods of rapid (< 10 min.) batch administration of calcein labels. The persistence of calcein labels is positively correlated with the mass and developmental stage of the individual at the time of marking. For larvae marked in later stages, the detection probability was 100% at metamorphosis and between 81-100% detectable in metamorphosed juveniles 146 days after marking. Larvae marked in early stages were 77% detectable 8 days after marking and 54% detectable upon metamorphosis. Calcein marking is a fast, reliable, non-invasive method for mass-marking amphibians that persists through metamorphosis with no adverse mortality or growth effects. This marking method is especially useful for species that are sensitive to handling and manipulation.

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

A.Z. Andis and David Skelly

Yale University, School of Forestry, New Haven, Connecticut, USA

Rapid, microgeographic divergence in a vernal pool amphibian metapopulation

Within a population, dispersal distances can vary over time and space in response to changing environmental conditions. Since both dispersal patterns and local environmental conditions can structure microgeographic divergence, we evaluated whether divergence patterns changed over time in a metapopulation of wood frogs (*Rana sylvatica*) by comparing phenotypes in 2001 and 2017. We further estimated whether distinctions in patterns of divergence at the two time points could be explained by changes in environment during the intervening period. Wood frogs breed in nonpermanent ponds; drying is often associated with loss of larval cohorts that fail to reach metamorphosis prior to pond drying. Previous research demonstrated microgeographic counter-gradient variation in these populations with respect to canopy cover over breeding ponds. We replicated this research by rearing embryos in a common garden to measure development rate in 1116 embryos representing 93 clutches from the same 12 ponds separated by less than 100 meters to over 5 kilometers. We estimated microgeographic variation as wright values for increasing dispersal kernels and compared the variation to data collected in 2001. There was no association between divergence and distance in either 2001 or 2017. In 2017, we found that microgeographic variation persisted in the metapopulation and was invariant to the assigned dispersal kernel distance. While the magnitude of variation was comparable between time points, the relationship between an environmental variable, canopy cover, and embryonic development rate changed. Our findings imply that, even when divergence persists over several generations, the drivers may shift.

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351 Lightning Talks II, Highland A, Saturday 14 July 2018

Nicole Angeli[1,2] and Lee Fitzgerald[2]

[1]*Auburn University, Auburn, Alabama, USA.* [2]*Texas A&M University, College Station, Texas, USA*

Repatriating species where threats still exist

A complex conservation challenge is how to repatriate extirpated species when persistent threats still exist in historic ranges. Even when threats persist at broad scales, reconfigured landscapes, such as when forests have regenerated, often contain patches of habitat for threatened biodiversity with relatively low levels of threat. On St. Croix, U.S. Virgin Islands, the St. Croix ground lizard (*Pholidoscelis polops*) was extirpated from the main island. The small Indian mongoose (*Herpestes auropunctatus*) caused the extirpation, probably in synergy with conversion of habitat to agriculture. Fortunately, the species persisted on two small cays and was later translocated to two islands. However, sugarcane cultivation ended by the 1950s, and forest and anthropogenic land cover types re-emerged. We predicted sufficient habitat for St. Croix ground lizards exists for repatriation to St. Croix comparing a map created in 1750 to the current landscape of St. Croix and finding statistical similarity. Based on a binomial mixture population model developed in the monitoring of the largest extant population, we estimated >142,000 lizards could inhabit protected areas that we ranked across St. Croix. Landscape transitions change the spatial configuration of threats to species and create opportunities for repatriation and rewilding. Threats such as invasive species may never be eliminated throughout species' historic ranges, or on islands, but it is important to recognize that the landscape of threats that drove extinctions is not static.

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

Nicole Angeli[1,2], Conor McGowan[3] and Anna Tucker[1]

[1]*Auburn University, Auburn, AL, USA.* [2]*Alabama Cooperative Fish and Wildlife Research Unit, Au, AL, USA.* [3]*Alabama Cooperative Fish and Wildlife Research Unit, Auburn, AL, USA*

Collaborative population modeling for the federal Species Status Assessments

To increase the transparency of decisions under the Endangered Species Act, the Fish and Wildlife Service (FWS) has developed the Species Status Assessment (SSA). Many FWS biologists tasked with developing SSAs must gather and synthesize data from many sources, are generally not trained in quantitative techniques, and are unsure what analyses are appropriate for the data. Reproducible, transparent modeling for conservation assessments are of central importance to conservation biology. Herein, we discuss completed and on-going projects to collaboratively assess the current and future status of species like Sonoran Desert Tortoises and Puerto Rican Boas with the FWS, academic biologists, and managers.

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

Carl Anthony

John Carroll University, University Heights, Ohio, USA

Edmund D. Brodie: Plethodontid Biologist

The most highly cited and visible work of Edmund "Butch" D. Brodie concerns the co-evolution of predators and dangerous prey. Thus, it surprises no one that Butch began his long career in salamander biology with his master's work on newt toxicity. What many followers of Brodie's research may not realize is that Butch was, and remains, a strong contributor to the biology of plethodontid salamanders. Butch's research program in plethodontid biology spans nearly 50 years and began with his dissertation work on the systematics of Western *Plethodon*. His more recent work has concerned systematics of tropical forms. In the intervening years, Butch tackled topics as varied as the evolution of mimicry and aposematism, community and foraging ecology, gland morphology, and of course, antipredator behavior. My master's research in the Brodie Laboratory at The University of Texas at Arlington examined the response of hymenopterans to surface mining. However, I spent as much time as possible in the Interior Highlands and Appalachians collecting and observing plethodontids. Butch encouraged this activity, involving me in a number of salamander projects that helped to place me as a PhD student in Robert Jaeger's laboratory. From there, I went on to study *Plethodon* of the Ouachita Mountains. I explore Butch's contributions to plethododontid biology with a focus on how his approach to research questions influenced on my own research in aggression, territoriality, and color polymorphism in *Plethodon*.

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367 Ichthyology Systematics II, Grand Lilac Ballroom South, Sunday 15 July 2018

Dahiana Arcila and James C. Tyler

Smithsonian Institution, Washington, DC, USA

Integrating molecules and fossils reveal multiple diversification shifts in marine fishes during the Cenozoic

Integrative evolutionary analyses based upon fossil and extant species provide a powerful approach for understanding past diversification events and for assessing the tempo of evolution across the Tree of Life. Here, we demonstrate the importance of integrating fossil and extant species for inferring patterns of lineage diversification that would otherwise be masked in analyses that examine only one source of evidence. We infer the phylogeny and macroevolutionary history of the Tetraodontiformes (triggerfishes, pufferfishes, and allies), a group with one of the most complete fossil records among fishes. Our analyses combined molecular and morphological data, based on an expanded matrix that adds newly-coded fossil species and character states. Beyond resolving the relationships and divergence times of tetraodontiforms with confidence, our diversification analyses detect a major mass-extinction event during the Paleocene Eocene Thermal Maximum (PETM), followed by a marked increase in speciation rates. While this pattern is consistently obtained when fossil and extant species are integrated, examination of the fossil occurrences alone failed to detect major diversification changes during the PETM. When taking into account non-homogeneous models, our analyses also detect a rapid lineage diversification increase in one of the groups (tetraodontoids) during the middle Miocene, which is considered a key period in the evolution of reef fishes associated with trophic changes and ecological opportunity. In summary, our analyses show distinct diversification dynamics estimated from phylogenies and the fossil record, suggesting that different episodes shaped the evolution of tetraodontiforms since the late Cretaceous.

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

Umilaela Arifin[1], Julian Glos[2], Djoko Iskandar[3] and Alexander Haas[1]

[1]Centrum für Naturkunde-Zoologisches Museum, Universität Hamburg, Hamburg, Germany.
[2]Biozentrum Grindel–Tierökologie & Naturschutz, Fachbereich Biologie, Fakultät für Mathematik, Informatik und Naturwissenschaften, Universität Hamburg, Hamburg, Germany.
[3]School of Life Sciences and Technology, Bandung Institute of Technology, Bandung, Indonesia

A glimpse of interaction dynamics among torrent–frog species in Sumatra, Indonesia

Bukit Barisan Selatan Mountain ranges, which stretches longitudinally in the island of Sumatra, provide numerous habitats (e.g., torrential streams habitat) for many different frog species living in this region. Three species which are usually recorded in such habitat are *Huia sumatrana*, *Sumaterana crassiovis*, and *Odorrana hosii*. The first two species have specialized larval form known as gastromyzophorous, which differentiate both species from *O. hosii*. During fieldwork in Sumatra from 2014–2015, we applied Visual Encounter Survey methods along the stream transect in Sumatra to document any cascade dwelling frogs in this type of stream habitats. We also recorded several ecological parameters (including distance from water and microhabitat) for each individual. Our analyses shows that there were indications of interaction dynamics among these three species within the torrents frogs' communities. In this very first ecological study for Sumatran torrent frogs, we present our preliminary observations on interaction dynamic within *Huia sumatrana*, *Sumaterana crassiovis*, and *Odorrana hosii* in Sumatran rainforest based on ecological data (distance from water and microhabitat) and propose further study on this topic.

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

Spencer Asperilla, Katie Brittain, Bridgette Ward and Gabriel Langford

Florida Southern College, Lakeland, FL, USA

A Survey of Parasites from *Anolis* Lizards on Andros Island, Bahamas: Do Ecomorphs Host Similar Parasite Assemblages?

The *Anolis* lizard ecomorphs of the Caribbean and Bahamian islands are a well-established example of both adaptive radiation and convergent evolution. However, due to a lack of parasite biodiversity surveys on these islands, it is unclear if the parasite fauna hosted by these lizards follow similar evolutionary pathways. This study attempts to determine if the parasites hosted by *Anolis* spp. display strict host specificity, which would indicate speciation events in-step with their hosts, or if the parasites have little specificity and are broadly distributed among the various lizard species. In 2015 and 2017, lizards were captured by hand and dissected as soon as possible after capture in three locations on Andros Island, Bahamas. First, an external exam was conducted to look for ticks and mites, then blood smears and fecal samples were taken to search for blood protozoans. Parasites and hosts were preserved and brought back to the Parasitology Lab at Florida Southern College. Preliminary results found the ground-trunk lizard, *Anolis sagrei*, to host nearly all species of parasites found in this study, whereas the treetop lizard, *Anolis smaragdinus*, hosted relatively few parasite species. We propose that this pattern is due to the parasites' intermediate hosts being ground-dwelling insects which would be more likely to consumed by ground-trunk lizards. Overall, our findings suggest that the parasites of *Anolis* display moderate levels of host specificity, thus some species may have speciated with their hosts, while others are generalists.

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434 NIA BEST STUDENT PAPER, Highland E., Friday 13 July 2018

Viviana Astudillo-Clavijo[1,2], Tobias Mankis[1] and Hernán López-Fernández[3]

[1]University of Toronto, Toronto, Ontario, Canada. [2]Royal Ontario Museum, Toronto, Onta, Canada. [3]University of Michigan, Ann Arbor, Michigan, USA

Field Records in Museum Collections Support Habitat as an Ecological Dimension of Diversification in the Adaptive Radiation of Geophagini Cichlids

Adaptive radiation, loosely defined as the diversification of an ancestor into descendent species adapted to diverse niches, is considered a foremost driver of species and phenotypic diversity. Geophagini, the largest tribe of riverine Neotropical cichlids, exhibits species and phenotypic diversification patters consistent with a continent-wide adaptive radiation. The early diversification of locomotor phenotypes towards different adaptive optima suggest that habitat may be one ecological dimension of adaptive diversification, since different locomotor strategies have major implications for habitat use. The collection of performance or ecological data for large numbers of species is impractical and therefore functional morphology has been a useful surrogate for ecological data in assessing macroevolutionary patterns of adaptation. Nonetheless, support for ecologically-driven adaptive evolution is strengthened if a correlation can be found between the measured phenotypes and the ecological variables for which those phenotypes are said to be adaptive. Field records archived in museum collections contain habitat records for hundreds of specimens and thus provide the opportunity to assess the phenotype-ecology correlation at a macroevolutionary scale. We test for an association between functional locomotor traits and structural habitat elements using standardized field records archived at the Royal Ontario Museum in order to assess whether habitat use may be an ecological dimension of diversification in the adaptive radiation of Geophagini.

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484 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Calder Atta[1,2], Darren Coker[1], Tane Sinclair-Taylor[1], Joseph Dibattista[1], Alexander Kattan[1], Alison Monroe[1] and Michael Berumen[1]

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Conspicuous and cryptic reef fishes from a unique and economically important region in the Northern Red Sea

Al Wajh lagoon in the Northern Red Sea contains a remote coral reef system that likely supports a novel fish community. The large (1500km^2), shallow (< 40m) lagoon experiences greater temperature and salinity fluctuations, and higher turbidity than most other Red Sea reefs. Since these conditions often influence coral communities and introduce physiological challenges, changes in reef-associated fishes are expected. We present much needed baseline data on fish biodiversity and benthic composition for this region. Underwater visual census of conspicuous fishes and standardized collections of cryptobenthic fishes were combined to provide a comprehensive assessment of these fish communities. We documented 153 fish species and operational taxonomic units, within 24 families, on a reef dominated by hard coral and soft sediment (39% and 32% respectively). The most diverse and abundant families were the Pomacentridae and Gobiidae, which contain several candidates for new species descriptions. Bray-Curtis dissimilarity distances for each site suggest a distinctive fish community within the lagoon, and coefficients of variation for each species show high variation in distribution across the lagoon. Species accumulation curves predict that additional sampling would document many more species throughout Al Wajh. Our findings provide the most extensive biodiversity survey of fishes from this region to date, provide a foundation for studying reef ecology in environments with high stressors on coral, and record the condition of the reef prior to major coastal development occurring in the near future.

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

Anna Ayvazyan[1], Davit Vasilyan[2,3] and Madelaine Böhme[1,4]

[1]University Tübingen, Tübingen, Germany. [2]JURASSICA Museum, Porrentruy, Switzerland. [3]Université de Fribourg, Fribourg, Switzerland. [4]Senckenberg Center for Human Evolution and Palaeoenvironment (HEP Tübingen), Tübingen, Germany

Morphology of the Pharyngeal Dentition of the Genus *Capoeta* (Cyprinidae) based on X-ray Computed Tomography: Implications for Taxonomy and Phylogeny

Capoeta is a herbivorous cyprinid fish genus, widely distributed in water bodies of Western Asia where they show a distinct biogeographic pattern with endemism to large fluvial drainage basins. As other cyprinids, the species of this genus are characterized by the presence of the pharyngeal dentition, which has taxonomic significance for this fishes. Despite this, the detailed morphology of the pharyngeal teeth, its interspecific and topologic variations, as well as the importance for taxonomy and phylogeny of the genus *Capoeta* is still not established. In the present study, we propose a new methodology based on the detailed 3-D morphology of the pharyngeal teeth of 10 extant *Capoeta* species. The results of this study show that the 3-D morphology of recent pharyngeal dentition of the genus provides important traits for the identification of isolated pharyngeal teeth at the generic and/or specific levels and has a potential phylogenetic signal. Both these patterns are very important for the taxonomy of cyprinid fishes and especially can be applied to fossil records.

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

Alan Babineau[1,2] and David Beamer[2]

[1]East Carolina University, Greenville, NC, USA. [2]Nash Community College, Rocky Mount, NC, USA

Testing the Utility of eDNA Detection for Species in Highly Turbid Coastal Streams

The collection of environmental DNA (eDNA) has been used successfully as a non-invasive, low impact sampling method for cryptic aquatic salamander species in mountain streams. We developed an eDNA sampling protocol aimed at detecting the presence of a NC Species of Special Concern, the Neuse River waterdog (*Necturus lewisi*). This species is endemic to the Neuse and Tar River drainages in Eastern North Carolina where it is sympatric with the closely related dwarf waterdog (*Necturus punctatus*) over most of *lewisi*'s range. We used transcriptome and genomic data to develop probes that were specific for each species. We used DNA extractions to confirm the specificity of the probes on a StepOnePlus real-time PCR system. We collected three 1L water samples per site from multiple streams that historically supported *Necturus lewisi*. The water from many of the sampled locations was highly turbid and often required multiple filter changes and many hours to filter a single 1L sample. Standard methods of real-time PCR for our eDNA samples failed due to PCR inhibition. Here we present some of our efforts to overcome PCR inhibition in these highly turbid waters.

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

Joseph Baecher and Stephen Richter

Eastern Kentucky University, Richmond, Kentucky, USA

Environmental gradients in old-growth Appalachian forest predict fine-scale distribution, co-occurrence, and abundance of woodland salamanders

Woodland salamanders are among the most abundant vertebrate animals in temperate deciduous forests of eastern North America. Because of their functional dominance in these ecosystems, woodland salamanders are responsible for the transformation of nutrients and translocation of energy between highly disparate levels of trophic organization: detrital food webs and high-order predators. However, the spatial extent of woodland salamanders' role in the ecosystem is likely contingent upon the distribution of their biomass throughout the forest. We sought to determine if natural environmental gradients influence the fine-scale distribution and abundance of Southern Ravine Salamanders (*Plethodon richmondi*) and Cumberland Plateau Salamanders (*P. kentucki*). We addressed this objective by constructing occupancy, co-occurrence, and abundance models from surveys within an old-growth forest in the Cumberland Plateau region of Kentucky. We found *P. richmondi* had a more restricted fine-scale distribution than *P. kentucki* (occupancy probability [ψ��] = 0.737) and exhibited variable abundance, from <250 to >1000 N•ha^{-2}, associated with increased soil moisture and reduced solar exposure due to slope face. While more ubiquitously distributed (ψ��= 0.95), *P. kentucki* abundance varied from <400 to >1000 N•ha^{-2} and was inversely related to increased solar exposure from canopy disturbance and landscape convexity. Our data suggest co-occurrence patterns of salamanders are primarily influenced by abiotic factors, and that populations likely occur independently, without evidence of competition. Given the realized role that woodland salamanders play in the maintenance of forest health, regions that support large populations of salamanders may provide enhanced support to the stability of the total forest.

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

Christina Baggett[1], Michael Fraker[1], Robert Denver[2], Barney Luttbeg[3] and Stuart Ludsin[1]

[1]The Ohio State University, Columbus, Ohio, USA. [2]University of Michigan, Ann Arbor, Michigan, USA. [3]Oklahoma State University, Stillwater, Oklahoma, USA

Performance Tradeoffs of Stress Hormone-mediated Antipredator Phenotypes in Wood Frog Tadpoles

Tadpoles exposed to predation risk display extensive antipredator phenotypic plasticity that enhances fitness by increasing the probability of survival. The induction of these responses, as well as their evolutionary and ecological significance, has been studied extensively. However, the underlying proximate mechanisms are largely unknown. Because these responses are employed with different lags to predator exposure and have different consequences to species interactions, it is critical that we learn how they are mechanistically integrated and what tradeoffs are implicated. Previous studies found that a stress hormone (corticosterone, CORT) mediates both behavioral and morphological responses to predation risk in ranid tadpoles and that a tradeoff exists between short- and long-term responses. Acute predation risk induces a reduction in CORT that permits a reduction in activity level, while chronic risk induces an elevation in CORT, promoting several morphological responses, but also a higher activity level. Previous work also showed that exogenous CORT elicited development of the antipredator tail morphology and increased locomotor activity; whereas, exposure to a corticosteroid synthesis inhibitor (metyrapone) blocked development of the tail morphology during concurrent predator exposure. We aim to quantify the development of the tadpole phenotype (specifically the transition from the initial behavioral response to the tail morphological response) under a range of ecological variables (predation risk, resource level), and to test the relative adaptiveness of the natural and artificially-induced phenotypes. Together, these experiments will test for a causal relationship between the tadpole neuroendocrine stress response and phenotypic expression, and whether the regulation is adaptive.

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

Troy Baird[1], Teresa Baird[1] and Richard Shine[2]

[1]*University of Central Oklahoma, Edmond, Oklahoma, USA.* [2]*University of Sydney, Sydney, NSW, Australia*

I Can See You Now: Influence of Vegetative Cover on the Social Dynamics of Male Eastern Australian Water Dragons

Physical attributes of local habitats may influence communication among individuals and have important effects on the social dynamics within complex animal societies. We compared the behavior of males living in the same confined population of eastern water dragons, one of Australia’s largest lizards, during two seasons when vegetative cover differed markedly. In 2009, horizontal visibility for lizards was limited and cover abundant owing to thick vegetative growth. Visibility was much higher and cover reduced seven years later (2016) because of human intervention to restore the native flora. The high lizard densities of 2009 were decreased by over 40% in 2016. There were 19% fewer females, but especially fewer (60%) males - both those that controlled territories and those vying to acquire defended areas some of which were confined to the underground drainage system. Males controlling territories in 2016 adopted different behavioral tactics than those in 2009, exhibiting lower rates of patrol and aggression under baseline conditions and less intense responses to temporary removal of individual territory owners. Instead, territory owners increased interactions with females, probably because male rivals could be signaled from a distance, especially from elevated perches (trees, rock walls). Our results suggest that variation in the environmental potential for visual signaling had significant effects on intra- and intersexual interactions and the intensity of costly aggression. Insights revealed by longitudinal observational research such as ours can be applicable to designing urban green areas that promote fitness, even in large conspicuous vertebrates such as water dragons.

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359 General Herpetology II, Highland B, Sunday 15 July 2018

Erica Baken and Dean Adams

Iowa State University, Ames, Iowa, USA

Repeated Evolution Across the Multiple Invasions of the Arboreal Microhabitat in Lungless Salamanders

For decades, biologists have strived to understand how and under what circumstances evolution is repeatable. The debate of contingency versus determinism is a perennial issue in evolution, and is informed by studying clades that have recurrently and independently faced the same evolutionary obstacle, providing a replicated evolutionary experiment. The family of lungless salamanders, Plethodontidae, are an ideal group with which to study this issue as different taxa have repeatedly colonized a diverse array of microhabitats. Plethodontids occupy terrestrial, aquatic, fossorial, saxicolous, and arboreal microhabitats, each of which present a unique set of selective pressures. The arboreal microhabitat is of particular interest due to the difficulties of climbing and desiccation avoidance in such an environment, leading us to investigate the question, “How, and under what circumstances, can plethodontids become arboreal?” To this end, we used a phylogenetically-informed approach to investigate which microhabitat types have transitioned towards arboreality and what effect these shifts have on morphological evolution. We found that at macroevolutionary scales, arboreal taxa appear to have evolved only from terrestrial lineages. This implies that some transitions between ecological regimes are inaccessible from an evolutionary perspective. With respect to morphology, arboreal and saxicolous lineages have a lower rate of morphological evolution than other lineages, even when only considering general body proportions. These findings indicate that the many evolutionary transitions to arboreality followed similar evolutionary paths, originating from terrestrial lineages and slowing morphological evolution once in the arboreal microhabitat, providing insights as to the circumstances under which evolution may be repeated.

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

Bryce Baker, Dustin Siegel and Jon Daven

Southeast Missouri State Univ., Cape Girardeau, Missouri, USA

Geographic variation in morphological traits of larval and paedomorphic *Ambystoma talpoideum*

Facultative paedomorphism is common in ambystomatid salamanders and the presence of paedomorphic phenotypes in populations are variable within species; e.g., *Ambystoma talpoideum*. It is currently unknown if morphological traits associated with paedomorphic individuals differ across a wide geographic range or if all converge on a similar phenotype. Three hypotheses were tested in the current study: 1) morphology differs between larval and paedomorphic *A. talpoideum*, 2) morphology differs between populations of *Ambystoma talpoideum* in both larvae and paedomorphs, and 3) paedomorphs are sexually dimorphic. To test these hypotheses, we measured five morphological traits of over 200 *A. talpoideum* specimens from two populations (one in South Carolina and one in Tennessee). We found that paedomorphic *A. talpoideum* had larger and longer heads in comparison to larval *A. talpoideum* after correcting for body size. These differences were consistent across both SC and TN populations. We found no difference in paedomorph *A. talpoideum* morphology across populations and no difference between males and females within populations. These results suggest convergence of morphological traits for larval and paedomorphic *A. talpoideum* across our two study populations. Paedomorphic salamanders are known to be efficient predators in aquatic communities. Therefore, larger heads in paedomorphs likely provide an advantage not only in predator-prey interactions, but also in interference competition with larval salamanders.

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462 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center; part of ASIH symposium: If Salamanders Could Speak, Saturday 14 July 2018

Kristin Bakkegard

Samford University, Birmingham, AL, USA

Chiggers, a lesser known threat to amphibian health

Chiggers are the larval form of trombiculid and leeuwenhoekiid mites which parasitize all terrestrial vertebrates. In anurans and caudates, chiggers burrow under the skin and can be seen by the naked eye as a moving red or orange dot, swollen nodules, skin lesions, or pustules. In summer 2013, 66% of 45 Northern Slimy Salamanders (*Plethodon glutinosus*) from north-central Alabama were infected with chiggers; one infected animal died shortly after collection. For the first time, in 20 years of field experience, I encountered chigger-infected salamanders, yet chigger-infected reptiles are not considered unusual. I conducted a comprehensive literature review on amphibians infected with chiggers in North America and discovered that the majority of the scientific literature on this topic is outside the traditional herpetological journals. Instead, the majority of work on chiggers and amphibians is published in the parasitological, entomological, natural history or zoo/wildlife pathology literature. This can be attributed to several factors – chiggers are small and difficult to identify, taxonomic keys are unclear, and the taxonomy for the entire order, including *Hannemania* and *Eutrombicula*, the two genera identified in the most infections, is difficult to follow and unresolved. Chiggers should be added to the list of factors contributing to amphibian decline. I also recommend that reports and studies of chigger infected amphibians, be, as oft is practicable, published in the herpetological literature to improve awareness and encourage further research into the contribution of chiggers and other multicellular parasites to amphibian decline.

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

Katherine Balasingham[1], Jake Daane[2], Matthew Harris[3] and Nathan Lovejoy[1]

[1]*University of Toronto, Scarborough, Canada.* [2]*Harvard, Boston, MA, USA.* [3]*Harvard Medical School, Boston, MA, USA*

Detecting evidence of positive selection in key osmoregulatory genes in freshwater and marine Beloniformes

Overcoming physiochemical barriers, such as differences in salinity, is a challenge for aquatic organisms. Evolutionary shifts between marine and freshwater habitats requires evolutionary changes in osmoregulation. Marine fish regulate to increase water uptake and remove intracellular ions to avoid dehydration, whereas freshwater fish need to excrete water and retain ions. Genes involved in regulating intracellular ion concentration and movement of water work to maintain internal ion and water balance. Evolutionary changes in these genes are likely associated with marine to freshwater habitat transitions, allowing freshwater adaption and speciation. We investigated selective pressures on several osmoregulatory genes in the Beloniformes (needlefishes, medakas, flyingfishes, and halfbeaks), an order that includes multiple marine and freshwater lineages. We used phylogenetic approaches to test for evidence of positive selection in candidate genes associated with osmoregulation.

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

Neil Balchan and Kevin Fraser

University of Manitoba, Winnipeg, Manitoba, Canada

Synchronous fall migratory movements in the red-sided garter snake (*Thamnophis sirtalis parietalis*)

Changes in movement and behavioural patterns are vital to a species' ability to inhabit a seasonally variable environment. In highly adverse or fluctuating conditions, a species' response must increase accordingly, with mass aggregations and migrations becoming common themes in several taxa. Long distance migratory movements are typically associated with endotherms, but such movements occur in a variety of taxa under necessitating circumstances. In central Manitoba, the red-sided garter snake (*Thamnophis sirtalis parietalis*) undertakes long distance migratory movements to travel between summer foraging habitat and winter communal hibernacula. While this phenomenon is unique among squamates, it remains relatively unstudied, with many of the factors relating to this movement being poorly understood. At the world's largest snake denning area near Narcisse, MB, we investigated: 1) fall movement timing, 2) changes in snake numbers over time at den sites, and 3) changes in body condition. Passive infrared camera traps were set in sub-highway snake tunnels to document movement events. Cameras revealed a movement interval from mid-August to early October, with 73% of snakes moving over a 10-day period. While microclimates among den sites varied, we found a strong relationship between snake numbers and air temperature. Individually marked snakes that were recaptured before denning (n=7) lost mass between sampling events (1%-9%). Our results suggest highly synchronous movements towards den sites with mass loss while snakes await ideal conditions for permanently remaining in hibernacula.

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

Carole Baldwin[1], Luke Tornabene[2] and D. Ross Robertson[3]

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

Below the Mesophotic

Mesophotic coral ecosystems, which occur at depths of ~40 to 150 m, have received recent scientific attention as potential refugia for organisms inhabiting deteriorating shallow reefs. These ecosystems merit research in their own right, as they harbor both depth-generalist species and a distinctive reef-fish fauna. Reef ecosystems just below the mesophotic are globally underexplored, and the scant recent literature that mentions them often suggests that mesophotic ecosystems transition directly into those of the deep sea. Through submersible-based surveys in the Caribbean Sea, we amassed the most extensive database to date on reef-fish diversity between ~40 and 309 m at any single tropical location. Our data reveal a unique reef-fish assemblage living between ~130 and 309 m that, while taxonomically distinct from shallower faunas, shares strong evolutionary affinities with them. Lacking an existing name for this reef-faunal zone immediately below the mesophotic but above the deep aphotic, we propose "rariphotic." Together with the "altiphotic," proposed here for the shallowest reef-faunal zone, and the mesophotic, the rariphotic is part of a depth continuum of discrete faunal zones of tropical reef fishes, and perhaps of reef ecosystems in general, all of which warrant further study in light of global declines of shallow reefs.

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

Suzana Bandeira[1,2], Aaron Bauer[1], Luis Ceriaco[3], Mariana Marques[3] and David Blackburn[4]

[1]Villanova University, Villanova, PA, USA. [2]Instituto Nacional da Biodiversidade e Areas de Conservacao, Luanda, Angola. [3]Museu de Natural e da Ciencia de Lisboa, Lisboa, Portugal. [4]Florida Museum of Natural History, Gainesville, FL, USA

The amphibians and reptiles from Malanje Province, Angola

Malanje province is one of the most herpetologically rich areas in Angola. It is dominated by the Miombo woodland Biome and includes important amphibian and reptile type localities such as Kalandula waterfall (formerly Duque de Braganca) and Pungo Andongo. However, many areas in Malanje have been inadequately surveyed. Between 2015 and 2017, we conducted several field trips in the province resulting in the collection of 33 herpetological taxa (14 frogs and 19 reptiles) from Cangandala National Park, including three species putatively new to science, eight new provincial records, and new records for rarely cited taxa in the country. Twenty-nine species (nine amphibians and ten reptiles) were collected from Kalandula waterfall and Pungo Andongo, and 44 taxa (nine frogs and 35 reptiles) were obtained during two trips to Lauca Dam, on the border of the province. In total 27 frogs and 50 reptiles of 35 and 68 previously recorded species were collected in Malanje, providing genetic, acoustic and morphological resources for ongoing and future systematic and providing an update basis for conservation management decisions.

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

William Barichivich[1], Jonathan Chandler[2], Pierson Hill[3], Kelly Jones[4], Marysa Milinichik[2], Katherine O'Donnell[1], Terry Peacock[2], Joseph Reinman[2], Brandon Rincon[4], Susan Walls[1], Kevin Enge[3], Anna Farmer[3], Thomas Gorman[4,5], Carola Haas[4] and Jeremy Preston[6]

[1]U.S. Geological Survey, Gainesville, FL, USA. [2]St. Marks National Wildlife Refuge, St. Marks, FL, USA. [3]Florida Fish and Wildlife Conservation Commission, Gainesville, FL, USA. [4]Virginia Tech, Blacksburg, VA, USA. [5]Washington State Department of Natural Resources, Chehalis, WA, USA. [6]Eglin Air Force Base, Niceville, FL, USA

Head-starting as a Conservation Tool for Flatwoods Salamanders: a Multi-stakeholder Perspective

The use of artificial propagation techniques to enhance recruitment of juveniles into wild populations, a practice known as "head-starting," is a widespread population supplementation tactic for imperiled species. In amphibians with complex life cycles, population sizes are generally considered to be regulated during the larval stage of development. Thus, the objective of head-start efforts for aquatic-breeding amphibians is often to increase metamorph recruitment into terrestrial adult populations. We used aquatic mesocosms to head-start larvae of the federally-endangered reticulated flatwoods salamander (*Ambystoma bishopi*) at Eglin Air Force Base (EAFB) and the federally-threatened frosted flatwoods salamander (*A. cingulatum*) at Apalachicola National Forest (ANF) and St. Marks National Wildlife Refuge (SMNWR). At SMNWR, mass at metamorphosis was significantly higher for larvae reared using a dried nutrient base of grass compared to one of leaf litter, whereas there was no significant effect of substrate type at ANF. At EAFB, head-started and naturally-emerging *A. bishopi* were of similar mass and snout-vent length, indicating that the environment of head-started individuals was likely similar to that of natural metamorphs. From 2015 to 2017, survival from time of introduction into mesocosms (as embryos or larvae) until metamorphosis was 54–97.8%, resulting in a total production of 1,130 metamorphs across all three sites. Our preliminary head-start efforts appear to be effective at rearing individuals through the vulnerable aquatic larval stage. However, complete success will depend on individuals returning as adults to breed for the first time, their continued breeding over multiple years and, ultimately, reproductive success of future generations.

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

Amanda Barker[1], Bryan Frazier[2], Douglas Adams[3] and David Portnoy[1]

[1]Texas A&M University-Corpus Christi, Corpus Christi, TX, USA. [2]South Carolina Department of Natural Resources, Marine Resources Research Institute, Charleston, SC, USA. [3]Florida Fish & Wildlife Conservation Commission, Fish & Wildlife Research Institute, Indian River Field Lab, Melbourne, FL, USA

Hybridization Between a Cryptic Species Pair, *Sphyrna lewini* and *S. gilberti*, in the western North Atlantic

Scalloped hammerheads (*Sphyrna lewini*) and Carolina hammerheads (*S. gilberti*) are cryptic species sympatrically distributed in the Atlantic Ocean off the southeastern United States. Currently the only morphological character used to differentiate between the species is the number of precaudal vertebrae. Therefore, we developed a panel of 1,490 diagnostic, nuclear-encoded single nucleotide polymorphisms (SNPs) that are fixed between the species. Individuals identified as *S. lewini* in the field were sequenced, 288 were confirmed to be *S. lewini* and 49 identified as *S. gilberti*. Visual inspection of fifteen ambiguous individuals revealed some individuals were heterozygous at nearly all diagnostic loci, indicative of first generation (F1) hybrids, and some individuals with approximately 75% alleles from one species 25% from the other species, indicative of backcrossing. A 1,000 base-pair fragment of the mitochondrial

control region was then amplified for 7 putative F1 hybrids and 8 putative backcrosses. All F1 hybrids had mtDNA haplotypes consistent with *S. gilberti*, indicating hybridization between female *S. gilberti* and male *S. lewini*.

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

Elizabeth Barron[1], Brad Moon[1] and David Penning[2]

[1]University of Louisiana at Lafayette, Lafayette, Louisiana, USA. [2]Missouri Southern State University, Joplin, Missouri, USA

When Push Comes to Shove: The Effects of Tunnel Width on Predation Performance in Kingsnakes

Pinioning is a predatory behavior used by many constrictor snakes where tight spaces limit their abilities to constrict. During pinioning, snakes use their surroundings to help subdue and incapacitate their prey. By pressing part of the body against a tunnel wall or other object and another part of the body against a prey animal such as a rodent, snakes can compress the prey and subdue or kill it. However, snakes probably encounter tunnels of different widths during foraging, which may affect their predatory movements to different degrees. We are quantifying pinioning performance of the Eastern Kingsnake (*Lampropeltis getula*) by using a pressure transducer to measure pinioning pressures. Specifically, we are testing how tunnel width affects maximum pinioning pressures. We expect that very narrow tunnels will elicit low pinioning pressures by severely limiting a snake's ability to form bends, very wide tunnels will elicit low pressures or coil formation, and tunnels of intermediate width will enable optimal pinioning performance. Our results will help reveal how pinioning behavior functions underground, where it is difficult or impossible to observe snake feeding the wild.

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

Henry Bart

Tulane University Biodiversity Research Institute, Belle Chasse, Louisiana, USA

The Value of Ichthyological Research Collections in Conservation Research

Natural history collections document centuries of biological collecting effort and changes in biotic communities during that time period. Collection data are frequently used in studies of ecological niche modeling involving one or small numbers of species. The data are seldom used in studies of species conservation because of concerns about sampling methods and sampling adequacy. The aim of this study is to demonstrate the value of collection data for assessing

trends in rare or imperiled species, using data mined from the Royal D. Suttkus Fish Collection. The samples involved were taken at the same sites at different dates, spanning 55 years (1950-2005). In most cases the collector was Royal D. Suttkus who sampled with students and other associates. In some cases, Suttkus collections are compared to other collectors. Gear types used in samples compared were the same, but sampling duration varied. To standardize sampling effort, samples collected in early time periods were randomly resampled to show how species accumulation changes as catch increases. The same method was applied to samples from more recent time periods and samples of equal catch from early and recent time periods were compared. The results suggest that resampling catch from large samples of long duration provides good baseline data for assessing how fish communities and species composition have changed over time. The study also suggests that modern sampling is frequently too short in duration and targeted on particular habitats and species to be representative of the fish communities present at a site.

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

Jeffrey Bartman and Katherine Greenwals

Eastern Michigan University, Ypsilanti, MI, USA

Population Genetics of Common Natricine Snakes Along an Urban-Rural Gradient in Southeast Michigan

Urban development provides intense challenges for wildlife. While some species can persist in urban areas, a clear understanding of population dynamics is lacking for many species of herpetofauna. We characterize individual health metrics and population genetic structure of two common urban residents, the Eastern Garter Snake (*Thamnophis sirtalis*) and the Northern Brown Snake (*Storeria dekayi*). In the spring and summer of 2017, we sampled 85 *T. sirtalis* (42 urban and 43 rural) and 63 *S. dekayi* (25 urban and 38 rural) along an urban-rural gradient in Washtenaw County, MI. Urban sites were located in city parks within Ann Arbor, while rural sites were located in outlying, heavily agricultural parts of the county. In addition, Ann Arbor is divided by the Huron River, which could potentially act as a wildlife corridor and mitigate negative effects of urbanization. Preliminary analysis shows that garter snakes in urban sites have significantly poorer body condition than snakes in rural sites. Genetic analysis is ongoing, but we predict that 1) urban populations of *T. sirtalis* and *S. dekayi* will be more structured in urban centers than in surrounding more natural landscapes, and 2) urban populations along the Huron River will be more connected than populations distant from the Huron River. Results from this study will be valuable for land managers and conservationists interested in the status of these ecologically important species.

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49 Herpetology Systematics, Highland B, Saturday 14 July 2018

Aaron Bauer, Ishan Agarwal and Luis Ceríaco

Villanova University, Villanova, PA, USA

Systematics of the *Hemidactylus* (Reptilia: Gekkonidae) of Sub-Saharan Africa

Hemidactylus is the second most species-rich genus of geckos and has radiated widely in Africa, tropical Asia, and the Palearctic. Although relationships among Indian and Arabian *Hemidactylus* have been well studied, only a few groups in sub-Saharan Africa have been investigated. We used a mulitlocus molecular phylogenetic approach to identify genetic diversity within two major groups of African *Hemidactylus*, the *H. mabouia* complex, and the West and Central African clade. *Hemidactylus mabouia* comprises a large number of geographically circumscribed species that share a similar morphology. Diversity in the group is lower in West and Central Africa than in southeastern Africa, although it appears that invasive populations of *H. mabouia* in the New World all represent a single Central African taxon. A clade of West and Central African *Hemidactylus* (exclusive of the *H. fasciatus* group) extends from southern Angola to the Western Guinean forest block. Allocation of names to lineages in this clade has historically been difficult and our results suggest extensive localized endemism, particularly from Angola to Cameroon, with multiple taxa in the *H. longicephalus*, *H. muriceus* and *H. echinus* species complexes. West Africa is also occupied by members of the *H. angularis* complex, which has its primary diversity in northeastern Africa. West, Central and southern Africa all exhibit previously unexpected *Hemidactylus* diversity.

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

Natalia Bayona-Vásquez[1], Travis Glenn[1], Manuel Uribe-Alcocer[2] and Píndaro Díaz-Jaimes[2]

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[2]Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autoónoma de México, Mexico City, Mexico

Population Genomics and Phylogeography of the Cosmopolitan Marine Pelagic Fish, Mahi-Mahi (*Coryphaena hippurus*)

Low levels of population genetic structure detected in widely distributed marine pelagic fishes have been attributed to processes such as, large effective population sizes, high capacity to disperse through migration and/or larvae drift which promotes gene flow between distant populations, and/or very recent population divergence events that can't be detected with a limited number of variable molecular markers. *Coryphaena hippurus* is a cosmopolitan fish found in tropical and subtropical waters, for which population genetic homogeneity has been reported. However with advances in protocols based on Next Generation Sequencing (NGS) it has become possible to detect subtle population genetic structure in other cosmopolitan pelagic species such as the yellowfin tuna. Here, we used ddRAD to develop a set of baits to screen more than a thousand variable nuclear loci in hundreds of individuals from around the globe using the method RADcap. We also assayed whole mitochondrial genomes in a more limited set of samples. We were able to assess the global population genetics and phylogeography of this ecologically and economically important species. Our results reveal the presence of at least three populations for *C. hippurus*, which corresponds to ocean basins Indo-Pacific, Atlantic and Mediterranean. The results highlight the importance of sea surface temperature breaks in South Africa and the Gibraltar Straight as biogeographic barriers and demonstrate how they modulate the distribution of the genetic diversity and demography of pelagic species.

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

Matthew Bealor[1], Victoria Kuhnel[2], Victoria Brady[1] and Kelsey Revicki[1]

[1]Rowan University, Glassboro, New Jersey, USA. [2]Drexel University, Philadelphia, Pennsylvania, USA

Bigger is Better: Dietary Quality Influences Bubble Nest Size and Mating Success of Male Siamese Fighting Fish, *Betta splendens*

Mating behavior of domestic *Betta splendens* involves females spending time near and under bubble nests constructed by males where females appear to inspect nests prior to mating. We hypothesized that females may use nest size, in part, to evaluate mate quality. We conducted standard dichotomous choice tests where we presented females with pairs of males matched for color and mass but that differed in the size of artificial nests provided (100 cm^2 vs. 25 cm^2 piece of bubble wrap). Females spent significantly more time associating and interacting with males displaying from large artificial nests over those provided with small nests. We also tested the effects of dietary quality on nest-building behavior. We compared mean bubble nest size between males fed a standard diet and those fed an enhanced diet for 21 days. During the final week, males were exposed to video playback of female mating behavior for two hours/day, during which nests were photographed and mean nest area was quantified using image analysis software. Males fed an enhanced diet initiated nest construction sooner (1.96 vs. 3.38 days), built significantly larger bubble nests (1304 vs. 591 mm^2), and maintained nests significantly longer (3.72 vs. 1.98 days) than males fed a standard diet. Females did not show significant mate preferences for enhanced diet or "healthier" males in the absence of bubble nests. Our results suggest that, at least with generally healthy males, female fighting fish rely heavily or solely on nest size to infer mate quality in order to select healthy mates.

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304 Herpetology Systematics, Highland B, Saturday 14 July 2018

David Beamer

Nash Community College, Rocky Mount, NC, USA

A Genomic Assessment of Diversity Within Waterdogs (*Necturus*)

Waterdogs (*Necturus*) are completely aquatic, paedomorphic salamanders distributed across the eastern United States. There are presently five or six species recognized by most authorities, however the number of species and species assignment of many populations has been problematic. To address the systematics and evolutionary history of these salamanders I sampled populations from each independent river drainage across their range. From each population I collected genomic data (~400 loci) and used this data to reconstruct a phylogeny within a likelihood framework and to produce an ASRAL species tree. This data reveals extremely limited divergence between populations including those currently recognized as different species. This result is surprising because many of the river drainages have entered the ocean independently for long periods of time and which seems at odds with the patterns detected in this data set. Usually limited genetic diversity is interpreted as being due to gene flow or recency of inhabitation. The biology of *Necturus* makes both of these unlikely scenarios and I present an alternative hypothesis that might explain the low genetic diversity detected in the present study.

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217 General Herpetology III, Highland B, Sunday 15 July 2018

Steve Beaupre

University of Arkansas, Fayetteville, AR, USA

Venomous Snakes in the Academic Environment: Toward Safer Protocols.

The use of venomous snakes in academic research poses safety concerns that affect a variety of stake holders including graduate and undergraduate students (and their families), faculty researchers, department chairs, Deans, Provosts, institutional compliance boards (IACUC), and funding agencies. Researchers that engage in such potentially risky work have a responsibility to conduct themselves in a safe manner that minimizes risk to themselves and stakeholders. At the University of Arkansas, we utilize a three-tiered safety approach (Equipment, Distance, Attention) in all research endeavors with venomous snakes. However, accidents can and will happen and it is important for the circumstances of accidents to inform and improve evolving safety protocols. Herein, I discuss the philosophy of snake safety and the basic safety protocols in place at the University of Arkansas. I describe several mishaps, and show how the circumstances and information from these mishaps have shaped both the equipment and procedures that we use. Finally, I attempt to put academic snakebite into broader realistic context relative to other animal research endeavors. Such grounding is especially critical due to more sensational expectations of the public with respect to the abilities and intentions of the snakes.

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184 General Herpetology II, Highland B, Sunday 15 July 2018

Noemi Becza, Emily Seiter, Sarah Bolton and Ralph Saporito

John Carroll University, University Heights, Ohio, USA

A New Method for Extracting Alkaloid Defenses from Poison Frog Skins

The skin of dendrobatid poison frogs contains a diversity of alkaloids that serve as a defense against predation and microbial infection. The ecology and evolution of these defenses are of particular interest to biologists, especially given the variation with frog species, sex, age, size, as well as geographic location and over time. To date, the extraction, identification, and quantification of alkaloids has relied on frogs being sacrificed, a non-preferred endpoint given the CITES protective status of dendrobatids. Although some studies have safely extracted alkaloids from frogs using a Transcutaneous Amphibian Skin Stimulator (TAS), this approach has been limited by providing only qualitative alkaloid data; however, this has never been tested. Herein, we quantitatively extract, identify, and compare alkaloid richness and quantity using a TAS method and standard method of whole skin extraction in the dendrobatid frogs *Oophaga pumilio* and *Oophaga granulifera* from Costa Rica. Our results suggest that alkaloid richness using the TAS method is almost identical to that obtained in whole frog skin extractions. Furthermore, the quantity of alkaloids measured using the TAS method ranges from 25%–50% of the total quantity measured in whole frog skin extracts; however, alkaloid quantity using the TAS method is largely proportional to the total quantity of alkaloid present in whole skin extractions. Our findings suggest that the TAS method can be used to extract, identify, and quantify alkaloid defenses in individual frogs, which may reduce the need to sacrifice as many frogs when studying the chemical ecology of dendrobatids.

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

Anat Belasen and Tim James

University of Michigan, Ann Arbor, MI, USA

Host genetics and ecological interactions structure amphibian skin microbiome diversity

The host-associated microbiome, the community of microbes living on/within an organism, has become a popular area of study in animal health research. However, it remains to be understood what role host genetics plays in determining microbiome assembly and diversity. Microbiome studies also rarely examine both eukaryotes and bacteria. In this study, we (1) determined the impacts of host genetics on the microbiome, and (2) examined the associations between bacterial and eukaryotic taxa. We sampled Brazilian land-bridge island frog (*Thoropa taophora*) populations that were previously shown to exhibit low genetic diversity relative to mainland populations. We examined the effects on the microbiome of two aspects of host

genetics: (1) neutral genetic diversity, and (2) genotype at an MHC immune locus, which we hypothesized would play a role in the ecological selection of microbes. Frogs from genetically diverse populations hosted a higher diversity of microbes, and frogs that were MHC heterozygotes hosted a higher proportion of likely commensal (non-parasitic) microbes. We then employed a network-based analysis to determine the positive and negative associations between bacterial and eukaryotic taxa across hosts. Specifically we were interested in testing whether bacteria previously shown to inhibit fungal growth were negatively associated with fungal diversity. Preliminary results suggest no negative associations between the presence of "antifungal" bacteria and the abundance of microbiome fungi. The results of this study contribute to our understanding of how host genetics and ecological interactions between microbes impact the structure of the host-associated microbiome.

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358 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Katherine Bemis

Virginia Institute of Marine Science, Gloucester Point, Virginia, USA

Biology and taxonomy of the Golden Puffer, *Chonerhinos naritus* (Richardson, 1848) (Tetraodontiformes: Tetraodontidae) from Southeast Asia

The Golden Puffer, *Chonerhinos naritus* (Richardson, 1848) occurs along the east coast of India and throughout Southeast Asia. Previous work has focused on the toxicity of this species because it is consumed in Malaysia as a local favorite food and is celebrated annually during the Pufferfish Festival. Its biology and morphology, however, are poorly known. It is rare in museum collections (< 100 specimens worldwide), but available specimens come from both freshwater and brackish-marine environments; it is thought to be anadromous because this distribution is related to spawning behavior. I studied 34 specimens of *C. naritus* from throughout its range to collect meristic and morphological data; I also studied the anatomy of one individual using CT scanning to investigate its internal anatomy. *Chonerhinos naritus* has several anatomical features that are unusual for tetraodontids, including a large nasal organ, three lateral lines, and four times the number of dorsal- and anal-fin rays as found in other members of this family. I developed a new range map documenting the distribution based on the specimens examined. My observations suggest that *C. naritus* is primarily piscivorous because stomach contents consist of chunks of fishes, including portions of fins, which it processes with its sharp beak. Piscivory is not widespread within Tetraodontidae: most species feed on hard-shelled prey, and the closest relatives of *C. naritus* (species of the freshwater genus Auriglobus) specialize on fruits and seeds.

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

Katherine Bemis and Eric Hilton

Virginia Institute of Marine Science, Gloucester Point, Virginia, USA

Tooth morphology, development, and replacement in the Longnose Lancetfish, *Alepisaurus ferox* (Aulopiformes: Alepisauridae)

The Longnose Lancetfish, *Alepisaurus ferox*, feeds on cephalopods and mesopelagic fishes using exceptionally large, fang-like teeth. We used dry skeletons, histology, and microcomputed tomography (CT) scanning to study a series of 40 specimens of *A. ferox* from the western North Atlantic and North Pacific oceans to describe its dentition and tooth replacement. The smallest teeth occur on the premaxilla. These teeth are conical in shape and uniform along the length of the premaxilla. The palatine and dentary have: 1) elongate and laterally compressed fangs; 2) tall, conical teeth that are not laterally compressed, and 3) a series of sharp triangular teeth that are slightly recurved. Despite differences in sizes and shapes of teeth, all are replaced extraosseously. The teeth develop in the oral epithelium on the lingual side of the tooth bearing bones. Functional teeth firmly ankylose to the bone of attachment through a ring of ossification that forms at the base of each tooth. Most striking is the horizontal formation of replacement teeth for the elongate palatine and dentary fangs, which rotate into place and subsequently ankylose to the bone of attachment. This is the first study to document replacement of large fangs in teleosts that are replaced extraosseously, although large fangs are rotated extraosseously in snakes. We compare this mode of tooth replacement to the intraosseous horizontal fang rotation found in the scombroid *Trichiurus lepturus*.

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

Michael Benard and Hilary Rollins

Case Western Reserve University, Cleveland, OH, USA

Variation in Larval-Stage Temperature has Carry-Over Effects on the Growth of Post-Metamorphic Wood Frogs (*Rana sylvatica*)

The temperatures that organisms experience early in development can have lasting effects on their phenotype, performance, and fitness. The effects of temperature on egg and larval development in amphibians is well-understood, with warmer temperatures accelerating development. However, few studies test whether egg-stage and larval-stage temperatures have carry-over effects beyond metamorphosis. We used a 2X2 factorial design in which we manipulated egg temperature (cool vs. warm) and larval temperature (cool vs. warm) in wood frogs (*Rana sylvatica*), and tested whether those treatments affected postmetamorphic growth rates and locomotor performance. Neither egg temperature nor larval temperature affected post-metamorphic endurance or maximum jumping distance. However, post-metamorphic growth rate was significantly affected by larval-stage temperature. Juvenile frogs that were raised in cool temperatures as larvae exhibited an increase in post-metamorphic mass of 5%. In contrast, the mass of juvenile frogs that were raised in warm temperatures as larvae increased after metamorphosis by 16%. Thus, the effects of warmer temperature during the larval stage carried past metamorphosis to increase post-metamorphic growth rates of juvenile

frogs. Limiting experiments to a single life stage may miss important carry-over effects. The potential for strong carry-over effects to exist is important to keep in mind when attempting to predict the likely effects of climate change on amphibians.

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

Michael Benard, Kacey Dananay and Hilary Rollins

Case Western Reserve University, Cleveland, OH, USA

Warmer Winters and Earlier Breeding Lead to Colder Temperatures Experienced by Larval *Ambystoma* Salamanders

Shifting phenology in a wide range of organisms is one of the best-described effects of climate change. For example, many spring-breeding amphibians are now breeding earlier in the year compared to past decades. Yet the consequences of many shifts in phenology are unknown. Do they allow species to buffer changes in temperature? Or do shifts in phenology expose species to different patterns of temperature? Here, we use a long-term study of a mixed population of smallmouth salamanders (*Ambystoma texanum*) and unisexual *Ambystoma* salamanders in northeast Ohio to investigate the effects of winter weather, the timing of breeding, and larval environmental conditions. Breeding date varied between years from late February to early April, and was tightly correlated with winter temperature. Salamanders bred earlier during warmer winters, and later during colder winters. Breeding date was also associated with temperature during the larval period. In years when salamanders bred earlier, their larvae experienced colder average temperatures compared to years when salamanders bred later. Thus, rather than buffering salamanders against warmer temperatures, earlier breeding exposed tadpoles to a different range of temperature. These results also provide a cautionary note to the many experimental studies that test for ecological effects of climate change on amphibian larvae by exposing larvae to warmer conditions. At least for early spring-breeding amphibians, climate change may result in colder larval temperatures due to shifts in phenology.

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

Abigail Berkey[1], David McLeod[2], William Flint[2], Oliver Hyman[2], Gregory Steffenson[2], Cerrie Mendoza[3], Rayna Bell[4], Daniel Mulcahy[4,5], Roy McDiarmid[4,6] and Steve Gotte[4,6]

[1]*Wilson College, Chambersburg, PA, USA.* [2]*James Madison University, Harrisonburg, VA, USA.* [3]*Eastern Mennonite University, Harrisonburg, VA, USA.* [4]*Smithsonian Institution, National Museum of Natural History, Washington, DC, USA.* [5]*Global Genome Initiative, Washington, DC, USA.* [6]*USGS Pawtuxent Wildlife Research Center, Washington, DC, USA*

Biodiversity Information Serving Our Nation (BISON): Adding New Tools to the Conservation Toolbox

Biodiversity Information Serving Our Nation (BISON) is a web-based resource that compiles and maps species occurrence data for taxa in the US and its outlying territories. BISON occurrence data are based primarily on whole, preserved museum specimens, and recent efforts are focused on obtaining information for type localities. Unfortunately, many historical type materials lack corresponding genetic samples and DNA extraction from formalin-fixed type materials (i.e. most herpetological specimens) is difficult. This limits contemporary molecular research questions and impedes conservation and management decisions. With this in mind we undertook a pilot project to develop a standardized model for adding genome-quality, topotypic specimen data to the BISON infrastructure, and extend this to the DNA Barcode of Life Database (BOLD). We resurveyed type localities of amphibians in Virginia, collecting high- quality voucher specimens, genome-grade tissue samples, and chytridiomycosis swabs from specimens representing one anuran and 13 salamander type localities (3 families, 6 genera, and 18 species). Our objectives for this study were threefold: 1) to provide a standardized model for collecting genome-quality, topotypic vouchers 2) to make DNA barcode data publicly available through the BOLD portal, and 3) to train undergraduate students in all aspects of the project from specimen collection to data processing and archiving. Ultimately, this project represents an important step towards developing a sampling protocol that could easily be adapted for use by other regional institutions to “crowd-source” the effort to obtain genome-quality, topotypic vouchers, and DNA barcode data from the type localities of all North American vertebrate taxa.

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482 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Highland A, Thursday 12 July 2018

Justin Bernstein[1], Callie Crawford[2], Sara Ruane[1] and Brooke Flammang[2]

[1]Rutgers University-Newark, Newark, New Jersey, USA. [2]New Jersey Institute of Technology, Newark, New Jersey, USA

Assessing the Functionality of Scale Keels in Reptiles

Keels are raised structures or ridges that are found on the scales of many squamate taxa. Morphological examinations have noted keels in species descriptions for centuries, and it is well known that there is variation in keel structure and number across different squamate lineages adapted to different environments, especially taxa associated with swimming and semiaquatic habitats. Although the presence of these keels is well documented, the functionality of keels remains poorly known for the majority of squamates. In this study we assess the functionality of scale keels in snakes using flow visualization methods. We first microCT scanned 15 snakes with smooth and keeled scales from different habitats (e.g., terrestrial, aquatic) and 3D printed the CT scans. The 3D models were then placed in a flow tank for volumetric particle image velocimetry analysis (3D PIV). The results of these analyses suggest that keels accelerate water flow around scales and may help to reduce drag. Future research will examine the microstructure of keeled and smooth scales in terrestrial and aquatic taxa to better understand the functionality of keels on reptiles in non-aquatic environments. This project represents the first study that investigates the function of keels and expands our knowledge on the evolutionary adaptations of squamates.

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439 ASIH STOYE GENERAL ICHTHYOLOGY IV, Highland E., Friday 13 July 2018

Maxwell Bernt[1], Victor Tagliacollo[2], Aaron Fronk[1] and James Albert[1]

[1]University of Louisiana at Lafayette, Lafayette, Louisiana, USA. [2]Universidade Federal de Tocantins, Palmas, Brazil

Diversification of the Ghost Knifefishes (Gymnotiformes: Apteronotidae)

The Apteronotidae is the most species-rich and morphologically-disparate family of electric knifefishes (Gymnotiformes), with roughly 100 species in 15 genera. Apteronotids are found throughout the humid Neotropics from Panama to northern Argentina, but are most diverse and abundant in the main channels of large rivers in the Amazon Basin. The presence of diverse, sympatric assemblages in deep river channels in conjunction with highly-disparate cranial morphologies is a pattern suggestive of an *in-situ* Amazonian radiation. We use a species-dense, dated phylogeny and biogeographic model testing to estimate ancestral ranges and ultimately infer the effects of geologic history on apteronotid evolution. Our results suggest apteronotids arose in the early-mid Oligocene, with most diversification occurring during or after the Miocene. Ancestral area estimation placed the origin of the family in the Western Amazon. Most clades are largely limited to the Amazon and Orinoco basins, with only relatively recent colonizations of other basins. One notable exception is the genus *Apteronotus*, which is the only clade to exhibit early vicariance or dispersal into the La Plata, Magdalena, and Maracaibo basins. We suggest that this more eurytopic clade's ability to survive outside of deep river channels has allowed it to spread and diversify across the continent. For the majority of Apteronotidae, diversification appears to be inextricably linked to the formation of the modern Amazon River system.

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149 General Herpetology II, Highland B, Sunday 15 July 2018

Catherine Bevier[1], Matthew Chatfield[2] and Cheryl Frederick[2]

[1]Colby College, Waterville, Maine, USA. [2]Unity College, Unity, Maine, USA

Assessing Amphibian Health in Maine

Global decline and extinction of amphibian populations have been attributed in part to emerging infectious diseases such as chytridiomycosis, caused by the chytrid fungus, *Batrachochytrium dendrobatidis* (Bd), and illness from ranavirus. Not all frog populations are at risk of these diseases. Many species, including the Green Frog, *Lithobates clamitans*, are carriers and remain seemingly resistant to developing the diseases caused by these pathogens. This resistance may be related to extrinsic factors of a frog's environment, the pathogen itself, or is an inherent character of the frog's innate immune system. Antimicrobial peptides (AMPs) produced in frog skin secretions and metabolites produced by beneficial bacteria in a frog's skin microbiome offer intrinsic protection against pathogens and are extremely variable among frog species. On the other hand, these disease resistant species may be vulnerable to sublethal effects of environmental stressors, including pathogen infection and human activity. We are monitoring populations of *L. clamitans* in three locations that vary in anthropogenic activity. Isolated island populations are not infected with either pathogen and have relatively low levels of skin immune defense. Inland populations from areas with more or less agricultural activity test positive for both pathogens but have a more diverse skin microbiome. We have also evaluated behavioral and morphological characters, including calling activity, breeding coloration, and symmetry, to determine if males in these populations exhibit signs of stress that could compromise immune defense or reproductive fitness.

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

Joe-Felix Bienentreu[1], Samantha Grant[2], Danna M. Schock[3], Christopher Kyle[2], Craig Brunetti[2] and David Lesbarrères[1]

[1]Laurentian University, Sudbury, Ontario, Canada. [2]Trent University, Peterborough, Ontario, Canada. [3]Keyano College, Fort McMurray, Alberta, Canada

Epidemiology and Identity of Ranaviruses in a Low-Diversity Northern Ecosystem

Emerging infectious diseases (EIDs) are recognized as a global threat to amphibians because outbreaks may lead to population die-offs, and possible species extinctions. Several morbidity and mortality events in Canadian amphibian populations have been linked to EIDs, but there have been few studies assessing the dynamics of EIDs in wild Canadian amphibians, especially in northern Canada. Thus, the true dimension of pathogen associated declines and die-offs is likely underreported. Our study closes important knowledge gaps on the epidemiology of *Ranavirus*, a genus of viruses known to cause lethal systemic infections in amphibians. Our study focused on wetlands north of the 59th parallel in northern Alberta and the Northwest Territories. We assessed *Ranavirus* presence, prevalence, and strain identity through non-lethal sampling methods, using molecular tools for pathogen detection and identification. We used genetic analyses combined with GIS data to investigate the pathogens spatio-temporal patterns. In 2015- 2017 we sampled a total of 2146 individuals at 20 sites (Wood Frog *Rana sylvatica*, n=1352; Boreal Chorus Frog *Pseudacris maculata*, n=642; Canadian Toad *Anaxyrus hemiophrys*, n=152). Our results show a widespread presence of the pathogen across the landscape, but most infected individuals have a low infection severity. Sequencing has led to the identification of a formerly unknown strain of *Ranavirus*, as well as a FV3-like strain. Laboratory-based studies are planned to further investigate patterns found in our wild populations.

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

Emily Bierbaum, Raul Diaz and Christopher Beachy

Southeastern Louisiana University, Hammond, Louisiana, USA

Comparative Morphology of Hand and Foot Skeletal Elements in *Amphiuma* Salamanders

The postaxial polarity skeletogenesis of salamanders limbs (Order Caudata) follows a reversed pattern compared to other extant tetrapod groups. Within the Order Caudata, the Family

Amphiumidae underwent the reduction of limbs. The three species within the family, *Amphiuma pholeter* (One-toed Amphiuma), *Amphiuma means* (Two-toed Amphiuma), and *Amphiuma tridactylum* (Three-toed Amphiuma), vary in digit number, yet their limb structures have not been compared. *A. tridactylum* is the basal species, so observing the skeletal elements could help understand the fate of the mesopodial elements and its influence on the digit number in the derived species *A. means* and *A. pholeter*. Wrist and ankle bones of tetrapods vary drastically, so I will clear and stain the limbs with alcian blue and alizarin red to examine the variation in skeletal composition of the three amphiuma species to understand the assembly of the autopodium, and how *A. means* and *A. pholeter* evolved from *A. tridactylum* to vary in digit number.

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286 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Corinthia Black and Jonathan Armbruster

Auburn University, Auburn, AL, USA

Shape Analyses of the Peckoltia Clade Using 3D Geometric Morphometric Techniques (Loricariidae: Hypostominae)

Loricariidae is the most species-rich family in the order of Siluriformes, with nearly 1000 species currently recognized. Commonly known as the suckermouth armored catfishes, the Neotropical family is known for their unique traits that include ossified dermal plates that cover the body, integumentary teeth known as odontodes on the plates and fin spines, and a ventral oral disk used in feeding and to adhere to objects in their habitats. The Hypostominae account for over a third of the loricariids and is the most geographically widespread and ecomorphologically diverse subfamily. Hypostominae can be divided into nine tribe-level clades, with the most genus-rich clade represented by the Peckoltia group. The Peckoltia consists of nine genera and 52 species, and includes several undescribed genera. In addition to morphological diversity, diets and habitat preferences vary greatly across Peckoltia. The goal of this study was to analyze body shape using 3D geometric morphometric analyses in a phylogenetic and ecological context. In the stereomorph package in R, 33 landmarks that represent key anatomical features were rendered into three-dimensional space. Additionally, curves outlining the mouth and oral disk were captured across 11 species, and shape variation was summarized through a principal component analysis. The most recent phylogenetic tree was pruned and overlaid onto the PCA using the R package geomorph. Trophic and ecological data was mapped to the phylomorphospace in the R package OUwie. Preliminary results will be presented.

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

David Blackburn[1], Christopher Austin[2], William Bemis[3], David Cannatella[4], Kevin Conway[5], Alison Davis Rabosky[6], Casey Dillman[3], Benjamin Frable[7], Richard Glor[8], James Hanken[9], Philip Hastings[7], Dean Hendrickson[4], Eric Hilton[10], Sarah Huber[10], Michelle Koo[11], Travis LaDuc[4], Katherine Maslenikov[12], Amy McCune[3], Heather Prestridge[5], Daniel Rabosky[6], Zachary Randall[1], Alan Resetar[13], Luiz Rocha[14], Mark Sabaj[15], Carol Spencer[11], Adam Summers[16], Luke Tornabene[12], Gregory Watkins-Colwell[17], Luke Welton[8] and Edward Stanley[1]

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The oVert Thematic Collections Network

The oVert (openVertebrate) Thematic Collections Network, funded by NSF, is a new collaborative initiative among museums across the U.S. that aims to CT-scan ~20,000 fluid-preserved specimens representing > 80% of the approximately 10,500 extant genera of vertebrates. This project is generating free, publicly available three-dimensional anatomical data housed in MorphoSource.org. This collection of digital imagery and three-dimensional volumes will be open for exploration, download, and use to address questions related to the discovery of new species, comparative anatomy and diversity, ontogeny and growth, and hypotheses of function and evolution. Our network of leading U.S, vertebrate collections is developing best practices and guidelines for high-throughput CT-scanning, including efficient workflows, preferred resolutions, metadata, and archival formats that optimize the variety of downstream applications. Using digitized collections data via iDigBio, we are locating data-rich specimens (e.g., geocoded locality data, associated tissues, or media files) in U.S. museum collections representing type species of extant genera. Our network of institutions then loans relevant specimens to six participating institutions to perform CT-scanning for this TCN. Since September 2017, the oVert TCN has provided on-line access to CT-scans representing 800 genera (~1,500 species) of fishes, amphibians, and reptiles via MorphoSource.org. In total, the ~2,140 media files (images and 3D models) representing these specimens have been viewed approximately 80,000 times and downloaded 7,000 times. In addition to digitization, we will work with investigators, students, and educators to facilitate research and education using these digital resources. Supported by NSF DBI-1701714.

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

Cory Blackwelder[1] and Christopher Murray[2]

[1]The University of Central Missouri, Savannah, TN, USA. [2]Tennessee Technological University, Cookeville, TN, USA

Morphological Plasticity in Larval Hylid Tree Frogs as a Function of Abiotic Factors

Frogs and tadpoles can accommodate large degrees of morphological plasticity. However, most studies have only been performed on changes due to predator cues. Little is known about how abiotic variables, such as flow, impact the morphology of these animals. *H. cinerea* were collected during amplexus and the eggs were housed into two tanks that were set up with no flow conditions, and two that were set up with flow. Multiple clutches of *H. chrysoscelis* were collected in 2017 and were distributed among one flow and one non-flow tank. Approximately 30 individuals were placed in each tank. *H. cinerea* exposed to flow were significantly more laterally compressed. *H. chrysoscelis* exposed to flow showed significantly more elongation. In the spring 2018 season, more *H. chrysoscelis* and *H. cinerea* will be collected and placed into tanks with flow and tanks without flow.

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

Devin Bloom[1], Michael Burns[2] and Tiffany Schriever[1]

[1]Western Michigan University, Kalamazoo, MI, USA. [2]Oregon State University, Corvallis, OR, USA

Evolution of Body Size and Trophic Position in Migratory Fishes: A Phylogenetic Comparative Analysis of Clupeiformes (anchovies, shad and allies)

Migration is a widespread phenomenon among animals and has a profound influence on the evolution of species traits. Diadromous fishes are an extreme example of migration, moving between marine and freshwaters, often traveling thousands of kilometers for feeding and reproduction. Diadromy has been linked to changes in feeding ecology, body size, and various life history attributes. However, most studies have focused on intraspecific variation and associated mechanisms. In this study we use phylogenetic comparative methods to analyze body size and trophic position across Clupeiformes (anchovies, herring, shad and allies), a large clade of fishes that includes both diadromous and non-diadromous species. We found that diadromous species are larger than non-diadromous species, but there is no difference in trophic position, and that these patterns are not due to common ancestry. Diadromous species show a decoupling of body size and trophic position, while all clupeiforms have a positive relationship between body size and trophic position. Using a model fitting approach, we detected a signal of strong selection driving diadromous fishes to different adaptive peaks than non-diadromous fishes for body size, but a single adaptive peak for trophic position. We suggest that diadromous fishes have evolved larger body size than obligate marine and freshwater species as an adaptation to maximize energy expenditure during long distance migration.

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

René Bolom-Huet[1], Eduardo Pineda[2], Jorge Galindo-González[1], Antonio Muñoz-Alonso[3] and Francisco Díaz-Fleischer[1]

[1]INBIOTECA/ Universidad Veracruzana, Xalapa, Veracruz, Mexico. [2]Instituto de Ecología AC, Xalapa, Veracruz, Mexico. [3]El Colegio de la Frontera Sur, San Cristóbal de las Casas, Chiapas, Mexico

New infection risk areas of the pathogenic fungus of amphibians: *Batrachochytrium dendrobatidis* in Mexico.

Chytridiomycosis is an emerging disease caused by the fungus *Batrachochytrium dendrobatidis* (Bd) and is a cause of the population decline of several amphibian species worldwide. In Mexico, its presence is related to the reduction of amphibian populations in the country, however, its geographical distribution remains unknown. In this work we integrated new field data with published records to obtain the current and potential distribution of Bd in Mexico. We also assessed the frequency of infections by vegetation type and land use, as well as the elevation gradient in which the records of chytridiomycosis were presented. Our results show a greater risk area of Bd infection, since its distribution is not limited to highlands and temperate zones, but includes lowlands, coastal zones, tropical dry forests and deserts, our results contrast with previous works that suggest the geographical range of the pathogen is restricted only to temperate and well-preserved habitats. This work contributes to the description of new chytridiomycosis risk areas and provides basic information for the management planning and conservation of amphibian populations.

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

Amaël Borzée and Yikweon Jang

Ewha Womans University, Seoul, Korea, Republic of

Segregated Evolutionary History Revealed by Brumation and Hibernation Habitat Selection of Two Closely Related Treefrog Species

Most amphibians are known for migrating between flooded habitats for breeding and dry habitats for non-breeding activities. However, not all species migrate between flooded and dry habitats, and this difference in closely related species may highlight divergent evolutionary histories. Through field surveys during brumation and overwintering periods, Harmonic

Direction Finder tracking in fall and spring, and laboratory behavioural experiments for brumation and hibernation, we demonstrated differences in seasonal migration and hibernation habitats between *Dryophytes suweonensis* and *D. japonicus*. We found that *Dryophytes japonicus* migrated towards forests for overwintering and migrated back to rice paddies for breeding in spring. In contrast, *D. suweonensis* was found to hibernate buried in the vicinity of rice paddies, its breeding habitat. We also found that the difference in migrating behaviour matched with variations in microhabitat use during brumation and hibernation between the two species. Our findings highlight different ecological requirements between the two species, which may result from the segregated evolutionary history of the two species, with speciation potentially linked to a species use of a new breeding habitat. Separately, use of rice paddies for both breeding and hibernation may be an additive factor for the endangered status of *D. suweonensis*, because of the degradation of hibernation sites in winter.

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

Renan Bosque[1], Justin Lawrence[1], Richard Buchholz[1], Guarino Colli[2], Jessica Heppard[1] and Brice Noonan[1]

[1]*University of Mississippi, Oxford, MS, USA.* [2]*Universidade de Brasília, Brasília, DF, Brazil*

Diversity of warning signal and social interaction influences the evolution of imperfect mimicry

Despite the expectation that mimics should closely resemble their models, many mimetic species appear to be poor mimics. This is particularly apparent in some systems in which there are multiple available models. However, the influence of model pattern diversity on the evolution of mimetic systems remains poorly understood. We tested whether the number of model patterns a predator learns to associate with a negative consequence affects their willingness to try imperfect, novel patterns. We exposed chickens to coral snake (*Micrurus*) colour patterns representative of South American areas that differ in model pattern richness, and then tested their response to the imperfect mimetic pattern of a widespread species of harmless snake (*Oxyrhopus rhombifer*) in different social contexts. Our results indicate that chicks have a great hesitation to attack when individually exposed to high model pattern diversity and a greater hesitation to attack when exposed as a group to low model pattern diversity. Individuals with a fast growth trajectory (measured by morphological traits) were also less reluctant to attack. We suggest that the evolution of new patterns could be favoured by social learning in areas of low pattern diversity, while individual learning can reduce predation pressure on recently evolved mimics in areas of high model diversity. Our results could aid the development of ecological predictions about the evolution of imperfect mimicry and mimicry in general.

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

Carly Boye[1], Luis Ceriaco[1], Edward Stanley[2], David Blackburn[2], Mariana Marques[3], Suzana Bandeira[4], Aaron Bauer[4] and Matthew Heinicke[1]

[1]University of Michigan-Dearborn, Dearborn, MI, USA. [2]University of Florida, Gainesville, FL, USA. [3]CIBIO Research Center in Biodiversity and Genetic Resources, Vairão, Portugal. [4]Villanova University, Villanova, PA, USA

Phylogeny of Scincine Skinks (Squamata: Scincidae) of Southern Africa and Angola

Sub-Saharan Africa contains a diverse assemblage of skink taxa, including representatives of five currently recognized subfamilies (Acontinae, Eugongylinae, Lygosominae, Mabuyinae, Scincinae). One of these subfamilies, Scincinae, has a broad distribution across Africa, Eurasia, and North America. Scincinae is represented in southern Africa and Angola by members of the genera *Feylinia*, *Melanoseps*, *Proscelotes*, *Scelotes*, *Sepsina*, and *Typhlacontias*, which display varying degrees of adaptation for burrowing. Recent field work has allowed us to obtain tissue samples for a number of species previously not included in phylogenetic analyses. Using these data, we sought to construct a more robust phylogeny of the group. DNA sequences were obtained for several mitochondrial and nuclear loci. This includes for the first time complete species coverage of *Sepsina*, which has been represented in published phylogenies by only a single taxon. Concatenated and coalescent phylogenetic analyses confirm that the constituent genera of southern African/Angolan scincines are reciprocally monophyletic, and that divergences among lineages occurred throughout the Cenozoic. The historical biogeography of the group in southern Africa is discussed in reference to these relationships and divergence times.

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650 Ichthyology Ecology and Ethology, Highland E, Sunday 15 July 2018

Laurel Brandsmeier[1] and Richard Mayden[2]

[1]HudsonAlpha Institute of Biotechnology, Huntsville, Alabama, USA. [2]Department of Biology, Saint Louis University, St Louis, Missouri, USA

Quantitative and Descriptive Analysis of the Spawning Behavior of the Ornate Minnow, *Codoma ornata* (Cypriniformes; Leuciscidae)

The Ornate Minnow, *Codoma ornata*, is endemic to Mexico, occurring in rivers of the Rio Grande Drainage or headwater tributaries of some Pacific Slope drainages. *C. ornata*, like many other leuciscid species lacks detailed descriptions of its reproductive behaviors. Observations and predictions (from phylogenetic inferences) have been contradictory, with some arguing that the species uses an egg clustering strategy similar to species of the genera *Pimephales* and *Opsopoeodus*, while others argue that it is a crevice spawner similar to species of *Cyprinella*. It has also been suggested that *C. ornata* may even display spawning plasticity. A series of controlled spawning experiments were video-recorded and quantitatively analyzed to determine the spawning strategy of the species and identify and describe specific spawning behaviors. With at least four other substrates to choose from, *Codoma ornata* spawned the majority of times (125 of 127) in narrow crevices between tiles, typical of the crevice spawning strategy. A new method of analyzing video using The Observer XT permitted investigations into questions regarding the frequency, duration, and latency of specific individual behaviors during spawning. Similar studies of other species can be extremely useful for investigating questions of homology and evolution of behavioral sequences.

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

Casey Brewster and Steve Beaupre

University of Arkansas, Fayetteville, Arkansas, USA

Addressing the Links between Woody Vegetation Encroachment and Reduced Reproduction in the Eastern Collared Lizard (*Crotaphytus collaris*).

Our previous research suggests that lizards inhabiting glades with high woody vegetation density (encroached glades) have reduced age-specific body size and fecundity compared to lizards in glades with low woody vegetation density (intact glades). Our previous findings suggest that lizards in encroached glades may experience some factor that reduces age-specific net energy budgets, in turn reducing annual fecundity. Here we address three potential mechanisms that could explain reduced energy budgets of *C. collaris* in encroached glades. First, arthropod densities were greater in encroached (1.2 arthropods/20m^2) than in intact (0.82 arthropods/20m^2) glades. Greater arthropod densities in encroached glades suggest that prey availability does not explain reduced energy budgets. Second, our data suggest that lizards in encroached sites have reduced movement rates (~36%) and shorter activity-time budgets (~24%), excluding increased energetic costs as an explanatory mechanism. Third, encroached glades imposed an approximate 23% decrease in suitable operative temperatures compared to intact glades. However, we found no difference in mean surface-active body temperature of lizards between encroached (mean = 37.2 °C, SD = 2.42) and intact (mean = 37.2 °C, SD = 2.57) glades. Instead, we found a difference in surface-activity times (~2.6 hrs./day). While in refugia (i.e. while inactive), lizards experienced cooler body temperatures (12-26°C) then while active (32.1-42.6°C) – and these body temperatures reduce digestion rates. Thus, our data suggest lizards in encroached glades experience reduced digestion rates for longer periods of the day than lizards in intact glades.

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

Michael Britton and Maureen Donnelly

Florida International University, Miami, Florida, USA

Metabolic ecology of amphibians across a 5,000 meter elevational gradient in the Peruvian Andes

The study of metabolism concerns the study of biological processes, their rates and

requirements, and how they change and interact in different contexts. It is a basis for understanding the energetic requirements of species and how these requirements are affected by environment and evolution. Metabolic measurements of amphibians were conducted at 10 field sites (between 200 meters above sea level and 5,500 meters above sea level) in the buffer zone of Manu National Park. Resting metabolic rates were determined by measuring the change in CO_2 over time with an infrared gas analyzer in a closed system where the amphibian was unmoving for at least 30 minutes. Measurements were taken at night and during the day at ambient temperatures to examine thermal sensitivity of metabolic rate. Results were analyzed at the species level, across elevational ranges, and among populations to examine variation. Additionally, phylogenetic analyses at the genus and family levels were used to examine the extent to which metabolic characteristics are constrained by evolutionary history. A total of 103 species of amphibians in 14 families, including anurans, salamanders, and caecilians, were found across the 5,000 meter gradient. There exists substantial variation of resting metabolic rate within both individual species as well at higher taxonomic levels. The variation might reflect plasticity in these characteristics, or genetic, heritable differences, and merits further study. These characteristics, their variation, and the potential for adaptation may be predictive for how amphibians, and which areas and species, will be affected by climate change.

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

Michael Britton and Maureen Donnelly

Florida International University, Miami, Florida, USA

Plaster models provide insight into the conditions of microhabitats across a 4,000 meter elevational gradient in the Peruvian Andes

Microhabitats provide important refugia for organisms to select favorable conditions and avoid unfavorable ones. The distribution, availability, and value of microhabitats vary greatly across time and space. However, the abiotic conditions of microhabitats are frequently not known and often not included in modeling studies of the distribution and environmental conditions experienced by various species. The use of physical models can be useful to estimate the actual conditions organisms experience across time in a variety of microhabitats. We used water-saturated plaster frog models to examine the importance of leaf litter microhabitats for amphibians across a 4,000 meter elevational gradient. Models were placed within the leaf litter and on top of the leaf litter with temperature data loggers, and changes in mass were measured daily. In combination with hanging temperature data loggers, this setup was used to examine the differences between ambient temperatures, amphibian body temperatures and water loss outside of the leaf litter, and amphibian body temperatures and water loss within the leaf litter. These studies will be increasingly important to assess the availability of microhabitats, their abiotic conditions, and their significance for a variety of taxa under current and future environmental conditions.

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639 General Herpetology II, Highland B, Sunday 15 July 2018

Colin Brocka and John Koprowski

University of Arizona, Tucson, Arizona, USA

Around the Watering Hole: Terrestrial Ecology of an Endangered Ambystomatid Salamander

Knowledge of ecological and behavioral processes are essential for the conservation of species at risk of extinction. Approximately one third of all amphibian species are threatened or endangered, and those with limited distribution or population size are particularly vulnerable. To develop effective conservation strategies for at-risk amphibians, managers need to understand their ecological requirements. The Sonoran tiger salamander (STS; *Ambystoma mavortium stebbinsi*) is a federally endangered subspecies found only in the San Rafael Valley of southeastern Arizona and northern Sonora, Mexico. The STS was listed as endangered in 1997 due to highly restricted distribution, dependence on human-constructed environments, invasive species, genetic swamping by non-native salamanders, and disease. Cattle tanks created by ranchers to hold water have replaced natural springs, and are now primary breeding sites for STS. The terrestrial life stage is the only means of responding to pond drying or die-offs and thus is critical to the maintenance of metapopulation dynamics. However, the ecology of metamorphosed salamanders outside of breeding tanks is virtually unknown. We are using radio-telemetry to assess STS terrestrial movement patterns, habitat preferences, and life history traits. Spatial information is important for wildlife managers to develop effective management strategies to conserve the Sonoran tiger salamander and other isolated amphibians.

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

Edmund Brodie III

University of Virginia, Charlottesville, VA, USA

Newts and the Snakes that Eat Them: Backstories of a Coevolutionary Arms Race

Studies of coevolution between garter snakes and their toxic newt prey led by the Elder Butch Brodie have generated over 50 publications, numerous PhD dissertations, and at least one over-viewed video clip of a barfing snake. The fabulous network of researchers he assembled spans a truly integrative range of biology from the level of protein structure and function, to population genomics, to patterns of phylogenetic diversity. The contributions of that team exemplify the power of understanding the natural history of organisms when the right questions are asked. From my unique vantage as a literal lifetime-collaborator, I will attempt to present a historical and personal perspective on some of the events and relationships that lie behind Brodie's published work on the evolution of tetrodotoxin toxicity and resistance.

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

Bob Brodman

Buena Vista University, Storm Lake, Iowa, USA

Do Amphibians Believe in Climate Change: The Tale of Research and Nature Interpretation in the National Parks.

Have you ever visited a National Park? If so then you probably walked thru a scientist's research site and did not even know it. Making visitors aware of the research going on in National Parks is the goal of the iSWOOP (interpreters and scientists working on our parks) program. I will tell the story of how my research on the effect of climate change on amphibians became a focus of education programs by park rangers at Indiana Dunes National Lakeshore.

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448 ASIH STOYE ECOLOGY & ETHOLOGY II, Highland C, Thursday 12 July 2018

Seth Bromagen and Michael Sukhdeo

Rutgers University, New Brunswick, New Jersey, USA

Community Ecology of Monogenea on Bluegill Sunfish (*Lepomis macrochirus*)

Monogeneans are direct life cycle parasites found throughout freshwater and marine ecosystems. In order to determine the ecological factors that shape communities of gill monogeneans, we sampled three New Jersey lakes for centrarchid fish, recovered parasites by dissection, and measured individual worms. We also investigated the effects of host density using mesocosm tanks to identify parasite population responses to host-specific stimuli. Overall, the data shows that monogenean abundance increased significantly in high host density tanks relative to wild parasite populations with both *Onchocleidus* sp. and *Actinocleidus* sp. growing larger populations. Abundance of *Urocleidus dispar*, common in natural lakes, showed no changes in abundance as host density increased, but this parasite was less prevalent (53%) in mesocosms when compared to natural populations (100%). There was a significant relationship between parasite size and parasite abundance; *Onchocleidus* sp. size increased with species abundance. These results suggest that transmission may be improved with higher host densities for some species more than others, and that transmission could be a more important limiting factor for those species than others in nature.

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

George Brooks[1], Jennifer Smith[1], Emmanuel Frimpong[1], Thomas Gorman[1,2], Houston Chandler[1,3] and Carola Haas[1]

[1]Virginia Tech, Blacksburg, VA, USA. [2]Washington State Department of Natural Resources, Castle Rock, WA, USA. [3]The Orianne Society, Tiger, GA, USA

Indirect Connectivity Estimates of Amphibian Breeding Wetlands from Spatially Explicit Occupancy Models

Metapopulation theory has become a leading paradigm in a breadth of ecological disciplines. In conservation science, metapopulation models are frequently used to explore the spatial

dynamics of organisms, and ultimately guide management decisions for threatened and endangered species. Pond-breeding amphibians are often touted as a classic example of metapopulation structure. Empirical assessment of this assumption however, is lacking for many species owing to the prohibitively high costs of movement studies. Spatially-explicit occupancy models provide an alternative method to evaluate metapopulation dynamics and directly translate to management recommendations. Here, we describe a dynamic, spatially explicit occupancy-based metapopulation model for the reticulated flatwoods salamander, *Ambystoma bishopi*. Models were constructed to evaluate the spatial distribution of salamanders across the landscape, rate of patch turnover, and connectivity between patches. To corroborate our findings, we compare estimates of patch-connectivity from the dynamic model with independent estimates derived from an eigenvector mapping approach. Both models predict a steep drop off in connectivity with increasing isolation and find no evidence of interactions between wetlands separated by distances greater than 1.5km. The best predictor of salamander occupancy status was the amount of understory vegetation in wetland basins. Understory vegetation represents egg-laying habitat and refugia for larvae, and hence should be targeted in future restoration efforts. In contrast, wetland size, water depth, and average hydroperiod had seemingly no influence on the distribution of flatwoods salamanders. The methodologies employed in this paper have broad applicability to studies of pond-breeding amphibians, particularly in situations where direct measures of dispersal are unobtainable.

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

George Brooks[1], Jennifer Smith[1], Thomas Gorman[1,2] and Carola Haas[1]

[1]Virginia Tech, Blacksburg, VA, USA. [2]Washington State Department of Natural Resources, Castle Rock, WA, USA

Discerning the Environmental Drivers of Annual Migrations in an Endangered Amphibian

Studies that discern the drivers of animal migrations are becoming increasingly common, reflecting growing concerns over climate-driven shifts in phenological patterns that can lead to phenological mismatches. Amphibians that breed in ephemeral wetlands are thought to be particularly vulnerable to phenological mismatches owing to the stochastic nature of their breeding habitat and trade-offs between adult survival and time necessary for larval development. Knowledge of the effects of climatic cues on amphibian breeding phenologies is necessary to evaluate the potential consequences of climate change and to inform conservation plans for at-risk species. Here we use six years of count data from drift-fences on Eglin Air Force Base, Florida, collected between 2010 and 2016, to model the phenology of flatwoods salamander (*Ambystoma bishopi*) breeding migrations. Daily values of temperature and precipitation were covariates, and Poisson and negative binomial error distributions were compared using an information-theoretic approach. We found that salamander movement was strongly tied to environmental cues. A proclivity to move over a medial range of temperatures

and precipitation result in a 'Goldilocks' set of conditions that facilitate migration. We also found evidence for endogenous drivers of movement, resulting in two peak movement dates over the course of each breeding season irrespective of environmental conditions. These results contribute to knowledge of flatwoods salamander behavior and provide managers with useful metrics to maximize the efficacy of conservation actions. More broadly, the methods employed within have utility to researchers to help predict the effects of climate change and tailor management strategies accordingly.

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267 ASIH STOYE ECOLOGY & ETHOLOGY II, Highland C, Thursday 12 July 2018

Taston Brookshire

Southeastern, Hammond, LA, USA

The Effects of Three Different Species of Leaf Litter on *Incilius nebulifer* Larval Growth, Development, and Survival.

Forest communities have been affected by anthropogenic change and shifts in species composition are rich in the literature. Species leaf litter varies drastically the farther one pans out on the phylogeny. Amphibian larvae are significantly affected by the substances from within leaf litter. Non-native species may have a differing effect on native fauna. An example of such a species in Louisiana is the Chinese tallow tree, *Triadica sebifera*. In this experiment two native tree species *Quercus nigra*, the water oak, and *Acer rubrum*, the swamp red *A. rubrum*, were compared to the non-native Chinese tallow. *Incilius nebulifer* larvae were placed into containers at three densities (5, 10, & 20 tadpoles) with one of the species of leaf litter from above. I've found that leaf litter causes significant variation in growth, development, and mortality. Also, a significant amount of the variation can be attributed to species of leaf litter. There was also a slightly significant species by density effect in the metamorphic analysis, signaling nonadditive effects. This study highlights the importance of understanding how aquatic systems are affected by allochthounous resources, and how the quality of leaf litter input could possibly mediate anuran larval fitness.

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

Donald Brown[1,2], Petra Wood[3], Yong-Lak Park[1], Sara Crayton[1], Lenza Paul[4] and Alice Millikin[1]

[1]West Virginia University, Morgantown, West Virginia, USA. [2]U.S. Forest Service, Northern Research Station, Parsons, West Virginia, USA. [3]U.S. Geological Survey, West Virginia Cooperative Wildlife Research Unit, Morgantown, West Virginia, USA. [4]National Park Service, New River Gorge National River, Glen Jean, West Virginia, USA

Assessment of Potential Indirect Impacts of Using Pesticides for Hemlock Preservation on Terrestrial and Semiaquatic Salamanders

Over the last half-century, the exotic invasive insect Hemlock Woolly Adelgid (HWA; *Adelges tsugae*) has killed hundreds of thousands of Eastern Hemlock (*Tsuga canadensis*) trees in the eastern United States. In response, federal and state agencies have initiated aggressive HWA control programs, primarily using soil and trunk injections of the pesticide imidacloprid. This control strategy has proven to be effective for reducing Hemlock mortality from HWA, but previous studies have shown application of the pesticide can have negative impacts on non-target invertebrate and vertebrate communities. Since 2006, approximately 700 hectares of Hemlock-dominated forest have been treated with imidacloprid in the National Parks of Southern West Virginia. In 2017, we used a control-impact design at 9 pairs of terrestrial, and 12 pairs of aquatic (i.e., stream), sampling sites to investigate if occurrence, abundance, and body condition of salamanders differed between control and treated areas. For both the terrestrial and aquatic sites, median observed species richness was equivalent between control and treated areas. Estimated abundances of 2 terrestrial salamanders, Eastern Red-backed Salamanders (*Plethodon cinereus*) and Slimy Salamanders (*Plethodon glutinosus*), did not significantly differ between control and treated sites. Body condition index comparisons between control and treated sites for 2 terrestrial and 5 semiaquatic salamanders indicated no significant differences. These preliminary analyses do not indicate that the HWA control program at the National Parks of Southern West Virginia is having measurable negative impacts on the salamander community. Additional research on potential temporal effects and salamander stress hormone responses will also be discussed.

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

Jason Brown[1] and Ana Carnaval[2]

[1]*Southern Illinois University, Carbondale, IL, USA.* [2]*City College of New York, New York, NY, USA*

A tale of two niches: concepts, methods, and quantifying evolution

Understanding and quantifying the factors governing distributions of species remains a fundamental aim across ecology and evolution. One broad field of study on this topic concerns quantifying the ecological niches of species, and comparing their niches to, usually, closely related species to assess how species niches evolve. In recent years, due to advances in methods that quantify species' distributions, studies on this topic have flourished. In this talk, I aim to shed light on: several key concepts, evaluate two methods, one which is novel, and discuss how these methods address the question of quantifying niche evolution.

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

Jason Brown[1], Dan Hill[2], Alan Haywood[2] and Ana Carnaval[3]

[1]Southern Illinois University, Carbondale, IL, USA. [2]Leeds University, Leeds, United Kingdom. [3]City College of New York, New York, NY, USA

PaleoClim.org: High Spatial Resolution Paleoclimate Surfaces for Global Land Areas

High-resolution, easily accessible paleoclimate data are essential for environmental, evolutionary and ecological studies across different disciplines. Here we present PaleoClim.org, which is a free database of downscaled palaeoclimate outputs at 2.5 minute resolution (~5km at equator) including surface temperature and precipitation estimates from snapshot-style climate model simulations using the Hadley Centre Coupled Ocean Atmosphere Model (HadCM3). The current database contains high spatial resolution data for three key time periods spanning the from 3.3 to 0.785 million years ago; specifically Marine Isotope Stage 19 (MIS19) in the Pleistocene (ca. 785 Ka), the mid-Pliocene Warm Period (ca. 3.264-3.025 Ma) and MIS M2 in the Late Pliocene (ca. 3.3 Ma).

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422 Herpetology Physiology, Highland C, Saturday 14 July 2018

William S. Brown[1] and Matthew G. Simon[2]

[1]Skidmore College, Saratoga Springs, NY, USA. [2]Fort Ann, NY, USA

Record Life Span in a Population of Timber Rattlesnakes (*Crotalus horridus*)

Reptiles that have evolved a long-lived life history typically display late age of maturity, low fertility, and high adult survival rates. These traits characterize many populations of *Crotalus horridus*. Associated with this suite of characteristics is longevity which is assumed to be lengthy, but this aspect has seldom been measured in a wild population of any long-lived snake. In this study, we report the ages of the longest-lived observed individuals in a wild population of *C. horridus* that has been continuously sampled from 1979 through 2017, a 39-year period. We recorded ages—based on rattle size at the initial capture—of all snakes recaptured in the most recent ten years (2008–2017) that had an estimated final age of at least 20 years (n=62). Recapture intervals averaged 21.5 (12–35) yr. At their initial capture, ages of snakes were 5.8 ± 3.5 (0–16) yr, and at their final recapture their ages were 27.3 ± 6.3 (20–51) yr. This analysis is not a description of the age structure of this population, but rather draws attention to selected individuals that exhibited the longest recapture intervals and ages. Among the 62 individuals thus aged, distributions were: 20–29 yr (n=43), 30–39 yr (n=16), 40–49 yr (n=2), and 50–59 yr (n=1). The record life spans were 41 years (in one male and one female) and 51 years (in one female).

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

Matthew Buehler[1], Todd Jackman[1], Jamie Oaks[2], Stacie Hathaway[3], Robert Fisher[3] and Aaron Bauer[1]

[1]*Villanova University, Villanova, Pennsylvania, USA.* [2]*Auburn University, Auburn, Alabama, USA.* [3]*United States Geologic Survey, San Diego, California, USA*

Patterns of Diversity and the Evolutionary Relationships of Sea Kraits (*Laticauda*)

The sea krait genus *Laticauda* comprises eight species, three wide ranging and five regional endemics, and is sister to all other members of the elapid subfamily Hydrophiinae. The genus has an enormous range extending from Myanmar in the west, to Niue Island in the south Pacific, and north to the Korean Peninsula. Molecular phylogenetic studies of sea kraits to date have not been taxon complete, nor have wide ranging taxa been deeply sampled. Additionally, gene sampling has primarily been of mitochondrial loci. We have sequenced both traditional and rapidly evolving nuclear loci for previously sampled and unsampled populations of wide ranging species of sea krait. We also include samples of the Niue endemic sea krait (*Laticauda schistorhynchus*), and show its relationship to other species for the first time using molecular phylogenetics. This research has implications for our understanding of species boundaries within the genus, and for helping to understand the early speciation events in the hydrophiine radiation.

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

Isabella M. Bukovich and M. Rockwell Parker

James Madison University, Harrisonburg, VA, USA

Assessing the fear of snakes in people

Ophidiophobia, the fear of snakes, notoriously presides as one of the most prominent phobias in human psychology. The role of snakes as predators of early mammals evidences not only a potential biological predisposition to fear or to learn to fear snakes but also serves to explain the multitude of adaptations enabling primates to evade snakes, as seen in human beings today. However, it appears less certain if this enhanced biological performance is also accompanied by enhanced (or inhibited) cognitive performance. As an Honors thesis student at James Madison University, I am attending JMIH to seek advice, suggestions, and criticisms of my prospective research project on the association between cognitive function—hypothetically in terms of memory, critical thinking, or problem solving—and ophidiophobia. Heightened cognitive performance in the presence of a snake is obviously adaptive by directly increasing one's fitness (e.g., potentially escaping an adept predator). Potentially, I could determine the continuum of fear intensity evoked by snakes and therefore identify a "fear optimum" as evidenced by best cognitive performance. Overall, the aim of this hypothetical research project is to garner a

deeper understanding of the implications of ophidiophobia apart from biological development; it serves to investigate the impact of the fear of snakes on the mind and its processes.

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390 Lightning Talks II, Highland A, Saturday 14 July 2018

Frank Burbrink, Marcelo Gehara and Edward Myers

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

Revisiting the phylogeography of the North American ratsnakes (*Pantherophis obsoletus* complex) using genomic data.

The origins of population structure and processes of speciation at biogeographic boundaries using genomic data are providing a solid foundation for understanding how biodiversity accrues regionally. The first estimates of phylogeographic structure for many snakes relied only on estimates from mtDNA, where conclusions over many taxa have supported the existence of several important biogeographic boundaries for generating diversity in the Eastern Nearctic. Unfortunately, while single genetic markers may have helped provide a basis for geographic structure of populations, estimates of divergence dates and demography are tenuous. Here, we revisit this topic by modeling the diversification and origins of the North American ratsnakes (*Pantherophis obsoletus* complex) using genomic data (UCEs) from ~300 samples liberally collected across their range. Using new models developed, in part, in our lab, we examine spatial distribution of lineages, timing and processes of divergence, and associated contributions of isolation by distance, ecology and barrier to understand the origins and diversity within this complex of snakes.

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

Luis Burgos[1], Karina Cervantes[2] and Emily Taylor[1]

[1]*California State Polytechnic University, San Luis Obispo, San Luis Obispo, CA, USA.* [2]*Allan Hancock College, Santa Maria, CA, USA*

Don't Hate, Thermoregulate: The thermal environment of *Sceloporus occidentalis*

We evaluated the thermal environment of the western fence lizard, *Sceloporus occidentalis*, on the central coast of California by quantifying the thermal quality of three different microhabitats and calculating the lizards' thermoregulatory accuracy. We looked at the most ecologically relevant microhabitats that lizards use for thermoregulation: sun, shade, and mixed sun and shade. To quantify the microhabitats, we built operative temperature models (OTMs) consisting of hollow copper cast lizard molds with data loggers that closely approximated the temperatures that a non-thermoregulating live lizard could experience. The thermal quality of each microhabitat was calculated as the difference between the lizards' preferred body temperature and the OTM temperature. Body temperature measurements of live lizards were obtained to evaluate their thermoregulatory accuracy, which was determined as the difference between their preferred temperature and field active temperature. On average throughout the

day, the basking habitat (OTMs in sun), was of the lowest thermal quality. The mixed and shade habitats were of higher quality. The lizards' body temperatures were most similar to OTMs in the mixed habitat, possibly because lizards shuttle between the sun and shade to thermoregulate. Using climate change predictions for the area, we show that lizards even in this relatively mild, coastal habitat could lose up to 3 hours of basking time. Availability of shade will be increasingly essential to optimal thermoregulation.

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

Ella Buring, Vanessa Gonzalzes and Daniel Mulcahy

Global Genome Initiative, NMNH, Smithsonian Institution, Washington, DC, USA

Lost and Found: Tuatara ND5 Gene Identified

Tuatara (*Sphenodon punctatus*) are relict reptiles that possess uniquely configured mitochondrial genomes, with several gene rearrangements, and lacking two tRNAs. Until recently, it was also believed that the Tuatara was missing the ND5 gene from its mitochondrial genome as well. However, our informatic and experimental data suggest otherwise. Here, we report the identification of a putative ND5 gene from a previously published transcriptome library of tuatara, which translates to amino acids only under the vertebrate mitochondrial genetic code; stop codons are present under the standard code. Our assembly coverage of the putative tuatara ND5 gene from the transcriptome library contains a partial tRNA-Leu at the 5' end and abruptly terminates at the 3' end. We were unable to find any flanking regions that would identify the location of the sequence within the tuatara genome. We conducted several phylogenetic analyses among Chordates using protein-encoding mitochondrial genes, including ND5, and a concatenated mitochondrial gene tree to verify the authenticity of the putative tuatara ND5 gene. We are now collaborating with others on a tuatara mitochondrial genome project and have been able to successfully amplify PCR products using primers designed from our putative tuatara ND5 gene, suggesting the presence of an ND5 gene. We will present our results and discuss possibilities for the location of the tuatara ND5 gene.

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13 Herpetology Reproduction, Highland C, Sunday 15 July 2018

Russell Burke[1], Beverly Clendening[1] and Alexandra Kanonik[2]

[1]Hofstra University, Hempstead, NY, USA. [2]American Littoral Society, Broad Channel, NY, USA

Long-Term Increases in Clutch Size in Common Snapping Turtles (*Chelydra serpentina*) and Diamondback Terrapins (*Malaclemys terrapin*)

Clutch size (CS) is a well-studied life history characteristic, and optimal egg size theory predicts CS should correlate positively with reproductive investment. Turtles are good subjects for studies of reproductive strategies because few turtle species exhibit parental care; therefore quantifying their short-term reproductive investment is mostly limited to measuring egg size

and number. Clutch size is usually reported as an average value for each turtle population, and where CS variation is noted, it is usually attributable to variation in adult body size. In two long-term studies of ecologically dissimilar species we detected a dramatic increase in CS in a Common Snapping Turtle (*Chelydra serpentina*) population and in a Diamondback Terrapin (*Malaclemys terrapin*) population. It is unknown whether these changes are due to either variation in adult body size or resource availability; but the temporal patterns we observed have apparently never been reported previously. These trends remain unexplained and should be explored further.

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281 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Thaddaeus Buser[1], Brian Sidlauskas[1] and Adam Summers[2]

[1]Oregon State University, Corvallis, OR, USA. [2]University of Washington, Seattle, WA, USA

2D or not 2D? Testing the utility of 2D vs 3D landmarks in geometric morphometrics of the sculpin subfamily Oligocottinae

We contrast 2D vs. 3D landmark-based geometric morphometrics in the fish subfamily Oligocottinae by using 3D landmarks from CT-generated models and comparing the morphospace of the 3D landmarks to one based on 2D landmarks from images. The 2D and 3D shape variables capture common patterns across taxa, such that the pairwise Procrustes distances among taxa correspond and the trends captured by principal component analysis are similar in the xy plane. We use the two sets of landmarks to test several ecomorphological hypotheses from the literature. Both 2D and 3D data reject the hypothesis that head shape correlates significantly with the depth at which a species is commonly found. However, in taxa that vary substantially in the z-axis, projection into a 2D plane sufficiently distorts differences among taxa to influence the outcome of the hypothesis tests regarding the relationship between mouth size and feeding ecology. Only the 3D data support previous studies that showed that positive correlation between mouth size and the percentages of elusive prey in the diet. When used to test for morphological divergence, 3D data show no evidence of divergence, while 2D data show that one clade of oligocottines has diverged from all others. This clade shows the greatest degree of z-axis body depth within Oligocottinae, and we conclude that the inability of the 2D approach to capture this lateral body depth causes the incongruence between 2D and 3D analyses.

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284 Lightning Talks II, Highland A, Saturday 14 July 2018

Thaddaeus Buser[1], Brian Sidlauskas[1] and Adam Summers[2]

[1]Oregon State University, Corvallis, OR, USA. [2]University of Washington, Seattle, WA, USA

Testing for sexual dimorphism in sculpin (Cottoidea: Oligocottinae) cranial weapons using 3D morphometrics

Many vertebrate groups have weaponized their skulls, with mammalian horns attracting the lion's share of attention from evolutionary biologists. Though some cranial weaponry aids defense, intraspecific combat appears to drive the evolution and elaboration of cranial ornaments in most terrestrial cases (e.g., Cervidae and Bovidae). Equally impressive weaponry adorns the heads of vertebrates that live below the waves, such as the sculpins (superfamily Cottoidea). The skulls of this diverse group of fishes bear antler-like preopercular spines of remarkable variation, but the reasons for the spines' origin and diversification remain unknown and untested. We use 3D morphometrics taken from reconstructions of micro computed tomographic data to quantitatively compare the shape of male versus female preopercular spines in sculpins of the subfamily Oligocottinae. Our results show evidence of sexual dimorphism in some species, with male preopercles showing reduced curvature of the preopercle bone itself and a shorter, straighter morphology of the uppermost preopercular spine. While preliminary, the dimorphism suggests that at least some sculpins fight with their spines, and that variation in reproductive behavior helped drive the morphological diversification of cottoid weaponry.

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324 ASIH STOYE ECOLOGY & ETHOLOGY II, Highland C, Thursday 12 July 2018

Nicholas Buss and Jessica Hua

Binghamton University, Binghamton, New York, USA

The relationship between amphibian biodiversity and disease outcome is modified by NaCl contamination

Infectious diseases are global threats to amphibian populations. However, theory suggests that shifts in amphibian diversity can modify disease outcome (i.e. dilution effect). For example, in more diverse amphibian communities, amphibian hosts that are less susceptible to parasite infection can act as 'decoys', diluting parasites away from more susceptible hosts reducing overall community infection loads. However, the evidence supporting the dilution effect has been equivocal, suggesting that other environmental factors may be contributing to the outcome of this proposed phenomenon. Chemical contaminants (i.e. road salts) can also shape disease outcome and may play a role in modifying the effect of amphibian community diversity on disease outcome. To understand how contaminants modify the predicted outcome of the dilution effect, we asked: (1) Does increased amphibian diversity buffer the overall community from trematode infection (i.e. dilution effect)? (2) Does NaCl enhance or suppress the dilution effect? In communities not exposed to NaCl, amphibians in single-species communities were similarly susceptible to trematode infection compared to multi-species communities (i.e. no dilution effect). However, in the presence of NaCl, the susceptibility of amphibian to trematodes was differentially modified. Peepers and wood frogs become 35% and 65% more susceptible to trematodes, respectively, while toad susceptibility was unaffected. Consequently, in NaCl-

contaminated, multi-species communities, toads served as 'decoys', diluting parasites away from the other hosts lowering overall community infection by 40% in more diverse communities. This work underscores the importance of considering environmental factors in evaluating the potential for increased biodiversity to buffer amphibian communities from infectious diseases.

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

Brett Butler, Aaron Bauer and Todd Jackman

Villanova University, Villanova, PA, USA

Evaluating Phylogeographic Barriers in Southwest African Skinks

The radiation of *Trachylepis* skinks across the southern Africa subcontinent provides an ideal system for studying phylogeography. Angola, in particular, has a heterogeneous landscape that supports the highest diversity of *Trachylepis* species in Africa. We conducted a comparative study examining the extent to which putative barriers, such as the Great Escarpment and the Cunene River, have shaped the population structure and speciation processes of multiple congeners in southwest Angola. For each species, a mutlilocus nucleotide dataset (16S, ND2, RAG-1, MXRA5, and EXPH5) was compiled to estimate phylogenies using Maximum Likelihood and Bayesian Inference. Population-level topologies and divergence dates were compared using hierarchical approximate Bayesian computation to test for parallel lineage splitting between taxa that might correlate with the proposed barriers. Results found inconsistencies in the levels of isolation spanning both barriers that may be attributed to differing levels of gene flow across the barriers in each species. Substantial population structure consistent with deep divergence was found in several widespread taxa including *T. sulcata* and *T. varia*, whereas other taxa such as *T. laevis*, *T. spilogaster*, and *T. punctualata* displayed more homogenous structure across the geographic features. North-south population divergence was found in Angolan *T. sulcata*, although it does not correspond to the hypothesized barrier of the Cunene River. In skinks, species boundaries rarely span the Angolan Great Escarpment, a testament to the steep environmental and elevational east-west gradient formed by the mountain range.

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

Sky Button[1], Adia Sovie[2], Cathryn Greenberg[3] and James Austin[2]

[1]Virginia Tech, Blacksburg, VA, USA. [2]University of Florida, Gainesville, FL, USA. [3]US Forest Service, Asheville, NC, USA

Modelling Habitat Preferences, Detectability, and Movement of a Fossorial Upland Snake

Occupancy modelling is often one of the only effective tools for studying the habitat preferences of cryptic species. Fossorial snakes are a prime example of this, because their secretive life histories make them difficult to detect, and make demographic studies unfeasible. Despite possibly being the only way to study most fossorial snakes, few studies have used occupancy models to assess the habitat preferences of these animals and determine which site variables and weather conditions maximize their detection. We sampled peninsula crowned snakes (*Tantilla relicta relicta*) using 24 groups of drift fences in longleaf pine-wiregrass sandhills in Ocala National Forest, and assessed how habitat characteristics and weather influenced occupancy, detection, colonization, and extinction rates using a robust sampling design and multi-season occupancy models. Peninsula crowned snakes were most likely to occupy recently burned sites, and were most easily detected during dry periods, and at sites with low leaf litter cover. We found no evidence that either rainfall or temperature influences fine-scale crowned snake movements, and suggest that these movements are either largely stochastic, or explained by unmodeled parameters. Our results are consistent with research suggesting that short return prescribed fires benefit fauna in central Florida's upland forests, and suggest that patterns of surface activity in peninsula crowned snakes may differ from those of other sympatric fossorial snakes that tend to be surface active following rains.

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

Jonathan Bynum, Zachary Nikolakis, Brian Crother and Kyle Piller

Southeastern Louisiana University, Hammond, LA, USA

Phylogeography of the Slender Glass Lizard (*Ophisaurus attenuatus*) complex.

The Slender Glass Lizard (*Ophisaurus attenuatus*) is a widespread species that occurs across the eastern United States from the Atlantic Slope to Kansas, Oklahoma and Texas and from Wisconsin to the Gulf Coast. It is currently comprised of two disjunct subspecies including the Western Slender Glass Lizard (*Ophisaurus attenuatus attenuatus*), the nominal member of this species complex and the Eastern Slender Glass Lizard (*O. a. longicaudus*). These subspecies are distributed disjunctly east and west of the Mississippi River. Previous work has indicated that there are a number of morphological differences between the subspecies, including differences in body length, width, and color morphology. Our goal was to generate DNA sequence data to assess divergence and gene flow among populations to assess the genetic distinctiveness between the subspecies. Here we present evidence for multiple genetically distinct lineages of *Ophisaurus attenuatus* within a phylogenetic framework.

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265 Lightning Talks II, Highland A, Saturday 14 July 2018

Jonathan Bynum[1], Stuart Wells[1], Joseph Incandela[1], Jennifer Lamb[1] and Christopher Beachy[2]

[1]Southeastern Louisiana University, Hammond, LA, USA. [2]Southeastern Louisiana, Hammond, LA, USA

The larval life history of the Southern Two-lined Salamander, *Eurycea cirrigera* (Caudata, Plethodontidae) in southern Louisiana

The family Plethodontidae has more diversity in life cycle than the other eight families of salamanders combined. There are three basic variations of life cycle: metamorphic, paedomorphic and direct-developing. Those plethodontid species that are biphasic differ from most amphibians in that larval growth is very slow and the larval period is long (9-60 months). There are few studies of species that occupy the coastal plain of the southeastern United States. We collected bimonthly samples of larval *Eurycea cirrigera* from a locality at Bogue Chitto State Park in Washington Parish, Louisiana for a full year cycle to estimate larval density, larval growth rate, timing of oviposition, timing of hatching and timing of metamorphosis. Larval growth is slow, although faster than many montane populations of *E. cirrigera*. Hatching takes place in early summer month in and metamorphosis occurs in late summer. We estimate the larval period to be 18-30 months.

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

Kip Callahan[1,2], Melissa Lech[1,3], Kyle Brown[1,2], J. Christopher Leaphart[2], Melissa Pilgrim[1,2] and Tracey Tuberville[2]

[1]USC Upstate, Spartanburg, SC, USA. [2]Savannah River Ecology Laboratory, Aiken, SC, USA. [3]Savannah River Ecology Laboratory, Spartanburg, SC, USA

Mercury and Cs-137 Concentrations Among Tissues of *Nerodia floridana* Inhabiting Former Nuclear Cooling Reservoirs

For contaminants that bioaccumulate, where they end up in an organism varies due to the interaction between biochemical properties of the contaminant and the organism's physiology. Studying this variation can help determine health risks for the organism and its predators. We investigated among-tissue distribution of radiocesium (Cs-137) and mercury (Hg) in *Nerodia floridana* (Florida Green Watersnakes) residing in former nuclear cooling reservoirs. Our goals were to 1) quantify Cs-137 and Hg concentrations among snake tissues and 2) determine which non-destructively sampled tissue (scale clips and tail tips) would best predict Hg concentrations in destructively sampled tissues (liver, muscle, and kidneys). We quantified snake whole-body Cs-137 concentrations. After dissecting snakes, we quantified Cs-137 and Hg concentrations in

harvested tissues. Six snakes had measurable Cs-137 body burdens; pooled liver samples had the highest Cs-137 concentration (2.6 Bq/g), followed by muscle (2.2 Bq/g) and kidney (1.9 Bq/g). Average Hg levels (in PPM wet weight) were highest in muscle (0.87±0.08), followed by kidney (0.49±.04), liver (0.47±.04), scale clip (0.24±0.06), and tail tip (0.25±0.06). Significant positive relationships between Hg concentrations in non-destructively sampled tissues and destructively sampled tissues indicate non-destructively sampled tissues can be informative indicators of Hg accumulation in *N. floridana*.

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

David Camak and Thomas Turner

University of New Mexico, Albuquerque, NM, USA

An Annotated SNP Assay for Assessment of Genetic Diversity in Gila Trout

Gila trout (*Oncorhynchus gilae*) is an endemic, cold-water fish species found in headwater streams in the southwestern US. Of five distinct evolutionary lineages of Gila trout, two show low genetic diversity and effective sizes associated with population bottlenecks. Some lineages are hypothesized to be locally adapted. Climate-change associated droughts and wildfire and nonnative introductions of Rainbow trout (*O. mykiss*) threaten this species. For effective conservation, it is imperative to understand sources of genetic variation available to effectively enhance probabilities of lineage resilience to disturbances. Using restriction-site associated DNA (RAD) sequencing approach and the Rainbow trout genome, we genotyped and annotated thousands of single nucleotide polymorphisms (SNPs) for all lineages of Gila trout and lineages of Rainbow trout likely stocked in local streams. We identified variable SNPs in presumably neutrally evolving and selected regions of the genome, targeting lineage-specific and species-specific loci. Samples were also genotyped using a 247 SNP panel designed for salmonids of the Columbia River Basin. Ultimately, this effort will yield a high-throughput assay to better understand the underpinnings of local adaptation and ecological and evolutionary effects of hatchery supplementation in an effort to project population persistence at the southern extreme of the range of salmonid fishes.

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520 Ichthyology Biogeography, Grand Lilac Ballroom South, Saturday 14 July 2018

Alexander Cameron[1], David Camak[1], Tyler Pilger[2], David Propst[1] and Thomas Turner[1]

[1]University of New Mexico, Albuquerque, New Mexico, USA. [2]FISHBIO, Chico, California, USA

Disentangling Natural Dispersal Versus Human-Mediated Introduction of the Longfin Dace (*Agosia chrysogaster*) Across the Trans-Continental Divide.

A long-standing objective of biogeography is to relate patterns of genetic diversity to historical and contemporary processes that influence the distribution of populations across a landscape. For some taxa, the role of human-mediated dispersal can confound the signal from natural processes and obscure understanding of a species' evolutionary history. *Agosia chrysogaster* is a small-bodied minnow native to the Upper Gila River basin in New Mexico. Accounts as early as the 1950's proposed that *A. chrysogaster* was recently introduced into tributaries of the Mimbres River and the Rio Grande. Human-mediated dispersal was hypothesized as a mechanism for crossing the trans-continental divide, but recent molecular evidence suggests that headwater capture events may have mediated the east to west movement of other fish taxa (e.g., *Pantosteus plebeius*). Therefore, it is plausible that populations of *A. chrysogaster* found east of the trans-divide were established via a similar headwater capture event as *P. plebeius* and not through human-mediated dispersal. We used two mitochondrial loci (ND4 and Cyt b) and a panel of ten microsatellite loci to examine historical and contemporary patterns of population structuring of *A. chrysogaster* in New Mexico to infer the mechanism of colonization across the trans-continental divide. We used Approximate Bayesian Computational approaches to evaluate competing hypotheses of recent introduction versus an older, natural event to account for its distribution east of the continental divide.

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335 Lightning Talks II, Highland A, Saturday 14 July 2018

Cooper Campbell and Hank Bart

Tulane University, New Orleans, LA, USA

Venom Gene Expression in *Noturus* Catfishes and their Response to Predators

Recent work has suggested fishes may be the most numerous venomous vertebrates on the planet, yet studies of piscine venoms are uncommon in the literature. Information is lacking not only on what venoms are produced by fishes, and how they affect their recipients, but also on how venom gene expression is regulated. Recent studies on venomous snakes have shown that differences in venom gene regulation and expression between species is high, suggesting that gene regulation and expression plays a large role in variation between venoms expressed by different species. This prompted the question, how does presence of predators influence venom gene expression in species that use venom as an anti-predator defense? Siluriform fishes are known for their well-developed sense of taste, and can detect the presence of both predators and prey. Since venom is produced solely for defense in catfishes, can its expression vary based on the presence or absence of a predator? For my study, I intend to test the transcriptomic response of multiple *Noturus* species to the presence of a predator. I intend to test both immediate response after the introduction of a predator cue and changes in the transcriptomic response over time, with a focus on transcripts of venom genes. By studying gene expression, I hope to obtain a better idea of how venom gene expression can vary in different species in response to predator presence.

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446 Herpetology Morphology II, Highland D, Sunday 15 July 2018

John Capano and Elizabeth Brainerd

Brown University, Providence, RI, USA

Morphology and kinematics of lung ventilation in the boid snake *Boa constrictor* and comparison with non-serpentine squamates

Ribs in snakes extend almost the entire length of their bodies and participate in numerous behaviors. Similar to other squamates, snakes continue to use rotations of their ribs to produce the volume changes responsible for ventilation of their lungs. Breathing kinematics in non-serpentine squamates are a combination of vertebral and sternal rib motions that are typically described as bucket-handle rotation about a dorsoventral axis, caliper rotation about a craniocaudal axis, and pump-handle rotation about a mediolateral axis. Snakes, however, breathe in complete absence of sternal ribs and breathe only with motions of their vertebral ribs. The objective of this study is to quantify the rib kinematics during lung ventilation in *Boa constrictor*, determine kinematic variation along the body, and compare the morphology and kinematics to non-serpentine squamates. We implanted radio-opaque markers into two vertebrae and their four corresponding ribs at anterior and posterior locations in three *B. constrictor*. We found that the rib kinematics of *B. constrictor* were almost equally dominated by bucket-handle and pump-handle rotations, with some contribution from caliper rotation. This is in stark contrast to the primarily bucket-handle rotations used by *Iguana iguana* and *Salvator merianae*, but remarkably similar to kinematics in *Varanus exanthematicus*. We also found that *B. constrictor* are capable of modular ventilation, with ribs in different regions capable of ventilation. Our findings suggest that muscular mechanisms and costovertebral articulations in snakes may influence their breathing kinematics and that their modular capacity may be functionally relevant to behaviors such as constriction, prey ingestion, and locomotion.

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

Gerardo Carfagno

Manhattan College, Riverdale, NY, USA

Microhabitat Use by an Urban Salamander Population

Many amphibians are thought to be threatened in the face of habitat loss, pollution, disease, and climate change. Given their sensitive physiologies, amphibians such as terrestrial salamanders can serve as indicator species for the health of an anthropogenically altered community. The red-backed salamander (*Plethodon cinereus*) can serve such a role, given its broad distribution and abundance in eastern North America. These salamanders could be adversely affected because of altered microclimates where urbanization has occurred. The goal was to document microhabitat use by this species in an urban landscape, and to compare use to salamanders

found in less urban locations. After locating a salamander in the field, several microclimate variables were measured. For each individual, these same measurements were taken at a randomly selected site to compare microhabitat used to microhabitat generally available. Data was collected both for salamanders found in an urban park in New York City, and for salamanders found in suburban locations outside of the city. Results show that there are some significant microclimate variables selected by salamanders relative to what is generally available, indicating that urban salamanders are choosing microhabitats with favorable characteristics. More surprisingly, while there are differences in the available habitats of the urban and suburban locations, there are no significant differences between the microclimates selected by urban and suburban salamanders. This result indicates that even urban salamanders may be able to locate ideal microhabitats. However, while urban salamanders may not be forced to occupy less suitable microhabitats, other factors could adversely affect these populations.

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

Brad Carlson[1], A.J. Belden[1], Joseph Pich[1] and Sasha Tetzlaff[2]

[1]Wabash College, Crawfordsville, IN, USA. [2]University of Illinois Urbana-Champaign, Champaign, IL, USA

Box Turtle Boldness is a Consistent Personality Trait Across Years, Age Classes, and Assay Conditions

Animal personality (or temperament) is present when individual animals vary in behavioral patterns in a consistent manner. Previous work demonstrated that wild, adult Eastern Box Turtles (*Terrapene c. carolina*) exhibited highly consistent antipredator behavior in response to human handling and confinement over the course of a month, reflective of the degree of boldness. This follow-up work validates and generalizes these conclusions. We first report that turtles encountered over multiple years exhibited significant repeatability in behavior across years, indicating that among-individual behavioral variation was not a result of transitory state differences. We tested whether young, laboratory-reared turtles exhibited similar personality differences despite a common environment. We found that boldness was repeatable to a similar extent in juveniles and adults, and rearing conditions had little effect on behavioral variation. This shows that personality differences are formed early in development and are not simply a consequence of differential life experiences in wild adults. Finally, we tested whether box turtle boldness in response to handling and confinement was correlated with their behavioral response to a more naturalistic threat, a simulated raccoon predator. We found that turtles that were bolder than conspecifics in response to confinement were also bolder in response to the simulated raccoon, though on average they were more cautious with the raccoon. Altogether, the high repeatability of box turtle boldness and its consistency across years, age classes, and measurement conditions suggests an excellent model for the study of personality in reptiles.

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

Nicholas Caruso[1], Christina Staudhammer[2] and Leslie Rissler[3]

[1]Virginia Polytechnic Institute and State University College of Natural Resources, Blacksburg, VA, USA. [2]University of Alabama, Tuscaloosa, AL, USA. [3]National Science Foundation, Arlington, VA, USA

Effect of climate-driven demographic variation on population growth in *Plethodon montanus* along an elevational gradient

Climate can influence amphibian life history; populations in cooler temperatures tend to have shorter breeding seasons, fewer clutches, slower growth rates, but larger body size, older age at maturity, greater number of eggs within a clutch and larger eggs. How this climate-driven variation in life history subsequently affects population growth through vital rates (survival, fertility, and transition rates) is crucial to understanding how future changes in climate can affect populations as well as the degree to which selection acts upon these traits. To determine the age structure, fertility, growth and survival rates of *Plethodon montanus* we combined results from a 4-year mark-recapture study with surveys of natural history collections. We used the relationship between these vital rates and climate to create demographic matrix models to understand how climate can influence population growth through its effects on vital rates along the elevational gradient. We then determined vital rate importance through simulations of vital rates and their uncertainty using a prospective perturbation analysis. Our results suggest that survival of the largest females is the most important vital rate for *P. montanus*. However, vital rate importance varied with climate and elevations. These results provide quantifiable estimates of the effect of the abiotic environment on montane salamanders and population growth and can inform predictions about how future climate changes may future populations.

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343 Ichthyology Biogeography, Grand Lilac Ballroom South, Saturday 14 July 2018

Tiago Carvalho[1] and Barbara Calegari[2]

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Historical Biogeography of Neotropical Freshwaters: a comparative approach using representatives of Doradoidea and event-based methods.

Lineage diversification of continentally distributed clades is often associated with allopatric speciation and thought to have played a major role in generating the diverse ichthyofauna in Neotropical freshwaters. Within Doradoidea families, several clades are distributed across Andes and the Parana/Paraguay-Amazon divide, which suggests that the Andean orogeny and the breakup of the subandean foreland basin were important in determining the modern distribution of these groups. An event-based method of ancestral range estimation was used to

investigate how these major events on South America have affected the distribution and diversity of these clades of Doradoidea. We test competing models of range evolution (e.g. DIVA-LIKE, DEC, BAYAREA-LIKE) and their variants with the additional founder-event parameter. Eleven discrete operational geographic units: Magdalena (MG), Maracaibo (MC), Orinoco (OR), Guianas (GU), Negro (NE), Western Amazon (WA), Eastern Amazon (EA), Tocantins-Araguaia (TO), Tapajós-Xingu (TX), Paraná-Paraguay and Southeastern Coastal (PP), São Francisco and Northeastern Coastal (SC). Ultrametric phylogenetic trees of species-comprehensive data sets containing 110 species of Auchenipteridae (of 123 known) and all known species of Aspredinidae were done using node dating (in BEAST 2.0) and calibration points within Siluriformes. The results suggests the importance of the rise of eastern Cordillera and Merida Andes at about 11 Ma and 8 Ma and several instances of dispersal to the Paraná-Paraguay from Western Amazon within different temporal ranges. Within Aspredinidae, estuary-dwellers may have invaded this habitat at around 23-50 Ma, which may be associated with marine continental incursions in the northwest portion of the continent.

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111 General Herpetology II, Highland B, Sunday 15 July 2018

John Cavagnaro

Villanova University, Villanova, PA, USA

Fluorescent coloration in reptiles and an amphibian from Namibia and southern Angola.

Externally visible biofluorescence is rare in tetrapods, known mainly from a few examples in birds. Recently, UV-induced fluorescence has been described in an amphibian species (the treefrog *Hypsiboas puncatatus*) and one genus of reptile (chameleons of the genus *Calumma*). In both cases the fluorescence may have a visual function, but this has not been confirmed with behavioral experiments, and the support from visual modelling is limited. Here I describe fluorescent color patches from several reptiles and one amphibian from the Namib desert region (Namibia and southern Angola), and discuss their potential role in visual signalling. I focus on three species in particular with regards to their fluorescent coloration: the gecko *Pachydactylus rangei*, which has a fluorescent side patch and eye ring; the lacertid lizard *Meroles suborbitalis*, which has a fluorescent tail; and a toad in the genus *Sclerophrys*, which has a fluorescent vocal sac. For my three focal taxa, the regions exhibiting fluorescence function as important signalling regions in related species. I use standardized full-spectrum photography and visual modelling to explore the contribution of the fluorescent pigment to the perception of the regions overall coloration. Fluorescent pigments may increase brightness as perceived by long-wavelength sensitive rods and cones, especially at dusk. In some cases, the UV-absorbance appears far more important than the fluorescent emissions, creating contrast with other UV-bright color patches and potential backgrounds.

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

Peter Cerda[1], Thomas F. Duda, Jr.[1,2] and Alison Davis Rabosky[1]

[1]University of Michigan, Ann Arbor, Michigan, USA. [2]Smithsonian Tropical Research Institute, Balboa, Ancón, Panama

Venom Expression Profiles of Rear-Fanged Snakes from Peru

One of the chief goals of evolutionary biology is to understand how variation in phenotypic traits among species arises. Venom is a toxic substance used by a variety of organisms for prey capture and/or defense. It is typically composed of direct gene products that interact directly with the organism's environment by disrupting physiological functions and varies in levels of complexity in several taxa. Several genetic and gene regulatory mechanisms contribute to the diversity of venoms among species as well as variation seen within species, such as strong positive selection, high rates of gene duplication and gene family turnover, and changes in gene expression. To understand how these toxic cocktails evolve, we must first know which toxins are present. Here I describe the venom expression profiles of several species of rear-fanged snakes, which until recently had been largely understudied. To do this, I extracted and sequenced mRNA from Duvernoy's gland tissues of species collected in Peru. I assembled and annotated the resulting transcriptomes to identify venom genes and gene families present and determined the expression level of each venom gene transcript. The results show a diversity of toxins present in species venom as well as a large number of unknown genes which may represent novel toxins. These results lay the groundwork for future work seeking to understand the evolution of these toxic cocktails.

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345 Herpetology Systematics, Highland B, Saturday 14 July 2018

Luis Ceríaco[1,2,3], Mariana Marques[4,3], Suzana Bandeira[2,5], Mathew Heinicke[1], Carly Boye[1], Edward Stanley[6], David Blackburn[6] and Aaron Bauer[2]

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A taxonomic review and phylogeny of the African Burrowing Skinks (Squamata: Scincidae: *Sepsina* Bocage, 1866)

Sepsina Bocage, 1866 is among the most poorly known genera of African skinks. Endemic to central and southwestern Africa and extending from Tanzania and the Democratic Republic of Congo (DRC) to Namibia, the genus currently comprises five recognized species – *Sepsina alberti* Hewitt, 1929; *S. angolensis* Bocage, 1866; *S. bayoni* (Bocage, 1866); *S. copei* Bocage, 1873; and *S. tetradactyla* Peters, 1874. While there are records of *S. tetradactyla* from DRC, Tanzania, Malawi and Zambia, the other four species are known only from a handful of localities in Angola and Namibia and remain taxonomically challenging. Most of the species, especially those endemic to Angola, have not been collected since their description in the 19th century and critical type material was lost in the fire that destroyed the collections of Museu Bocage (Lisbon) in 1978. Our recent field research in Angola and Namibia provide new specimens for these poorly known taxa. We present a study of the systematics of *Sepsina* based on external and internal morphology, including from x-ray computed tomography (CT-scanning), and molecular phylogenetic analysis that allows for an integrative taxonomic revision. Our new data confirm the monophyly of the genus using molecular data, and we provided detailed morphological diagnosis for the five recognized species of *Sepsina*, and contribute to our understanding of the biogeography of southwestern African.

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

Mariana Marques[1,2], Luis Ceríaco[3,2], Suzana Bandeira[3,4], Ishan Agarwal[5], Nuno Ferrand de Almeida[6] and Aaron Bauer[5]

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Serra da Neve: Herpetofauna Diversity of southwest Africa's least known Inselberg

Serra da Neve is an Inselberg in the northern limit of Namibe Province, Southwestern Angola, and is the second highest peak (2489 m) in Angola. Until very recently this mountain has remained completely unexplored in terms of its biodiversity, although, given its isolation, area (approx. 5000 km^2) and biogeographic patterns of the surrounding areas, it has always been considered a place of special biogeographic interest. In 2016 we conducted the first herpetological survey of the Serra da Neve Inselberg, and the preliminary results suggest the presence of a diverse and rich diversity of amphibians and reptiles, including new species to science and various lineages of species occurring in the surrounding areas. The herpetofauna of the mountain includes both taxa that are typically found in the higher elevation areas of the Angolan plateau, as well as those that are more xeric, lower elevation and commonly found in the Pro-Namib region of both Angola and Namibia. This poster presents some of these novelties and gives a preliminary overview of the biogeographic significance and context of Serra da Neve Inselberg and the surrounding areas of Southwestern Angola.

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

Jackie Childers[1], Sebastian Kirchhof[2] and Aaron Bauer[3]

[1]Museum of Vertebrate Zoology, UC Berkeley, Berkeley, CA, USA. [2]Museum für Naturkunde, Berlin, Germany. [3]Villanova University, Villanova, PA, USA

Phylogeography and Systematics of the Namaqua Sand Lizard *Pedioplanis namaquensis* and the Specific Recognition of a Long-Synonymised Taxon from Namibia

The Namaqua Sand Lizard (*Pedioplanis namaquensis*) is a widespread species that occurs in arid habitats throughout southern Africa. It is a member of the Lacertidae, a speciose family of lizards that has radiated extensively into nearly every habitat throughout the African subcontinent. Recent phylogenetic studies within the genus have resulted in new species' discoveries and revealed major genetic breaks that show strong geographic structuring. While ecological or physical barriers have been implicated in driving speciation within this group, a lack of fine-scale geographic sampling has hindered efforts to precisely identify specific biogeographic barriers. Samples were collected from localities in South Africa, Namibia and Botswana, and sequenced using 1,938 bp derived from two mitochondrial markers and 1,997 bp from three nuclear markers. Our results show that *P. namaquensis* consists of two highly divergent, geographically distinct lineages separated by the Orange River. Analyses of population structure show that the river appears to act as a hard barrier along the western border of Namibia and South Africa, but sampling localities further inland show genetic admixture between the two lineages, as well as sympatric occurrence of the two clades. Given our results, herein we elevate the northern lineage to a distinct species.

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

Sam Chin[1,2], John Waldman[3] and Elizabeth Alter[1]

[1]York College, New York, NY, USA. [2]CUNY Graduate Center, New York, NY, USA. [3]Queens College, New York, NY, USA

Surveying Fish Community Composition of the Hudson and Bronx River Systems Using Environmental DNA

The least observed fish are often of the highest concern. Populations in decline may be spared from extirpation through habitat protections and catch restrictions, while invasive species may provoke rapid eradication efforts. Environmental DNA (eDNA) methods appear to be well-suited to the task of monitoring species present in low abundances. Rather than depending on chance encounters with fish themselves, eDNA methods detect and identify fragments of DNA that are left behind in water or soil. Due to the efficiency of PCR, even trace amounts of fish DNA can yield positive detections. We tested the efficacy of eDNA as a tool for surveying fish by using it to determine the composition of the fish communities of the Hudson River Watershed and the Bronx River. Water samples were collected from 11 tributaries and 2 main stem sites in the Hudson system, and from ten sites spanning the whole length of the Bronx River. DNA extracts from water samples were processed using a metabarcoding approach designed to amplify, sequence, and identify DNA from all vertebrates. Species lists produced by

metabarcoding were compared to those produced by previous visual and capture-based surveys in order to evaluate the performance of the eDNA method. The broad spatial and taxonomic range of this study should make it a useful baseline for future studies of the Hudson and Bronx, or any of the taxa detected.

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389 Herpetology Physiology, Highland C, Saturday 14 July 2018

Manisha Choudhury[1], Ryan McCleary[2], R. Manjunatha Kini[3] and Devadasan Velmurugan[1]

[1]University of Madras, Guindy Campus, Chennai, India. [2]Stetson University, DeLand, FL, USA. [3]National University of Singapore, Singapore, Singapore

Determination of structure-function relationships of orphan group I three-finger toxins from elapid snake venoms using molecular modeling approaches

Toxins from snake venoms have diverse functions, including pro- and/or anti-coagulant capabilities that help snakes incapacitate and capture prey. Recent proteomic studies of the venom of the Indian cobra, *Naja naja*, identified peptides belonging to orphan group I of the three-finger toxin (3FTx) family, a group of snake venom toxins that include some known to disrupt the blood clotting cascade. To characterize the protein to which these peptides belong, we cloned and sequenced a 261 bp cDNA transcript derived from venom RNA that encodes a mature protein 65 amino acid residues in length. The translated sequence is identical to a protein previously described in venom from *Naja atra*. This protein (here termed najalexin) was also found to have high sequence similarity with ringhalexin from *Haemachatus hemachatus* and a hypothetical protein from *Ophiophagus hannah* (ophiolexin). Predictive molecular modeling demonstrated similar structural organization among the three proteins, and in silico protein-protein docking studies indicate that the proteins bind the tissue factor-factor VIIa complex within the blood clotting cascade, resulting in an inhibition of factor X activation. Eight specific amino acid residues were implicated in this hemostatic activity using protein modeling software.

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34 SSAR SEIBERT CONSERVATION I, Highland B, Thursday 12 July 2018

Kristina Chyn[1] and Te-En Lin[2]

[1]Texas A&M University, College Station, Texas, USA. [2]Taiwan Endemic Species Research Institute, Jiji Township, Nantou County, Taiwan

Projecting Roadkill Risk for Endemic & Native Island Herpetofauna

Herpetofauna have some of the highest recorded levels of road mortality globally and are the most threatened group of terrestrial vertebrate taxa, but road ecology studies are typically lacking. Due to their spatially-complex lifestyles, diverse life-histories, and urgent need for conservation research, herpetofauna are ideal for studying road zone effects across multiple scales. However, they are often understudied in road ecology as they pose little threat for

motorists and are often difficult to accurately and safely assess. As it is unrealistic to monitor all roads to determine which roads are most risky for wildlife mortality, I use species distribution models (SDMs) to analyze and project roadkill risk for wildlife across a road network. I am working with researchers from the Taiwan Endemic Species Research Institute who manage an extensive citizen science roadkill-monitoring group, the Taiwan Road Observation Network (TaiRON), and experts from the Australian Research Council Centre of Excellence for Environmental Decisions (ARC-CEED) to develop roadkill risk models. I use roadkill observation data and environmental covariates in SDMs to create projections and maps of roadkill risk for Taiwan and Australia's wildlife.; though both are islands with high endemism, modeling with their dissimilar ecosystems and human impacts helps broaden the applicability and impact of my research. These risk projections identify areas of high and low roadkill risk, as well as the environmental variables that strongly contribute to risk outcomes for herpetofauna. This allows transportation managers and researchers to identify key locations of high roadkill risk for mitigation and further monitoring.

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

Megan Civitello[1], Robert Denton[1], Michael Zasloff[2] and John Malone[1]

[1]University of Connecticut, Storrs, Connecticut, USA. [2]Georgetown University School of Medicine, Washington D.C., District of Columbia, USA

Comparative Analysis of Frog Skin Transcriptomes suggests Novel Immune Functions in *Mantella betsileo*

The skin secretions of many frog species contain antimicrobial peptides (AMPs) that function to fend off a wide range of infectious microorganisms. However, it was recently discovered that the skin of Madagascar poison frogs (*Mantella*) secretes a novel, bile-acid derived molecular compound named tauromantellic acid, raising new questions as to the function of this compound and whether AMP genetic elements remain present in *Mantella*. To understand AMP expression among frogs, we assembled the skin transcriptome of *Mantella betsileo* and compared it to skin transcriptomes from 11 other species across the phylogeny of frogs. Our analyses revealed the absence of AMPs in *M. betsil*eo but a diversity of AMPs and AMP expression levels in other species. For bile acid, many bile acid pathway genes were expressed in all frog skin transcriptomes. However, one gene critical to the function of the bile acid pathway (CYP7A1) was highly expressed exclusively in the skin of *M. betsileo*. This specific gene catalyzes the first reaction in the cholesterol catabolic pathway in the liver and is the rate-limiting step in the regulation of bile acid synthesis. This suggests that the bile acid pathway is functional in the skin of *Mantella* and may replace AMPs for normal defense function, which would provide a unique mode of frog skin defense not previously described. The transcriptome of *Mantella* will facilitate new comparative analyses to better understand the complexity of frog skin defense molecules, their evolutionary origin, and potential applications as therapeutic agents for human health.

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320 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS, Empire Hall South – JF Rochester Riverside

Convention Center, Friday 13 July 2018

Meaghan Clark[1], Maria Akopyan[2,1], Gideon Bradburd[3], Andres Vega[4] and Jeanne Robertson[1]

[1]California State University, Northridge, Northridge, CA, USA. [2]Cornell University, Ithaca, NY, USA. [3]Michigan State University, East Lansing, MI, USA. [4]AMICOR, Tibás, Costa Rica

Orange to Purple: Evolutionary history of red-eyed treefrogs in a hotspot of color pattern diversity

Linking phenotypic variation to underlying genetic diversity contributes to our understanding of how evolutionary forces affect natural populations. We investigate the genetic structure and evolutionary history of red-eyed treefrogs (*Agalychnis callidryas*) occupying six regions along the Pacific coast of Costa Rica, where a phenotypic cline extends from the north (orange legs) to the south (purple legs), with intermediate color patterns in central regions. We hypothesize that patterns of color variation in intermediate central regions could be explained by the retention of ancestral and/or novel color polymorphism, or by hybridization between divergent populations that meet at secondary contact zones. We used a SNP dataset generated by RAD-sequencing to analyze population genetic structure. Comparison of inter-population ancestry and admixture proportions did not reveal evidence of hybridization at contact zones between color patterns. Instead, we detected a pattern of genetic isolation by distance that is discordant with color boundaries. These incongruent patterns suggest the possibility of selective pressures acting on color pattern along the Pacific Coast. Overall, our data support that color-pattern variation is due to differential retention of polymorphism as opposed to recent introgression.

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

Olivia Clark[1], Juan Daza[1], Ian Brennan[2], Mark Hutchinson[3] and Aaron Bauer[4]

[1]Sam Houston State University, Huntsville, Texas, USA. [2]The Australian National University, Canberra, Australia. [3]University of Adelaide, Adelaide, Australia. [4]Villanova University, Philadelphia, Pennsylvania, USA

Distinct Patterns of Skull Morphology among Australian Legless Lizards (*Aprasia*: Pygopodidae)

Aprasia is a genus of miniaturized pygopods from Australia that indisputably exhibit the most extreme skull morphologies for any known gecko. Some of the autapomorphies of this group include several convergent characters with scolecophidian snakes such as the outer shell bone arrangement in the snout, extreme reduction of teeth, lateral closure of the braincase, and a lower jaw that is shorter than the cranium. The genus today includes 14 species of fossorial or semifossorial lizards, but only three of them have been studied osteologically. Using XRCT scans of 27 specimens, we found that the skulls show two alternative construction patterns. When these patterns were mapped into concatenated tree of mtDNA and nDNA, we found two distinctly different patterns: 1) A basal pattern where the braincase is supported by the pterygoid bones via the epipterygoid (as in the vast majority of squamates) and 2) a derived pattern where the braincase contacts the frontal bone via a hypertrophied parabasisphenopid

rostrum, with no support of the pterygoids due to a reduction of the epiterygoids. This second pattern is present today exclusively in Western Australia, while the basal patterns are found throughout the country. It has also been suggested that perhaps the *Aprasia* specimens from Western Australia will consist of all “long-nosed” specimens, which so far are considered to be the more fossorial species. Their counterparts found throughout the rest of the Australian continent are known to have a more basic, round-nosed morphology.

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105 Herpetology Physiology, Highland C, Saturday 14 July 2018

Rulon Clark[1], George Bakken[2] and Hannes Schraft[1]

[1]San Diego State University, San Diego, CA, USA. [2]Indiana State University, Terre Haute, IN, USA

Are Warmer Pit Vipers Less Sensitive to Infrared Radiation?

Some species have evolved unique sensory systems that allow them to see the world in fundamentally different ways. Pit vipers possess extraordinarily sensitive infrared radiation detectors that essentially operate as an extension of the visual system, allowing them to see temperature contrast in their environment. Although some details of the physiology and neuroanatomy of this system have been worked out, there are still basic properties of this sensory channel that remain mysterious. For example, although behavioral studies have suggested that IR sensitivity increases when the pit organ is cooler, this relationship is the opposite of predictions from typical thermal reaction norms and from the positive temperature response profile of TRPA1, the ion channel thought to be the molecular mechanism underlying thermal contrast detection. We implemented a behavioral assay to systematically explore the interacting effects of thermal contrast and body temperature in a captive colony of Pacific rattlesnakes (*Crotalus oreganus*). Although we found the expected strong increases in snake responsiveness with both positive (target warmer than background) and negative thermal contrast, the effect of body temperature was the opposite of predictions based on thermal reaction norms and ion channel sensitivity: cooler snakes responded much more strongly to thermal contrast. Because the temperature of the pit membrane has little effect on net thermal radiation exchange, we know of no physical or biological properties of the pit organ system that can explain this result. Clearly, additional behavioral and molecular studies are necessary to understand the basic properties of this unique sensory system.

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294 Lightning Talks II, Highland A, Saturday 14 July 2018

Rute Clemente-Carvalho, Peiwen Li, Hannah Driver, Cora Jennings, Peter van Coeverden de Groot and Stephen Lougheed

Queen's University, Kingston, ON, Canada

Genetic Insights Into Lake Whitefish of the Lower Northwest Passage

Northern regions have been disproportionately impacted by climate change, which is causing shifts in the geographical ranges of some species. However, climate change may also create some economic opportunities for northern peoples facilitating greater access to fishing areas in

areas like the Lower Northwest Passage (LNWP). The Lake Whitefish (*Coregonus clupeaformis*) is one LNWP species that might be suitable for a commercial fishery; however, its taxonomy presents challenges as there has multiple morphotypes/species. To develop a cogent, sustainable fisheries plan we must be able to identify these putatively distinct taxa. To this end, we examined 120 individuals from three LNWP sites: Legendary River, Back River, and Kaleet River. We surveyed variability in mitochondrial DNA sequence from the Cytochrome Oxidase I (n=120) and 8 microsatellites loci (n=60). In CO1, we found four distinct genetic clusters, two for *C. sardinella*, one for *C. clupeaformis* and one for *C. autumnalis*. Pairwise p-distances showed the following ranges: 0-0.9% within *C. sardinella* , 1.1-1.5% between *C. clupeaformis* and *C. sardinella*, 1.7–2% between *C. clupeaformis* and *C. autumnalis*, and 0.9-1.3% between *C. sardinella* and *C. autumnalis*. Analyses of DNA microsatellites showed three clusters, with some individuals assigned to different clusters as defined a priori based on COI sequences. These results imply hybridization within the LNWP and highlight the importance of undertaking taxonomic studies before any commercial fishery is developed. Future work will incorporate morphological data and additional nuclear markers including SNPs.

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

Rebecca Clemons, Anat Belasen and Timothy Y. James

University of Michigan, Ann Arbor, MI, USA

Host Ecology and Habitat Fragmentation Impact Bd Prevalence in the Brazilian Atlantic Forest

Since its recent discovery in the late 1990s, the fungal parasite *Batrachochytrium dendrobatidis* (Bd) has been implicated in the global decline of amphibians. Bd preferentially thrives in colder, wetter environments. Although these environmental preferences are well-established, it remains to be understood how human alteration of natural habitats may impact Bd infection dynamics. In the Brazilian Atlantic Forest, a hotspot for frog diversity, human activity has caused the widespread fragmentation of important amphibian habitats. The remaining amphibian populations in habitat fragments are small and isolated compared to those found in preserved continuous habitats. This fragmentation may increase disease prevalence due to increased host stress. However, fragmentation may also lead to the loss of species from the frog host community which may alter infection dynamics if Bd exhibits preferences for certain host species and/or ecologies. We used molecular assays (qPCR) to quantify the infection prevalence and load of samples collected from a diversity of amphibians in terrestrial and aquatic habitats found within both fragmented and continuous areas. Our data indicate trends toward higher prevalence of Bd in frogs found in fragmented habitats, as well as a lower prevalence of Bd in frogs that live and breed in drier, terrestrial environments. Understanding which populations of frogs are at increased risk of Bd infection will inform conservation efforts for declining amphibian populations worldwide.

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

Ian Clifton and Jeanine Refsnider

University of Toledo, Toledo, OH, USA

Phenotypic variation along an elevational gradient in a montane lizard community (San Juan County, UT)

Climate varies widely along elevational gradients on relatively small ecological scales. In general, temperature decreases and becomes more stochastic as elevation increases. This extensive climatic variation can mean conspecifics in populations at different elevations experience vastly different climatic regimes, potentially leading to substantial shifts in phenotypic means among populations. We collected morphological and physiological (specifically thermal sensitivity and performance) data from lizards within a montane lizard community to identify phenotypic patterns and to determine if the observed patterns are consistent among species. Four phrynosomatid lizard species (*Phrynosoma hernandesi*, *Sceloporus tristichus*, *Sceloporus graciosus*, and *Uta stansburiana*) were sampled from populations at varying elevations over four years (2014-2017). We found a range of morphological differences when comparing high and low elevation populations in all species sampled; however, differences tended to be inconsistent among species. On the other hand, only populations of *S. tristichus* exhibited significant differences in thermal sensitivity, with lower elevation *S. tristichus* having a higher critical thermal maximum than their higher elevation conspecifics. We also found evidence of variation in endurance, though, once again, patterns were inconsistent among species.

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629 General Herpetology I, Highland B, Sunday 15 July 2018

Anthony Cobos[1], Robert Espinoza[1], L. Lee Grismer[2], Shahrul Anuar[3] and Evan Quah[3]

[1]California State University Northridge, Northridge, CA, USA. [2]La Sierra University, Riverside, CA, USA. [3]Universiti Sains Malaysia, Penang, Malaysia

Convergent Evolution in Morphology, Physiology, and Performance among Malaysian Cave-Dwelling Geckos

Cave life is associated with novel adaptations for coping with the unique challenges of a troglodytic lifestyle. Such specializations are expected given the distinct environments and abrupt transition associated with caves relative to surrounding areas. For example, caves are devoid of light, stable in temperature and humidity, and scarce in resources, leaving few niches for organisms to occupy. We therefore expect cave-adapted species to converge on a common suite of specializations relative to their forest-dwelling relatives. Our study compares morphological, physiological, and performance differences between cave-dwelling Banded

bent-toed geckos and their closest forest-dwelling relatives living in the surrounding forests (*Cyrtodactylus pulchellus* complex). Specifically, we tested for convergence in gecko morphology, resting metabolism, and clinging performance. We hypothesized that cave-dwelling species (n = 3) would exhibit (1) convergent adaptations in morphology, (2) lower rates and variance in metabolism given their narrower abiotic niches, and (3) a greater clinging performance to cave substrata (limestone karst) relative to forest-dwelling species (n = 4). Cave-adapted forms had greater body-size corrected palmar/plantar surfaces than forest forms. Cave-dwelling species also had significantly lower mass-specific rates of resting metabolism and outperformed forest-dwelling *Cyrtodactylus* in cling-performance trials. Our study shows that cave-dwelling species appear to have independently evolved these diverse adaptive traits supporting convergence of a cave-adapted phenotype for Banded bent-toed geckos.

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

Marlon E. Cobos[1] and Roberto Alonso Bosch[2]

[1]University of Kansas, Lawrence, Kansas, USA. [2]Havana University, Havana, Havana, Cuba

Multiscale Analyses Reveal Importance of Breeding Sites for a Critical Endangered Cuban Toad's Conservation in the Face of Global Change

Global change includes climate change, sea-level rise, and land-use change, among others, as significant threats to biodiversity. These changes are usually studied across broad extents, and understanding their potential effects on endangered species with restricted ranges is challenging. *Peltophryne florentinoi* is an endangered coastal Cuban toad, and despite its potential vulnerability, few efforts have focused on threats to its survival in the face of global change. Current and future threats from global change to this species were evaluated using multiscale GIS and statistical approaches. Climate change effects were assessed comparing the species niche with six future (2050) climate configurations in its distribution range. Sea-level rise risks were evaluated by simulating potential coastal inundation under three sea-level rise scenarios. Recent land-use changes were quantified using forest cover loss information between 2000 and 2015. Within the species' habitat, warmer and drier conditions can be expected in the future. Sea-level rise will not have direct impacts on the species habitats; however, occasional inundations and saltwater intrusion could present additional stressors. Although ~2% of the forest cover has deteriorated in the species' habitat and its surroundings during 2000–2015, deforestation trends are variable during this period, and future forest cover losses can be expected. In the face of these threats, and in view of colonization of new areas being unlikely, indirect and additive negative effects can be expected. These impacts will most probably be observed during the larval stage of this toad; hence, breeding sites constitute a key element in this species' conservation.

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

Hannah Cohen and Emily Kane

Georgia Southern University, Statesboro, GA, USA

Local Adaptation of Morphology and Diet Does Not Predict Feeding Behavior in Guppies (*Poecilia reticulata*)

Organisms face many challenges, including predation and resource availability, and these pressures can change across spatial gradients. For example, where predation pressures are low, increased population density increases intraspecific competition for prey. However, how these changes in selective pressures lead to local adaptation, particularly in feeding behaviors, needs further exploration. In Trinidadian guppies a shift in selective pressure toward resource competition in low predation environments has resulted in local adaptation of many traits, including jaw morphology and diet. But whether these changes result in local adaptation of feeding behaviors remains unclear. No difference between populations in suction feeding performance suggests an inability to adapt their feeding behaviors. But as guppies' natural feeding mode is biting, this alternative behavior could reflect this adaptation. If selective pressures cause changes in resource use that drive adaptation for feeding, then low predation guppies should have stronger biting kinematics compared to high predation guppies. We filmed individuals from replicate low and high predation populations using a high-speed camera while they fed from an agar substrate using biting. Preliminary data suggests that there is no local adaptation in biting performance due to the environment, in agreement with previous work on suction feeding performance. The lack of adaptation suggests potential unexplored effects, such as a many-to-one mapping of morphological traits to behavior or selection pressure on morphology may not be due to feeding.

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298 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Karly Cohen and L. Patricia Hernandes

The George Washington University, Washington, DC, USA

Functional morphology of the epibranchial organ of *Hypophthalmichthys molitrix* (silver carp)

Incredibly invasive Asian carp are destroying ecosystems throughout the United States by outcompeting native species. Their ability to feed so efficiently within eutrophic environments is due to their highly modified gill rakers and complex epibranchial organ. Epibranchial organs are paired food-aggregating organs located ventral to the neurocranium in certain teleostean fishes. These structures have independently evolved multiple times and range in complexity

from small slits to intricate spiraling diverticula, epibranchial organs are morphologically diverse across filter-feeding fishes. Despite this morphological diversity and broad distribution, the epibranchial organ of silver carp is morphologically distinct. Here we present data on the functional morphology of the epibranchial organ in adult silver carp and how the epibranchial organs in silver carp differ from those is other filter feeding teleosts. Unlike other epibranchial organs, the gill rakers that extend from branchial arches 1-5 are greatly modified as they curve into the body of the epibranchial organ. Throughout ontogeny the epibranchial organ becomes more complex with the gill rakers becoming increasingly incorporated into the overall structure. Increased complexity coincides with histological changes to supporting cartilaginous structures and an increase in innervation. By early juvenile stages, the epibranchial organ is fully functional. The adult epibranchial organ forms a multiple-looped structure that efficiently moves food from each of the gill rakers to the pharyngeal jaws. This detailed anatomical investigation has yielded a functional hypothesis of the epibranchial organ in silver carp.

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306 General Ichthyology I, Grand Lilac Ballroom South, Sunday 15 July 2018

Karly E. Cohen[1], L. Patricia Hernandez[1], Callie H. Crawford[2] and Brooke E. Flammang[2]

[1]The George Washington University, Washington, DC, USA. [2]New Jersey Institute of Technology, Newark, NJ, USA

Modeling silver carp filtration using µCT and 3D PIV

Invasive Silver carp are thriving in eutrophic environments in the United States due to efficient filter-feeding mechanisms. Like many filter-feeding fishes, silver carp utilize modified gill rakers to filter out particles from the incoming streamline of fluid; however, unlike other fishes, silver carp gill rakers are fused together to form highly porous, channeled filtering plates. This filtering morphology captures particles ranging from 4-80 µm, which may help explain how this species can outcompete native fishes. While some descriptive studies exist no work has yet described the mechanism behind silver carp filtration. Here we investigate the hydrodynamics of silver carp filter feeding using volumetric Particle Image Velocimetry (3D PIV). Fixed gill rakers and 3D models (based on 10µm and 28µm µCT scans of adult Silver carp and its sister species Bighead carp) were placed in a recirculating flow tank. Neutrally-buoyant 50µm particles were illuminated by a 50mJ-100Hz Nd:YAG pulse laser focused into a 14cm x 14cm x 14cm volume using an optic and mirror system, tracked and processed using V3V software, and resulting vector information was analysed in Tecplot. Using 3D PIV, we tracked particle and fluid interaction from the surface of the gill raker through the various sized pores along the filter. Based on results from these multiple PIV studies and morphological analyses, we find that the morphology on the outer face of the gill raker plates quickly organizes flow across the entirety of the filtering surface and initiates strong vortical flow, likely accounting for particle capture and retention.

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300 Ichthyology Systematics II, Grand Lilac Ballroom South, Sunday 15 July 2018

Kathleen Cole[1] and Lynne Parenti[2]

[1]*University of Hawaii at Manoa, Honolulu, HI, USA.* [2]*Smithsonian Institution National Museum of Natural History, Washington, DC, USA*

Gonad morphology of *Rhyacichthys aspro*: a proposed template for comparative reproductive morphology among gobioid fishes

Histological and ultrastructure studies have significantly advanced our understanding of gonadal morphology and putative homologies across teleost fishes. Similar comparisons of informative traits at lower taxonomic levels may also enlighten our understanding of phylogenetic relationships among more restricted taxon groupings. The Gobioidei is one of the two largest vertebrate taxa (Nelson et al., 2016) and exhibits considerable variation in morphology of the male reproductive system. Much of the available information on reproductive morphology is limited in scope and taxonomically diverse, constraining our understanding of gobioid reproductive system evolution. We carried out a detailed histological examination of reproductive morphology, using a "basal" gobioid, *Rhyacichthys aspro*, to identify potential informative characters that could be used to test existing phylogenetic hypotheses for Gobioidei. We found that adult females exhibit an elaborate fimbriate pad associated with the urogenital papilla, which has not previously been reported among gobioids. The male reproductive complex is partitioned into an elongate secretory lobe, and a smaller spermatogenic lobe which arises from the former, with sperm exiting the gonadal complex by a series of dedicated, intralobar, collection channel systems. The male reproductive system appears to reflect a lobular construct with different regions exhibiting different lobular modifications. In the course of this study we recognized a clear need for more consistency in fine-scale descriptions of gobioid reproductive morphology, and propose some new, anatomically descriptive and unambiguous terminology in order to identify possible homologies for future comparisons among other gobioid taxa.

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

Bruce B Collette[1] and Katherine E Bemis[2]

[1]*Smithsonian Institution, Washington, D.C., USA.* [2]*Virginia Institute of Marine Science, Gloucester Point, VA, USA*

History of the monographic series “Fishes of the Western North Atlantic”

With the establishment of the Sears Foundation of Marine Research at Yale University in 1937, funds became available for publication of a comprehensive account of western Atlantic fishes to replace Jordan and Evermann’s 1896-1900 Fishes of North and Middle America. Accounts in Fishes of the Western North Atlantic covered taxonomy, biology, distribution, with illustrations

of each species. Part One, lancelets, cyclostomes, and sharks was published in 1948. Part Two, Sawfishes, etc. in 1953; Parts Three and Four, Soft-rayed bony fishes in 1963 and 1964; Part Five, Iniomi in 1966; Part Six, halosaurs to grenadiers in 1973; Part Seven, Myctophiformes in 1977; Part Eight Sticklebacks and pipefishes in 1982; and Part Nine, eels in two volumes, in 1989. Twenty-nine years later, we have completed the final volume on Beloniformes, Part Ten. The gap in completion was mostly caused by the deaths of two previous flyingfish experts, Bob Gibbs and Nik Parin. This gap has now been filled by Ilia Shakhovskoy. But why is this the last volume? Times have changed. We have Google and other electronic sources of information. And the supply of ichthyologists interested in summarizing all available information about the groups of fishes that they study seems to have evaporated. Are there other explanations?

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

Kevin Conway[1] and Dustin Siegel[2]

[1]Texas A&M University, College Station, TX, USA. [2]Southeast Missouri State University, Cape Girardeau, MO, USA

Enlarged and highly mobile male genital papilla in the miniature Southern Australian clingfishes of the genus *Parvicrepis* (Teleostei: Gobiesocidae)

Male members of the Southern Australian clingfish genus *Parvicrepis* (1 described and 2 undescribed species) exhibit an enlarged and highly mobile genital papillum. Preliminary investigation of this structure using a combination of light and scanning microscopy has revealed a complicated network of collagen fibers surrounding an ovoid central canal (sperm duct). A dense network of collagen fibers (with fibers running parallel to the long axis of the papillum) is located ventral to the central canal and may function as an internal supporting structure. Preliminary observation of movement of the papillum and differences in collagen fiber arrangement along the length of the papillum demonstrate that movement may be restricted to the rostral/caudal axis. We predict that this mobile structure may be involved in delivering sperm directly to the female reproductive tract (i.e., internal fertilization). Internal fertilization is rare within the Gobiesocidae and has been reported previously only from the South African endemic clingfish *Eckloniaichthys scylliorhiniceps*.

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

Robert D. Cooper and H. Bradley Shaffer

UCLA, Los Angeles, CA, USA

The Effect of Pond Hydroperiod and Larval Density on Hybrid Tiger Salamander Success

The California tiger salamander (*Ambystoma californiense*) is an endangered species that is experiencing rapid introgression from non-native alleles throughout its range. Efforts to control this spread have largely been ineffective, necessitating research into novel methods of management. Previous mesocosm experiments coupled with field observations have shown that artificially longer hydroperiods are advantageous to hybrid genotypes, and suggest that reducing hydroperiod may remove or even reverse the hybrid advantage. We constructed 18 experimental ponds to evaluate this potential management strategy. Here we present data on two facets of this ongoing project. First, we present hydrologic data from the ponds which are used to parameterize a predictive model for pond hydroperiod based on weather and pond geometry. Second, we present phenotypic data from hybrid salamanders that have developed at different larval densities across a range of hydroperiods. We use these data in conjunction with a recently developed integral projection model to determine the effects that altered ponds may have on demography in the wild. These results provide insight into the effect of hydroperiod manipulation on hybridization in tiger salamanders, and on the ecological effects of hydroperiod more generally on larval development and metamorphosis in this endangered species.

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

Joel Corush[1], Jen-Chieh Shiao[2], Todd Pierson[1], Jie Zhang[3] and Benjamin Fitzpatrick[1]

[1]University of Tennessee, Knoxville, TN, USA. [2]National Taiwan University, Taipei, Taiwan. [3]Institute of Zoology, Chinese Academy of Sciences., Beijing, China

The effects of an amphibious life history on the population structure of a mudskipper (*Periophthalmus modestus*) in East Asia.

Amphibious fishes are those that require an aquatic and terrestrial portion of their life cycle. While many fishes can persist on land for a limited period of time, few species have an obligate terrestrial life history stage. Many species of mudskippers in the family Gobidae (subfamily: Oxudercinae) are obligate amphibious. This obligatory phase comes with a geographical restriction to mudflat habitats during breeding when adults build burrows in the mud to lay their eggs. While they do not have obligate juvenile or adult stages out of water, some of these fishes tend to spend the majority of their time out of the water. This out of water phase limits movement to very specific terrestrial habitat for a portion of the fish's life and should be reflected in the population structure of the species. We examined the shuttles hoppfish (*Periophthalmus modestus*) with respect to its population structure throughout its range of the East and South China Seas. Over 250 individuals were collected from 10 populations across mainland China, Hainan island, Taiwan, Okinawa and central Japan. We used a new targeted capture sequencing method, RADcap, to sequence 1000 loci from each individual. We found that, based on genetic variation and structure analysis, these fish are connected across large

areas of continuous coastal areas and across small spans of water. However, restricted long-distance dispersal across water results in fragmentation of the species' population structure. These results are consistent with the hypothesis that a limited dispersal phase significantly affects population structure in fishes.

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216 General Ichthyology I, Grand Lilac Ballroom South, Sunday 15 July 2018

Matthew Craig[1] and Wm. Leo Smith[2]

[1]NOAA National Marine Fisheries Service, La Jolla, CA, USA. [2]University of Kansas, Lawrence, KS, USA

Groupergate: On the reluctance to recognize the non-monophyly of the "Serranidae".

More than a decade ago we published a data-rich analysis of percomorph relationships based on genetic sequence analysis that unequivocally demonstrated the non-monophyly of the family "Serranidae". Since that time, many researchers (primarily from the United States) have chosen to ignore that study, and instead have argued that the "Serranidae" are monophyletic using what can only be described as "special pleading." In this presentation, we describe the history of the "Serranidae", discuss various phylogenetic hypotheses that have been presented since our previous paper, and demonstrate the inadequacies of the most recent classification of fishes in its ability to test the monophyly of the "Serranidae".

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168 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Callie Crawford[1], Zachary Randall[2] and Brooke Flammang[1]

[1]New Jersey Institute of Technology, Newark, NJ, USA. [2]Florida Museum of Natural History, Gainesville, FL, USA

These Fins Were Made for Walking: Tetrapodal Morphology of Balitorid Fishes

Balitoridae, the hillstream loaches, is a family of cypriniform fishes living in high-flow streams and rivers of South and Southeast Asia. There are currently 16 recognized genera including a monotypic blind cave genus, *Cryptotora*. Previous work found that the cave loach, *Cryptotora thamicola*, was capable of terrestrial walking with a tetrapod-like walking gait. This gait is due, in part, to having a robust pelvic morphology rigidly attached to the vertebral column via sacral ribs – a trait previously thought to be specific to tetrapods. Further examination of the skeletal morphology of other balitorids has shown a spectrum of pelvic robustness with fishes having pelvises and sacral ribs similar to *Cryptotora thamicola* at one end and others with more stereotypically fish-like pelvises and ribs at the other. Here, we explore the pelvic morphology

of closely related genera within Balitoridae. Further work will use kinematics and electromyography to compare the weight-bearing walking capabilities of three different pelvic morphs. The expected outcome is that a more robust connection between the vertebral column and the pelvis, e.g. more similar to the morphology observed in *C. thamicola*, will correspond to an increased ability to bear weight and thus increased capacity for walking.

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510 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Lyda Crawford

Tulane University, New Orleans, LA, USA

Comparing Follicle Cell Processes Across Chondrichthyan Orders

The chondrichthyan fishes are an excellent model to investigate the evolution of live bearing. The major stages in the transition from egg laying to placental live birth can be found in this evolutionarily old class. The diversity of reproductive modes permits us to follow the logical stages in anatomical adaptations of extant species to better understand how the female reproductive system adapted to these strategies. Viviparity allows the maternal organism to protect her offspring by keeping them inside her body and providing increased nutrients, thus, the neonates will be large at birth. One potentially important aspect in the shift from egg-laying to viviparity and towards producing large offspring is the increase in size of the unfertilized egg (oocyte). Some of the chondrichthyan species produce very large eggs, such as the dogfish sharks (*Centrophorus* sp.) whose oocytes reach 10 cm in diameter at ovulation. More yolk stored within the oocyte, means more nutrition available to the developing embryo. A variety of studies have addressed aspects of matrotrophy in chondrichthyan fishes but very little have addressed how large eggs develop within the ovary. In the chondrichthyan fishes there may be a novel set of structures that play a role in vitellogenesis, Follicle Cell Processes (FCP). To date, papers that have addressed the presence FCP are purely morphology based and have covered relatively few species. The present paper aims to address the gap in understanding over how vitellogenin moves between follicle cells and the developing oocyte across Chondrichthyes.

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

James Creed[1,2], Matthew Aardesma[3,2] and Melanie Stia[2]

[1]York College/CUNY, Jamaica, NY, USA. [2]AMNH, New York, NY, USA. [3]Montclair State University, Montclair, NJ, USA

Beyond the cave: The genetic basis of troglomorphy across highly divergent fish lineages

Fishes dwelling in caves and other low-light environments have evolved a distinct set of features (“troglomorphy”), generally considered to be adaptations to a lightless or light-poor environment. These features, which include eye loss as well as enhancements in other aspects of sensory anatomy (e.g. lateral line), exemplify the process of convergent adaptive evolution.

Cave fishes such as *Astyanax mexicanus* have emerged as model organisms for studying the processes that result in so-called "degenerative" evolution. However, eye loss and laterosensory enhancements are not limited to cave organisms, and in fact occur across numerous fish lineages. In particular, this phenomenon has been identified in a diverse set of fish species that are endemic to the lower Congo River. To investigate the genetic basis of troglomorphy, we sequenced the genome of *Lamprologus lethops*, the blind cichlid, and compared it with published genomes from other cichlid species and with *Astyanax mexicanus*. Our analyses reveal both similarities and differences with regard to genome-level changes linked to troglomorphic phenotypes; for example, different loss-of-function mutations are present in the Oca2 gene in both lineages, very likely contributing to loss of pigment. Likewise, we observe degenerative mutations in genes related to eye loss, circadian rhythm and satiety/feeding control in *L. lethops*, some of which have been implicated in *A. mexicanus* behavior and physiology. Finally, we put forward a framework for comparative research across both deep and shallow branches in the vertebrate tree of life to better understand the convergent evolution of troglomorphy.

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

James Creed[1], Kimberly Bernotas[2], Elizabeth Alter[1,2] and Melanie Stiassny[2]

[1]York College/CUNY, Jamaica, NY, USA. [2]AMNH, New York, NY, USA

Morphometric analysis of an unusual specimen of cichlid in the genus *Teleogramma* (Teleostei, Cichlidae)

The Congo River is one of the world's largest rivers. It is a hotspot for fish species diversity and harbors a large number of endemic species, likely due to its unique hydrology and geography, which includes rocky-strewn shores and fast-flowing water. The cichlid genus *Teleogramma* is endemic to the Congo, and a number of species in this genus show adaptations to fast-flowing water. However, the number of species in the genus remains unknown. New specimens in the cichlid genus *Teleogramma* were collected in the middle Congo River in 2015-2017; these specimens showed unusual morphology and coloring, and a preliminary genetic analysis indicates they are differentiated from other *Teleogramm*a species. We compared body shape between these new specimens and two described species of *Teleogramma* (*T. monogramma* and *T. obamaorum*) using a program called MorphoJ, which can be used to perform geometric morphometric analysis. We discuss the similarities and differences in morphometric measurements in these new specimens and comment on its validity as a potential new species of cichlid.

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258 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Highland A, Thursday 12 July 2018

Hayley Crowell and Emily Taylor

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

Eat, Prey, Live: Comparative Thermal Ecology and Energy Requirements of Coastal and Inland Populations of Pacific Rattlesnakes (*Crotalus oreganus*)

Understanding the effects of changing temperatures on ectothermic species is crucial if land managers and researchers are to make informed decisions about how to mitigate the predicted loss of diversity as a result of anthropogenic climate change. Using body temperature data from free-ranging snakes, the field metabolic rates, and therefore basic energetic requirements, can be calculated to determine average annual energy expenditure of a given ectotherm. The goal of this study is to use field active body temperature data from four distinct populations of *Crotalus oreganus* from central California (two inland and two coastal) to compare average body temperatures, estimated metabolic rates and annual energy expenditure across varying habitat types. Snake body temperature data were collected via internal implantation of Thermochron iButton temperature loggers from 2006 to 2017 during the snakes' active season (April-Oct). Despite dramatically different ambient temperatures at the field sites, snakes at inland and coastal sites thermoregulate such that they experience similar mean daily body temperatures. However, inland snakes are significantly larger in mass than their coastal counterparts and therefore have higher overall metabolic rates. Operative temperature models were used throughout each of the four field sites in order to characterize microhabitat temperatures available and calculate thermal quality of the landscape. In combination with predicted increases in ambient temperature, probable changes in body temperatures, activity times, and energy requirements were extrapolated for each site through the year 2100.

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

Joe Crowley

Ontario Ministry of Natural Resources and Forestry, Peterborough, Ontario, Canada

Increasing the Resilience of Northern Populations: Protection and Recovery of Ontario's Herpetofauna

The effects of climate change on amphibian and reptile populations remain poorly understood, and the direction and magnitude of these effects will vary from species to species. An overall trend toward northward shifting ranges is expected for many species. Thus, the conservation of genetically diverse source populations at the northern extent of species' ranges is particularly important in light of climate change. However, over half of Canada's amphibian and reptile species (55 of 102 species) are listed as species at risk under Canada's Species at Risk Act, and declining or isolated populations make these species particularly vulnerable to the effects of climate change. Further to this, much of southern Canada is highly developed and densely populated by humans, which may present a barrier to the northward dispersal and expansion of species. Ontario has a number of legislative and policy tools that are helping to address these challenges. For example, species at risk legislation and associated funding is playing an instrumental role in recovering Ontario's amphibian and reptile species, and protecting and re-connecting the habitats on which they depend. This presentation will provide an overview of the key protection and recovery efforts for amphibians and reptiles in Ontario, with a focus on how they support the resilience of northern populations and facilitate potential range expansion in northern latitudes.

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207 ASIH: If Salamanders Could Speak Symposium, Grand Lilac Ballroom North,

Saturday 14 July 2018

Paul Cupp, Jr.

Eastern Kentucky University, Richmond, KY, USA

Unken Reflexes in a Cryptic Salamander, *Aneides aeneus*

Green salamanders, *Aneides aeneus*, exhibit a number of postures that may enhance their survival and ability to reproduce. Some individuals were observed in substrate avoidance postures that resemble unken reflexes in which all or some limbs are raised off the substrate and often at a level above the head. The head and tail were elevated in some cases. Being cryptic, warning coloration and toxic skin secretions are not present. The body surface area that is in contact with the substrate is significantly reduced which allows the salamander to minimize contact with potentially harmful "dirty" or excessively wet substrates. Dirty substrates would include bacterial or fungus-laden areas that salamanders may encounter during spring and fall migrations. Also, extended periods of rainfall resulting in water standing in crevices may subject some *A. aeneus* to overhydration. In ten instances (equally divided in lab and field), individual *A. aeneus* were observed in wet rock crevices exhibiting postures where limbs were raised as in unken reflexes thereby significantly reducing exposure of the skin to wet substrates. One salamander shifted to an alternate posture in which all four feet were in contact with the substrate with limbs extended, and the mid-body arched above the substrate. Slight changes in posture may provide for fine control of dehydration or rehydration rates to optimize body water content. Postural adjustments may allow terrestrial salamanders, such as *A. aeneus*, to remain in home crevices thereby reducing exposure to predation, and avoid harmful substrates.

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

Joseph Cutler[1], Brian Sidlauskas[2], Hans Mipounga[3] and Jean Herve Mve Beh[3]

[1]UC Santa Cruz, Santa Cruz, CA, USA. [2]OSU, Corvallis, OR, USA. [3]CENAREST, Libreville, Gabon

Dam, Dam, Dam - Balancing Fish Biodiversity and Hydroelectric Development in Gabon

Gabon is rapidly developing, and the government plans a four-fold increase in hydropower production by 2020. 42 potential dam sites have been identified, including several on the mainstem Ogooué River - the fourth largest river in Africa. Hydroelectric dam development in Gabon threatens the >350 freshwater fish species, moreover several of the proposed dam sites have never been sampled by ichthyologists. To assess the impacts of hydropower development at three proposed dam sites, my team and I sampled fish biodiversity in three river systems the Komo, Ngounie, and Louetsi. Our baseline assessment provides a two-season snapshot of the freshwater biodiversity at and around, three impending dam sites. Over the course of four months, we collected 12,000 fish specimen, representing at least 150 fish species including several new to science. I will present the results from our sampling expedition, the implications of hydropower development in the Louetsi, Komo, and Ngounie Rivers, and how we will use our data and strategic planning to balance development goals while simultaneously protecting freshwater biodiversity in Gabon.

91 Herpetology Morphology I, Highland D, Sunday 15 July 2018

Domenic D'Amore[1], Megan Harmon[1], Stephanie Drumheller[2] and Jason Testin[3]

[1]Daemen College, Amherst, NY, USA. [2]University of Tennessee, Knoxville, TN, USA. [3]Iowa Western, Council Bluffs, IA, USA

Determining Shape- and Size-Heterodonty in Members of Crocodylia Using Geometric Morphometrics

Modern crocodylian dentition has been referred to as “homodont,” “pseudoheterodont,” or “heterodont” depending on the study, but few of these studies have actually measured the teeth in question. Our goal was to quantify dental morphology in a multispecific sample of extant and extinct members of Crocodylia using geometric morphometrics. Intact teeth from 39 dry-skull/fossil specimens were photographed, adding up to over 1,250 teeth. The margins of each tooth were traced and converted into semilandmarks in TpsDig2.6. A generalized least squares Procrustes superimposition was performed, and centroid size was calculated. Heterodonty was analyzed through principal components analysis, Foote’s morphological disparity, and regression analysis. Results indicated shape and size were developmentally decoupled in crocodylians; size-heterodonty typically manifested as three size undulations along the tooth row, and shape-heterodonty reflected a significant linear transition from caniniformy to molariformy. Teeth significantly differed by position according to ANOVA. Variability in heterodonty allowed individuals to be organized into dental categories based on similarities. Most crocodylians reflected a “generalist” dental condition, with crowns ranging from moderate-caniniform to moderate-molariform. In members of Caimaninae and *Crocodylus porosus*, this was coupled with high size-heterodonty and large pseudocanines. Longirostrine species had more caniniform teeth overall, with *Gavialis gangeticus* being the least heterodont. *Alligator mississippiensis* crowns were generally more molariform than almost all crocodyloids. *Alligator sinensis* and *Osteolaemus tetraspis* uniquely possess hypertrophied distal crowns similar to fossil globidont taxa, but differ in having greater shape heterodonty. Further studies should investigate the effects of allometry and captive rearing.

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202 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Noah Daun, Justin Kowalski, Maxfield JonasKrueger, Jeanne Thibodeau and Justin Sipiorski

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

Morphometric variation in *Etheostoma exile* in lotic and lentic environments in Wisconsin

The Iowa Darter (*Etheostoma exile*), native to the state of Wisconsin, is a member of Percidae and makes up an important part of the benthic community in many lakes and streams. Iowa Darters are also an important indicator species of good water quality and have a high index of biotic integrity (IBI) value. They are notable because they are one of a few Wisconsin darter species found in both lotic and lentic environments. Even though Iowa Darters are fairly common and widely distributed throughout the northcentral United States and central Canada, little ecological research has been done concerning this species. Our past research on over 650 individuals collected throughout Wisconsin over the past 65 years, showed that Iowa Darters have length based growth. We wanted to continue this research to determine if growth differs between lotic and lentic populations. We used standard truss measurements to determine if morphologies differed between the populations. We also calculated gonadal-somatic index (GSI) for each population. We then compared the GSI's of the lotic and lentic populations to determine if there was a difference in reproductive investment between populations. PCA analysis on the morphometric data also shows population-specific morphological differences. Understanding differences in growth between Iowa Darter populations in lotic and lentic environments could help us to further understand this important indicator species and help future managers understand what makes this species a potentially important member of aquatic foodwebs.

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

Hayden Davis, Aaron Bauer and Todd Jackman

Villanova University, Villanova, PA, USA

Examining the Bornean *Cyrtodactylus* Radiation and the Karst-dwelling Morphology

Cyrtodactylus is among the most well-studied gekkonid genera in Southeast Asia, yet knowledge of the genus within Borneo is limited and out-of-date. For example, of the nearly 250 described *Cyrtodactylus* species, only nine have been recorded from Borneo, despite the island's large size and centralized placement within Sundaland. A high degree of genetic and morphological specialization has been recorded in the group, especially within the limestone-karst ecosystems of mainland Southeast Asia. We studied similar ecosystems within Sarawak, East Malaysia, Borneo, where karst habitats are prevalent. We assembled a multi-locus (ND2, RAG1, and MXRA 5) dataset incorporating new Bornean collections, including two new species, and published *Cyrtodactylus* sequences to provide better resolution for the relationships in the Bornean clade. Additionally, we developed a morphological dataset that included karst and forest-dwelling species from Sundaland to test for convergent evolution in karst ecosystems. The terrestrial connection between East and West Malaysia until the Early Pliocene, makes the inclusion of the Bornean clade of *Cyrtodactylus* essential to accurately understanding the evolutionary and biogeographic history of the genus.

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

Matthew Davis

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

Evolutionary Relationships and Classification of Lizardfishes (Aulopiformes) Using Genomic and Morphological Data

This study focuses on the morphologically diverse and species-rich (~282 species) marine lineage of lizardfishes (Aulopiformes). Aulopiform species possess morphological adaptations (e.g., bioluminescent organs, fang-like teeth, hermaphroditism) that have been hypothesized to have resulted from selective pressures found in their respective habitats that range from inshore to the deep-sea. In this study, the patterns and processes of diversification among aulopiform fishes are investigated with a densely-sampled hypothesis of evolutionary relationships inferred from ultraconserved elements, protein-coding gene fragments, and morphological data. This evolutionary framework represents the first genome-scale phylogenetic analysis of lizardfishes and provides new insights into the evolution and classification of aulopiform fishes.

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

Juan D. Daza[1], Aaron M. Bauer[2], Edward L. Stanley[3], Arnau Bolet[4,5], Blake Dickson[6] and Jonathan B. Losos[6,7]

[1]Sam Houston State University, Huntsville, Texas, USA. [2]Villanova University, Villanova, Pennsylvania, USA. [3]Florida Museum of Natural History, Gainesville, Florida, USA. [4]University of Bristol, Bristol, United Kingdom. [5]5Institut Català de Paleontologia Miquel Crusafont, Barcelona, Cataluña, Spain. [6]Harvard University, Museum of Comparative Zoology, Cambridge, Massachusetts, USA. [7]Washington University, Saint Louis, Missouri, USA

An enigmatic miniaturized and attenuate complete lizard from the Mid-Cretaceous amber of Myanmar

We report the discovery of a new genus and species of amber-preserved lizard from the mid-Cretaceous of Myanmar. The fossil is one of the smallest and most complete Cretaceous lizards ever found, preserving both the articulated skeleton and remains of the muscular system and other soft tissues. Despite its completeness, its state of preservation obscures important diagnostic features. Nonetheless, an apomorphy-based study of this specimen, as well as comparative data on trunk elongation in squamates, provisionally suggests its allocation to the Anguimorpha. If this taxonomic allocation is correct, this fossil would represent the first anguimorph in amber and the smallest ever recorded. It further emphasizes the role of amber inclusions in expanding our understanding of the diversity of Cretaceous lizard communities.

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

Luiz Jardim de Queiroz[1,2] and Juan Montoya-Burgos[1,3]

[1]*Department of Genetics and Evolution. University of Geneva., Geneva, Switzerland.* [2]*Science without Borders/CNPq, Brasília, Brazil.* [3]*Institute of Genetics and Genomics of Geneva (IGE3), Geneva, Switzerland*

Origin of the Remarkable Genetic Diversification in the Widespread Amazonian Fish *Triportheus albus*

Understanding the processes that give rise to genetic diversity in the Amazon is challenging due to the vast scale, the environmental richness and the outstanding biodiversity. We addressed this issue by determining the genetic structure of the Amazonian fish *Triportheus albus* and assessing the role played by multiple structuring factors. The results revealed a strong structuration with three geographical groups: two populations in Andean-born rivers (whitewaters) and a population spread in geographically disjointed black-/clearwater tributaries. A distance-based Redundancy Analysis (db-RDA) identified, for the first time, multiple factors driving the genetic diversification in this species, including geographical distance, waterfalls, water colour, floodplain size and flooded forest composition. Variance partitioning tests quantified the relative importance of these explanatory factors. Moreover, historical processes during the Pleistocene might also have played a role in the structuration of *T. albus*. The dry periods of the Pleistocene could have caused a partial disconnection between the Upper and the Lower Amazon mainly due to the decrease in the outflow, triggering an allopatric divergence in fish populations. Since the Upper Amazon was probably dominated by whitewaters (as is the currently case) and the Lower Amazon by black-/clearwaters (including the main channel of the Amazon River), the allopatric divergence would have been reinforced by ecological adaptation, explaining why both populations avoid mixing nowadays after secondary contact. We suggest that the multifactorial processes highlighted here may account for the high speciation rate characterising the Amazonia.

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

Lesley de Souza[1], Donald Taphorn[2] and Jonathan Armbruster[3]

[1]*Field Museum, Chicago, IL, USA.* [2]*None, Belleville, IL, USA.* [3]*Auburn University Museum of Natural History, Auburn, AL, USA*

Review of *Ancistrus* (Siluriformes: Loricariidae) from the northwestern Guiana Shield with description of six new species

The northwestern Guiana Shield (Essequibo, Orinoco, Branco, and upper Rio Negro) was found to contain 11 species of *Ancistrus*, six of which are new. We additionally examine *A. brevifilis* from the Río Tuy of Venezuela. The species in the region can be broken up into dorsoventrally flattened species (*A.* new species 1, *A. lithurgicus*, and *A. macropthalmus*), small white to yellow-spotted species (*A.* new species 2, *A. nudiceps*, and *A.* new species 3), long-jawed species (two new species), and large white-spotted species (*A. brevifilis, A. leucostictus*, *A.* new species 6, and *A. triradiatus*). *Ancistrus triradiatus* is variable, and evidence is available to suggest that it is a species complex. Distributions of *Ancistrus* support the Proto-Berbice hypothesis as *A.* new species 6 is found in the upper reaches of the Ventuari, Caura, and Caroni rivers, which were thought to have once flowed into the Proto-Berbice while *A. triradiatus* is present lower in the systems. In addition, although *A. nudiceps* does not appear to have split once the Takutu River

was captured by the Branco, the progenitor of *A. leucostictus* and *A.* new species 6 did speciate with the species on either side of the Rupununi Portal differing significantly in their mitochondrial Cytochrome *b* sequences. *Ancistrus nudiceps* can often be found in lowland conditions, and likely the flooded Rupununi Savannah is not a barrier for the species while it is for *A. leucostictus* and *A.* new species 6, which are found in riffles.

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470 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Emily DeArmon and Matthew Davis

St. Cloud State University, St. Cloud, Minnesota, USA

Evolutionary Relationships of Dragonfishes (Stomiidae) with a Survey of the Anatomical Variation of Bioluminescent Barbels

Dragonfishes (Stomiidae) are a species-rich lineage of deep-sea fishes (~302 species) that have a worldwide distribution. Prior studies have hypothesized that marine lineages living in open-ocean habitats may exhibit lower species richness due to a reduction in genetic isolation among populations. The observed high species richness of dragonfishes indicates that this lineage is undergoing genetic isolation in the deep sea, and previous studies have indicated that the family Stomiidae is diversifying at a rate that is significantly higher than expected given their clade age. This increase in diversification has been attributed to their anatomically species-specific bioluminescent barbels, which are sometimes sexually dimorphic and exhibit tremendous anatomical variation among the various species of dragonfishes. This research focuses on investigating the evolution of dragonfishes and the anatomical variation of their bioluminescent barbels. The evolutionary relationships among the family Stomiidae is inferred from a combination of ultraconserved elements (UCEs) and protein-coding gene fragments. Character evolution of features associated with the bioluminescent barbels are investigated across the dragonfish radiation.

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

Jennifer Deitloff[1], H. Nate Rainey[1], Samantha P. Wesnak[2,1], Jacob Fetterman[3,1], Kelsey Young[1] and Todd Pierson[4]

[1]Lock Haven University, Lock Haven, PA, USA. [2]Cornell University, Ithaca, NY, USA. [3]Louisianna State University, Baton Rouge, LA, USA. [4]University of Tennessee, Knoxville, TN, USA

Intraspecific Variation in Mate-Guarding Behavior Is Correlated with Morphology in Males of *Eurycea wilderae*

Salamanders exhibit a wide variety of mating systems and characteristics, including variation in tactics used to find or acquire mates. Specifically, species within the *Eurycea bislineata* complex exhibit a continuum of male morphologies. During this study we examined behavior of *Eurycea wilderae*, focusing on differences in behavior between the two different male morphologies common in this species. One form possesses long cirri and a slender head (cirriferous), and the other form has a larger, robust head (previously described as Morph A in *E. wilderae*). We also used geometric morphometrics to quantify head shape differences between these male morphs and between sexes. We tested the following hypotheses: (1) Morph A males would display mate-guarding behaviors, but males with the cirriferous morph would not; (2) the cirriferous morph would prefer areas containing female pheromones; and (3) morphology and mate-guarding behavior would be correlated with males who have wider heads displaying higher levels of aggression. We found support for the first and third hypotheses. In regard to detection of pheromones, male salamanders preferred areas with scents of other salamanders, but they had no preference for male or female pheromones, and the morphs did not differ in ability to detect the presence of pheromones. This study demonstrates that the relationship previously described between male morphology and mate strategy in other *Eurycea* species holds true for *Eurycea wilderae*. We hope to continue to explore the differences in mating strategies within *Eurycea* in the future.

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

Robert Eugene del Carlo[1], Jessica S. Reimche[2], Michael T.J. Hague[3], Edmund D. Brodie, Jr.[4], Normand Leblanc[1] and Chris R. Feldman[2]

[1]University of Nevada, Reno - School of Medicine, Reno, Nevada, USA. [2]University of Nevada, Reno, Reno, Nevada, USA. [3]University of Virginia, Charlottesville, Virginia, USA. [4]Utah State University, Logan, Utah, USA

Arms Race Penalties: The biophysical costs of adaptive mutations in a complex organism

The interaction between garter snakes (*Thamnophis*) and toxic newts (*Taricha*) is a model system of predator-prey coevolution. At the interface of this coevolutionary interaction are the snake voltage-gated sodium channels, Na_V proteins, and the newt's sodium channel toxin, Tetrodotoxin (TTX). Na_V proteins are responsible for the first electrical event initiating nerve impulses and fast muscular contractions. TTX ligation to the channel pore prevents sodium ion movement through the membrane, thereby abolishing excitability, and leading to numbness, paralysis, and eventually death by respiratory arrest. TTX has independently served as an agent of selection on several *Thamnophis* species that prey on sympatric *Taricha*. *Thamnophis atratus* and *T. sirtalis* have independently evolved adaptive mutations in the outer pore of the skeletal muscle channel, $Na_V1.4$. The amino acid substitutions reduce the affinity of TTX to the pore, thereby providing physiological resistance to TTX. Here, we show that these same mutations actually reduce sodium channel performance, despite their adaptive value in reducing TTX ligation to the pore. This channel hypofunction also appears to explain dramatic reductions in skeletal muscle performance (force and speed) in snakes that carry these naturally occurring channel mutants. We suggest that the proximate cause of these tissue performance deficits is reduced excitability imparted by reduced unitary sodium conductance and a shift in $Na_V1.4$ steady-state kinetics. These findings may influence higher order phenomena such as the organism's capacity to evade predation, which in turn, may provide a traceable explanation for the geographic mosaic distribution of toxin resistance phenotypes across the landscape.

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257 Lightning Talks II, Highland A, Saturday 14 July 2018

Naomi Delventhal[1] and Lynne Parenti[2]

[1]*University of Manitoba, Winnipeg, MB, Canada.* [2]*National Museum of Natural History. Smithsonian Institution, Washington DC, USA*

Comparative Morphology of the Female Urogenital Papilla of Seven Species of *Callogobius* (Teleostei: Gobiidae)

The gobiid genus *Callogobius* contains over 40 nominal species and at least 25 undescribed species. These are small to medium-sized, typically brown-barred gobies that inhabit tropical and subtropical Indo-West Pacific shallow marine and brackish environments. The monophyly of *Callogobius* is well-supported by the shared presence of raised ridges of sensory papillae in a particular pattern, yet the taxonomy is not well understood, due to the large number of species and the difficulty in distinguishing them. One structure that shows interspecific variation within *Callogobius* is the female urogenital papilla. Using scanning electron microscopy (SEM), we photographed the female urogenital papilla of seven species of *Callogobius* as well as the basal gobioid, *Rhyacichthys aspro*. We describe several morphologies, including broad with little texture (*C. mucosus*), broad, bilobed with deep textured ridges (*C.* cf. *maculipinnis* and *C.* cf. *centrolepis*), broad with a distal nubbin (*C.* cf. *hasseltii*), pear-shaped with an imbedded distal nubbin (*C. okinawae*), and broad with hook-shaped distal lateral projections encircling finger-like processes (*C. flavobrunneus* and *C. sclateri*). The female urogenital papilla of *R. aspro* is much more ornate, having broad lateral flaps, and distal projections in a variety of sizes, both branched and unbranched. Our evidence suggests that urogenital papilla morphology has taxonomic and phylogenetic information, and we encourage broader examination of urogenital papillae characters in gobioid systematic studies.

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

Joseph DeMarchi[1], Carl Anthony[1], Cari-Ann Hickerson[1] and Matthew Venesky[2]

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

The effects of temperature on *Batrachochytrium dendrobatidis* resistance and heart rate in unstriped and striped Eastern Red-backed Salamanders, *Plethodon cinereus*

Temperature can change the outcome of host-parasite interactions. How temperature affects these interactions is not always straightforward because host and parasite species may differ in their optimal temperatures. The amphibian fungal pathogen *Batrachochytrium dendrobatidis (Bd)* is one such parasite whose optimal temperatures for growth are 15°C-25°C. Many amphibian immune responses are more effective in warmer temperatures, but this may not be universal for cool adapted amphibians because temperatures exceeding an amphibians' optimal range can inhibit immune function. Thus, warm temperatures do not always favor amphibian *Bd* resistance. We examined how temperature affects *Bd* infection and heart rate of Eastern Red-backed Salamanders (*Plethodon cinereus*) from a color polymorphic population in northeast Ohio. Equal numbers of each morph were split into warm or cold temperature gradients and challenged with either *Bd* or a control. Striped salamanders at our locality tolerate colder temperatures relative to the unstriped morph, therefore we predicted striped salamanders to have lower *Bd* infection and heart rate at cooler temperatures. We found a significant interaction between morph and temperature on *Bd* abundance: resistance increased across a gradient from cool to warm in unstriped individuals, whereas striped individuals maintained high resistance across temperature gradients. We also found an interaction between pathogen treatment and temperature on heart rate: heart rates of infected salamanders were greater at warm temperatures compared to that of non-exposed and non-infected salamanders. Our results suggest pathogen induced changes in heart rate and morph specific differences in *Bd* resistance as functions of temperature.

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

Joe DeMarchi, Andrew Britton, Kaylee O'Donnell and Ralph Saporito

John Carroll University, University Heights, Ohio, USA

Behavioral Avoidance to UV-B Radiation in Two Neotropical Frogs from Costa Rica

Tropical frogs experience damaging effects from exposure to UV-B radiation, and some diurnally active, aposematic species exhibit avoidance behaviors to high levels of UV-B. To determine if similar behaviors are present in other diurnal frogs, we experimentally compared UV-B avoidance in two common species of neotropical diurnal frogs – *Oophaga pumilio*, an aposematic poison frog and *Craugastor bransfordii*, a cryptic leaf litter frog – in response to different levels of UV-B. Wild-caught frogs were tested in experimental arenas fitted with filters that permitted different levels of UV-B transmission. Our results demonstrate that both species equally avoid high levels of UV-B, suggesting that avoidance behaviors are common to different species. Although limited in scope, the findings of our study suggests that UV-B avoidance may be a behavioral adaptation common to all diurnal frogs.

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95 Herpetology Genetics I, Highland D, Sunday 15 July 2018

Rob Denton and John Malone

University of Connecticut, Storrs, Connecticut, USA

Assembly of the African Bullfrog (*Pyxicephalus adspersus*) Genome and History of Vertebrate Sex Chromosomes

Gene dosage causes distinct challenges during vertebrate sex chromosome evolution, but our understanding of dosage solutions has been limited by 1) the lack of heteromorphic genome sequences from species at the base of Tetrapoda and 2) underrepresentation of lineages where there are independent instances of sex chromosome evolution. Frog sex chromosomes offer an ideal system for advancing our understanding of genome evolution and function because of their variety of sex determination systems and diversity of sex chromosome maturation states. To understand what sequences have become sex-linked, we have sequenced and assembled the genome of *Pyxicephalus adspersus*, an amphibian with heteromorphic ZW sex chromosomes. Our assembly is highly contiguous with 99% of sequences arranged and annotated in 14 scaffolds, each corresponding to a single chromosome. By comparing sequencing depth between female and male, and validating chromosome assignments with targeted PCR and qPCR experiments, we identified the W- and Z-chromosomes and their underlying genes and sequences. Comparing sex chromosome sequences in *Pyxicephalus* to other vertebrate species revealed that one-copy Z-linked sequences are homologous to substantial portions of the therian X chromosome, suggesting repeated evolution of similar sequences for sex chromosome function. The genome assembly of *Pyxicephalus* fills an important gap at the base of tetrapods for understanding sex chromosome evolution. Comparing patterns of expression for sex-linked genes across the evolutionary history of vertebrates opens new opportunities for studying sex chromosome evolution, dosage compensation, and the mechanisms that generate heteromorphic sex chromosomes.

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

Robert Denton[1,2], Ariadna Morales[2] and Lisle Gibbs[2]

[1]University of Connecticut, Storrs, CT, USA. [2]Ohio State University, Columbus, OH, USA

Evolutionary History of the Nuclear Genomes Trapped in a Polyploid Salamander Lineage

Quantifying genetic introgression between sexual species and polyploid lineages traditionally thought to be asexual is an important step in understanding what factors drive the longevity of putatively asexual groups. However, the presence of multiple distinct subgenomes within a single lineage provides a significant logistical challenge to evaluating the origin of genetic variation in polyploids. Here, we measure the extent and tempo of introgression over the evolutionary history of an allopolyploid lineage of all-female salamanders (genus *Ambystoma*) and two ancestral sexual species. We collected variation from more than a thousand ultraconserved element loci using a reference mapping method developed for polyploids. Then we inferred subgenome specific patterns of variation in the all-female lineage by gauging support for sets of historical models that reflected different patterns of introgression and divergence. Our analyses support a scenario in which the genomes sampled in unisexual salamanders were present in the lineage ~3.4 million years ago, followed by an extended period of divergence. Recent secondary introgression has occurred at different times between each sexual species and their representative genomes within the unisexuals during the last 500,000 years. Sustained introgression of sexual genomes into the unisexual lineage has been the defining characteristic of their reproductive mode, but this study provides the first evidence that unisexual genomes have also undergone long periods of divergence without introgression. The alternating periods of divergence and introgression between unisexual salamanders and their sexual relatives could reveal the scenarios in which the influx of novel genomic material is favored.

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543 General Herpetology II, Highland B, Sunday 15 July 2018

Thomas DeWitt

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

Evolvable multi-moment phenotype distributions account for 73% more variation in fitness than otherwise can be explained

Data from mosquitofish, snails, fungi, and flies illustrate the likelihood of evolvable multi-moment trait distributions and indicate the likelihood of phenotypic plasticity of these complex traits. A trait distribution is the probability density function, **PDF**, of phenotypes that can be developed by a genotype. Each is characterized by a mean, variance, skewness, and kurtosis and any of these may differ by genotype and environment. Thus, to the extent these PDF traits and their plasticities are heritable and differ in fitness realized, they may evolve. I present a suite of data on PDF heritability, fitness differences, and fitness function matching. PDF matching with fitness functions suggests evolutionary adaptation. Results strongly evinced each component of multiple-moment evolution described above. Thus, we found a positive result in every instance we tested. What is more surprising was the large magnitude of effects. Traditional analysis (lacking a multi-moment PDF perspective) underestimated selection and heritability of trait means (genotypic values) by 9 and 68 %, respectively. The mean-centric approach in evolutionary genetics and ecology besides reducing accuracy also fails to reveal complex and biologically meaningful aspects of the systems being studied. Examples are given from the empirical systems mentioned. Evolutionary adaptation, therefore, may be more deeply complex and fascinating than we know.

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

Thomas DeWitt

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

Old typologies must die: Phenotypic plasticity in the real world produces traditional specialists and generalists, plus unique nontraditional, integrated strategies

There is a long history of ecological and evolutionary theory addressing adaptation of and competitive interactions between specialists and generalists. Often, this body of thought posits that generalists master no specific niches but can exploit multiple niches. When phenotypic plasticity is conceptually inserted into the body of theory, we generally assume the plastic genotypes produce "near specialists". But if environmental variation is fine-grained (experienced within generations over time or space), then the competing environmental influences might be thought to produce intermediate, hence generalist phenotypes. A radical alternative relative to current thought is that plasticity could produce a unique phenotype not seen among specialists or generalists. Or, plastic development of multiple traits may enact complex forms of trait integration. I present data from mosquitofish and snail experiments demonstrating that plasticity in response to fine-grained environmental variance produces some phenotypic elements that meet the generalist criterion of intermediacy. However, in systems tested, plasticity also produced unique phenotypes. Thus, evolutionary adaptation to complex ecologies may be more deeply complex and deeply fascinating than we know.

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

Matthew Dickson[1], Heather Liwanag[2], Aaron Bauer[3] and Robert Espinoza[1]

[1]California State University, Northridge, Northridge, CA, USA. [2]California Polytechnic University, San Luis Obispo, San Luis Obispo, CA, USA. [3]Villanova University, Villanova, PA, USA

Getting comfortable in your own skin: Morphological variation in the epidermis of an invasive reptile in response to novel climates

Invasive species often serve as natural experiments that allow us to observe how species respond to novel environments, leading to a better understanding of the process of adaptation over short timescales. Recent studies of invasive lizards have documented rapid adaptive evolution within relatively few generations following introduction. Mediterranean House Geckos (*Hemidactylus turcicus*) first established in southern Florida ~100 years ago. Since then, they have colonized 25 states across a diversity of climates in the US. Our previous studies

found that lab-acclimated geckos from distinct climates (desert, Mediterranean, subtropical, and continental) exhibit adaptive differences in physiology. Specifically, at high body temperatures, geckos from hot, dry climates have rates of evaporative water loss (EWL; body-mass adjusted) from a third to half that of geckos from humid climates. Most EWL occurs cutaneously via diffusion through the integument; however, no one has quantified cellular changes in the epidermis in response to climatic variation. Three cell layers in the squamate epidermis are hypothesized to retard EWL: the alpha and beta keratin layers, and the lipid-rich mesos layer. We hypothesized that in arid climates all three layers would be thicker via increasing the number of cell layers and/or cell volume. We are using electron microscopy to compare the ultrastructure of the epidermis at the surface (scalation) and the three cellular layers for 12 MHG populations representing two extreme climates (desert and subtropical; $n = 6$ populations/climate) to identify the features of the epidermis that contribute to EWL adjustment in this widespread invasive reptile.

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

Devin DiGiacopo, George Meindl, Kirsten Prior and Jessica Hua

Binghamton University, Binghamton, New York, USA

Invasive-Invasive Facilitation Across Ecosystems Enhanced by a Common Anthropogenic Contaminant

Human activities are rapidly changing natural environments, often with harmful consequences for native communities. For instance, global warming, invasive species, and environmental contaminants have been cited as major contributors to global amphibian declines. Invasive species can pose a broad range of threats to native communities, including altering the chemical environment. These novel, abiotic conditions are predicted to be stressful for native taxa, potentially facilitating future invasions by other stress-tolerant invasive species (i.e., invasional meltdown). However, few environments are free of other anthropogenic stressors, which likely mediate these species interactions. For example, chemical contaminants have been shown to favor stress-tolerant invasive species over native species. Thus, to examine if facilitation between invasive species is enhanced in polluted environments, we tested how leachates from invasive plants and road salt (NaCl) impacted a native (leopard frog; *Lithobates pipiens*) and invasive (African clawed frog; *Xenopus laevis*) amphibian. Leopard frogs reared in invasive plant solutions hatched faster and grew to a smaller tadpole size than those reared in native plant solutions. Conversely, hatching rate and size were unaffected in African clawed frogs, suggesting that they were more tolerant of the abiotic conditions imposed by invasive plants than leopard frogs. Leopard frogs were also less tolerant of NaCl when reared in invasive plant solutions than native plant solutions, while African clawed frogs were more tolerant when reared in invasive plant solutions. Collectively, these findings demonstrate that chemical contaminants may augment the facilitative relationship between invasive species, highlighting the negative implications of co-occurring anthropogenic stressors.

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

Casey Dillman[1] and Eric Hilton[2]

[1]Cornell University, Ithaca, NY, USA. [2]Virginia Institute of Marine Science, Gloucester Point, VA, USA

Nuclear DNA Sequences and their bearing on our understanding of the history and Relationships of Sturgeons (Acipenseriformes: Acipenseridae)

Sturgeon are endemic to the Northern Hemisphere where 25 species survive, though many are considered critically endangered. Much of the biology of sturgeon make them absolutely fascinating animals for study, not the least of which is their genome; where variable levels of ploidy are exhibited. Extant members of this clade possess either tetra- (4n), octo- (8n), and either a 12n or 16n genome size. This condition clearly complicates data collection and more importantly inferences of phylogenetic relationships of species from a nuclear DNA perspective. Previous work with six nuclear loci has shown variability between orthologous and paralogous copies of loci in the North American river sturgeons (*Scaphirhynchus*) and therefore utility in these loci for exploration of phylogenetic reconstruction across Acipenseridae. Gene tree and Species Tree results will be presented and discussed.

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

David Dimitrie[1], Michael Benard[1] and David Burke[2]

[1]Case Western Reserve University, Cleveland, Ohio, USA. [2]The Holden Arboretum, Kirtland, Ohio, USA

Response of American Toads (*Anaxyrus americanus*) to Experimental Elevation of Soil pH in Acidic Hardwood Forests of Northeast Ohio

Anthropogenic activities can lead to acid deposition, resulting in the acidification of forest ecosystems. Applications of Hi-Ca lime to soil can be used to facilitate forest recovery from historic acidification. Although studies have examined how some organisms respond to these management strategies, few studies have addressed the effects on amphibians and their invertebrate prey. We assessed American toad (*Anaxyrus americanus*) survival and growth in northeast Ohio forests that have been treated for nine years with Hi-Ca lime to elevate soil pH. Field enclosures were constructed within both lime-treated forests (mean pH 6.0) and forests with untreated soil (mean pH 4.4), and four post-metamorphic toads were placed into each enclosure. We measured toad survival and growth after 25, 60, and 90 days. Invertebrates were sampled both before toads were placed into enclosures and after 90 days to assess prey availability. We found no difference between the two soil treatments in toad survival or growth throughout the study. Invertebrate abundances also did not differ between soil treatments. Toad mass after 90 days was positively correlated with number of Collembola collected in invertebrate samples on day 90, regardless of soil treatment. Our study provides evidence that elevating soil pH via Hi-Ca lime does not have direct effects on post-metamorphic toad survival or indirect effects on growth mediated by prey availability. Understanding the implications of soil liming within acidic hardwood forests may provide managers with better insight into how this long-term treatment may affect not only anurans but other forest floor consumers as well.

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

Dawn Dittman

USGS, Cortland, New York, USA

A Lake Sturgeon Restoration Experiment in the Genesee River, Rochester, NY.

An applied test of stocking as a Lake Sturgeon (*Acipenser fulvescens*) management action was initiated in the Genesee River, NY, where the population was extirpated. This restoration project was designed as an investigation of the fate of the 1,900 YOY juveniles released in 2003 & 2004. We assessed the retention of these fish in the juvenile rearing habitat of the lower Genesee River (2003 – 2016) using a mark-recapture technique. The sturgeon received year class identifying scute marks. Lake Sturgeon were subsequently captured using gill nets and given unique tags. The numbers of Lake Sturgeon in the river were relatively high for the first six years, with over half of the stocked fish still in residence. Attrition is due both to mortality and emigration from the nursery habitat into near shore areas of Lake Ontario. Ten years post release, there were 150 to 300 Lake Sturgeon in the river. Even in 2016, they had not completely left the river, seven resident fish were recaptured in October. After the capture of three adult males in Spring 2016, the next step in this experiment is to focus on the likely return in 2020 of the first reproductive females. Assessment of these returning fish will give a measure of stocked YOY survival to adults and their expected contribution to recovery of a Lake Sturgeon population in the Genesee River. This research provides critically needed milestones for the assessment of reintroduction as a restoration management action for Lake Sturgeon.

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

Dawn Dittman, Marc Chalupnicki and Phyllis Randall

USGS, Cortland, New York, USA

Fish Habitat Quality, Distribution, and Modeling in the Genesee River, Rochester, NY

The Genesee River NY is one of the major tributaries to Lake Ontario. In the past, the 6 km up to the Lower Falls from Lake Ontario have been spawning habitat for migratory sport fish and species of concern, including walleye, several salmonid species, catfish, and sturgeon. This river mouth is the site of an ongoing experiment in Lake Sturgeon (*Acipenser fulvescens*) restoration. We conducted a long term systematic sampling of the fish habitat, the large bodied fish community (collected with gill nets), and the benthic invertebrate community 1999-2016, at fixed sites. More intensive systematic (0.5 km intervals) benthic habitat sampling was included in 2004, 2010, and 2011. Habitat variables were, depth, flow, temperature, oxygen, pH, bottom hardness, and sediment grain size. We applied kriging analysis to model distribution of habitat measurements and the benthic macroinvertebrate indices, using ESRI ArcMap 9.2. We applied the results to calculate habitat suitably indices (HSI) for the critical migratory fish in this river mouth and the observed distributions of the most abundant target fish species. The majority of the 6km is suitable as juvenile Lake Sturgeon habitat, with good water quality, soft substrate and abundant macroinvertebrate food. Other fish species had more mixed suitability results. Understanding the longer term quality factors and distribution of fish habitat in the lower Genesee River is part of the environmental stewardship of the Rochester Embayment Area of Concern as habitat and native fish communities are restored to improve ecosystem health for wildlife and people.

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

Ken Dodd[1] and Corey Anderson[2]

[1]University of Florida, Gainesville, Florida, USA. [2]Valdosta State University, Valdosta, Georgia, USA

Amphibian Immigration and Emigration at a Temporary Pond in the Florida Sandhills

Temporary ponds are important breeding sites for many amphibians and may serve as refugia for species crossing unfavorable habitats while dispersing. In this study, we examined the immigration and emigration patterns of six amphibian species from October 1985 through September 1990 at an isolated temporary pond in a sandhills community in north central Florida, USA. Our results indicated that the circular distribution of amphibian captures around the pond was often non-uniform, especially when capture distributions were pooled over multiple years or multiple species. Species captured more frequently tended to be found at a wider range of directions moving into and out of the pond. Many species exhibited complex multimodal distributions, with potential shifts in modal directions from year to year. Interspecies variation in the frequency of dispersion at different angles into and out of the pond basin was common and likely reflected species-specific movement capabilities. Nonrandom dispersal at our study site suggests that species may be moving to and from specific habitat types, such as nearby wetlands or terrestrial habitats used for foraging or refuge. The extensive interspecific variation in amphibian movement patterns seen at Breezeway Pond and observed in other studies, coupled with the potential for widespread and long-range dispersal, suggest that large areas of habitat should be protected to ensure the survival of amphibians breeding in temporary ponds from stochastic and long-term effects of climate change and isolation.

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162 Ichthyology Ecology and Ethology, Highland E, Sunday 15 July 2018

Terry Donaldson

University of Guam Marine Laboratory, MANGILAO, Guam, USA

Male Territory Swamping in a Lek-like Mating System Increases Courtship Success in a Fish Spawning Aggregation

A number of reef fish species that form spawning aggregations utilize a lek-like mating system in which males establish temporary courtship territories that they defend against rival males while attracting females to spawn. At a resident spawning aggregation site located at Finger Reef, Guam, male *Cheilinus trilobatus* (Labridae) holding territories along the outer edge of the site experience significantly greater courtship success compared with males holding territories within the site's interior. Males holding edge territories are always successful in defending these territories from intruding males, even when they are engaged in courtship. Recently, however, increases in the number of males present at the spawning aggregation site have resulted in an increase in the number of territory intrusions during courtship periods. These intrusions "swamp" a normally successful male's territory and make defense difficult. Multiple intruders not chased away or simply returning after being chased then court and spawn with females that arrive within the territory. Costs to the territory holder include lost courtship opportunities because of territorial interactions that interrupt courtship and reduced reproductive success because intruding males court successfully with females that visit the male's territory and deprive him of the opportunity to do so.

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164 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Highland D, Thursday 12 July 2018

Caroline Dong[1,2], Claire McLean[1,2], Adnan Moussalli[2] and Devi Stuart-Fox[1]

[1]The University of Melbourne, Parkville, Victoria, Australia. [2]Museum Victoria, Carlton, Victoria, Australia

Genomic and Phenotypic Patterns Across a Contact Zone of Colorful Agamids

In the study of speciation dynamics, contact zones are of great interest because they function as natural laboratories, particularly when lineages are at an intermediate stage of divergence. Further, coloration is thought to be a promoter of speciation for species that use color traits in mate choice, male-male competition, and species recognition. The tawny dragon, *Ctenophorus decresii*, is a compelling study system comprising two divergent lineages, with lineage-specific sexual coloration, that hybridize in a contact zone. We used ddRADseq to identify SNPs and investigate genome-wide patterns of divergence. We characterized the geographic extent of hybridization and shape of the genomic cline across the contact zone. In addition, we characterized hybrid phenotype across the contact zone and found a steep cline with genetic hybrids more strongly resembling one parental lineage. Ongoing research in this study system to clarify contact zone dynamics and genomic regions associated with coloration will contribute to our understanding of the role of coloration in speciation.

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

Erica Donlon and Marcelo Melo

Instituto Oceanografico, Universiadde de São Paulo, São Paulo, SP, Brazil

Palaeogeographical Evolution of the Central Atlantic coast of South America, from the Last Glacial Maximum (Pleistocene) to the Present

The Pleistocene (2.6Ma–11.7ka BP) is characterized by the many glacial cycles giving rise to sea level fluctuations. During the Last Glacial Maximum (17–19ka BP), the glaciers were at their largest, dropping the sea level 115–130 m and exposing most of the continental platform. Using ArcGIS, we created maps of eastern South America between the Orinoco and La Plata rivers (8°40′N-35°00′S) to evaluate how the variation of the sea level affected the coastline, and infer the paleobasins of coastal streams. Both in the North, between the Guyanas and Maranhão, and in the South, from the Abrolhos Bank to the La Pata river, the continental shelf is broad. The coastal drainages expanded their areas as far as 340 km and the coastal islands became embedded in the continent, allowing a free transit of freshwater species. In Northeastern Brazil, between Ceará and Central Bahia, the continental shelf is extremely narrow and the paleobasins expanded their areas only from 10 to 50 km. However, in the marine environment, the areas where the coral reefs in Northeastern Brazil are located nowadays became completely exposed, and the suitable area for coral reefs were restricted to small portions along the break of the continental shelf. On the other hand, the seamounts along the Brazilian Equatorial Margin and the Vitoria-Trindade chain formed oceanic islands and shallow areas that served as stepping stones for the reef organisms to colonize Atol das Rocas, Fernando de Noronha, and the Trindade Island.

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

Paul D'Ortona and Scott McRobert

Saint Joseph's University, Philadelphia, PA, USA

The Effect of Sex and Shoal Size on Shoaling Behavior in *Poecilia reticulata*

Shoaling behavior is thought to provide numerous benefits to individual fish, including reduction in the risk of predation and increasing the opportunity to find potential mates. Two phenomena, the oddity effect and confusion effect, which affect predation risk, depend on shoalmate phenotype and number of fish in the shoal. In sexually dimorphic fish, like guppies, males having bright coloration and females having cryptic coloration, may face the dilemma of swimming with the phenotypically distinct members of the opposite sex, reducing the benefits of the confusion effect, and incurring risks from the oddity effect when choosing shoalmates. We examined the effect of sex and shoal size on shoaling behavior in adult guppies by calculating net preference scores for same-sex and opposite-sex shoals of varying sizes for intraspecific shoals, in dichotomous choice tanks. In intraspecific tests, both males and females showed a significant preference for small same-sex shoals (1 - 3 guppies). However, no preference was shown between same-sex and opposite-sex shoals of 6 guppies. These results suggest that shoalmate choice decisions differ depending on shoal size. Swimming with smaller numbers of fish may enhance the negative effects of the oddity effect, thus requiring phenotypic matching. Swimming in larger shoals may enhance the benefits of the confusion effect, thus enabling fish to join mixed-sex shoals.

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

Dana Drake, Sean Giery and Mark Urban

University of Connecticut, Storrs, CT, USA

Metabolic Rates of Larval Spotted Salamanders: Interpopulation Variation and the Influence of Predator Presence

Metabolic rates are expected to be relatively constant within species. We believe there may be several factors that affect metabolic rates of larval salamanders on a smaller scale, including predator presence. We hypothesized that there would be interpopulation variation in metabolic rates of larval Spotted Salamanders (*Ambystoma maculatum*), and that a main contributing factor to this variation would be the presence of larval Marbled Salamanders (*A. opacum*), a predator of larval Spotted Salamanders known to affect their foraging and growth rates. We present results and analyses of metabolic rates measured on over 500 larval Spotted Salamanders from 24 populations in central Connecticut, USA, including larvae from ponds with and without larval Marbled Salamanders.

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

Peter Ducey

SUNY Cortland, Cortland, NY, USA

Adaptation and Homology in Salamander Antipredator Behaviors and Tail Autotomy

Over 40 years ago, E. D. Brodie, Jr., began the scientific examination of the defenses used by salamanders against their predators. In the intervening decades, research by Brodie and his colleagues has given us a depth of understanding for these animals rarely seen in science. As with most phenotypic traits that directly affect individual survivorship, the phylogenetic distributions of antipredator behaviors in salamanders are indicative of both homoplasy and homology. The adaptive nature of many reportedly defensive behaviors is supported by evidence of individual variation in behavior, as well as correlations of that variation with measureable differences in survival. The presence of similar behaviors in separate salamander lineages suggests that these behavior patterns evolved during independent natural selection events, leading to homoplasy. However, some aspects of antipredator behavior also show evidence for homology. Such evidence includes examples of behavior pattern conservation within certain clades of salamanders and observations that suggest the evolutionary re-purposing (exaptation) of specific responses and motor patterns from other functions (e.g., locomotion and mating) into antipredator defense.

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

Thomas Duchak and Russell Burke

Hofstra University, Hempstead, New York, USA

Nesting Site Alterations Facilitate Successful Nesting Attempts in Wood Turtles, *Glyptemys insculpta*

In northern New Jersey, substrates of many turtle nesting areas are strewn with cobbles from past glaciations. Glacial till, along with vegetation, often hinders the ability of nesting wood turtles, *Glyptemys insculpta*, to excavate nests and consequently increases failed nesting attempts and time at nesting sites. Risk of predation and illegal collection are likely heightened in turtles that spend several days or even weeks attempting to nest unsuccessfully in exposed areas. Furthermore, gravid females that cannot find suitable nest sites may eventually jettison their eggs as captive turtles do when keepers fail to provide laying media. To facilitate nesting and inform management strategies during a multi-year wood turtle nesting study, we altered the grounds of a former stone quarry that attracts ≈30 nesting wood turtles annually. In 2013, we tilled the quarry to soften the ground and remove vegetation. Then, we delimited four adjacent 80m^2 nesting plots and designated them as control and experimental plots in an alternating fashion. In the experimental plots, we excavated the original rocky sediment and replaced it with sand. In subsequent years, we tilled all plots to delay succession and keep soft sediments exposed. Besides annual tilling, the control plots were not manipulated. From 2013-2017, we monitored the quarry for nesting wood turtles. We found that more failed nesting attempts occurred in the control plots and more nests were successfully laid in the experimental plots. From these results, we conclude that nesting site management may be beneficial for turtle populations in areas with rocky soils.

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

Andrew M. Durso[1,2], Isabelle Bolon[3] and Rafael Ruiz de Castañeda[3]

[1]*University of Geneva, Geneva, Geneva, Switzerland.* [2]*Max Planck Institute for Biogeochemistry, Jena, Thüringen, Germany.* [3]*Institute of Global Health, University of Geneva, Geneva, Geneva, Switzerland*

Snapp: A Medical Decision Support Tool for Snake Identification based on Artificial Intelligence and Remote Collaborative Expertise

Snakebite is the second most deadly neglected tropical disease, responsible for a dramatic humanitarian crisis in global health. Snakebite causes over 100,000 human deaths and 400,000 victims of disability and disfigurement globally every year affecting poor and rural communities in developing countries, which host the highest venomous snake diversity and the highest burden of snakebite due to limited medical expertise and access to antivenoms. Antivenoms can be life-saving when correctly administered but, since many are species-specific, this depends first on the correct identification of the biting snake. Snake identification is challenging due to snake diversity and incomplete or misleading information provided by snakebite victims or bystanders to clinicians, who generally lack the knowledge or resources in herpetology. To reduce potentially erroneous and/or delayed healthcare actions, and taking advantage of the expansion of mobile technologies in developing and emerging countries, we are developing Snapp, the first medical decision-support mobile app for snake identification based on artificial intelligence and remote collaborative expertise in herpetology. Our app will combine computer vision with the expertise from a network of herpetologists to identify photos of snakes, particularly supporting victims and clinicians when urgent and reliable snake identification is needed.

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447 Reptile Ecology II, Highland A, Sunday 15 July 2018

Andrew M. Durso[1,2], Lorin A. Neuman-Lee[3], Gareth R. Hopkins[4] and Edmund D. Brodie Jr.[5]

[1]*Max Planck Institute for Biogeochemistry, Jena, Thüringen, Germany.* [2]*University of Geneva, Geneva, Geneva, Switzerland.* [3]*Arkansas State University, Jonesboro, Arkansas, USA.* [4]*University of Melbourne, Melbourne, Victoria, Australia.* [5]*Utah State University, Logan, Utah, USA*

Stable Isotope Analysis suggests that Tetrodotoxin-resistant Common Gartersnakes (*Thamnophis sirtalis*) rarely feed on Newts in the Wild

Most toxin-resistant predators do not feed exclusively on toxic prey, and may still suffer costs from doing so. We investigated the diets of Common Gartersnakes (*Thamnophis sirtalis*) at a site in central Oregon where they have high levels of resistance to tetrodotoxin, which is found at high levels in the skin of sympatric Rough-skinned Newts (*Taricha granulosa*). Because snake diets are difficult to quantify using traditional means, we used data from stable isotopes to estimate the proportion of gartersnake diets made up of six prey types, including newts, which allowed us to increase our sample size from 2 to 44. Our estimate for the proportion of *T. sirtalis* diet made up of *T. granulosa* at this site is 3.2% (95% credible interval = 0.1-17%). Instead, *Ambystoma* salamanders were predicted to be the most important prey, followed by slugs, *Pseudacris* chorus frogs, and mice, with a very minor role for earthworms. We saw little evidence for intersexual differences in diet. Our results agree with scattered data from other studies that even though Common Gartersnakes are physiologically capable of consuming toxic prey, they do not often do so, suggesting that even a generalist predator can be exposed to very strong selection and exert reciprocal selection on rarely eaten, chemically defended prey.

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

Julia Earl

Louisiana Tech University, Ruston, LA, USA

Relative Importance of Different Ecological Pressures to Tadpole Survival, Growth, and Development

Natural populations are affected by many environmental variables that alter survival, growth, and developmental rates. Many observational studies and experiments have demonstrated the importance of competition, predation, resources, habitat, and chemical and thermal environments. However, the relative importance of these different variables remains unclear, as experiments typically examine only one or two mechanisms at a time. Here, I simultaneously examine the relative importance of all of these mechanisms for tadpole survival, growth, and development using a mesocosm experiment. Mesocosms were placed within forest and clearcuts, and plant litter input was manipulated. Mesocosms were naturally colonized by predators and competitors. I introduced tadpoles and assessed survival and time and size at metamorphosis using three species: wood frogs, American toads, and southern leopard frogs. I created seven models representing different mechanisms to examine which best predicted tadpole performance using AIC. For wood frog survival, water quality and thermal models were competing for best model, showing a positive relationship between survival and tannin concentration and a negative relationship with pH and temperature. American toad survival was lower with higher dragonfly larval density. Wood frogs and American toads had longer body lengths with grass litter than leaf or no litter. Wood frog developmental time was longer in mesocosms with cooler temperatures. These results highlight the importance of water quality, temperature, and predation to tadpole survival, though the variable with the best predictive power varied by species. However, for size at metamorphosis, resource type was similarly important for two different tadpole species.

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331 ASIH STOYE GENERAL ICHTHYOLOGY II, Grand Lilac Ballroom South, Thursday 12 July 2018

Diego J. Elias and Prosanta Chakrabarty

Louisiana State University, Baton Rouge, LA, USA

Comparative Phylogeography of Freshwater Fishes in Northern Central America.

Central America harbors a unique and diverse assemblage of freshwater fishes dominated by the families Cichlidae and Poeciliidae. Recent work has concluded that Central America is more complex in terms of biogeographic realms than previously hypothesized. In Northern Central America, geological features such as the Isthmus of Tehuantepec have acted as a phylogeographic break. Previous work recovered that freshwater fishes from this area do not possess congruent phylogeographic patterns. The objective of the current project is to evaluate if species with different natural histories have responded in a congruent fashion to historical geological and to more recent (Pliocene-Pleistocene) climatic events in Northern Central America. We evaluated pattern of genetic diversity of seven species of freshwater fishes: three cichlids, three poeciliids and one characid using mitochondrial markers. We evaluate if the recovered genetic structure is correlated with differences in morphology (e.g., size and body-shape) using phylogenetic generalized least squares analysis. Our work provides empirical data to disentangle the relative importance of the roles played by historical geological and climatic events and by natural history traits in shaping diversity across Northern Central America. This study also demonstrates how differences in phenotypes can impact the ability of species to maintain gene flow across previously recognized phylogeographic breaks, leading to concordant/discordant patterns when comparative phylogeographic analyses are performed with organisms that possess different natural histories.

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333 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Diego J. Elias[1], Caleb D. McMahan[2] and Prosanta Chakrabarty[1]

[1]Louisiana State University, Baton Rouge, LA, USA. [2]The Field Museum of Natural History, Chicago, IL, USA

Molecular and morphological assessment of *Trichromis salvini* in Northern Middle America.

Trichromis salvini is a cichlid of the tribe Heroini that is distributed from Southern Mexico to Northern Guatemala and Belize. Despite its widespread distribution across this complex geological region, the genus *Trichromis* is monotypic. This is in contrast to other cichlid genera possessing several species in the same geographic region (e.g *Thorichthys*). Therefore, the objectives of this study are 1) to identify patterns of genetic variation of *T. salvini* using mitochondrial and nuclear markers and 2) to assess the degree of morphological variation across the lineages recovered across Northern Middle America. Our preliminary molecular analysis recovered three independent lineages of *T. salvini* across its distribution: one lineage in the Petén lake district and Northern Belize, one lineage in Southern Belize and Izabal lake and one lineage in La Pasion river system and intermontane region of Guatemala. Finally, we use morphological data in an effort to understand the degree of phenotypic variation across the distribution of lineages recovered in Northern Middle America. Our work provides evidence of unrecognized diversity within *T. salvini* and advances our understanding of the diversity of freshwater fishes in this region.

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546 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION & BEHAVIOR, 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

Erica Ely[1,2] and Chris Feldman[1]

[1]University of Nevada Reno, Reno, Nevada, USA. [2]California Academy of Sciences, Herpetology, San Francisco, California, USA

Feeding Behavior of *Thamnophis* (Colubridae) in the Sierra Nevada and Lower Cascade Mountain Ranges of California

Thamnophis is a wide-ranging, abundant and ecologically important group of North American snakes. Previous studies have indicated that most *Thamnophis* species are generalist predators, consuming the most abundant prey available, which can vary spatially and temporally. Here, we investigated the dietary habits of three sympatric *Thamnophis* species (*T. couchii, T. elegans* and *T. sirtalis)* in the Sierra Nevada and Lower Cascade Mountain Ranges of California. We assessed diet habits by examining stomach contents of preserved museum specimens collected across this geographic range, over the past 120 years, as well as reputable observations. Feeding frequency was overall low, and most specimens with stomach contents contained a single-prey item. We discuss how the dietary habits of *T. couchii, T. elegans and T.*

sirtalis vary across latitude, ontogeny, seasons and in relation to each other. This study provides insight to niche partitioning of sympatric, ecologically similar snakes, as well as adds to the growing evidence of ecological plasticity of *Thamnophis* species across North America.

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

David Ensminger, Tracy Langkilde, Dustin Owen, Kirsty MacLeod and Michael Sheriff

Pennsylvania State University, University Park, PA, USA

Effects of Maternal Stress on Egg Allocation and Offspring Physiology in a Free Living Lizard

The physiological impact of stress and its adaptive potential are areas of interest in the fields of ecology and biology, as we are in a time of increased anthropomorphically induced perturbations. In addition to mediating the link between environmental variability and organismal plasticity, such as changes in behavior and fitness, glucocorticoids (GCs) are also a mechanistic translator between mothers and their offspring. We tested the hypothesis that GCs will alter maternal physiology as well as egg allocation and offspring physiology. We treated wild caught gravid female eastern fence lizards (*Sceloporus undulatus*) daily with transdermal applications of GCs at an ecologically relevant dose (GC response similar to a fire ant attack) from capture to ovoposition. Eggs were collected and incubated until hatching. We found that stressed mothers laid eggs that had less protein but more lipids and GCs. Maternal stress altered offspring HPA-axis, decreasing baseline and ACTH-induced GC levels. These results suggest that stress experienced by a gravid female has ecologically relevant effects on hatchling physiology which may be mediated by changes in the metabolism and egg allocation of the gravid female.

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

James Erdmann

Wyoming Game and Fish Department, Laramie, Wyoming, USA

Aggressive anglers, seductive serpents, and titillating toads: A discussion of luring and prey manipulation strategies

When a predator hunts a cryptic or mobile prey item, it has two general options: actively seek out the prey or remain stationary and wait for prey to approach. In the latter case, predators employ an assortment of strategies to increase the encounter rate of their prey-to-be. Perhaps the most recognizable of these strategies is the lure, wherein the predator creates some

attractive stimulus to their potential prey, causing the prey to unwittingly approach the predator. However, the literature is equivocal on what constitutes a lure, as well as how to go about testing it. I critique the conditions when the term 'lure' is applied and suggest ways of quantitatively measuring it against behavioral alternatives to create a more robust foraging theory.

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

Taylor Eubank[1], Juan Diego Daza[1] and Aaron M. Bauer[2]

[1]Sam Houston State University, Huntsville, Texas, USA. [2]Villanova University, Villanova, Pennsylvania, USA

Alternative gaits in gekkotans explains femoral morphology

The typical sprawling gait of gekkotans predicts the femoral head to be perpendicular to the main axis of the shaft of the bone, and to be inserted into the pelvis in a lateral facing acetabulum. However, gekkotans develop other gaits (semi-sprawling and nearly parasagittal gaits). We studied femur morphology in 12 species of limbed gekkotans. Skeletonized femora were photographed using a Leica microscope equipped with a digital camera. Dorsal images, in which both the femoral head and the trochanter were visible, of all bones were taken. For each bone, the internal angle formed by the intersection of two imaginary lines 1) between the distal condyles and trochanter, and 2) between the femoral head and the trochanter. The internal angle was higher in species with a sprawling position (e.g., *Homonota fasciata*), whereas the angle was lower in species with a more parasagittal or crouching gait (e.g., *Pristurus carteri*). In addition to changes in the femoral head angle, we also noted that the distal condyles experience rotation, which indicates rotation on the knee joint axis with respect to the hip joint. Since it is virtually impossible to detect both rotation of the femoral head and the distal condyles using 2D images, we will continue this project using 3D morphometric analyses using anatomical landmarks.

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

Adriana Eugene[1], Alexandra Kanonik[2] and Russell Burke[1]

[1]Hofstra University, Uniondale, NY, USA. [2]American Littoral Society, Highlands, NJ, USA

The Effects of Plastic and Metal Predator Excluders on Diamondback Terrapin (*Malaclemys terrapin*) Nest Temperatures, Hatching Success, and Hatchling Sex Ratios

Turtles are among the most threatened vertebrate groups, and conservation efforts to protect turtle populations commonly include the use of predator excluders to protect nests from predation. The use of predator excluders has been shown to dramatically reduce nest predation by human-subsidized predators. However, there is a wide diversity of predator excluder designs yet the potential effects of predator excluder designs on turtle incubation conditions and secondary effects are little explored. Ideal predator excluders should have minimal effect on the incubation temperature of the nest to reduce alterations on hatchling success and sex ratios. Most turtle species have temperature dependent sex determination (TSD). If predator excluders alter nest temperatures significantly, especially during the temperature sensitive period, they may influence hatchling sex ratios. Alterations in hatchling sex ratios could severally harm turtle populations in the near future due to a small number of females being available for reproduction. It is desirable to determine which predator excluder design has the least effect on the incubation conditions to minimize effects on hatching success, hatchling sex ratios and hatchling survivorship. We tested the potential effects of two commonly used predator excluder designs on incubation temperatures of Diamondback Terrapin (*Malaclemys terrapin*) nests in Jamaica Bay, New York. We measured nest temperatures throughout the incubation period but focused on the temperature sensitive period, when sex is determined. We found that neither predator excluder model affected the temperature at which the nests incubated, hatching success or hatchling survival.

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

Allyson J. Evans[1], Carlos David De Santana[2] and Casey B. Dillman[1]

[1]Cornell University, Ithaca, NY, USA. [2]Division of Fishes, Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington, D.C., USA

Comparison of Sexually Dimorphic Snout and Tooth Morphology in *Sternarchogiton nattereri* and *Sternarchorhynchus roseni* (Gymnotiformes: Apteronotidae)

Several species of South American knife fish within the family Apteronotidae exhibit secondary sexual dimorphism in their snout and jaw structure. Documented observations of sexually dimorphic dentition have been limited to few genera which exhibit hypertrophied teeth of the dentary or premaxilla, including *Sternarchogiton* and *Sternarchorhynchus*. In this study, we used micro-computed tomography (CT) to examine differences in snout and tooth morphology in one male and one female specimen of *Sternarchogiton nattereri* and *Sternarchorhynchus roseni.* Mature males of *S. nattereri* are characterized by a prominent outgrowth of teeth on the premaxilla and enlarged, medially-oriented teeth arranged in multiple rows along the dentary. Female *S. nattereri* lack premaxillary teeth and possess smaller, medially-oriented teeth confined to a single row along the dentary. Mature males of *S. roseni* are characterized by numerous enlarged teeth attached to the interior surface of the dentary. Dentary teeth of females are much smaller, conical, and confined to two rows. Both males and females possess small premaxillary

teeth that are recurved posteriorly. Further examination of jaw and snout morphology will be discussed.

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

Annette Evans[1], Elizabeth Jockusch[1], Mark C. Urban[1], Brenna Forester[2], Caitlin Fisher-Reid[3] and Bradley Cosentino[4]

[1]University of Connecticut, Storrs, Connecticut, USA. [2]Colorado State University, Fort Collins, Colorado, USA. [3]Bridgewater State University, Bridgewater, Massachusetts, USA. [4]Hobart and William Smith Colleges, Geneva, New York, USA

Does Land Use Buffer Evolutionary Responses to Climate Change by a Polymorphic Salamander?

A myriad of biotic and abiotic factors can act simultaneously to amplify or dampen the selective pressures imposed by climate change and the ecological responses of species. Given this multifaceted nature of selection, we need to understand how the joint operation of multiple major disturbances, like land use change and climate, interact in their effect on population evolutionary responses. Terrestrial amphibians, such as plethodontid salamanders, are expected to be particularly sensitive to multiple environmental stressors given their limited dispersal capabilities and need to maintain cool, moist skin for respiration. Previous research on the response to environmental stressors by the polymorphic salamander *Plethodon cinereus* suggests that both cool climates and forest cover are associated with higher frequencies of striped color morphs at broad spatial scales. However, at the regional New England scale, recent population resurveys reveal no changes in morph frequencies over the past 40 years despite substantial changes in climate. One potential explanation is that changes in forest cover over the same period have buffered populations from the impacts of climate change. We used structural equation models (SEMs) to examine if land use and climate change affect the evolution of *P. cinereus* color polymorphisms in New England by comparing historical and resurvey data. Our results shed light on the importance of simultaneously examining multiple environmental stressors when evaluating and predicting species evolutionary responses to climate change.

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244 General Ichthyology I, Grand Lilac Ballroom South, Sunday 15 July 2018

Kory Evans[1], Lesley Kim[2], Brian Schubert[2] and James Albert[2]

[1]University of Minnesota, St. Paul, MN, USA. [2]University of Louisiana at Lafayette, Lafayette, LA, USA

The mighty mandible: Mosaic evolution facilitates trophic specialization in electric fish skulls

Mosaic evolution allows functional specialization of organismal traits that are subject to differing levels of selection or constraints, and can result in differential rates of phenotypic evolution among traits. Here we use three-dimensional geometric morphometrics, biomechanics, stable isotope analysis, and gut-content analysis to study mosaic shape evolution in the skulls of 20 species of navajine electric fishes. We quantify the multivariate rates of shape evolution for three modules within the skull (face, braincase, and mandible), and assess their functional interactions with trophic ecology. We also use biomechanics to estimate the performance of the mandible, and its relationship to trophic ecology. We find that the mandible evolved nearly five times faster than other skull modules, and that mechanical advantage of the mandible is linked to trophic position. We also find that mechanical advantage and trophic position best fit an Orenstein-Uhlenbeck model of trait evolution, suggesting the presence of adaptive optima. We hypothesize that the mandible is more evolutionarily labile than other modules and is capable of mounting a larger response to directional selection resulting in its elevated rates of shape evolution relative to other skull modules and ultimately, a pattern of mosaic evolution among several regions of the navajine skull.

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

Teah Evers and Jennifer Deitloff

Lock Haven University, Lock Haven, PA, USA

Assessment of the Density, Spatial Distribution and Movement Patterns of *Plethodon cinereus* (Eastern Red-backed Salamander) Using Spatial Capture-Recapture

Plethodon cinereus (Eastern Red-backed Salamander*)* is a terrestrial salamander commonly found in the Eastern United States. This species is territorial and will defend areas against conspecifics through aggressive behavior. The extent to which males and females defend territories, spatially distribute themselves, and disperse needs to be further explored. We examined the density, spatial distribution and movement patterns of both males and females of *P. cinereus* in their natural habitats using artificial cover boards and spatial capture-recapture methods. We tested the following hypotheses: (1) males will have larger foraging areas than females and (2) both males and females will display site fidelity by remaining within the same plot and the same area within a plot. We marked individuals using four colors of Visual Implant Elastomer Tags in order to create a unique color code for each individual. We calculated a home range size and an activity center for each individual based on their movement patterns. Of the 110 individuals, 65 were only captured once while 45 were recaptured at least once. Densities varied across plots. Comparison of mean distance moved showed that gravid females moved slightly more than males and that both males and gravid females, on average, moved more than non-gravid females, but these differences were not significant. Based on the number of recaptures and the individual spatial history, analyses indicated that both males and females of *P. cinereus* display site fidelity. Estimating population density and understanding movement patterns can provide insight into intraspecific interactions among individuals within a population.

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

Vincent Farallo[1], Martha Muñoz[1] and Donald Miles[2]

[1]Virginia Tech, Blacksburg, VA, USA. [2]Ohio University, Athens, OH, USA

Niche evolution varies depending on geographic scale: Implications for climate change

Climate change is altering species distributions, and even causing extirpation events. One way to assess the impacts of climate change includes understanding the evolutionary history of species climatic niches. Specifically, we would like to know whether species niches are conserved or divergent across evolutionary timescales. In turn, we can leverage this information to predict whether species will be able to track habitats or even expand into new habitats as conditions change. The ways in which micro- and macro-geographic patterns of niche evolution relate, if at all, remain largely unknown. Resolving these patterns would greatly enrich our ability to predict species' responses to global climate change. Here we compared micro- and macroclimate niche evolution in 18 species of plethodontid salamanders. We tested for niche lability using phylogenetic signal, which indicates whether variation among species in climatic traits is correlated with relatedness (higher signal) or evolves independently of relatedness (lower signal). The results showed that patterns of niche conservatism are impacted by the geographic scale of the analysis. Microclimatic variables exhibit stronger phylogenetic signal, indicating that relatedness and phylogenetic inertia shape niche evolution at the microgeographic scale. In contrast, patterns of macroclimatic variation exhibited no phylogenetic signal, indicating high niche lability and no impact of relatedness on variation. Importantly, we discovered that patterns of niche evolution are inverted at distinct geographic scales. As such, it is important for microclimatic measurements to be included in studies of niche evolution and the impacts of climate change.

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368 Herpetology Reproduction, Highland C, Sunday 15 July 2018

Terence Farrell[1], Sarah Smiley[1], Amber Clark[1] and Craig Lind[2]

[1]Stetson University, DeLand, FL, USA. [2]Stockton University, Galloway, NJ, USA

The Effects of Supplemental Feeding of Pregnant Pygmy Rattlesnakes (*Sistrurus miliarius*) on Reproductive and Neonate Traits

Pregnant vipers are often thought to be anorexic while pregnant but the information on this topic is largely anecdotal and does not address the adaptive significance of the cessation of foraging. We experimentally determined if pregnant snakes would feed, and if so, how energy intake in the last six weeks of pregnancy affected reproductive females and their offspring. We

field-collected 27 pregnant *S. miliarius* in June and July of 2017 and held them in field enclosures until parturition. Each female was randomly assigned to either the unfed control treatment or the supplemental feeding group. All 12 pregnant females in the supplementally fed group ate at least once when offered a leopard frog. Females consumed between one and four frogs. The total wet weight of prey consumed by each female was, on average, equal to 54.7% of their initial body mass. Supplementally fed females had significantly higher mean postpartum body condition index but did not more closely attend to their neonates. In the supplementally fed group, 42% (5 of 12) of females failed to produce a viable litter, while none of the unfed females failed to produce a litter. Feeding pregnant females did not significantly affect the mass, length, swimming speed, or frequency of caudal luring of their neonates. Our results indicate that the physiological demands of feeding may be in conflict with the physiological demands of late-stage pregnancy, and that feeding may have deleterious impacts on the reproductive success of pregnant females.

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568 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Dario Faustino-Fuster[1,2], Rafael Angrizani[1] and Luiz Malabarba[1]

[1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil. [2]Museo de Historia Natural (UNMSM), Lima, Lima, Peru

Description of two new heptapterid species (Siluriformes: Heptapteridae) from the Uruguay River basin belonging to *Heptapterus* clade

Heptapteridae is a monophyletic group with 217 species, widely distributed in the Neotropical region. We herein describe two new species from the Rio Uruguai basin. Morphometric (44) and meristic (34) data were taken with caliper and stereomicroscope. Counts and descriptions of osteological features were made from cleared and stained specimens and X-ray images. DNA was extracted from specimens, and analyzed using two mitochondrial (COI and cytb) and one nuclear (RAG2) genes. Analyses were conducted using both Maximum Likelihood and Bayesian Inference methods. In a preliminary molecular analysis we found them related to *Rhamdioglanis* and *Heptapterus*. The two new species and *Chasmocranus lopezae* can be distinguished from *Rhamdioglanis* by the absence of anterior process in the last neural and hemal spines of caudal vertebrae (*vs.* presence of anterior process in the last neural and hemal spines of caudal vertebrae); from *Heptapterus* by having 54-60 vertebrae (*vs.* 43-45 vertebrae) and 12-14 anal fin rays (*vs.* 15-23 anal fins rays). The two new species can be distinguished from *Chasmocranus lopezae* by having 10-13 dorsal procurrent rays on caudal-fin (*vs.* 16-19 dorsal procurrent rays on caudal-fin) and additional morphometric data; the new species A is distinguished from the new species B by having 44-45 vertebrae (*vs.* 43 vertebrae) and six unbranched anal-fin rays (*vs.* five unbranched anal-fin rays). Distribution of the new species are restricted to Uruguay River basin in Brazil, being the new species A found in the lower Uruguay River and the new species B in the upper Uruguay River.

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

Matthew Fedler, Coleman Sheehy and Kenneth Krysko

University of Florida, Gainesville, Florida, USA

High Levels of Genetic Divergence within the Genus *Rhineura* Confounded by Secretive Life History and Morphological Conservatism

The monotypic amphisbaenian genus *Rhineura* (*floridana*) has long been an enigma to herpetologists due to its difficulty to collect, secretive life history, and superficial lack of morphological variation across its range. Several studies have attempted to identify diversity within the genus. However, these studies have either lacked the technology (genetic sequencing and GIS software) needed to differentiate lineages in close geographic proximity that have been isolated for millions of years (Zug 1968), or they lacked genetic samples representing the entire range of *R. floridana*. Our study combines variable morphological traits from over 150 specimens with an increased breadth of genetic sampling in an attempt to identify lineages that may represent distinct taxa. Our results identify five distinct lineages and support Zug's initial hypothesis that the Lake Wales Ridge (LWR) lineage is distinct from the rest of *R. floridana*, though Bayesian analysis indicates the divergence occurred much earlier than he suspected. Three lineages of *R. floridana* each contain relatively low amounts of genetic diversity. However, the LWR and Central Peninsula populations contain high levels of diversity, which could indicate secondary isolation events. After assigning lineages based on genetic data (rather than geographic distance), analysis of external morphology provides a well-supported suite of diagnostic characteristics of the LWR lineage. Similarly, osteological data obtained from CT scans further support the divergence and could indicate adaptive evolution to more efficiently utilize different habitat types.

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

Miranda Figueras[1], Kent Hatch[2], Beverly Roeder[3] and Russell Burke[1]

[1]*Hofstra University, Hempstead, NY, USA.* [2]*LIU Post, Brookville, NY, USA.* [3]*Brigham Young University, Prove, UT, USA*

Metabolic rates, Q_{10} coefficients, and reaction norms of hatchling turtles: Comparisons with behavior

Interspecific comparisons of physiological parameters, such as metabolic rates and temperature regulation, with ecological parameters such as activity patterns and thermoregulatory behavior, often demonstrate that physiology and behavior co-evolve to meet ecological challenges. Hatchling turtles are vulnerable to abiotic hazards such as temperature extremes and desiccation, as they have high surface area-volume ratios, poor locomotor abilities, and cannot easily dig deeply into substrate. Measuring metabolic rates (SMR), Q_{10} coefficients, and reaction norm patterns among hatchlings of eleven species allowed us to test for a correlation with post-hatching activity associated with overwintering patterns, between turtles that dramatically differ ecologically. The metabolic rates of hatchlings were measured as the rate of oxygen consumption (VO_2) at 20, 22, 24, 26, 28, and 30°C, using closed–flow respirometry. We performed Kendall's Coefficient of Rank Correlation tests to compare SMRs at 24°C, 26°C and 28°C to our predicted SMR rankings, based on overwintering strategy. We calculated Q_{10}s for each species using SMR values at 20°C and 30°C and visually inspected reaction norms. Predicted patterns were different from observed reaction norms and there were no significant relationships between our predicted SMR species rankings and actual SMR rankings. However, we determined SMRs for hatchlings of eleven species of turtles (5 of which occur primarily outside temperate North America), including both suborders and seven families, some of which are very poorly known. Further investigation of these patterns, especially additional Testudinidae, Trionychidae, and the tropical Chelydridae, are likely to be productive.

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

João Pedro Fontenelle[1], William Crampton[2] and Nathan Lovejoy[1]

[1]University of Toronto Scarborough, Toronto, ON, Canada. [2]University of Central Florida, Orlando, FL, USA

Master of (n)One? Phylogeny and Population Structure in the Neotropical Electric Fish genus *Steatogenys* (Gymnotiformes: Hypopomidae) Across Different Water-Types.

The Amazon river basin is composed of rivers with different physicochemical properties, which are reflected in their colors. White water rivers (flowing out of Andean erosion zones) are neutral in pH and high in sediments, and contrast with black water systems (flowing from sedimentary lowlands, are low in sediments, and are acidic) and clear water rivers (which originate on pre-Cambrian shields, are low in sediments, and have neutral pH). Environments with different physicochemical properties may interrupt gene flow between populations. To investigate how water types affect population structure, we use the genus *Steatogenys* (Boulenger, 1898) as a model system. *S. elegans* and *S. duidae* are widely distributed across the Amazon and occur in the three water types, while *S. ocellatus* is restricted to central upper Amazon black water rivers. We generated a phylogeny for the three valid species of *Steatogenys* using both mitochondrial and nuclear genes, evaluated the phylogeography of *S. duidae* and *S. elegans,* and tested for environmental significance using multivariate statistics. Our analyses confirm reciprocal monophyly for each recognized species of *Steatogenys*, and show evidence for three sympatric lineages within *S. elegans*. One of these lineages is widely distributed across

water types, one is associated with black and clear water, and the last is associated with white water habitats. This suggests that water type plays a role in Neotropical fish diversification.

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567 Herpetology Morphology II, Highland D, Sunday 15 July 2018

Cliff Fontenot[1], Sydney Ferguson[1] and Helen Plylar[2]

[1]Southeastern Louisiana University, Hammond, LA, USA. [2]Florida Institute of Technology, Melbourne, FL, USA

Comparison of the Role of Spectacle/Cornea Curvature in Vision Among Colubrid snakes from Southeastern Louisiana

Vertebrates have eyes that generally contain two refractive elements, the cornea plus and internal lens. In snakes, the spectacle and cornea function as one, as both have the same refractive index as water (1.33). Because refraction occurs only when adjacent media have different refractive indices, the spectacle/cornea functions as a lens in air, but that refractive power is lost when diving underwater, imposing defocus. Whether interspecific variation in spectacle curvature exists is unknown. We hypothesized that terrestrial snakes may have a greater corneal curvature (and so more power) because they rarely dive underwater, but that semi-aquatic snakes should have less curvature (and so less to loose when diving). To test these hypotheses, we determined the relationship between body size and spectacle curvature for a variety of colubrid snakes, and compared among species and ecotype (aquatic vs terrestrial).

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

Jessica Ford

McGill University, Montreal, QC, Canada

Methods for raising toad tadpoles in experimental mesocosms

Mesocosm studies are extremely important for better understanding the ecology of many aquatic organisms, including larval amphibians. Mesocosms provide an important middle ground between low realism but high control lab experiments, and high realism but low control field experiments. However, in order to study an organism in a mesocosm, it needs to be able to survive in that environment. Previous studies involving toad tadpoles in mesocosms have found that they had an extremely high mortality, compromising the ability to study them. Traditionally, mesocosms containing tadpoles have been deep, high nutrient environments. The Fowler’s toad (*Anaxyrus fowleri*), however, breeds in shallow, sandy, usually oligotrophic ponds. I tested whether the use of a low nutrient substrate, such as sand, would allow for a higher survivorship of toad tadpoles in mesocosms. I raised tadpoles of the abundant American

toad (*Anaxyrus americanus*) and the locally endangered Fowler's toad (*Anaxyrus fowleri*) in 30 100 US Gallon mesocosms in Long Point, Ontario. By mimicking the natural environment of the Fowler's toad in mesocosms, I was able to raise the Fowler's toad tadpoles with a 90.8% survivorship. The American toad tadpoles were raised at two densities, and had the highest survivorship at a density of 100 tadpoles per mesocosm (1 tadpole per US Gallon or 3.7 L). This research has applications in any study housing these species in mesocosms, as well as for captive breeding conservation efforts for these toads and similar species.

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

María J. Forzán[1], Joe-Felix Bienentreu[2], Danna M. Schock[3] and David Lesbarreres[2]

[1]Cornell University, Ithaca, NY, USA. [2]Laurentian University, Sudbury, ON, Canada. [3]Keyano College, Fort McMurray, AB, Canada

Mortality due to ranavirus infection in Boreal chorus frog, *Pseudacris maculata*, tadpoles: histopathology and diagnostic stains

Dead and moribund Boreal chorus frog (*Pseudacris maculata*) and wood frog (*Rana sylvatica*) tadpoles were found in late June 2017 at three separate locations in the Northwest Territories, Canada. Skin hemorrhages were noted in most affected tadpoles. A subset of 19 tadpoles was collected, fixed in 10% formalin, and processed for routine histologic examination as well as immunohistochemical (IHC) and *in situ* hybridization (ISH) staining for ranaviruses. A PCR test for ranaviruses (Iridoviridae) from a tail clip obtained prior to fixation was positive in all tadpoles. All but one tadpole had histopathologic lesions consistent with ranavirus infection, i.e. skin and oral mucosa necrosis, branchial epithelium necrosis and renal tubular and hematopoietic necrosis. All lesions were associated with intense IHC and ISH staining. When budding limbs were present, skeletal and connective tissues were often undergoing necrosis and were intensely positive for ranavirus with IHC staining. Necrosis of the liver and pancreas was rare and mild with occasional cellular debris suggesting inflammation; inclusion bodies in the liver were only definitively present in two tadpoles. Gastrointestinal and thymic necrosis were rare and very mild, but there was common IHC staining for ranavirus in the mesothelium, thymic medulla and, occasionally, brain. This first report of mortality due to systemic ranavirosis in Boreal Chorus frogs demonstrates their susceptibility to infection and describes the lesions associated with it. It also confirms the viability of using special IHC and ISH stains to confirm infection and determine the extensive dissemination of ranaviruses within a host.

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73 General Ichthyology I, Grand Lilac Ballroom South, Sunday 15 July 2018

Claire Fox and William Bemis

Cornell University, Ithaca, NY, USA

Benthic walking and body form in three families of Flatfishes (Pleuronectiformes: Achiridae, Cynoglossidae, and Pleuronectidae)

Flatfishes have an anatomically and functionally unique form of walking locomotion based on median fins in direct contact with the substrate. Previous research on six species of pleuronectid flatfishes documented that all species converge successive portions of their dorsal and anal fin rays to form functional "fin-feet" that push posteriorly in a wave against the substrate to propel the animal forward. Coordinated movements of fin-feet produce a symmetrical walking gait if the fin-feet in the dorsal and anal fins travel in the same direction, or rotational movements if the fin-feet travel in opposite directions. Morphologically similar species employ different modes of substrate locomotion: some walk using continuous movements of fin-feet whereas others pause between waves of movement to produce a bounding gait. Here, we add new kinematic analyses of benthic locomotion in two derived flatfish families: suction-cup shaped Achiridae (Hogchoker, *Trinectes maculatus*), and highly elongated Cynoglossidae (Black cheeked Tonguefish, *Symphurus plagiusa*). We recorded videos of both species in top and side views in aquaria and analyzed body and fin velocity using DLTdv5 for MATLAB. Additional kinematic analyses include: functional area of median fins during walking; testing gait symmetry; number of simultaneous fin-feet; distances between fin-feet; range of motion of fin-rays; and degree of convergence between fin rays. Using landmarks and meristic data from x-ray imagery we compare key morphological features related to locomotion including fin-ray number, fin-ray length, and overall body form. CHF supported by NSF GRFP; research support from the Raney Fund and Lerner-Gray Grant for Marine Research.

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

Elyse Freitas[1], Aniruddha Datta-Roy[2], Praveen Karanth[2] and Cameron Siler[1]

[1]Sam Noble Museum, University of Oklahoma, Norman, Oklahoma, USA. [2]Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India

Historical Biogeography and Cryptic Diversity of Lygosomine Skinks in the Old-World Tropics

The skink genera *Lygosoma*, *Mochlus*, and *Riopa* comprise a closely-allied group of Old World, semifossorial lizards distributed throughout much of Africa, India, Indochina, and the Sunda Shelf. Although they are all elongate-bodied, species in these genera exhibit diverse body forms, from large and robust to small and gracile, making them an interesting group in which to study patterns of diversification across a geographically complex region of the planet. Preliminary species tree reconstructions for this group indicate that multiple dispersal events to and from disparate biogeographic areas have occurred, including between India and Indochina, and between Indochina and the Sunda Shelf. Employing morphological and multi-locus datasets with broad, geographic sampling, I am conducting a phylogenetic and biogeographic study of *Lygosoma*, *Mochlus*, and *Riopa* to address the following hypotheses: (1) Southeast Asia represents the origin of diversity of this group of skinks, and clades have dispersed multiple times out of

this region, (2) the early diversification of *Riopa* in India occurred during the Eocene, originating from a Southeast Asian ancestor, (3) African *Mochlus* originated from an Indian ancestor, and (4) significant levels of cryptic lineage diversity exists across Southeast Asia. Understanding historical and contemporary patterns of lineage diversity within this group of skinks can provide insights into the macroevolutionary factors that have shaped vertebrate communities across the Old-World tropics.

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

Connor French and Jason Brown

Southern Illinois University, Carbondale, IL, USA

Phylogeography of a Recently Diverged Poison Frog Species Group (Genus: *Ameerega*)

Speciation is not a linear process. The path from genetic overlap to complete genetic and reproductive isolation is often interspersed with repeated introgression events. These events lead to complicated genetic histories, which are difficult to resolve with a traditional bifurcating phylogeny. The Amazon rainforest at the foot of the Andes contains exceptionally high diversity, much of it recent. The complex geology of the Andes and paleoclimate fluctuations preclude complex dispersal scenarios. This, in turn, has contributed to idiosyncratic speciation modes among shallowly-diverged Amazonian taxa. The poison frog genus *Ameerega* recently radiated throughout the Andes and Amazon (MRCA ~8.7 mya), with some taxa diverging as recently as the late Pliocene and early Pleistocene. Some species-level relationships remain poorly resolved, especially among recently diverged taxa. Here, we address the phylogenetic relationships among three recently diverged Peruvian *Ameerega* species (*A. cainarachi, A. petersi,* and *A. smaragdina*), using multiple species tree methods, including one that accounts for a reticulate history. We complement species tree analyses with morphological and niche overlap analysis to better resolve species boundaries. In addition, we consider the relative contributions of isolation-by-distance and isolation-by-environment to the spatial genetic structure of these species. We uncover a complex evolutionary history among the three *Ameerega* species and shed light on the geographic and environmental contributions to their speciation.

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

Aaron H Fronk, Maxwell J Bernt and James S Albert

University of Louisiana at Lafayette, Lafayette, Louisiana, USA

Ancestral Ranges and Geographic Range Evolution of Electric Ghost Knifefishes (Gymnotiformes: Apteronotidae).

Apteronotidae is a clade of Neotropical electric fishes distributed throughout northern South America and Panama. A lack of fossils in this group invites alternative biogeographic methods to calibrate the phylogenetic tree and thereby inform historical biogeography. Here we constructed a Maximum Likelihood tree for 43 apteronotid species representing all but two recognized genera, using molecular sequence data from seven genes (5052 bp), nuclear and mitochondrial. Geographic information was obtained from museum records and publications, and geographic ranges organized by major river basins. Data were analyzed using the software package BioGeoBEARS, which uses Maximum Likelihood to estimate ancestral geographic distributions and modes of geographic range evolution using three macroevolutionary parameters: speciation, extinction, and dispersal. The tree was time-calibrated using two cis-trans Andean sister species pairs, calibrated by the rise of the Eastern Cordillera of Colombia at c. 11 Ma. The results show strong support for an Eocene-Oligocene (45+/- 15 Ma) origin of Apteronotidae in the Western Amazon, and Oligocene-Miocene dates (35 +/- 15 Ma) for tribe-level divergences, including the origin of the Navajini, a clade specialized to inhabit deep river channels. The results are consistent with diversification of apteronotid and navajine lineages in association with the formation and fragmentation of the Pebas mega-wetland system and origin of the modern transcontinental Amazon River system.

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620 NIA BEST STUDENT POSTER, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

César Fuentes

School of Biology, Faculty of Chemical Sciences and Pharmacy, University of San Carlos of Guatemala, Guatemala, Guatemala

Long time, no see: A revision of historical records of sawfishes (Pristidae) in Guatemala

Sawfishes (Pristidae) are considered threatened with a concerning conservation status over their distribution due to overfishing and habitat reduction. Two species are recorded from Guatemala: *Pristis pristis* and *P. pectinata.* Despite their conservation status in Guatemala the research of these species is scarce. Although worldwide there is an augment of the conservation efforts in Guatemala there has not been an effort to update the information regarding records and their conservation status. Therefore, the objective of this work is to update the distributional records and to compile historical records of fishes of the family Pristidae in Guatemala. I compile nine records: seven records were from the Caribbean Sea and two from the Pacific Ocean. Additionally, three records were found that do not possess voucher specimens. This work provides information that highlights the concern on the conservation status of these fishes in Guatemala. More research and conservation actions for sawfishes

should be taken to update conservation status on Central America and improve our knowledge of these fishes in the region.

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376 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Giovanni Fuentes[1], Sean Harrington[2], David Blackburn[1] and Daniel Paluh[1]

[1]University of Florida, Gainesville, Florida, USA. [2]University of Hawaii at Manoa, Honolulu, Hawaii, USA

Comparative Morphology of Rattlesnake Cranial Diversity: Influence of Phylogeny, Ecology, and Modularity

A fundamental goal of evolutionary biology is to classify patterns of diversity and identify the processes responsible for shaping those patterns. The vertebrate skull is often considered to be modular and partitioned into semi-independent blocks of traits, and these modules may be differentially influenced by historical constraints and selective pressures. We investigated the diversity of rattlesnake skulls (*Crotalus* and *Sistrurus*) using high-resolution x-ray micro-computed tomography. Our objectives were to characterize the morphology of individual cranial elements across species and determine 1) if overall skull shape is associated with habitat utilization or diet and 2) if certain elements or modules of the skull are more variable across lineages than others. Despite their similar overall body forms, rattlesnakes occupy a variety of habitats. The 47 taxa range from tropical savannahs, desert dunes, and high elevation rock outcrops to temperate deciduous forest. Diet is also variable across species, with some species specializing nearly exclusively on mammals while others include larger portions of lizards and other ectothermic prey in their diets. Preliminary results demonstrate that small-bodied, rock habitat specialists have repeatedly evolved relatively longer and narrower skulls than large-bodied species that occupy a diversity of environments. Structures associated with feeding (e.g., maxilla, pterygoid, dentary) appear to be more labile across species than the posterior region of the skull. Future research directions include quantifying morphological variation using 3D geometric morphometrics and testing how diets and habitats influence rates of evolution and phenotypic optima using phylogenetic comparative methods.

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

Rory Fuller and L. Michael Romero

Tufts University, Medford, MA, USA

Differences in the stress response of the painted turtle, *Chrysemys picta*, across sites of varying anthropogenic disturbance

Urbanization and related anthropogenic stressors present an array of distinctive challenges for many extant species. However, many studies have shown conflicting information on how vertebrates respond to these stressors, necessitating further research into the reason for and nature of differing stress responses. As an initial step toward this goal, we sought to determine whether eastern painted turtles (*Chrysemys picta picta*) in eastern Massachusetts displayed substantial differences in their stress responses at three sites of greatly differing urbanization. Painted turtles represent an excellent subject for this study due to their long lives, high adult survivability, and relatively high site fidelity compared to more classical subjects of field stress physiology, such as birds. We trapped turtles at these locations for two summers, taking blood samples and behavioral data for comparison. Blood samples were used for analysis of glucocorticoid levels and various metabolic and immune function markers known to be related to stress physiology. Behavioral data consisted of observations and timing of escape behaviors post-handling. We discovered significant variation in glucocorticoid secretion patterns between sites, which were consistent between years. We also show potential signs of differences in immune system functionality between the sites, as well as in some escape behaviors. We conclude that the eastern painted turtle appears responsive to the presence of urbanization and therefore makes an excellent candidate for further investigations into differential responses to anthropogenic stressors.

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

Emily Funk and Amy McCune

Cornell University, Ithaca, NY, USA

Gene expression patterns underlying gas bladder evolution in ray-finned fishes

Study of the origin of evolutionary novelties, such as jaws and limbs, is central to understanding the history of life. With advancements in developmental genetics, we can investigate the genetic underpinning of evolutionary novelties, their origins and subsequent transformations. The gas bladder, derived from lungs of the bony vertebrate common ancestor, originated as a novelty within ray-finned fishes and is important for efficient buoyancy control. As homologous organs, the gas bladder and the lungs share many similarities; however, the defining difference between them is the location of budding from the anterior foregut; gas bladders bud dorsally and lungs bud ventrally. We are investigating whether the inversion of budding location is paralleled by a dorsoventral inversion of gene expression patterns. Bowfin (*Amia calva*) are ideal to study early evolution of the gas bladder because they are a deeply-branching lineage that diverged soon after gas bladder origination and possess a dorsal gas bladder. To capture transcriptome-wide expression during bowfin gas bladder development while maintaining dorsoventral spatial information, we used laser-capture microdissection to

isolate the dorsal and ventral foregut tissue from 3 developmental stages spanning bowfin gas bladder budding. We separately sequenced expression profiles for each tissue and identified genes differentially expressed between dorsal and ventral foregut. Subsequently, we characterized at what stage and tissue known lung-regulatory genes are expressed during bowfin gas bladder development and whether they are differentially expressed across the dorsoventral axis in the same or opposite (i.e. inverted) direction.

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

Nicole Fusco[1], Ellen Pehek[2] and Jason Munshi-South[1]

[1]Fordham University, Bronx, New York, USA. [2]New York City Parks Department, New York City, New York, USA

Genetic Connectivity of Stream Salamander Populations within Stream Systems in the New York City Metropolitan Area

The Northern two-lined salamander (*Eurycea bislineata*) plays an important ecological role in Northeastern forests yet they are incredibly susceptible to human disturbances due to a reliance on both terrestrial and aquatic habitats for survival, dispersal, and reproduction. Published results show that decreased canopy cover, a high presence of invasive predators, and alterations to water chemistry, can restrict movement and reduce the abundance of salamanders within stream systems. To understand if urbanization in and around New York City is affecting Northern two-lined salamander (*Eurycea bislineata*) populations, we investigated population structure, genetic diversity, and isolation-by-distance (IBD) within an urban, suburban, and rural stream habitat. Despite differing levels of urbanization within each habitat, results show fine-scale genetic structure within each stream network, suggesting that urban habitats may still play a role in maintaining some genetic connectivity. Yet there is significantly lower genetic diversity (H_O and p) and greater genetic differentiation between streams within the urban watershed as compared to the suburban and rural sites. Additionally, IBD is governing the spatial patterns of populations to a greater degree in the urban habitat than in the suburban habitat. Whereas, IBD is not a significant factor contributing to population isolation in the rural watershed. These results demonstrate that urbanization affects gene flow in stream salamanders in highly urbanized stream networks. Overall, we need to maintain connectivity within and between branches of stream systems to sustain healthy salamander populations within freshwater aquatic ecosystems.

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

Brian Gall[1], Yiyuan Li[2], Michael Pfrender[2] and Edmund Brodie[3]

[1]*Hanover College, Hanover, IN, USA.* [2]*University of Notre Dame, Notre Dame, IN, USA.*
[3]*Utah State University, Logan, UT, USA*

Diffuse Coevolution? Tetrodotoxin and Insecticide Resistance in Egg Predators of the Rough-Skinned Newt (*Taricha granulosa*)

Coevolution is typically viewed as shaping traits between pairs of closely interacting species. Yet, a single species may interact with dozens of others at each of several life-history stages, all of which could impose differing levels of selective pressure on a trait. Newts possess large quantities of Tetrodotoxin (TTX) in their skin and females deposit this toxin in their eggs. Caddisfly larvae (Order: Trichoptera) have been found to eat these toxic eggs. Here we present behavioral and genetic evidence that caddisflies sympatric with newts are resistant to TTX, as well as pyrethroid insecticides. We discuss the potential for these additional species to impose selective pressure on newts and the general implications for the coevolutionary interaction revolving around tetrodotoxin.

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

Gennesee Garcia[1], John Nolan[2], Hayley Crowell[2] and Emily Taylor[2]

[1]*Cal Poly San Luis Obispo, San Luis Obispo, California, USA.* [2]*Cal Poly San Luis Obispo, San Luis Obispo, California, USA*

It's a Snake-Eat-Snake World: Quantifying Pacific Rattlesnake (*Crotalus oreganus*) Responses to Kingsnake (*Lampropeltis californiae*) Stimuli

It is well known that kingsnakes (*Lampropeltis spp.*) often engage in ophiophagy and their presence can elicit extreme responses from possible prey species (primarily pit vipers). Rattlesnakes have been shown to utilize chemosensory cues to detect kingsnakes, but it is not known whether they can also do so using visual cues. Furthermore, small rattlesnakes respond more readily to kingsnake chemosensory cues than large rattlesnakes, perhaps because they are more easily predated. We observed the responses of rattlesnakes to various kingsnake stimuli and related them to the individual rattlesnakes' size to quantify the effect of kingsnake presence on rattlesnakes at various stages of their ontogeny. Pacific rattlesnakes (*Crotalus oreganus*) were presented with live kingsnakes, visual kingsnake models, or swabs of kingsnake scent, and behavioral responses were recorded in both field and laboratory settings, including body bridging, body jerks, body flips, expansion, head hiding, and fleeing. We will present preliminary data on how stimulus type (live kingsnake, kingsnake model, or kingsnake swab), setting (field or lab), and rattlesnake body size affect the snakes' behavioral responses. Smaller rattlesnakes are expected to display more frequent and pronounced behavioral responses to the kingsnake stimuli. Chemosensory stimuli are expected to have a greater impact on rattlesnake responses than visual stimuli. Determining when rattlesnakes are most vulnerable to kingsnake

predation can give researchers greater insight into predator-prey interactions and aid in determining which cues prey species use to assess threats in their surrounding environments.

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440 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Jennifer Gardner and Luke Tornabene

University of Washington, Seattle, WA, USA

Iodine-based contrast-enhancing staining methods for visualization of soft tissues of snailfishes (Family: Liparidae) through CT-Scanning

The oVert Thematic Collections Network is an NSF funded endeavor to produce publicly available 3D scans across the vertebrate tree of life via X-ray computed tomography (CT). To date, CT scans of fishes typically capture dense structures such as bone, but diffusible iodine-based contrast enhanced CT (diceCT) can produce 3D scans of soft tissues. The majority of scans produced by oVert will be skeletons, but production of diceCT scans of select taxa are also an important component of this initiative. This method has been especially useful for projects focused on soft tissues, like looking at brain evolution across vertebrate lineages. While published works referencing diceCT from many different vertebrate taxa, including fishes, currently exist, published protocols or guidelines for iodine staining of fishes are lacking. The work presented here tests protocols for staining fishes, specifically snailfishes of the family Liparidae. Snailfishes from multiple genera (*Liparis* and *Careproctus*) were stained using different stain concentrations, formulations (aqueous versus in ethanol), and timings to determine the optimal protocol for a range of sizes of liparids. The methods developed here focus on the tradeoffs between optimizing visualization of tissues, minimizing degradation of specimens (including desiccation and long-term stain retention), and minimizing overall cost (including time required and chemicals used). From making specimen selection easier by detailing specimen condition before and after staining, to removing some of the guesswork around time of stain diffusion based on specimen size, this work aims to make future diceCT scanning of other fishes simpler, more efficient, and more repeatable.

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

Shana Geffeney[1], Gabriela Toledo[2] and Charles Hanifin[1]

[1]Utah State University Uintah Basin, Vernal, UT, USA. [2]University of Virginia, Charlottesville, VA, USA

Understanding evolution through natural experiments: Tetrodotoxin resistance in snakes

A diverse array of species has evolved resistance to toxins that target proteins critical for nervous system function such as ion channels. Understanding the mode and tempo by which ion channels evolve resistance to toxins can inform our understanding of how proteins respond to selection from multiple sources. Tetrodotoxin (TTX) is a well-studied example of a toxin that cripples nerve and muscle cell function by binding to and blocking the outer pore of voltage-gated sodium ion channels (VGSCs). Early work demonstrated that extreme TTX-resistance evolved in garter snakes by a few key changes in the TTX-binding site of VGSCs. These key changes are found in other species that have independently evolved resistance to TTX, including newts and octopuses. This convergence suggests common structural and functional constraints shape evolutionary change of VGSCs. Recent data gathered from a constructed native snake channel demonstrate that a single shared change in the outer pore causes the greatest increase TTX resistance and dramatically disrupts some aspects of channel function, voltage-dependence of activation and slow inactivation. This change, however, has minimal effects on other channel functions. Other shared changes are compensatory and recover functional disruptions without altering TTX resistance. These results suggest adaptive evolution of proteins is constrained by functional costs but that extreme phenotypes can evolve through combinations of progressive substitutions that increase resistance and compensatory substitutions that mitigate costs.

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

Marcelo Gehara and Frank Burbrink

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

Comparative Historical Demography of Amphibians and Reptiles from Northeastern Brazil

The northeast of Brazil is mostly covered by Seasonally Dry Tropical Forests, known as Caatinga, a xeric vegetation characterized by strong seasonality and unpredictable droughts. Palynological evidence suggests that the Caatinga experienced an increase in aridity during the Pleistocene. If this increase was important for the diversification of associated xeric-adapted species, simultaneous population expansions should be evident at the community level. Here we analyzed the demographic history of 7 reptiles and 4 amphibians associated with the Caatinga in a hierarchical approximate Bayesian computation (hABC) framework to test for simultaneous demographic expansion. We found a strong signal of synchronous population expansion in the Late Pleistocene, supporting the hypothesis of an increase in total area of the Caatinga during this time. This expansion likely enhanced the formation of communities adapted to high aridity and seasonality and caused regional extirpation of taxa adapted to mesic forest.

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

Marina Gerson

Stanislaus State University, Turlock, CA, USA

Homage to GE Hutchinson or Are there still so many kinds of animals? Long term studies needed.

Long term studies are key to assessing changes in community structure. Data are lacking for most localities despite an urgent need for information in the light of rapid habitat degradation and loss related to human activity. The VertNet Database reports one amphibian record comprising a species of toad and 67 records of reptiles comprising 13 species from the Turtle Mountains desert region near Needles, San Bernardino County, California, USA. These records span a timeframe between 1910 and 1994. My preliminary survey data from June 2015, 2016, and 2017 documented continued presence of six of these species and one additional species, with two of these observed only in one survey year. Outside of designated survey times, I documented three additional species at the locality. These data support the notion that dedicated survey efforts are required to capture complete community data; annual June visits are planned into the foreseeable future. Only long term data sets can reveal ongoing changes to community structure. Despite the lack of short-term publication prospects, new assistant professors should consider targeting a locality for annual surveys in order to develop a longitudinal data set while traversing the path to tenure and promotion.

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

Michael Ghedotti[1], Hannah DeKay[1], Josephine Gruber[1], W. Leo Smith[2] and Matthew Davis[3]

[1]Regis University, Denver, CO, USA. [2]University of Kansas, Lawrence, KS, USA. [3]St. cloud State University, St. Cloud, MN, USA

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

Bioluminescence, the generation of light by living organisms, is widespread in fishes but light organs are often poorly known. The luminous roughies (genera *Aulotrachichthys* and *Paratrachichthys*) have a light organ in the region of the anus that houses bacteria in the genus *Photobacterium*. In this study we seek to determine the anatomic structure of the bioluminescent organ in two species *Aulotrachichthys prosthemius* and *Paratrachichthys fernandezianus* and shed light on its likely evolution. We used histological sectioning and gross dissection to explore the anatomy of the bioluminescent organs and we used a DNA sequence dataset to generate a phylogeny for the group. The bacterial bioluminescent organs in the luminous roughies are derived from pouching of the terminal intestine and the bacterial housing components are restricted to the region around the anus. This anatomy in the context of the phylogeny suggests that the bioluminescent organs of the luminous roughies arose via a single evolutionary transition along with a far more anterior position of the anus. Continuing work is needed to have a reasonably complete understanding of bioluminescence evolution in this group.

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578 Ichthyology Systematics II, Grand Lilac Ballroom South, Sunday 15 July 2018

Ava Ghezelayagh[1], Carole Baldwin[2], Raymond Simpson[1] and Thomas Near[1]

[1]Yale University, New Haven, CT, USA. [2]National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

Revising Perciformes: Molecular Evidence of Non-monophyly in the Mail-cheeked Fishes (Scorpaeniformes) and the Sea Basses and Groupers (Perciformes: Serranidae)

Positioned within the unresolved “bush at the top” of the teleost tree, Perciformes (the “perch-like” fishes) is a species-rich lineage of percomorph fishes. Discovered and delimited primarily through molecular phylogenetic analyses, there is no identified morphological synapomorphy for the clade. In the present study, we inferred Bayesian and maximum likelihood phylogenies for representatives of 71 perciform families and 238 genera utilizing sequences for 10 nuclear genes (*enc1*, *glyt*, *myh6*, *plag12*, *ptr*, *rag1*, *sh3px3*, *sreb2*, *tbr1* and zic1). Our newly-generated phylogenetic trees reaffirm most of the perciform relationships hypothesized in previous molecular studies and provides further support for the non-monophyly of Scorpaeniformes, as traditionally delimited, and the nesting of its taxa within Perciformes. This study also includes the broadest sampling to-date of Serranidae (sea basses and groupers), one of the most species-rich percomorph families that have long been hypothesized as paraphyletic. With representative species from all five hypothetical serranid subfamilies, our phylogenies reconfirm the paraphyly of Serranidae and provide strong support for six lineages containing serranids: 1.) Serraninae as previously delimited, 2.) Anthiinae (to the exclusion of *Acanthistius* and *Trachypoma*), 3.) Epinephelinae (to the exclusion of *Niphon*), 4.) *Niphon* as the sister lineage of Percidae, and 5.) *Hemilutjanus* that resolves outside of Perciformes and as sister lineage of Polyprionidae. Our results provide a foundation to incorporate morphological characters in a phylogenetic-based classification of perciform teleosts.

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326 Ichthyology Systematics II, Grand Lilac Ballroom South, Sunday 15 July 2018

Sarah Gibson

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

The Evolutionary Relationships of the Order †Redfieldiiformes (Osteichthyes, Actinopterygii)

Fishes of the order †Redfieldiiformes (~22 genera, 26 species) are an extinct group of stem ray-finned fishes found globally (e.g., Australia, Madagascar, Morocco, North America, South Africa) in geologic deposits from the Early Mesozoic. The order †Redfieldiiformes are one of a few stem actinopterygian lineages present in the Early Mesozoic, prior to the neopterygian radiation of the Late Triassic and Early Jurassic, and are often found in abundance in certain deposits after the extinction events of the Late Permian and Mid-to-Late Triassic. Redfieldiiforms possessed a fusiform body shape, thick enameled (ganoid) scales covering the entire body, fixed maxillae and premaxillae, more upright jaw suspensoria, prominent and often tuberculated snouts, and reduction in the dorsal lobe of the caudal fin (hemiheterocercal). Some redfieldiiform fishes also possess unusual or novel patterns of pores along the sensory line canals of the skull. The evolutionary relationships within the †Redfieldiiformes were last examined over thirty years ago and have never been assessed via a quantitative phylogenetic analysis. Redfieldiiform fishes are reexamined in this study, with updates to the anatomical and morphological descriptions of certain taxa. Parsimony and maximum-likelihood analyses support a monophyletic †Redfieldiiformes with two families, †Brookvaliidae and

†Redfieldiidae. The order †Redfieldiiformes is closely related to the †Scanilepiformes, †Perleidiformes, and †*Mesopoma*. A new classification of the †Redfieldiiformes is presented.

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384 Reptile Ecology II, Highland A, Sunday 15 July 2018

Sean Giery[1] and James Stroud[2]

[1]University of Connecticut, Storrs, CT, USA. [2]Washington University in St. Louis, St. Louis, MO, USA

Trophic Ecology of the Brown Anole (*Anolis sagrei*): Niche Compression in Species-Rich Communities

Detailed assessment of the trophic ecology of *Anolis* lizards has fundamentally shaped our current understanding of how communities form, function, and evolve (e.g., partitioning, expansion, and complementarity). Despite these early advances and continued efforts to understand the trophic niche of anole lizards, a systematic review has yet to be performed. Similarly, thorough examination of intraspecific niche variation in any widespread anole species is lacking. Here, I assemble published and unpublished data on the dietary and structural niche of brown anole (*Anolis sagrei*) populations. These data, collected from populations spanning their huge geographic range (e.g., Florida, The Bahamas, Greater Antilles, Swan Islands, Bermuda, Taiwan, and Hawaii), reveal substantial interpopulation variation in trophic ecology. Intriguingly, our analysis reveals a clear pattern of increased Trophic Niche Width (TNW) where brown anoles coexist with congeners (e.g., *A. grahami*, *A. equestris*, *A. distichus*) and/or other members the diurnal insectivorous lizard guild (e.g., *Leiocephalus carinatus*). This positive relationship between TNW and guild richness is largely incongruent with expectations based on contemporary niche theory that suggests population resource use is more narrowly 'subsetted' as interspecific competition increases. However, our data are consistent with a little-used model of resource use that may deserve more attention - niche compression. In this talk I will share these results and discuss how niche compression might alter our understanding of the role of interspecific interaction in ecology and evolution.

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

Emilia A.R. Gildemeister and Aaron M. Sullivan

Houghton College, Houghton, NY, USA

Do Allegheny Mountain Dusky Salamanders (*Desmognathus ochrophaeus*) Learn to Associate Non-Predatory Smooth Greensnakes (*Opheodrys vernalis*) with Threat?

Learning benefits organisms through increases in foraging success, reproductive output, and predator detection. The capacity to recognize and assess predators via chemical stimuli may be especially beneficial for amphibians, whose populations are declining globally due to a variety of environmental changes. With this study, we attempted to train Allegheny Mountain Dusky Salamanders (*Desmognathus ochrophaeus*) to associate non-predatory Smooth Greensnakes (*Opheodrys vernalis*) with stimuli from predation events by pairing conspecific damage-released cues with snake kairomones. Salamanders were collected from wooded areas of the campus of Houghton College and randomly assigned to one of six treatment groups: three controls (distilled water, damage-released cues, and aqueous rinses of *O. vernalis*) were used to establish baseline levels of locomotor and foraging activity, whereas three experimental groups varied the amount of time that salamanders were exposed to the paired chemical stimuli (48 h, 96 h, and 144 h) in an attempt to assess the effect of exposure duration on the learned response. The foraging of trained salamanders exposed to kairomones from *O. vernalis* was observed in the laboratory at night. Our results show no significant locomotor or foraging differences between the control and experimental treatments, suggesting a lack of learning by *D. ochrophaeus*. This may indicate the inability for associative learning by *D. ochrophaeus*, which is inconsistent with other studies of amphibian learning, or limitations on the types of associations that can be formed. Alternatively, the lack of pronounced behavioral responses to the damage-released stimuli could partially account for the results of this study.

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287 ASIH STOYE GENERAL ICHTHYOLOGY I, Grand Lilac Ballroom South, Thursday 12 July 2018

Matthew Girard

University of Kansas, Lawrence, KS, USA

Untangling threadfins: Relationships of Polynemidae using a total evidence approach

Polynemids are best known for their numerous, elongated, thread-like lower pectoral-fin rays. Also known as the threadfin fishes, the Polynemidae consists of eight genera and 42 species that can be found in a diversity of habitats throughout the world’s tropics. Despite substantive taxonomic work across the family or in particular geographic regions, our current knowledge of polynemid evolution is limited. Preliminary investigations and prior work on threadfin systematics have shown phylogenetic discrepancies in the family’s sistergroup, with little work being done on the clade’s intrarelationships. Fortunately, previous studies have depicted a wealth of external anatomical characters in the fins and scales, with a trend toward reduced eye size. In light of these features and their potential utility as a source of phylogenetically informative characters, an expanded survey of the variation in polynemid skeletal systems will be conducted. These data will be combined and analyzed with DNA sequence data to work toward a well-supported phylogeny of the Polynemidae.

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113 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Highland D, Thursday 12 July 2018

Jessica Glass[1,2], Richard Harrington[1], Brant Faircloth[3] and Thomas Near[1]

[1]Yale University, New Haven, CT, USA. [2]South African Institute for Aquatic Biodiversity, Grahamstown, South Africa. [3]Louisiana State University, Baton Rouge, LA, USA

Phylogenomics of carangiform evolution using ultraconserved elements

Carangiformes is a clade of approximately 170 marine species that exhibit substantial morphological and ecological diversity, including species such as the jacks, scads, pompanos, billfishes, and remoras. Many carangiforms are large predators; ecologically significant for coral reef and coastal ecosystems; and economically important in recreational, commercial, and artisanal fisheries throughout the world. A number of molecular phylogenetic studies have brought into doubt the monophyly of several genera, as well as the relationships among major carangiform subclades, including monophyly of the most species-rich subclade, Carangidae. Previous molecular studies have either lacked sufficient taxonomic coverage or sampled too few loci to adequately resolve carangiform phylogeny. We sought to resolve taxonomic relationships within Carangiformes through genomic sequencing of ~1200 ultraconserved DNA elements (UCEs). Using this molecular dataset, which sampled 80% of the recognized carangiform species, we performed fossil-calibrated divergence dating in order to assess timing of carangiform diversification. The data strongly support the paraphyly of multiple traditional taxonomic groups, including Carangidae, *Alepes*, *Carangoides*, *Caranx*, and *Seriola*. A re-evaluation of morphological trait variation is needed to assess congruence with phylogenies inferred from molecular data. Our results provide new insight on the phylogenetic relationships of Carangiformes and the timing of carangiform evolution in the context of significant historical events such as the Cretaceous-Paleogene extinction. By mitigating taxonomic uncertainty in an important percomorph clade, we aim to more accurately characterize teleost biodiversity, a pressing issue in the face of increasing anthropogenic disturbances on marine ecosystems.

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232 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Jessica Glass[1,2], Scott Santos[3], John Kauwe[4] and Thomas Near[1]

[1]Yale University, New Haven, CT, USA. [2]South African Institute for Aquatic Biodiversity, Grahamstown, South Africa. [3]Auburn University, Auburn, AL, USA. [4]Brigham Young University, Provo, UT, USA

Long live the kingfish: phylogeography of an iconic sportfish, the Giant Trevally (*Caranx ignobilis*)

The Giant Trevally (*Caranx ignobilis*), also called the Giant Kingfish, inhabits the Indo-West-Pacific and is a top predator associated with rocky and coral reefs. *Caranx ignobilis* is coveted by recreational fishermen and heavily targeted by small-scale and commercial fisheries throughout its range. We investigate the genetic structure of *C. ignobilis* across the full extent of its range using double digest restriction enzyme-associated DNA sequencing (ddRADseq). We sampled 140 individuals from multiple Indo-Pacific localities spanning Australia, Japan, South Africa and the Red Sea. Results indicate genetic admixture in the western Indian Ocean and genetically distinct populations in the western Pacific. The observed genetic homogeneity across the western Indian Ocean is interesting in light of recent acoustic tagging studies that indicate a high level of territoriality, which would presumably result in geographic structuring of genetic variation. Future research will incorporate samples from additional localities throughout the Indo-Pacific, with the objectives of identifying potential phylogeographic breaks, population bottleneck or expansion events, modeling the direction and magnitude of gene flow, and determining the functional roles of loci under selection. Understanding the population structure of *C. ignobilis* is essential for the sustainable management of this understudied species in the Indian and Pacific Oceans.

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374 Herpetology Systematics, Highland B, Saturday 14 July 2018

Richard Glor

University of Kansas, Lawrence, KS, USA

Speciation in the Hispaniolan Bark Anole (*Anolis distichus*)

The Hispaniolan Bark Anole (*Anolis distichus*) is a widespread and highly polymorphic lizard with more than a dozen subspecies. My laboratory's prior research suggests that this species includes populations at various stages of the speciation process. These populations often exhibit some degree of ecological, phenotypic and genetic differentiation, but hybridize where they come into contact. Along hybrid zones, we have found evidence for reduced gene flow and intrinsic reproductive isolation. We have recently sequenced and assembled whole genome sequence data for this species, and are currently using this genome to identify the genomic basis for species differences and speciation. Our research suggests that geographic isolation and ecological specialization both contribute significantly to anole speciation, and that species divergence is restricted only to portions of the genome.

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279 Lightning Talks II, Highland A, Saturday 14 July 2018

Brad M. Glorioso[1] and J. Hardin Waddle[2]

[1]U.S. Geological Survey, Wetland and Aquatic Research Center, Lafayette, LA, USA. [2]U.S. Geological Survey, Wetland and Aquatic Research Center, Gainesville, FL, USA

A Decade of Turtle Capture-Mark-Recapture in a Small Urban Pond Complex

Turtles are among the longest-lived vertebrates, and as such, it is important that studies examining survival be conducted for as long as possible. We have conducted an ongoing 10-year capture-mark-recapture study of the aquatic turtle assemblage in an urban landscape in Lafayette, Louisiana, USA. The manmade pond complex, built in the 1990s, lies within meters of a busy four-lane divided road on the University of Louisiana at Lafayette's Research Park. From 2009–2018, we captured aquatic turtles using two methods (deep-water crawfish nets and standard three-ring hoop nets) using a robust design, where we had five consecutive sampling days (secondary periods) each year in May (primary periods). We have captured over 100 individual Red-eared Sliders, 20 Eastern Musk Turtles, and just a few individuals of several other species. We captured more female Red-eared Sliders than males, but this was not significantly different from equality. We have recaptured nearly 50% of individual Red-eared Sliders in subsequent years after initial capture. Deep-water crawfish nets were much more effective, compared to hoop nets, at capturing turtles in our study. Continued investigation into this urban turtle population will enable us to refine our estimates of survival and compare them to populations studied in more natural habitats.

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

Christopher Goatley and Stephen Wroe

University of New England, Armidale, NSW, Australia

Micro-CT Scanning Techniques to Study the Ecology of Small Vertebrates

In recent years, micro-computed tomography (micro-CT) scanning has become more accessible for use in biological studies. It now offers relatively quick, cost-effective and non-destructive opportunities to visualise internal morphological structures of specimens. Where micro-CT data is beginning to prove exceptionally useful for studying the anatomy and taxonomy of specimens, it has, until recently, been largely overlooked by ecomorphological studies. With this poster I aim to show how this innovative technique can be applied to better understand the functional ecology of small vertebrates in a broad, comparative framework. I will present a brief description of how micro-CT scanning works, and some considerations that must be taken into account during basic scanning. I will then introduce the advantages of diffusible iodine contrast enhanced CT (DiceCT) techniques, to visualise soft tissue structures. Finally, using small fishes as a model system, I will showcase how micro-CT scanning can be used to directly identify the functional roles of fishes through dietary analyses, and indirectly assess functional capabilities through the application of morphological techniques including biomechanical modelling. This poster will provide a detailed background on the potential application of increasingly available micro-CT data, with the goal of increasing the uptake of this technique among researchers in different fields of vertebrate ecology.

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163 Ichthyology Ecology and Ethology, Highland E, Sunday 15 July 2018

Christopher Goatley[1], Simon Brandl[2], David Bellwood[3] and Luke Tornabene[4]

[1]University of New England, Armidale, NSW, Australia. [2]Simon Fraser University, Vancouver, BC, Canada. [3]James Cook University, Townsville, QLD, Australia. [4]University of Washington, Seattle, WA, USA

Cryptic Biodiversity: Community Composition of Cryptobenthic Reef Fish Faunas

Cryptobenthic reef fishes have typically been defined as fishes under 50mm long that have cryptic colouration or behaviour, and are associated with the benthos. Wherever they have been studied, these fishes numerically dominate coral reef fish communities in terms of both their abundance and diversity. Yet, despite this prevalence, these fishes are both poorly defined and, due to the difficulty of sampling them, the number of places that cryptobenthic reef fishes have actually been censused remains remarkably small. In this presentation, I will focus on the potential treasure-trove of biodiversity represented by cryptobenthic reef fishes. I will begin by highlighting the trends in rates of descriptions of fishes which gives us a broad introduction to how many species may be left to describe. I will then move on to discuss the findings of a recent field trip to one of the best studied reef systems in the world, and one of the few places that cryptobenthic reef fishes have been studied: Lizard Island on the Great Barrier Reef. Remarkably, and somewhat worryingly, in just 10 days sampling we found that many of the current identifications of common taxa are incorrect. Even more compelling, was that on this short field trip we found numerous taxa never reported from this location, and even entirely new species. This presentation will provide a broad overview of a poorly known reservoir of biodiversity and introduce techniques which can be employed to explore new communities in new locations around the world.

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

Cody Godwin[1], Chris Murray[1], J. Sean Doody[2], Simon Clulow[3] and Dave Rhind[4]

[1]Tennessee Technological University, Cookeville, Tennessee, USA. [2]University of South Florida Saint Petersburg, Saint Petersburg, Florida, USA. [3]University of Newcastle, Newcastle, New South Wales, Australia. [4]Monash University, Clayton, Victoria, Australia

Observation on Australia’s Largest Lizard, The Perentie (*Varanus giganteus)*

Australia is home to the world’s third largest lizard, the perentie (*Varanus giganteus).* While the species is an icon of the outback and an important apex predator, very little is known about their life history in the interior. Here, I present observations on an interior population including

movement patterns and habitat preference after a six-week preliminary field season. The study was performed in the Northern Territory of Australia in mid summer. Baited camera traps and baited live traps were deployed to identify preferred sites and areas to focus search efforts. Perentie were detected via driving and hiking surveys and captured with noose poles. Perentie of appropriate size were radio tagged and tracked daily. Cameras were placed at active burrows to assess haul in and haul out times. A total of 13 perentie were detected with five captures, two observations and six individuals discovered on camera traps. All size groups were discovered during the survey from hatchlings to large adults. Of the five perentie captured, three were large enough to be outfitted with a radio telemetry tags. Perentie do not create their own burrows and use rock crevices and rabbit warrens for refuge. Movement appears to be crepuscular with burrows used to escape the heat of the day. Perentie exhibits site recidivism and will use specific rock crevices repeatedly. Future work will include boosting the sample size, tracking during different seasons and comparing sex specific movement patterns.

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

Alexandra Gonzalez and Jennifer Dever

University of San Francisco, San Francisco, California, USA

Seeing Red: Analyzing IUCN Red List Data of Amphibians in Southeast Asia

In the midst of the current sixth mass extinction event which is now underway, it appears that amphibians are one of the most impacted vertebrates. Over 7,500 amphibian species are listed on the IUCN Red List of Threatened Species (an assessment tool which provides species' conservation status, perceived threats, and distribution range). While it is well-known that populations under multiple stressors are more likely to undergo significant declines, there are limited resources available for visualizing how these threats may work synergistically and interact within a species' range. This is especially the case for Southeast Asian amphibians, which much less attention has been paid as compared to other parts of the globe. Additionally, the IUCN Red List provides a description of threats affecting species and categorizes species into Red List Categories. However, this data is not easily accessible for wide-scale analyses. The aims of this project were as follows:
(1) utilize bioinformatics to increase accessibility to IUCN Red List data and (2) analyze the IUCN data repository to identify trends in amphibians of Southeast Asia.

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

Alexandra Gonzalez and Jennifer Dever

University of San Francisco, San Francisco, California, USA

Visualizing Threats of Amphibians in Southeast Asia

In the midst of the current sixth mass extinction event which is currently underway, it appears that amphibians are one of the most impacted vertebrates. Over 7,500 amphibian species are listed on the IUCN Red List (an assessment tool which provides species' conservation status, perceived threats, and distribution range). The primary threats amphibians face include habitat loss, disease, invasive species, pollution, climate change, overexploitation, natural disasters and human disturbance. While it is well-known that populations under multiple stressors are more likely to undergo significant declines, there are limited resources available for visualizing how these threats may work synergistically and interact within a species' range. This is especially the case for Southeast Asian amphibians, which much less attention has been paid as compared to other parts of the globe. Using code previously developed to increase the accessibility of IUCN threat data, various threats affecting amphibians of Southeast Asia are plotted by species range.

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

Sebastian Gonzales, Hayley Crowell and Emily Taylor

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

A Comparative Study of Home Range and Movement Patterns Between Coastal and Inland Pacific Rattlesnakes

Few studies have compared home range size among different populations of snake within a given species. In this study, we compared the home ranges and movement patterns of coastal and inland populations of adult, male Pacific rattlesnakes (*Crotalus oreganus*). Using radio telemetry, we tracked 28 male snakes (n/coastal=15, n/inland=13) from April to October of 2017 in four study sites throughout central California. Our four field sites included one inland and one coastal northern site in San Luis Obispo County as well as an inland and coastal site in Santa Barbara County to examine possible differences in movement patterns between each location based on climate. Individuals were tracked 4-5 times per week at random times throughout the day, and location was recorded via handheld GPS. We will present data on the home range sizes as well as timing and length of movement bouts. Increased movements typically occur during the mating season, while male snakes are searching for mates. Apart from the mating season, the snakes stay in small home ranges, with short infrequent movements. This is particularly true during the cool winter months while many *C. oreganus* over-winter underground. We will present data about the relationship between spatial ecology and climate in these four populations.

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572 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Allex Gourlay, Kurvin Li, Daniela Brouwer and Robert Drew

University of Massachusetts Dartmouth, North Dartmouth, MA, USA

Skin Mucous Proteome of the Clark's anemonefish (*Amphiprion clarkii*) while

Interacting with Different Sea Anemone Species

When an anemonefish (clownfish) encounters a host sea anemone, they often engage in a behavior called "acclimation," in which they gradually increase physical contact with a potential host. The purpose of this acclimation behavior is unclear, given that naïve anemonefish are usually protected from host anemone species, even if the fish have never before encountered sea anemones. We hypothesized that anemonefish use acclimation to regulate the mucous proteome to suit diverse host species that differ widely in toxicity and adhesiveness. To test this hypothesis, we used LC-MS/MS to compare the mucous proteomes of naïve Clark's anemonefish (*Amphiprion clarkii*) to fish associating with one of two natural hosts: the bubbletip sea anemone (*Entacmaea quadricolor*, Family Actiniidae) or the more venomous carpet anemone (*Stichodactyla* sp., Family Stichodactylidae). There were no significant differences in peptide content or quantity between naïve and associating anemonefish, or between fish associating with different species. There were also no differences in the post-translational modifications detected by this technique which included oxidation, acetylation, and deamidation of glutamine. Preliminary comparisons with the mucous proteomes of non-symbiotic fish species also did not reveal any obvious differences associated with symbiosis with sea anemones. We therefore conclude that this symbiosis does not depend upon changes in the quantities of peptides in the mucus, but instead likely involves some other aspects of the anemonefish's mucus.

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396 Reptile Ecology II, Highland A, Sunday 15 July 2018

Sean Graham and Crystal Graham

Sul Ross State University, Alpine, Texas, USA

Amphibians and Reptiles as Prey of the Loggerhead Shrike in West Texas

While the ecological impacts of apex predators are well known, the trophic effect of secondary consumers ("mesopredators") is less well known and more difficult to quantify. Loggerhead shrikes are small predatory birds that are common secondary consumers in open habitats throughout the United States. Loggerhead shrikes are generalist predators on arthropods and small vertebrates and important selective agents on these animals. However, the net impact of their predation on small animals has not been quantified. We surveyed an active shrike larder (a barbed wire fence) in West Texas once per month during 2014-2017 to quantify the seasonal abundance and identity of shrike prey. We also studied prey turnover time weekly during 2017 to estimate the total number of prey captured at this location. 1061 individual prey items were collected during 34 surveys. Shrikes preyed upon 13 taxa of arthropods and 13 species of amphibians and reptiles, and several unidentified species of small mammals and birds. Incidence and diversity of impaled prey was highest during October-December. Orthopterans (mostly grasshoppers) were the most abundant impaled prey, followed by Coleopterans and lizards. Our estimates of predation rates suggest impaled prey turnover time at this larder is rapid, so that our monthly collections are indicative of about one week of predation by the local population of shrikes. In addition, shrikes often consume prey immediately and only impale a small subset of their prey. Therefore, the number of prey killed by shrikes is considerably higher than the total numbers reported here.

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

Sean Graham[1], Richard Kline[2], David Steen[3] and Crystal Kelehear[4]

[1]Sul Ross State University, Alpine, Texas, USA. [2]University of Texas Rio Grande Valley, Brownsville, Texas, USA. [3]Georgia Sea Turtle Center, Jekyll Island, Georgia, USA. [4]Smithsonian Tropical Research Institute, Ancon, Panama

Description of an extant Salamander from the Gulf Coastal Plain of North America: the Reticulated Siren, *Siren reticulata*.

The Sirenidae family contains a number of eel-like salamanders currently restricted to North America. Despite their apparent abundance throughout the southern United States and their status as some of the world's largest amphibians, the biology, ecology, and phylogeography of this group is poorly-known. In this study we use morphological and genetic evidence to describe a long-suspected species from southern Alabama and the Florida panhandle; a species we name the Reticulated Siren, *Siren reticulata*. Future studies will enable more precise phylogenetic information about *S. reticulata* and will almost surely reveal additional undescribed species within the family.

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

Alejandro Grajal-Puche, Christopher Murray, Donald Walker and Tania Datta

Tennessee Tech University, Cookeville, TN, USA

The Structure and Function of Microbial Communities within Alligator Nesting Ecosystems: A Comparative Approach Across Ecological Scales

Recent publications have highlighted the ecological significance of both the endo- and exogenous microbiome. Thus, the characterization of microbial assemblages, across focal scales, and elucidation of environmental drivers behind microbial communities can further scientific understanding of pattern-driven ecological phenomena. Many questions remain regarding the formation and functional role of a host's microbiome, especially within understudied taxonomic classes, such as Reptilia. Crocodilians are keystone reptiles, which are crucial to the resiliency of the ecosystems they inhabit. Utilizing high-throughput DNA sequencing, I have categorized the microbiome of wild American alligator (*Alligator mississippiensis*) nests, the alligator eggshell surface, and surrounding nest habitat. In addition, I have identified which environmental variables influence the associated alligator-nest microbial assemblage and predicted the functional role of core microbial members. These results reflect a single sampling season and location. We will be expanding our sampling effort to an additional five sample sites to determine spatiotemporal microbial variations. With these findings, I address ecological scaled-

based questions, add to the scientific understanding of ecosystem dynamics, and establish baseline modeling predictions of microbial community shifts due to altered environmental variables.

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

Brian Gratwicke[1], Anna E Savage[1,2], Matthew H Becker[1,3], Blake Klocke[1,4] and Robert C Fleischer[1]

[1]Smithsonian Conservation Biology Institute, Washington, DC, USA. [2]University of Central Florida, Orlando, FL, USA. [3]Liberty University, Lynchberg, VA, USA. [4]George Mason University, Fairfax, VA, USA

Panama Amphibian Rescue and Conservation Project

The Panama Amphibian Rescue and Conservation Project cares for a living collection of 12 amphibian species at risk of extinction from the amphibian chytrid fungus in Panama. The collection is cared for by 11 fulltime staff in a 450 square meter facility at the Smithsonian Tropical Research Institute. The purpose of this and similar Amphibian Ark projects around the world is to buy us time to figure out how to mitigate the disease threat. Our initial research focused on understanding the microbiome of amphibian skin and how the microbiome of highly susceptible species might be modified to confer protection from disease. We even tried genetically modified core skin microbes to produce known antifungal metabolites. In addition to a probiotic approach to disease mitigation, we sought to understand the genetic mechanisms underlying differential disease outcomes in partially susceptible species. We have not yet identified any specific mitigation approaches likely to improve the host's ability to survive a Bd infection, but the captive breeding program is now producing surplus animals allowing us the start release trials. These trials will help us to observe disease dynamics in the released frogs and the native amphibian community, and understand how climatic variables might influence persistence. One potential release strategy could be to identify potential climatic refugia where animals will have a higher probability of persistence. An adaptive management approach to these experimental release trails will also help us to improve release-trial efficacy with non-disease-related questions.

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

David Green

McGill University, Montreal, QC, Canada

Cold Comfort: Amphibians in winter.

Northern amphibians are dormant for most of the year while weather conditions are too cold for surface activity. To survive a long period of winter dormancy, the animals must

physiologically "stop the clock" and reside where it is just cold enough to minimize metabolic rate but not cold enough to kill them. They need to seek refuge sites with sufficient humidity and available oxygen for them to maintain a metabolism low enough to allow them to live for an extended period of time entirely off stored fat reserves. They should, therefore, alter their active season behaviour as winter approaches to seek out favourable overwintering sites where they are unlikely to be disturbed or die. As spring approaches, though, they have to be able to respond to indications of the return of warmer conditions on the surface. Although the cues triggering the onset of winter dormancy and the animals' behaviour during winter dormancy remain largely a mystery, the conditions associated with the animals' breaking their winter dormancy and re-emerging onto the surface in spring are becoming increasingly better understood. Re-emergence is tied, first, to changes in subsurface conditions and, then, by the re-appearance of springtime atmospheric conditions that allow for the resumption of surface activity.

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78 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Highland A, Thursday 12 July 2018

Aaron Griffing[1], Sanger Thomas[2], Daza Juan[3], Stuart Nielsen[1], Edward Stanley[4] and Tony Gamble[1,5,6]

[1]Marquette University, Milwaukee, Wisconsin, USA. [2]Loyola University in Chicago, Chicago, Illinois, USA. [3]Sam Houston State University, Huntsville, Texas, USA. [4]Florida Museum of Natural History, Gainesville, Florida, USA. [5]Bell Museum of Natural History, Saint Paul, Minnesota, USA. [6]Milwaukee Public Museum, Milwaukee, Wisconsin, USA

Embryonic development of a parthenogenetic gecko (*Lepidodactylus lugubris*) with special reference to adhesive toepads

One goal of evolutionary developmental biology (evo-devo) is to understand the role of development in the origin of phenotypic novelty and convergent evolution. Squamates are an ideal clade to study this topic as they are species-rich and exhibit a suite of diverse morphologies — many of which have evolved independently multiple times. In particular, geckos are extraordinary models for squamate evo-devo due to their phylogenetic position as the sister clade to most other squamates. Therefore, by including geckos in comparative evo-devo studies, one can encompass nearly all squamate diversity. Here we characterize the embryonic development of a gecko with adhesive toepads, *Lepidodactylus lugubris*, with a non-gecko squamate exhibiting an independent evolution of adhesive toepads, *Anolis sagrei*. *Lepidodactylus lugubris* is an ideal evo-devo model because it is parthenogenetic, easily kept in a laboratory setting, and there is a suite of resources being developed. We harvested 170 embryos of *L. lugubris* throughout embryonic development, characterized developmental events, and compared the timing and pattern of toepad development with that of *A. sagrei*. We find broadly similar patterns of toepad development between the two species, suggesting remarkable convergence in the developmental pathways underlying toepad development. This embryonic staging table will serve as a foundational tool to study convergent evolution of adhesive toepads and other questions concerning squamate evolution and development.

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

Michael Grundler

University of Michigan, Ann Arbor, MI, USA

Patterns of ecological specialization in colubrid snake diets

I use data on snake feeding observations gathered from dissections of museum specimens and the published literature to address two hypotheses regarding the evolution of ecological specialization in colubrid snake diets along a temperate to tropical gradient. More than 8000 predator-prey observations from 350 colubrid snake species reveal substantial variation in snake diets but do not indicate that rates of ecological specialization are higher in tropical snakes than in temperate snakes or that more specialized feeding ecologies are less evolutionary labile than more generalized feeding ecologies.

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198 ASIH STOYE GENERAL ICHTHYOLOGY II, Grand Lilac Ballroom South, Thursday 12 July 2018

Anna Gruszkiewicz and Kyle Piller

Southeastern Louisiana University, Hammond, Louisiana, USA

Analysis of Body Size Evolution and Diversification Rates in the Family Poeciliidae (Cyprinodontiformes)

From the guppy to the whale shark, one of the most interesting characteristics of animal diversity is the wide range of body sizes. Body size can play a vital role in the ecology, life history, physiology, and niche partitioning of a species. Previous studies have found that many freshwater fish species exhibit a phyletic shift toward smaller body size over evolutionary time potentially due to the invasion of small streams and subsequent isolation. This body size trend raises interesting questions about the potential correlation between diversification rates and the rate of body size evolution. This study examines this relationship within Poeciliidae. Poeciliidae is a highly speciose (> 250 species) group of live bearing New World fishes ranging from the southern US to southern regions of South America and the Antilles. Within the family, species richness as well as average standard length (SL) vary widely among genera. For this study, ultra-conserved elements (UCEs) were used to produce a new phylogeny for Poeciliidae including 82 species that represent 24/29 total genera. Diversification rates and body size evolution were inferred using multiple phylogenetic comparative analyses. It was predicted that poeciliid species would exhibit a correlation between body size evolution and diversification rates and a general shift toward smaller body size over evolutionary time. The results from this study will be presented.

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

Wilson Guillory[1], Jason Brown[1], Connor French[1], German Chavez[2], Rudolf von May[3], Jennifer Serrano-Rojas[4], Ignacio De la Riva[5], Jose Padial[5], Andrew Whitworth[6], Migeul Trefaut Rodrigues[7], Stefan Lötters[8], Steffen Reichle[9], Ivan Prates[10] and Evan Twomey[11]

[1]Southern Illinois University, Carbondale, IL, USA. [2]CORBIDI, Lima, Peru. [3]University of Michigan, Ann Arbor, Michigan, USA. [4]Universidad Nacional San Antonio Abad del Cusco, Cusco, Peru. [5]Museo Nacional de Ciencias Naturales, Madrid, Spain. [6]University of Glasgow, Glasgow, United Kingdom. [7]University of Sao Paulo, Sao Paulo, Brazil. [8]Universitat Trier, Trier, Germany. [9]Museo de Charupas, Santiago de Chiquitos, Bolivia, Plurinational State of. [10]Smithsonian National Museum of Natural History, Washington, DC, USA. [11]Vrije Universiteit Brussel, Brussel, Belgium

Resolving species relationships in the Amazonian Poison frog genus *Ameerega* using ultraconserved elements

Ameerega is a relatively large (~32 species) genus of poison frog in the family Dendrobatidae, ranging throughout the Amazon but with especially high diversity in the eastern foothills of the Peruvian Andes. Despite high interest in dendrobatids, the taxonomy and systematics of *Ameerega* are still in flux. Several phylogenies of the genus have been produced, but with a highly divergent array of topologies, leading to systematic inconsistencies and uncertainty as to the monophyly of several species. Previous trees have also generally been produced using only a few mitochondrial genes, thus not accounting for potential gene/species tree discordance. To resolve these issues, we produced a comprehensive species tree of *Ameerega* using subgenomic data derived from sequence capture of ultraconserved elements (UCEs).

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

Jennifer Gumm

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

Evolution and Function of Coloration in Darters (genus *Etheostoma*)

Darters of the genus *Etheostoma* are a group of colorful freshwater fishes that occur in the Southeastern US. Herein, I highlight several integrative studies aiming to uncover the causes and consequences of elaborate coloration in this group. First, behavioral studies have shown that color is used by females and males for mate choice. Work in this group provides evidence for a link between sexual selection and behavioral isolation, and by extension for a role of sexual selection in speciation. Combining reflectance spectrophotometry with comparative phylogenetic methods shows that coloration has high evolutionary lability, suggesting that color may be influenced by ecological factors that are not phylogenetically conserved. Interpreting visual signals also relies on the corresponding visual system. Using physiological tools to describe the spectral sensitivity of fish visual systems, shows differences in peak absorbance of visual pigments among species and individuals within a species. Additionally, intraspecific variation may have implications for visually based behaviors such as female and male preferences for color, which may contribute to reproductive isolation between species.

Using molecular genetics to examine visual pigment genes (opsins) provides strong evidence that structural genetic changes (i.e. changes in amino acid sequences) and regulatory genetic changes (i.e. gene expression) both underlie variation in darter visual systems. Examining the signal, the receiver, and the function of coloration provides a comprehensive understanding to the sensory ecology of these fishes and demonstrates how evolutionary processes acting on genes, mediated by physiological systems and behavioral interactions, can lead to an increase in biological diversity.

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

Joe Gunn[1], Leah Berkman[2] and Lori Eggert[1]

[1]University of Missouri, Columbia, MO, USA. [2]The Missouri Department of Conservation, Columbia, MO, USA

Validating the Taxonomic and Distributional Status of the Neosho Smallmouth Bass (*Micropterus dolomieu velox*)

Smallmouth Bass (*Micropterus dolomieu*) are economically important as a sportfish, accounting for a multi-billion-dollar angling industry in the United States alone. Thus, stocking has become increasingly common. The taxonomic status of *M. dolomieu* is controversial. Two subspecies are currently recognized: the Northern Smallmouth Bass (*M. d. dolomieu*), whose native range extends north and east of the Mississippi River, and the Neosho Smallmouth Bass (*M. d. velox*), which is restricted to the Arkansas River Basin. Although they are allopatric, their distinction is based primarily on a few morphological traits, such as the number of soft dorsal fin rays, predorsal contour, and body size. The taxonomic relationship between these subspecies has not been adequately resolved on a molecular level. Because mixing of genetically unique populations can lead to hybridization or, in extreme cases, loss of species-wide diversity, it is vital to consider genetic distinctions within *M. dolomieu* when restocking fisheries. To investigate the taxonomic and distributional status of *M. d. velox* in Missouri, Arkansas, and Oklahoma, we measured levels of genetic differentiation at 14 microsatellite loci among samples collected from the putative native ranges of both subspecies. With these results as a guide, we identified 95 samples representing relatively high genetic divergence and evaluated genome-wide differentiation between subspecies using double-digest RAD sequencing (ddRAD-seq). Our genomic analysis lays the groundwork for an assessment of population structure at thousands of single nucleotide polymorphisms (SNPs), which will allow us to evaluate the taxonomic and distributional statuses of the *M. dolomieu* subspecies.

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

Jacquelyn Guzy[1], Kelly Halloran[1], Jessica Homyack[2] and John D. Willson[1]

[1]University of Arkansas, Fayetteville, AR, USA. [2]Weyerhaeuser Company, Centralia, WA, USA

Population biology of Ouachita Dusky Salamanders (*Desmognathus brimleyorum*) in a managed forest landscape.

Salamander populations can play a key role in the function and diversity of temperate forest ecosystems. However, the population parameters of salamanders residing in forests managed for timber production are generally unknown. We conducted a capture-mark-recapture (CMR) study at three streams within intensely managed pine forests in the Ouachita Mountain region of Arkansas from March 2015-October 2016. Specifically, we used robust design CMR models to explore the effects of seasonal, site, and age-class variation on the capture probability, recapture probability, temporary emigration, abundance, and apparent survival of a stream salamander, *Desmognathus brimleyorum*. We found evidence of significant seasonal variation in temporary emigration rates, which were lowest in late spring and highest in the winter months. Our estimates of mean salamander density (1.31 individuals/m^2, adjusted to account for temporary emigration and conditional capture probability) and apparent survival (46%) were comparable to those of other *Desmognathus* species. This suggests that streams in forests managed for even-aged timber production can support viable, dense populations of salamanders comparable to those in protected forests. Understanding the dynamics of such populations may help inform future assessment, monitoring, and conservation of stream-associated salamanders.

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

Michael Hague[1], Chris Feldman[2], Edmund Brodie, Jr.[3] and Edmund Brodie III[1]

[1]University of Virginia, Charlottesville, VA, USA. [2]University of Nevada, Reno, NV, USA. [3]Utah State University, Logan, UT, USA

Convergent adaptation to dangerous prey proceeds through the same first-step mutation in the garter snake *Thamnophis sirtalis*

Convergent phenotypes often result from similar underlying genetics, but recent work suggests convergence may also occur in the historical order of substitutions en route to an adaptive outcome. We characterized convergence in the mutational steps to two independent outcomes of tetrodotoxin (TTX) resistance in separate geographic lineages of the common garter snake (*Thamnophis sirtalis*) that coevolved with toxic newts. Resistance is largely conferred by amino acid changes in the skeletal muscle sodium channel (Na_V1.4) that interfere with TTX-binding. We sampled variation in Na_V1.4 throughout western North America and found clear evidence that TTX-resistant changes in both lineages began with the same isoleucine-valine mutation (I1561V) within the outer pore of Na_V1.4. Other point mutations in the pore, shown to confer much greater resistance, accumulate later in the evolutionary progression and always occur together with the initial I1561V change. A gene tree of $Na_V1.4$ suggests the I1561V mutations in each lineage are not identical-by-decent, but rather they arose independently. Convergence in the evolution of channel resistance is likely the result of shared biases in the two lineages of *T. sirtalis*—only a few mutational routes can confer TTX resistance while maintaining the conserved function of voltage-gated sodium channels.

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340 ASIH STORER HERPETOLOGY, 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

Joshua M. Hallas[1], Chris R. Feldman[1], Edmund D. Brodie III[2], Michael E. Pfrender[3], Edmund D. Brodie Jr[4] and Thomas L. Parchman[1]

[1]*University of Nevada, Reno, Nevada, USA.* [2]*University of Virginia, Charlottesville, Virginia, USA.* [3]*University of Notre Dame, Notre Dame, Indiana, USA.* [4]*Utah State University, Logan, Utah, USA*

Adaptive variation in the Sierra garter snake (*Thamnophis couchii*): The influence of biogeography and genetic structure on patterns of TTX-resistance

Most species consist of multiple, genetically differentiated populations that may also experience different abiotic conditions and community interactions. Despite the importance of a population genetic perspective for understanding geographic variation in coevolution, few studies have thoroughly examined the role of population genetic structure underlying geographic mosaics of coevolution. Here, we quantified phenotypic variation and population genetic structure in the Sierra garter snake (*Thamnophis couchii*) using over 26,000 genome-wide single nucleotide polymorphisms. Our goal was to understand the geographic scale at which gene flow might be reduced among populations, and allow for independent local adaptation in response to variation in the tetrodotoxin (TTX) defense of their Pacific newt (*Taricha*) prey. We documented pronounced geographic variation in TTX-resistance, with snakes from the southern regions of the Sierra Nevada displaying higher TTX-resistant phenotypes than those in the north. In addition, phylogenomic analyses recovered relationships among clades strongly associated with geographic and phenotypically distinct regions. Even though we recovered fine scale population genetic differentiation at the level of neighboring watersheds, explanation of genetic distances among populations is confounded by the influences from both geography and phenotype. This does, however, give evidence that the geographic scale in which adaptive phenotypic variation can arise and persist is likely narrow.

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

Brian Halstead[1], Patrick Kleeman[2] and Jonathan Rose[1]

[1]*USGS WERC, Dixon, CA, USA.* [2]*USGS WERC, Point Reyes, CA, USA*

Time-to-detection Occupancy Modeling: An Efficient Method for Analyzing the Occurrence of Amphibians and Reptiles

Occupancy models provide a reliable measure of species distributions while accounting for imperfect detectability. The cost of accounting for false absences is that occupancy surveys typically require repeated visits to a site or multiple-observer techniques. More efficient methods of estimating detection probabilities would allow more sites to be surveyed, resulting in greater information about the ecological processes leading to occupancy. Time-to-detection surveys allow the estimation of detection probability based on a single site visit by one observer, and therefore might be an efficient technique for herpetological occupancy studies. We evaluated the use of time-to-detection surveys to estimate the occupancy of pond-breeding amphibians at Point Reyes National Seashore, California, USA, including variables that affected detection rates and the probability of occurrence. We found that detection times were short enough to reliably estimate the probability of occurrence of four of five pond-breeding amphibians at Point Reyes National Seashore, and that survey and site conditions had species-specific effects on detection rates. In particular, larger sites resulted in reduced detection rates for Sierran Treefrogs (*Pseudacris sierra*) and Rough-skinned Newts (*Taricha granulosa*). Probability of occurrence was negatively related to the presence of fish for these species, and positively related to grazing within the watershed for California Red-legged Frogs (*Rana draytonii*). Pond area also negatively affected Sierran Treefrog occurrence. Time-to-detection surveys can provide an efficient method of estimating detection probabilities and accounting for false absences in occupancy studies of reptiles and amphibians, allowing researchers to study a wider area for the same cost.

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

Gregor Hamilton[1], Alex Cameron[1] and Randy Jennings[2]

[1]*University of New Mexico, Albuquerque, NM, USA.* [2]*Western New Mexico University, Silver City, NM, USA*

Identification of whiptail lizards (*Aspidoscelis*) using multivariate analysis of a morphometric dataset.

Whiptail lizards of the genus *Aspidoscelis* can be difficult to identify, especially for museum specimens where color is often leached and formalin fixation makes genotyping difficult. The ranges of the three parthenogenetic species of *Aspidocelis* intersect in an ecotone along the Gila River in Southwest New Mexico: *A. sonorae* (Sonoran Spotted Whiptail)*, A. flagellicauda* (Gila Spotted Whiptail)*, and A. exsanguis* (Chihuahan Spotted Whiptail). Typically, these unisexual species can be distinguished as adults using the following morphological attributes: *A. exsanguis* is heavily spotted on dorsal stripes, on the base of the tail, and on the dorsal surface of the thighs, *A. flagellicauda* has 2 pre-anal scales as well as spots touching dorsal stripes, and

A. sonorae has three pre-anals with spots seldom touching dorsal stripes. However, intraspecific variation in these diagnostic characters makes identification of variant individuals challenging and is further compounded by specimen preservation. The Gila Natural History Collection at Western New Mexico University in Silver City, NM, possesses many specimens of these three species that could not be identified confidently and catalogued. To address this, we collected a morphometric dataset of 14 continuous and 7 binary characters, including scale counts, spot counts, and spot and stripe presence/absence data (n=337). We then implemented a multivariate approach to identify characteristics that enabled the assignment of unknown individuals (n=207) to species using a training data set (n=72) generated from catalogued specimens of each species.

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

Kathryn Hamilton[1], Shannon O'Leary[1], Kyle Piller[2], Kevin Conway[3] and David Portnoy[1]

[1]Texas A&M University - Corpus Christi, Corpus Christi, TX, USA. [2]Southeastern Louisiana University, Hammond, LA, USA. [3]Texas A&M University, College Station, TX, USA

Phylogenetic relationships within the genus *Erimyzon* (Family: Catostomidae) based on mitochondrial and nuclear loci

Erimyzon is a genus in the family Catostomidae, currently consisting of four described species: *E. oblongus* (Eastern creek chubsucker), *E. claviformis* (Western creek chubsucker), *E. sucetta* (lake chucksucker), and *E. tenuis* (sharpfin chubsucker), all native to North America. Most studies of catostomid phylogenetics focus on resolving relationships among genera and higher taxonomic groups. Due in part to the fact that catostomids are polyploid, previous studies have relied mainly on mitochondrial markers and inconsistencies between various studies are likely due to a combination of the loci used and limited taxon sampling. While the genus *Erimyzon* is consistently recovered as monophyletic, in a recent study, *E. oblongus* was not monophyletic; a result that could be due to misidentification, presence of cryptic lineages, incomplete lineage sorting, and/or hybridization/introgression. Because the genus *Erimyzon* has not been thoroughly examined genetically, and there may be unrecovered lineages in the genus, we amplified mitochondrial and nuclear markers in multiple individuals of each of the four currently recognized species to reconstruct phylogenetic relationships among them. This research is an important first step towards a better understanding of evolutionary relationships in the genus *Erimyzon*.

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

Paul Hampton

Colorado Mesa University, Grand Junction, CO, USA

Is Foraging Ecology an Overlooked Influence on Organ Position in Snakes?

Sea snakes have relaxed selection on cardiovascular function because low gravitational forces and water pressure in the marine environment place little stress on blood pressure homeostasis. Relative heart position in sea snakes is quite variable among species considering that the environmental influence on cardiovascular function should be similar. Sea snakes are diverse with respect to foraging ecology, which may be driving morphological diversification. I measured the position of the heart, liver and small intestine in sea snakes both by linear measurements on specimens and axial position (vertebral counts) determined from radiographs. The relative position of the organs was compared between species that forage for prey in either open habitats or burrows. Results will be discussed.

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

Paul Hampton[1] and Jesse Meik[2]

[1]Colorado Mesa University, Grand Junction, CO, USA. [2]Tarleton State University, Stephenville, TX, USA

Trophic Morphology and Prey Shape in Snakes

As gape-limited predators, head morphology in snakes should be strongly correlated with prey shape. In particular, specialization on elongate versus robust prey should result in divergent head morphologies, because under these circumstances the jaw would be subject to opposing functional demands. We compiled detailed dietary data for 70 species of snakes from 8 families, and evaluated head morphology and integumentary distension (through dorsal scale counts) for each of these species in order to characterize morphological differences between robust and elongate prey specialists. In addition, we evaluated whether shifts in diet were associated with shifts in speciation rate. Principal components analysis demonstrated that dietary specialists are positioned at the extremes of head morphospace, and moreover that integumentary distension was correlated with prey specialization. While results of this study support the general agreement that robust prey consumers have relatively large gapes and increased skin distension, we also find that elongate prey specialists possess unique adaptations to preferred prey shape.

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498 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center; part of ASIH symposium: If Salamanders Could Speak, Saturday 14 July 2018

Charles Hanifin and Shana Geffeney

Utah State University, Vernal, UT, USA

Toxicity, Resistance, and Protein Evolution: What Can We Learn from Newts and Snakes?

Natural product toxins provide powerful empirical systems to explore biological processes on multiple levels including large-scale ecological interactions, micro evolutionary processes and organismal physiology. Newts of the genus *Taricha* and their snake predators (Genus: *Thamnophis*) are engaged in a coevolutionary arms race in which reciprocal evolution drives increased TTX toxicity in newts and increased TTX resistance in snakes. To use TTX as a defense, *Taricha* newts must concentrate TTX in their tissues and also be resistant to the toxin. Here we will report results associated with the adaptive evolution of TTX-resistance in both snakes and newts. Our results show that TTX-resistance is ancient and ubiquitous in the modern-newt clade and that the molecular basis of TTX resistance in snakes and newts is strikingly convergent. In both groups, TTX-resistance results from similar substitutions in their VGSCs. This convergence likely results from shared constraints on channel function. Empirical manipulations of snake channels demonstrate that a single shared change in the outer pore of highly resistant snakes and all modern newts causes the greatest increase TTX resistance. Furthermore the first change along the path to resistance is shared in both newts and snakes but may occur in response to selection on organismal performance rather than resistance to TTX. Lastly, the identification of single “super-resistant” mutation in snakes indicates that snakes may have a simple path to resistance and explain why snakes appear to be the only winners in their arms races with newts.

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

James Hanken, Stephen Turney and Linda Ford

Harvard University, Cambridge, MA, USA

Unlocking the Vault: Mass Digitization and Imaging of Historical Slide Collections for use in Comparative Biology

Natural history museums hold vast collections of glass microscope slides amassed from a variety of sources over the last 100 or more years. These slides were prepared in association with a variety of botanical and zoological studies but were especially important for studies of fishes, amphibians and reptiles. While such collections represent a unique and irreplaceable resource for studies of integrative and comparative biology, most are fragile or otherwise difficult to access and work with. Hence, they are largely ignored by contemporary researchers. We have developed a cost-effective, high-throughput and semi-automated workflow for digitally scanning and displaying slides of many different sizes characteristic of the collections of the Harvard Museum of Comparative Zoology, which is

applicable to like collections at other institutions. The resulting high-resolution digital images, each depicting the contents of an entire slide, may be accessed via a customized web application that allows a variety of kinds of image analysis and data capture. Ready access to these historically and scientifically rich data sources will enable fruitful and timely collaborations between natural history museums and other branches of biology, such as neuroscience, physiology, developmental biology, functional morphology and ecology, and complements the growing number of digital-image repositories available via the Internet.

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

Maggie Hantak[1], Robert Page[2], Paul Converse[1], Carl Anthony[3] and Shawn Kuchta[1]

[1]Ohio University, Athens, OH, USA. [2]Texas A&M University-San Antonio, San Antonio, TX, USA. [3]John Carroll University, University Heights, OH, USA

The Relationship Between the Genetic Structure, Landscape Ecology, and Color Polymorphism in the Eastern Red-backed Salamander (*Plethodon cinereus*)

An underexplored question in color polymorphic species pertains to how phenotypes are maintained among populations. Mechanisms that maintain polymorphisms include negative frequency dependent selection, spatiotemporal variation in selection, and gene flow among populations. Investigating these mechanisms in multiple populations provides insight into the processes influencing geographic variation in genetic structure and color morph frequency. The Eastern Red-backed Salamander (*Plethodon cinereus*) is widely distributed in northeastern North America and contains two common color morphs (striped and unstriped). Currently, the evolutionary processes that maintain the polymorphism are not well understood. Using microsatellite loci, we investigated whether patterns of morph frequency variation conformed with patterns of population structure in Ohio. In addition, we examined whether genetic distance, landscape variables, or geographic distance had a stronger relationship with morph frequency variation. Our results demonstrate clear population structure with three genetic clusters, one of which is monomorphic for the striped morph. There was no relationship between genetic differentiation and morph frequency variation. Instead, we found that genetic distance was most correlated with ecological and landscape features, and morph frequency variation was most correlated with geographic distance and waterway barriers. Gene flow alone does not appear to maintain the polymorphism in *P. cinereus,* rather a balance between gene flow and selection likely maintains the two color morphs. Overall, our study provides critical information on the role of gene flow and natural selection in the evolution and maintenance of this color polymorphism, and links patterns of genetic differentiation with an understanding of the ecology of *P. cinereus*.

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26 Herpetology Physiology, Highland C, Saturday 14 July 2018

Rebecca Hardman[1], Kendall Oziminski[1], Laura Reinert[2], Louise Rollins-Smith[2], Kelly Irwin[3] and Debra Miller[1]

[1]*University of Tennessee, Knoxville, Tennessee, USA.* [2]*Vanderbilt University, Nashville, Tennessee, USA.* [3]*Arkansas Game and Fish Commission, Little Rock, Arkansas, USA*

Hellbender skin antimicrobial peptides show variable inhibition against chytrid fungus (*Batrachochytrium dendrobatidis*)

Hellbenders (*Cryptobranchus alleganiensis*) are large aquatic salamanders from the eastern USA and have experienced considerable population declines in both Ozark and Eastern subspecies, *C. a. bishopi* and *C. a. alleganiensis*, respectively. *Batrachochytrium dendrobatidis (Bd)* is a fungal skin pathogen of concern as it is present in wild hellbender populations and is known to cause mortality in captivity during times of stress. Furthermore, ulcerative non-healing lesions have been frequently observed in *C. a. bishopi* adults alongside high prevalence of *Bd*. Antimicrobial peptides (AMPs) secreted on the skin are an important component of amphibian innate immunity and may be a factor in manifestation of observed lesions. For instance, frog AMPs have demonstrated growth inhibition of *Bd* in vitro and, in some species, have been linked to variable resistance. Our objective was to determine if hellbender AMPs exhibited anti-*Bd* activity and if inhibition correlated to subspecies. We challenged *Bd* zoospores against serial concentrations of field collected Hellbender AMPs and found significantly higher *Bd*-inhibition from *C. a. alleganiensis* compared to *C. a. bishopi* with an MIC50 of 250 and 2500 ug/mL, respectively. Although we were unable to evaluate effects of *Bd* infection status on AMP activity, AMPs from ranavirus negative animals had significantly higher inhibition than those from ranavirus positive animals within *C. a. alleganiensis* populations (MIC50 75 and 400 ug/mL, respectively). Our study is the first to report hellbender AMPs with inhibition against *Bd* and that factors such as infection status and subspecies can affect peptide quality and risk for chytridiomycosis.

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

Mallory Harmel, Hayley Crowell and Emily Taylor

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

50 Shades of Clay: Rattlesnake Coloration Affects Detection by Predators

Crypsis, or the ability of an animal to avoid detection by other animals, is strongly related to the organism's coloration. Southern Pacific Rattlesnakes (*Crotalus oreganus helleri*) vary in coloration within and among populations, suggesting selection on coloration within specific habitats and environments. The purpose of this study was to investigate the effect of coloration on likelihood of being attacked by a predator, on latency to attack, and to observe where on the snake body predators tend to attack. Clay snake models representing four commonly observed color morphs of rattlesnakes (light, dark, intermediate color with white pattern, intermediate color with dark cream pattern) were placed in grassy and wooded habitats at a reserve in central coastal California, and marks made on the models by predators' teeth, beaks, and claws were quantified. We found that model type was a significant predictor of the overall number of attack marks, with dark colored snakes being attacked significantly more often than light-colored snakes. The latency to attack did not differ significantly among model types. Model type was related to where on the models the marks were made although the location of the marks on the models was not significantly different. Our data show that coloration can play a

large role in crypsis, and suggest that dark-colored rattlesnakes, which have the most contrast with the golden-colored grasses and therefore have the lowest crypsis, are most at risk from predation.

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

Richard Harrington[1], Thomas Near[1], Brant Faircloth[2] and Matt Friedman[3]

[1]Yale University, New Haven, CT, USA. [2]Louisiana State University, Baton Rouge, LA, USA. [3]University of Michigan, Ann Arbor, MI, USA

Swimming in Data: Addressing Pelagaria Relationships with Phylogenomic Datasets

Pelagaria is a clade of fishes that was discovered on the basis of molecular phylogenetic analyses. This group represents a largely pelagic, marine radiation of approximately 270 species classified in 16 families that previously had been hypothesized to belong to multiple percomorph suborders. Its members include the scombroids (e.g., tunas and mackerels,) and stromateoids (e.g., butterfishes and driftfishes), as well as Icosteidae (Ragfish), Chiasmodontidae (swallowers), Bramidae (pomfrets) and Caristiidae (manefishes). Pre-molecular, morphology-based hypotheses of intra- and inter-relationships of Pelagiaria groups were by no means settled, and increasingly larger and taxonomically more inclusive molecular datasets have yet to converge on well-supported topologies, with the exception of strong support for monophyly of the crown group. We gathered sequence data for more than 1,000 ultraconserved DNA elements (UCEs) in order to assess molecular support for relationships among the Pelagaria subclades, and to incorporate fossil information into a phylogenetic framework for analyses of diversification and patterns of morphological evolution. As in previous molecular phylogenetic analyses, we find support for an early, rapid radiation of major Pelagaria clades. Our analyses of UCE loci show strong support for some previous morphological hypotheses of relationships, but also reveal strong support for new relationships among major subclades, and some areas in the phylogeny that are characterized by high levels of incongruence among loci. These results provide directions for future efforts to investigate morphological and molecular data in order to resolve relationships among the subclades of Pelagaria.

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264 Herpetology Systematics, Highland B, Saturday 14 July 2018

Sean Harrington[1], Jordyn de Haan[2], Lindsey Shapiro[3] and Sara Ruane[4]

[1]University of Hawaii, Honolulu, HI, USA. [2]LSU, Baton Rouge, LA, USA. [3]Briarcliff High School, Briarcliff Manor, NY, USA. [4]Rutgers University, Newark, NJ, USA

Habits and characteristics of arboreal snakes worldwide: arboreality constrains body size and has complex effects on lineage diversification

Arboreal lifestyles represent common and major habitat shifts among snakes. Major habitat shifts are often facilitated by particular traits that confer advantages in the new environment. Although studies have examined the habits and characteristics of arboreal snakes at the level of

individual species or small clades, a broad survey has never been performed across all snakes. We surveyed the literature to identify all known arboreal snakes and summarize their general characteristics. We then tested for associations between diversification rates and arboreal habits and reconstructed ancestral states using the HiSSE approach. Finally, we tested for an association between body size and arboreality by fitting multi-peak OU models. We found that generally, arboreal snakes are most frequently nocturnal, oviparous, reptile eating, brown/banded/patterned snakes inhabiting the Neotropics (assessing each trait individually, not jointly). The effect that arboreality has on diversification depends on how data are coded, but when comparing primarily arboreal snakes to all others, we identified an increase in diversification rates associated with arboreality, consistent with previous findings. Our OU models showed that arboreal snakes tend to be larger than non-arboreal snakes, that rates of body size evolution are generally slower in arboreal snakes, and arboreal body sizes are pulled more strongly toward their optimum than in non-arboreal snakes. These results suggest that arboreal snake lineages may diversify more rapidly than non-arboreal lineages, even though morphological evolution is more constrained.

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271 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Highland D, Thursday 12 July 2018

Pamela Hart-Burress[1], Matthew Niemiller[2] and Prosanta Chakrabarty

[11]*Louisiana State University, Baton Rouge, LA, USA.* [2]*University of Alabama in Huntsville, Huntsville, AL, USA*

Phylogenomics of the Amblyopsidae (Percopsiformes)

Cave-obligate organisms long have captured the imagination and interest of scientists and the general public, yet their evolutionary histories and modes of subterranean adaptation are still poorly understood. The endemic North American Amblyopsidae fishes are one of very few families across the fish Tree of Life to contain both surface- and cave-dwelling members; thus, this group is ideal for comparative studies of cave adaptation. Morphological and molecular datasets have presented conflicting evolutionary relationships within the Amblyopsidae, particularly with respect to the placement of eyed species in relation to the blind, cave-obligate taxa. Molecular phylogenies indicate a possible subterranean ancestor for one eyed genus, suggesting the regeneration of eyes and re-invasion of surface habitat. Morphological topologies recover a continuum of forms, progressing from surface to cave without re-evolution. To further elucidate phylogenetic relationships within the Amblyopsidae, we collected genomic data from over 700 ultraconserved element (UCE) loci from 119 samples representing all described taxa as well as additional undescribed lineages. Each of the three states of troglomorphy (surface, cave-utilizing, and cave-obligate forms) was sampled for this study. This work will provide insight into the patterns and modes of cave adaptation.

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

Jordan Hartley and Dustin Siegel

Southeast Missouri State University, Cape Girardeau, MO, USA

Comparison of pelvic and genital kidney glomeruli in *Eurycea longicauda*

Salamanders possess kidneys with two distinct regions: a caudal pelvic part and cranial genital part. Nephrons of the pelvic region are only responsible for urine formation and transport. Nephrons of the genital region transport sperm from the testes to the Wolffian ducts. However, they possess all the same functional regions found in pelvic kidney nephrons that are involved with urine formation and transport; i.e., renal corpuscles, proximal tubules, distal tubules, and collecting ducts. Thus, past researchers hypothesized that nephrons of the genital kidneys possess dual function: sperm transport and urine formation/transport. However, this hypothesis has never been tested. Considering size of glomeruli is directly related to the total amount of blood plasma filtered into the Bowman's space, we tested the hypothesis that nephrons of the genital kidneys have reduced urine formation function by comparing glomeruli size between nephrons of the pelvic and genital kidney regions in *Eurycea longicauda* with general histological techniques. Glomeruli of the pelvic kidneys were significantly larger than those measured from the genital kidneys. Greatest cross sectional surface area of pelvic kidney glomeruli averaged 7,822.83 mm. Genital kidney glomeruli averaged 1,669.35 mm. In conclusion, although structurally similar at the histological level, it appears that nephrons of the genital kidneys have decreased urine formation function based on glomerular size comparison between pelvic and genital kidneys.

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

Malorie Hayes and Jonathan Armbruster

Auburn University, Auburn, Alabama, USA

A New Genus of Minnow in West Africa (Cypriniformes, Cyprinidae, Smiliogastrini)

The monophyletic *Enteromius jae* species group (*E. jae, E. condei, E. nounensis*, and *E. parajae*) is a group of African small barbs that represents a new genus that we will describe as *Baka*. *Baka* occurs in coastal rivers of Cameroon and Gabon as well as the Dja River (Congo River tributary). *Baka* can be separated from all other African small barbs based on the following combination of characters; from *Barboides* by having a pigmented pseudotympanum (vs. not pigmented with fat globules); from *Clypeobarbus* by lacking a cleithral mark and having lateral-line scales the same height as all other scales (vs. dark line present along the posterior edge of the pectoral girdle and a midlateral row of enlarged, pigmented scales); from *Enteromius* by having an incomplete lateral line, possessing a pseudotympanum, having reduced numbers circumorbital bones (vs. an often complete lateral line, no pseudotympanum, and a complete series of circumorbital bones); from *Pseudobarbus* by having eight dorsal fin rays (vs. seven dorsal fin rays); and from the cave barbs (*Caecobarbus* and *Barbopsis*) by fully developed eyes and pigment (vs. no eyes and lacking pigmentation). A molecular phylogeny is also presented demonstrating the placement of *Baka* in the context of *Enteromius* and other African taxa.

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

Kirsten Hecht[1,2], Katie Stofer[1] and Max Nickerson[2,1]

[1]University of Florida, Gainesville, FL, USA. [2]Florida Museum of Natural History, Gainesville, FL, USA

Public Engagement of Herpetologists: Attitudes and Scope

Scientists' public engagement (PE) is a popular topic in the greater science community due to general concerns about public scientific support, attitudes towards science, and changes in scientific funding requirements. Herpetofauna specifically stands to benefit from PE, as direct exposure can improve attitudes and conservation behavior of participants towards uncharismatic species. Despite potential advantages, little research has focused on herpetologists' PE. We plan to assess the current scope of herpetologists' PE activities, investigate factors associated with their participation in PE, and compare these factors with those in the broader scientific community. We expect that conservation-oriented herpetologists will share similar PE factors but will exhibit an additional factor related to their understanding of the public's role in conservation. Based on previous research, our theoretical framework will utilize an adapted version of the Theory of Planned Behavior, which states that an individual's attitudes about a behavior, social pressure to perform that behavior, and an individual's perceived control over that behavior, for example resources and ability, predict an individual's intention to participate in a behavior. We will conduct 25-minute semi-structured qualitative interviews with ~15 herpetologists expressing varying interest in PE. We will code and analyze transcripts using thematic analysis with expected and emergent codes. Results will be used to design a broader survey consisting primarily of closed-ended questions which will be distributed through herpetological organizations. Survey results will be analyzed with descriptive and inferential statistics. This study will help identify barriers to PE by herpetologists, ultimately improving conservation outcomes of herpetofauna.

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

Kirsten Hecht[1,2], Lori Williams[3], Stephen Nelson[4], Thomas Floyd[5], Shem Unger[6] and Jeremiah Cronin[2]

[1]University of Florida, Gainesville, FL, USA. [2]Florida Museum of Natural History, Gainesville, FL, USA. [3]North Carolina Wildlife Resources Commission, Fletcher, NC, USA. [4]Zoo Knoxville, Knoxville, TN, USA. [5]Georgia Department of Natural Resources, Forsyth, GA, USA. [6]Wingate University, Wingate, NC, USA

Common Mudpuppies (*Necturus maculosus*) Not Common in Southern Blue Ridge Streams.

While the Common Mudpuppy (*Necturus maculosus*) is considered common throughout most of its North American range there are relatively little data to support the claim, especially within Southern Appalachia. From 2000-2016, we sampled 163 streams in eastern Tennessee, northern Georgia, and western North Carolina using several methods to determine presence/absence of Common Mudpuppies in lotic systems as well as to collect information on basic life history traits and habitat use. During 5,697.5 survey hours and 2,998 trap nights, we located a total of 115 individuals (64 in TN, 51 in NC, and 0 in GA). While locally abundant in some drainages, *N. maculosus* was not detected in many waterways (especially in NC and GA), and we had low catch per unit effort (CPUE) and trapping success. Both immature and mature Mudpuppies were found, along with five nests. We had the most success using the snorkeling with rock turning method and found most animals under rocks in runs and pools. Overall our efforts demonstrate that *N. maculosus* is potentially not common in Southern Appalachia and further research on this species and its status is warranted. Specific research needs include, but are not limited to, continued distributional surveys, habitat use (specifically, micro-habitat and potential use impounded waters and deeper riverine pools), diet, density, and movement.

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

Brandon Hedrick[1], Samantha Cordero[2], Patrick O'Roark[2] and Edward Watt[2]

[1]Harvard University, Cambridge, MA, USA. [2]Hitchcock Center for the Environment, Amherst, MA, USA

How Did the Salamander Cross the Road? Improvements to Older Amphibian Culverts

Roads create barriers to wildlife migrations, leading to habitat segmentation and road mortality. Erecting barrier fences and wildlife tunnels has become a common way to address these problems. The first amphibian tunnels in the United States were installed in 1987 in Amherst, Massachusetts to aid in the annual migration of the spotted salamander, *Ambystoma maculatum*, across a busy road. The salamanders hibernate on the eastern side of the road and move to the marshy breeding area on the western side of the road in mass during rainy nights in early Spring. An initial assessment of the tunnels' functionality in 2016 suggested that only 11% of the salamanders were still using the tunnels successfully, while 45% were scaling the barrier fences and the remaining 44% were reaching the tunnels, but balking upon approach. We have designed a three-year study using these tunnels to determine if it is possible to retrofit older amphibian tunnels cheaply to increase salamander use without necessitating costly full-scale renovations. In 2017, we repaired the fencing and added a light to the far side of one of the tunnels to discourage balking (anecdotal evidence suggested that salamanders balked less when confronted with a light at the far side of the tunnel). Although fewer salamanders scaled the fencing, there was no significant difference in the percentage of salamanders that balked. For Soring 2018 we have constructed ramps leading down to the tunnels designed to raise the energetic cost of balking at tunnel entrances.

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

Matthew Heinicke[1], Luis Ceriaco[1], David Blackburn[2] and Aaron Bauer[3]

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

Evaluating Evidence for the Arid Corridor Hypothesis in Angola's Herpetofauna

The herpetofauna of Angola is unique in sub-Saharan Africa because it includes a complete faunal turnover from arid-adapted taxa in the south to tropical taxa in the north. Many of the "southern" taxa are more closely related to geographically distant species from East Africa rather than species from intervening parts of Central Africa. This pattern may have arisen from species dispersing across intermittent arid corridors across Central Africa beginning in the Miocene, or alternatively as a result of more circuitous connections among populations via southern Africa, where many of the same arid-adapted species also occur. Through recent field work in Angola, we have obtained genetic samples suitable for testing the viability of the arid corridor hypothesis in a number of widespread amphibian and reptile lineages. We performed phylogenetic and phylogeographic analyses for many of these widespread lineages including *Sclerophrys*, *Tomopterna*, *Acanthocercis*, *Agama*, *Boaedon*, *Chondrodactylus*, *Hemidactylus*, *Pachydacylus*, and *Trachylepis*. Our results suggest that arid-adapted taxa in Angola are typically, but not always, most closely related to congeners found further to the south and that the arid-adapted herpetofauna is dominated by taxa that colonized via a southern, not central, route.

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

Patricia Hernandez[1], Stephanie Keer[1], Catherine May[2], Sarah McMenamin[2] and Karly Cohen[1]

[1]George Washington University, Washington, DC, USA. [2]Boston College, Boston, MA, USA

Anatomical assessment of the adult skeleton of thyroid-ablated zebrafish, *Danio rerio*

Thyroid hormone is critical for the normal development and regulation of a variety of cellular and organismal processes, particularly those involving normal skeletogenesis. Mouse and rat models have been traditionally used to study thyroid hormone, but the fast generation time and ease of genomic manipulation of zebrafish makes them an excellent tool to investigate the effects of thyroid hormone disruption. Therefore, a thorough anatomical assessment of the differences in the adult hypo-, eu-, and hyperthyroid zebrafish is important for those who wish to use zebrafish as a model organism for thyroid research. We study the effects of thyroid alteration on skeletal development using both transgenic hypothyroid and mutant hyperthyroid lineages of *Danio rerio*. Our anatomical examination has shown that in hypothyroid zebrafish, developmental anomalies include the parietal and frontal bones failing to properly fuse, and the radials of the pectoral girdle undergoing improper ossification. In addition, hyperthyroid

zebrafish exhibit greatly enlarged neural spines, haemal spines, and dentaries. By thoroughly investigating and comparing the anatomy of hypo-, eu-, and hyperthyroid zebrafish, we are better able to understand the role of thyroid hormone in skeletal development in vertebrates in general.

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525 Herpetology Genetics I, Highland D, Sunday 15 July 2018

Obed Hernandez-Gomez[1], Steven Kimble[2], Jessica Hua[3], Vanessa Wuerthner[3], Devin Jones[4], Brian Mattes[5], Rickey Cothran[6], Rick Relyea[5] and Jason Hoverman[7]

[1]University of California, Berkeley, Berkeley, CA, USA. [2]Towson University, Towson, MD, USA. [3]Binghamton University, Binghamton, NY, USA. [4]University of South Florida, Tampa, FL, USA. [5]Rensselaer Polytechnic Institute, Troy, NY, USA. [6]Southwestern Oklahoma State University, Weatherford, OK, USA. [7]Purdue University, West Lafayette, IN, USA

Local adaptation of the MHC class IIβ gene influences the susceptibility to a common parasite in amphibians

The major histocompatibility (MHC) genes code for membrane-bound proteins that are involved in parasite/pathogen recognition. The link between the MHC and immunity makes these genes an important genetic marker to evaluate in systems where infectious disease is associated with population declines. Amphibians are an ideal model to test the role of the MHC in infectious disease resistance, as parasites and pathogens currently threaten populations worldwide. We evaluated the importance of the MHC in resistance to trematodes, a common amphibian parasite. We characterized the diversity of MHC class IIβ and 14 microsatellite loci, average trematode loads, and average tolerance to pesticides in 14 populations of wood frogs (*Lithobates sylvaticus*) in northwestern Pennsylvania. To explore local adaptation in the MHC IIB, we quantified genetic differentiation of MHC IIB and microsatellite markers (Fst). In addition, we evaluated the associations between MHC IIB diversity and trematode prevalence or tolerance to pesticides. Populations where individuals shared more alleles were associated with higher trematode loads than populations with an even distribution of alleles. This suggests that individuals possessing common MHC IIB alleles are more susceptible to trematode infection. In addition, we noted a positive association between MHC IIB diversity and tolerance to pesticides, suggesting that processes which influence the evolution of pesticide tolerance (e.g., proximity to anthropogenic environments) may similarly affect immune-related traits. As such, future research should investigate the mechanisms through which anthropogenic and natural factors shape the evolution of the MHC, such as the prevalence of other parasites in the environment.

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

Melanie Herrera[1,2], Antony Harold[1], Carly Gramling[1] and Madison Martin[1]

[1]College of Charleston, Charleston, SC, USA. [2]University of Maryland, College Park, MD, USA

Diversity and Abundance of Early Life History Stages of Fishes Associated with Algal Beds Dominated by *Gracilaria vermiculophylla*

Diversity and abundance of juvenile and sub-adult stages of estuarine fishes has been well studied overall, although that of earlier, post-metamorphic juveniles has not. Benthic microhabitats are thought to be important resources during early life history. These habitats in estuaries of the southeastern United States have become dominated by the invasive red alga *Gracilaria vermiculophylla*, with native species of algae reduced. In order to probe the effects of bottom coverage of benthic algae on diversity we compared two microhabitats that occur over sand/silt bottom in Charleston harbor, during June and July 2017: dense assemblages dominated by *G. vermiculophylla* (≥80% coverage) and sparse assemblages (≤20% coverage). A 15 foot long fine-meshed (1/16") beach seine was dragged along a transect 15 meters in length. All fishes captured were identified to the lowest taxonomic level possible and standard length recorded. A total of 3,305 fish specimens were caught, with 2944 (19 species total) of those from dense sites (top five in decreasing rank of abundance: *Menidia menidia, Anchoa mitchilli, Fundulus majalis, Syngnathus* sp., and *Bairdiella chrysoura*) and 361 (21 species) from sparse sites (decreasing rank: *A. mitchilli, Syngnathus* sp., *M. menidia, B. chrysoura*, and *Trachinotus carolinus*). Dense sites support much higher abundances in comparison to sparse but with much less living space available. It is yet to be determined whether the explanation for the high abundances in dense algal beds is related to structural complexity, abundance of food resources, predator avoidance, or some other factor.

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

Paul Hime[1,2], Shem Unger[3], Steven Price[2], Jeffrey Briggler[4], Lori Williams[5], Michael Freake[6], Andrea Drayer[2], Amy McMillan[7], Mary Foley[8,2], Emily McCallen[9], Dale McGinnity[10], John Groves[11], Emily Lemmon[12], Songlin Fei[9], Rod Williams[9] and David Weisrock[2]

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What the Hellbender?! Genomic Perspectives on the Evolutionary History of *Cryptobranchus*.

Identifying the demographic and historical forces which have shaped contemporary patterns of biodiversity is a primary aim of modern phylogeography. Central to these efforts, is the desire to objectively test hypotheses about lineage boundaries in dispersal-limited taxa. We investigate range-wide phylogenetic relationships and putative species boundaries in the imperiled North American hellbender salamander (genus *Cryptobranchus*), integrating comprehensive geographic sampling and dense sampling of the nuclear genome in a model-based statistical framework. Phylogenomic analyses of 194 individual hellbenders from 14 states have revealed extensive population genetic differentiation within and between major watersheds and suggest the presence of multiple, deeply divergent, reproductively isolated lineages of hellbenders. Our results suggest that *Cryptobranchus* contains as many as four cryptic lineages which are broadly

aligned with the major continental watersheds of eastern North America. Do these different lineages of hellbenders actually represent distinct species? We demonstrate that rates of effective gene flow between these lineages are up to four orders of magnitude lower than rates of gene flow within lineages, and that these putative species exhibit genealogical exclusivity across the genome. These findings have significant implications for delimiting species with genomic data, and imply that the current hypothesis of a single hellbender species may warrant reconsideration. This work also has applied conservation implications for hellbenders in that, regardless of the true number of hellbender species, given current trends, a model of zero *Cryptobranchus* species may be impossible to reject in the foreseeable future.

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

Amanda Hipps and Jon Moore

Florida Atlantic University Honors College, Jupiter, Florida, USA

Filling in the Data Gaps: The Vertebrate and Invertebrate Gopher Tortoise Burrow Commensals in Southeast Florida

The gopher tortoise, *Gopherus polyphemus*, is a keystone species that digs extensive burrows providing a novel microhabitat also used by over 360 other vertebrate and invertebrate species. Limited information is available regarding gopher tortoise burrow commensal species in southeast Florida, especially regarding invertebrates. This study investigates the gopher tortoise burrow commensals at six sites in subtropical southeast Florida, consisting of three pine flatwoods and three scrub habitats with varying degrees of habitat management. Vertebrate commensal species are identified using a burrow scoping system and game cameras. Several methods are being employed to collect invertebrate species to aid in their identification, consisting of insect pitfall traps, baiting with gopher tortoise feces, burrow facade traps, UV light, mesh tents, and active searching at burrow entrances. This project is ongoing and preliminary results will be presented. The objective of this research is to compile an account of vertebrate and invertebrate species dependent on gopher tortoise burrows in this region, accumulate information on threatened, endangered, and invasive species, add to the distributional information on obligate invertebrate species, and to present information to land managers concerned with maintaining biodiversity.

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

Matthew Holding[1,2], Darin Rokyta[1], Mark Margres[1] and Lisle Gibbs[2]

[1]Florida State University, Tallahassee, FL, USA. [2]Ohio State University, Columbus, OH, USA

Assessing biotic and abiotic drivers of venom divergence among populations of the Northern Pacific rattlesnake (*Crotalus oreganus*).

Identifying the biotic and abiotic correlates of population divergence in functional traits can provide insights into the evolutionary mechanisms that generate local adaptation among populations. Venom is used by snakes to capture prey, and shows significant divergence among populations of the same species in many taxa, yet the underlying causes of this general pattern remain unclear. Here, we assess patterns of population differentiation in venom protein expression in Northern Pacific rattlesnakes (*Crotalus oreganus*) from 13 locations across California. We then evaluate the relative importance of major biotic (prey species community composition), abiotic (temperature, precipitation, and elevation) and genetic (genetic distance based on RADseq loci) factors as correlates of population divergence in these venom phenotypes. Environmental and genetic data all explain a significant amount of population divergence in venom but vary in their relative importance. Surprisingly, genetic differentiation among populations was the best predictor of venom divergence accounting for 46% of overall variation, whereas differences in prey community composition and abiotic factors explained smaller amounts of variation (23% and 19%, respectively). The association between genetic differentiation and venom composition may reflect an isolation by environment effect where selection against recent migrants is strong, producing a correlation between neutral genetic differentiation and venom differentiation. Our analyses suggest that even coarse estimates of prey community composition can be useful in understanding the potential selection pressures acting on patterns of venom protein expression.

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194 General Herpetology I, Highland B, Sunday 15 July 2018

Iris Holmes, Daniel Rabosky and Alison Davis Rabosky

University of Michigan Museum of Zoology, Ann Arbor, MI, USA

Relationship of host genetic diversity to microbiome diversity in squamate reptiles

Gut microbiomes are critical to the survival of multicellular animals. They help the host digest their food, resist invading pathogens, and synthesize critical nutrients. The gut microbiome of snakes and lizards is little studied relative to other vertebrates, but the physiological flexibility of squamates (for example clonal lineages and multiple evolutions of viviparity, among others) makes them an intriguing potential study system for host-microbiome interactions. The gut microbiome interacts with the host primarily by communicating with the host immune system, although many other host metabolic processes are also involved. Correlative evidence suggests that more diverse gut microbiomes improve host health, although the mechanism behind this effect are not fully understood. The diversity of mammal gut microbiomes show a slight correlation with increasing host genetic diversity. Squamates have a greater range of heterozygosity levels than are displayed in mammals, including several clonal lineages that should have near zero between-individual heterozygosity. I present a study of a community of squamates that includes two clonal lizards and ten sexually reproducing species that cover a four-fold range of average heterozygosity. We find no consistent effect of host heterozygosity on gut microbiome diversity.

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

Chace Holzheuser[1], Bruce Means[2], Brooke Talley[3] and Karen Lips[1]

[1]University of Maryland, College Park, MD, USA. [2]Coastal Plains Institute, Tallahassee, FL, USA. [3]Florida Fish and Wildlife Conservation Commission, Tallahassee, FL, USA

Assessing Distribution and Abundance of the Southern Dusky Salamander (*Desmognathus auriculatus*) in Florida: Population Surveys, Habitat Analysis, and Disease Status.

Once considered an abundant salamander across its range in Georgia, Florida and Alabama, the Southern Dusky Salamander (*Desmognathus auriculatus*) cannot be found at many historic locations. In 2016 we calculated the historic distribution of this species in Florida from field notes and museum data, and conducted a statewide resurvey of historic localities to determine the current distribution, population abundances, and disease status. We swabbed 628 museum specimens and 50 wild caught individuals for amphibian chytrid (*Bd*), and analyzed historic versus current distribution with GIS. Analysis of capture effort at 7 sites in Florida between 1969-1977 shows a decline of 1.29 salamanders hr^{-1} yr^{-1} (p-value = 0.011), until reaching zero at all sites by 1977. From June 2016 – July 2017, we spent 155.75 hours searching 123 sites in 14 river basins. We encountered SDS in 7 sites (5.7%) within 3 habitat patches with a combined area of ~513 km^2, or <1% of its original distribution. Of the 50 field swabs we collected, 1 was *Bd*+ (2%; 95% CI: 0-11.47%). We tested 142 museum swabs of this species but found only 1 *Bd*+ (0.7% 95% Cl: 0-4.28%). We show that declines began by at least the 1960s, although we are unable to identify a cause. Identifying the extent of losses and current distribution is critical for informing state agencies, IUCN and ESA on the species conservation status. Determining the timing, locations and patterns of population declines can help identify potential causes and possible recovery and mitigation actions.

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344 SSAR SEIBERT CONSERVATION I, Highland B, Thursday 12 July 2018

Charlene Hopkins, Shawn Kuchta and Willem Roosenburg

Ohio University, Athens, Ohio, USA

How to Build a Better Ecopassage: Evaluating Amphibian Use and Preference of Various Ecopassage Designs

As roadways impact amphibian and reptile population sizes, disrupt connectivity, and degrade habitat, mitigation measures are increasingly being implemented. Barrier-ecopassage systems are a common strategy used to mitigate roadway impacts. Barriers limit access to roadways and may direct animals toward ecopassages, which are corridors designed to conduct animals safely over or under the roadway. We assessed use and preference of various ecopassage parameters by utilizing manipulative choice experiments and an observational choice experiment along a two-lane highway in southeastern Ohio. Using amphibians, and some reptiles, we tested preference for the aperture size of passages, levels of sky exposure in the passages, and

maintenance of ability to see across the passage. Testing animals throughout 2017, we found that amphibians prefer passages that are 100cm wide, provide 90% sky exposure, and maintain full sight across the passage. The results from the manipulative and observational experiments did not vary significantly, and our observational experiment was able to reduce mortality along the roadway stretch where it was in place. These findings have potential implications for the implementation of future barrier-ecopassage mitigation projects.

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

Gareth Hopkins[1,2], Susannah French[2] and Edmund D. Brodie, Jr.[2]

[1]University of Melbourne, Melbourne, VIC, Australia. [2]Utah State University, Logan, UT, USA

Interacting effects of salinity and temperature on amphibians: exploring the potential for adaptation in a changing world

To accurately predict the impact of environmental change, it is necessary to assay effects of key interacting stressors on vulnerable organisms such as amphibians, and the potential resiliency of their populations. Yet, for the most part, these critical data are missing. We examined the effects of two common abiotic stressors predicted to interact with climate change, salinity and temperature, on the embryonic survival and development of rough-skinned newts (*Taricha granulosa*) from populations differing in their history of exposure to these stressors. We found that salinity and temperature significantly interacted to affect newt embryonic survival and development, with the negative effects of salinity most pronounced at temperature extremes. We also found significant variation among, and especially within, populations, with different females varying in the performance of their eggs at different salinity–temperature combinations, possibly providing the raw material for future natural selection. Our results highlight the complex nature of predicting responses to climate change in space and time, and provide critical data towards that aim.

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278 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center; part of ASIH symposium: If Salamanders Could Speak, Saturday 14 July 2018

Gareth Hopkins[1], Jasmine Maftei-Muirson[2], Seamus Doherty[2], Gina Mincham[2] and Craig Williams[2]

[1]University of Melbourne, Melbourne, Victoria, Australia. [2]University of South Australia, Adelaide, South Australia, Australia

Amphibian adaptability to global environmental change: salinity tolerance in the common Australian froglet *Crinia signifera*

Ecosystem disturbance through urbanisation and agriculture, coupled with anthropogenic climate change, poses a pervasive threat to ecosystem health. On face value, increasing salinisation of both soils and waterways has the potential to render habitats unsuitable for amphibians. However, some species are known to exist in brackish and saline habitats, which suggests the capacity to adapt to salinisation. To assess this adaptability, we examined current brackish habitat utilisation by a common Australian froglet, *Crinia signifera*, and determined the tolerance of eggs and tadpoles of this species to acute and chronic exposure to brackish water. *C. signifera* were found to lay eggs in brackish water, and through laboratory experiments we determined that short term survival in water up to 7.5 ppt salinity is common. Chronic exposure experiments demonstrated that *C. signifera* can successfully complete larval development to metamorphosis in brackish water (up to 5.0 ppt) and that there is some initial evidence of growth and development trade-offs for salinity tolerance.

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

Christopher Howey[1] and Erika Snyder[2]

[1]University of Scranton, Scranton, PA, USA. [2]The Pennsylvania State University, University Park, PA, USA

Substrate type affects scent-trailing behavior of timber rattlesnakes

Animals can obtain social information from monitoring chemical cues within their environment left behind by conspecifics, competitors, predators, or prey. Whereas many studies have addressed the ability for snakes to trail scents within a laboratory along a homogenous substrate (butcher paper), our objective was to determine if the scent-trailing behavior of a snake was affected by changes in substrate type. We brought 5 gravid timber rattlesnakes (*Crotalus horridus*) into the laboratory where each gave birth to an average 9 neonates. After each neonate shed, we conducted Y-maze trials. For each trial, the Y-maze floor was covered in either paper, sand, leaf litter, or burnt leaf litter. The scent of the mother was applied down one arm of the Y-maze. Prior to each trial, we replaced the substrate and scent. Each neonate was tested on each substrate. Neonates non-randomly chose the arm with the mother's scent 87% of the time when tested on paper ($P < 0.001$) and 73% of the time when tested on sand ($P < 0.011$). When tested on leaf litter and burnt leaf litter, neonates chose the arm with the mother's scent 67% and 53% of the time ($P < 0.068$ and $P < 0.715$ respectively). Substrate affects the ability for neonates to scent trail their mother. In a natural setting, the rocky substrate coupled with leaf litter near den sites may facilitate this scent-trailing behavior. However, as prescribed fire becomes a more popular forest management tool, care should be taken in where this tool is applied.

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

Jessica Hua and George Meindl

Binghamton University, Binghamton, NY, USA

Effect of Different Cold-temperature Regimes on Compensatory Larval Growth, Development, and Susceptibility to Road Salt and Parasites in *Lithobates sylvaticus*.

Environmental conditions early in development can alter amphibian fitness or performance later in life. For example, during embryonic stages, early spring-breeding amphibians can be exposed to a diversity of cold-temperature regimes (pulse vs. press) that may differentially affect growth and development. Amphibians can counteract the negative effects of poor embryonic conditions by accelerating larval growth and development. However, these compensatory responses may lead to costs that hinder the ability for amphibians to respond to other stressors. We investigated how different embryonic thermal regimes affect compensatory larval growth and development and larval responses to contaminant and parasitic stressors. Towards this goal, we exposed *Lithobates sylvaticus* embryos to three thermal regimes: Control (20C), press-of-cold (4C), and pulses-of-cold (4C/20C). We then conducted three tolerance assays by exposing tadpoles from each thermal regime to NaCl (3d and 17d post-hatching) and an amphibian parasite (echinostomes-24d post hatching). We found: (1) No evidence of compensatory growth- tadpoles reared in 4C and 4C/20C were consistently smaller than tadpoles reared in 20C. (2) Evidence of compensatory development in tadpoles exposed to the 4C/20C treatment, but not in the 4C treatment. (3) Tadpoles reared in the 4C treatment were initially more susceptible to NaCl, but this effect disappeared by 17d. (4) The reduction in mass caused by the 4C and 4C/20C treatments indirectly facilitated tadpoles by making them less susceptible to parasites. These results demonstrate that variation in cold-temperature regimes can lead to unique direct and indirect effects on larval growth, development, and performance.

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

Sarah Huber[1], Katherine Maslenikov[2], Andrew Williston[3], Eric Hilton[1], Adam Summers[2] and David Blackburn[4]

[1]Virginia Institute of Marine Science, Gloucester Point, VA, USA. [2]University of Washington, Seattle, WA, USA. [3]Harvard University, Cambridge, MA, USA. [4]University of Florida, Gainesville, FL, USA

oVert Deep Dive: Ontogenetic Series of Fishes

The non-destructive nature of CT-scanning makes it appealing for studying ontogeny in groups for which early developmental material is rare, and it has been successfully used for studying the ontogeny of many vertebrates that have relatively gradual developmental shifts, including

mammals and birds. Many groups of vertebrates that have not been the focus of this type of imaging (e.g., fishes and amphibians) undergo major ontogenetic changes during development. For many taxa in these groups it is not possible to capture the morphological diversity of a particular species by scanning a single adult specimen. Within the framework of the oVert Thematic Collections Network, we will identify taxa, with input from the ichthyological community, for which it would be advantageous to CT larval or juvenile material to capture otherwise unobtainable anatomical data from rare specimens (legacy scans), to produce anatomical data for key taxa (basal ray-finned fishes) or to highlight the radical ontogenetic transformations that occur in fishes. We will leverage the excellent collections of marine and freshwater larval fishes at VIMS, UW and MCZ to provision the oVert database with ontogenetic data. Based on preliminary collection surveys, we have identified over 250 taxa for which ontogenetic material is available. Traditional CT scanning methods are sufficient for examining early development in highly ossified taxa, and we will explore contrast enhanced scanning for less ossified specimens. We expect that resulting scans will become a remarkable educational tool for showcasing the radical metamorphoses that occur in many vertebrates. Supported by NSF DBI-1701714.

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

Lily C. Hughes

George Washington University, Washington, DC, USA

Comprehensive phylogeny of ray-finned fishes (Actinopterygii) based on transcriptomic and genomic data

Our understanding of phylogenetic relationships among bony fishes—half of all living vertebrates— has been transformed by analysis of a small number of genes, calling into question many traditional groupings based on morphology, but uncertainty remains around critical nodes. Additionally, fish molecular phylogenies are particularly prone to biases due to undetected paralogy, given the history of whole-genome duplications at the base of the vertebrate and teleost fish radiations. We leveraged 144 genomes and 159 transcriptomes (130 newly sequenced) to investigate fish evolution with an unparalleled scale of data: >0.5 Mb from 1,105 exon sequences from 303 species, representing 66 out of 72 ray-finned fish orders. This set of exon markers was filtered against paralogy based on explicit tests to detectwhole-genome duplications among vertebrates, eliminating many loci initially identified as single-copy based on a few genomes. Our results further consolidated the backbone of the ray-finned fish phylogeny with genome-wide data, and gene genealogy interrogation settled some long-standing uncertainties, such as the branching order at the base of the teleosts, among early euteleosts, and the massive percomorph radiation in a hypothesis testing framework that accounts for gene tree error.

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485 ASIH STOYE GENERAL ICHTHYOLOGY I, Grand Lilac Ballroom South, Thursday 12 July 2018

Elizabeth Hunt[1], Stuart Willis[2], Kevin Conway[3] and David Portnoy[1]

[1]Texas A&M University - Corpus Christi, Corpus Christi, Texas, USA. [2]California Academy of Sciences, San Francisco, California, USA. [3]Texas A&M University, College Station, Texas, USA

Phylogenomics of pufferfish in the genus *Sphoeroides* (Tetraodontiformes, Tetraodontidae)

Species-level phylogenies are critical for studying mechanisms of diversification, but challenges to accurate inference abound, some of which can be addressed with genomic methods. While there have been previous investigations into the phylogenetic relationships of fishes in the family Tetraodontidae, a diverse group of derived percomorph fishes, there has yet to be an extensive investigation into the relationships within the genus *Sphoeroides*. The diversity of *Sphoeroides* is primarily within the western Atlantic and eastern Pacific in shallow waters, with the exception of *S. pachygaster* which is found circumglobally in deeper water of the continental shelf. In order to better understand mechanisms driving speciation in this group we generated data from ultraconserved DNA elements (UCE) using hybrid enrichment. We targeted 500 loci in order to assess the phylogenetic relationships among 13 of the 23 currently recognized species of *Sphoeroides*, with a special focus on putative sister species from the Gulf of Mexico that are distributed on either side of an apparent biogeographic break.

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

Nicholas A. Huron, S. Blair Hedges and Matthew R. Helmus

Temple University, Philadelphia, PA, USA

Extinctions Point to Different Levels of Morphological and Functional Role Diversity Loss in a Genus of Island Lizards

Functional diversity (FD) loss is a central concern under the current mass extinction. FD reflects unique roles species with different traits play in ecosystems. Because traits mediate ecological interactions, if organisms with uncommon traits go extinct, loss of unique interactions could follow. For example, large-bodied species are extinction-prone, and their loss catalyzes cascading effects on ecosystems. Here, we estimated past, present, and future FD loss for an imperiled Caribbean lizard clade, *Leiocephalus* (curly-tailed lizards). We first asked how *Leiocephalus* morphological FD evolved in the past. We measured external traits for extinct/extant species, constructed a phylogeny, and fit models of adaptive trait evolution to these data. Second, we estimated the change from past to present-day morphological FD and from present to future FD if all threatened species go extinct. Finally, we built an interaction database from mined literature and asked if unique interactions are lost due to extinction. All *Leiocephalus* are ground-foraging and xeric-adapted species, and morphological FD evolution was explained by weak

stabilizing selection toward a single adaptive optima. However, significant interspecific variation exists in morphological FD, and this diversity is being lost. Extinct species were larger than extant species, and if threatened species go extinct, ca. 53% more morphological FD will be lost, mostly on Hispaniola. By contrast, we estimate that few unique interactions will disappear. This discrepancy between morphological FD erosion with minimal loss of species interactions emphasizes the importance of evaluating biodiversity across several dimensions to prioritize conservation efforts and avoid irreversible changes to sensitive ecosystems.

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

Carl Hutter and Rafe Brown

University of Kansas, Lawrence, KS, USA

A new and freely available exome sequence capture probe set of 10,000 loci for all frogs

The widespread use of high-throughput sequencing technologies has led to new challenges for biodiversity researchers in designing projects and deciding which method to use to sequence reduced portions of the genome. Targeted sequence capture is one method shown to work well across divergent taxa at a lower cost; however, this requires a specifically designed probe set for the focal taxon, which is largely unavailable for frogs. Herein, we introduce and demonstrate the utility of a new and publicly available sequence capture probe set and data analysis pipeline for all frogs. We provide a modular, large, and flexible set of probes for ~13,000 loci that unifies all previous sequencing work on frogs by including legacy loci previously used in phylogenetic studies in frogs (e.g. Sanger Loci, AHE, UCEs). The probe set is designed to be modular, such that subset of the loci can be selected and used based on the type of research question and taxonomic scale being addressed. Finally, we evaluate our sequence capture results using multiple phylogenetic scales, evaluating the number of loci captured per taxa, the sensitivity and specificity of the sequence capture, assess percentage completeness across different values, and demonstrate the utility of exon and intron sequence across these phylogenetic scales.

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

Saidee Hyder[1], Jon Davenport[1] and Josh Ennen[2]

[1]Southeast Missouri State University, Cape Girardeau, Missouri, USA. [2]Tennessee Aquarium, Chattanooga, Tennessee, USA

Preliminary assessment of movement ecology in a West Tennessee population of Alligator Snapping Turtles (*Macrochelys temminckii*)

Alligator snapping turtles (*Macrochelys temminckii*) are experiencing population declines throughout their range; this decline is primarily due to habitat fragmentation and overexploitation. Currently, one of the only known populations in West Tennessee is being monitored in order to understand the habitat preferences and spatial use of *Macrochelys temminckii*. This population is composed of subadult turtles that were previously released and monitored as hatchlings. Currently, little data is available for the subadult life stage of *Macrochelys temminckii* in comparison to hatchling and adult life stages. We hypothesized that the home range size will have increased since estimates taken from hatchlings and that turtles will select warmer microhabitats with a high percentage of tree cover. Preliminary data shows that the mean home range size for this first field season is 0.38 +/- 0.16 hectares. The mean distance moved per day by a turtle is 2.37 +/- 0.85 meters with trends showing differences in microhabitat. There also appears to be a correlation between the distance moved and water temperatures, with longer distances and more movements associated with warmer water temperatures. Continued monitoring of the habitat preferences and spatial use of this population will aid in future reintroductions and management protocols within West Tennessee. This study will also provide updated data for the IUCN in a state with currently little information available on *Macrochelys temminckii*.

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

Atsushi Ishimatsu[1], Van Hieu[1] and Karen Martin[2]

[1]Nagasaki University, Nagasaki, Japan. [2]Pepperdine University, Malibu, CA, USA

Patterns of Fish Reproduction at the Air-Water Interface

Although fishes by nature are aquatic, many species expose their embryos to air during incubation. We examine the ecological context of reproduction by fishes at the air-water interface, whether or not the adults breathe air. Seven modes are described, with examples from taxa of teleost and primitive species from fresh water, estuaries and sea water. Mode 1 is the most common type of reproduction by fishes at the air-water interface, marine teleosts that spawn in water onto a substrate surface, on vegetation, or other objects that will later be exposed to air tidally. In Mode 2, some fishes emerge from water to oviposit beneath a substrate or on vegetation above the water line. Mode 3 is annual fishes that bury eggs in temporary pools that evaporate seasonally. Mode 4 fishes spawn buoyant eggs on a water surface surrounded by vegetation. Mode 5 fishes construct foam nests on hypoxic water. Mode 6 mudskippers excavate burrows and store air in a subterranean chamber. Mode 7 combines Modes 5 and 6, placing demersal eggs on foams inside a nesting burrow. The widespread, variable nature of fish reproduction at the air-water interface across a broad taxonomic spectrum indicates repeated independent evolutionary events and strong selection pressure for fishes to protect their propagules from hypoxic waters or aquatic predators. Air-breathing by adult fishes appears to be de-coupled from air exposure of developing embryos, and no primitive fishes are known to place their propagules where they will be exposed to air.

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

Kathleen Ivey and Emily Taylor

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

Turn Up The Heat: Thermal Ecology of the Endangered Blunt-nosed Leopard Lizard (*Gambelia sila*)

Recognizing how climate change will impact populations can aid researchers and managers in making decisions about how they will approach conservation of endangered species. By projecting how the accelerated rate of anthropogenic climate change will interact with a species' thermal ecology, we can predict the likelihood of extirpation of endangered populations and identify methods for mitigating the effects of climate change. The Blunt-nosed Leopard Lizard (*Gambelia sila*) is a federally endangered lizard found in the arid grasslands of the San Joaquin Valley and Carrizo Plain. It has been extirpated from most of its range due to habitat destruction and alteration. We collected data on the field-active body temperatures of *G. sila*, combined with operative temperatures, preferred body temperatures, and thermal tolerance data for the population, that allows us to (1) calculate the number of hours that lizards are currently thermally constrained, (2) project how this number will change in the future as ambient temperatures rise, and (3) assess the importance of shade-providing shrubs in the current and projected future thermal ecology of *G. sila*. I will be presenting preliminary data on the thermal ecology of the blunt-nosed leopard lizard.

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

Carl Jacobsen[1], William Flint[2] and Donald Brown[1]

[1]West Virginia University, Morgantown, WV, USA. [2]James Madison University, Harrisonburg, VA, USA

Projected Current and Future Habitat for the Cow Knob Salamander (*Plethodon punctatus*).

The Cow Knob Salamander (*Plethodon punctatus*) has a narrow distribution at the high elevations of Shenandoah and Great North Mountain. Given their small distribution and specialized habitat requirements, *P. punctatus* is considered a species of special concern in both Virginia and West Virginia. Previous studies have predicted that the climatic niche for this species will be eliminated by 2050 due to climate change. We sought to expand on these studies by using a species-specific approach and a robust occurrence data set to identify habitat variables that are the strongest predictors of the environmental niche for *P. punctatus*.

Additionally, we created a habitat suitability model that can be used to facilitate the discovery of new populations. We used a maximum likelihood approach (package maxlike) to model the structural and climatic niche for this species. We explored the effects of climate change using an ensemble of 37 global climate models produced for the IPCC 5th assessment report and statistically downscaled using SimClim. Our results indicate that elevation, aspect, and hill shade are the best predictors for structural niche, while mean annual temperature and mean precipitation in the warmest quarter are the best predictors of climatic niche. Further, our climatic niche model predicts a drastic reduction in suitable habitat for this species by 2050 due to warmer annual temperatures.

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584 ASIH STOYE GENERAL ICHTHYOLOGY IV, Highland E., Friday 13 July 2018

Francesco Janzen[1], William Crampton[2], Mark Sabaj-Pérez[3], Javier Maldonado-Ocampo[4] and Nathan Lovejoy[5]

[1]University of Ottawa, Ottawa, Ontario, Canada. [2]University of Central Florida, Orlando, Florida, USA. [3]The Academy of Natural Sciences of Drexel University, Philadelphia, Pennsylvania, USA. [4]Pontificia Universidad Javeriana, Bogotá, Capital District Cundinamarca, Colombia. [5]University of Toronto Scarborough, Toronto, Ontario, Canada

Molecular Phylogeny of the Weakly-electric Knifefishes of Central and South America (Gymnotiformes, Actinopterygii)

The Neotropical knifefish order Gymnotiformes, comprises 200+ species divided into five families. These fishes have a distribution that includes Central and South America, and inhabit a variety of freshwater habitats. Gymnotiforms are capable of producing and detecting species-specific electrical signals using specialized electric organs and electroreceptors. For these reasons, knifefishes are excellent models for studying biogeography, speciation, and the evolution of communication. However, these studies rely on a clear understanding of gymnotiform phylogeny. To date, attempts at resolving the internal relationships of the Gymnotiformes have yet to produce an unambiguous, well-supported species-level phylogeny. In order to resolve the phylogeny of Gymnotiformes, we used 197 species representatives from nearly all recognized clades and combined molecular data for seven nuclear and two mitochondrial genes. We performed maximum likelihood and Bayesian analyses to produce phylogenies of the order. We found support for the monophyly of all families within Gymnotiformes. Of note was the prevalence of paraphyly and polyphyly of the genera and recognized major clades found within the Apteronotidae. *Sternarchogiton* is polyphyletic as *Sternarchogiton preto* is sister to all other species of Navajini. *Porotergus* and *Apteronotus* are also polyphyletic, indicating a need for some *Apteronotus* species to be reclassified as *Porotergus*. The genera *Sternarchorhynchus* and *Adontosternarchus* were strongly supported as monophyletic. We propose two new major clades within Apteronotidae based on our results: a Leptorhynchini clade containing *Apteronotus leptorhynchus* and close relatives, and a *Platyurosternarchus* clade. Our study provides a robust phylogenetic framework for future evolutionary and ecological investigations of gymnotiform fishes.

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

Rebecca Jasulevicz and Aaron Bauer

Villanova University, Villanova, PA, USA

A Bolder Shoulder: Pectoral Girdle Morphology in Geckos

Geckos utilize a variety of substrates and have developed morphological adaptations to facilitate effective locomotion across them. Morphology of the pectoral girdle reflects these adaptations. The pectoral girdle articulates the forelimbs with the axial skeleton, plays a role in defining locomotor capabilities, and provides attachment points for musculature associated with locomotion, ventilation, and feeding. Micro-CT data was used to assess morphological variations in the pectoral girdles of arboreal, terrestrial, and rock-dwelling gecko species across the six limbed families within Gekkota. Reduced interclavicles are more common in arboreal geckos, whereas terrestrial and rock-dwelling geckos more often possess wider transverse processes on these elements. The scapulocoracoid complex is variable across the families, but distal ossification of the epicoracoid is more often seen in arboreal species, and the suprascapula is more heavily ossified in terrestrial and rock-dwelling species. The shape of the clavicles is also highly variable, although with some evidence of phylogenetic signal.

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

Kyle Jaynes[1], David Blackburn[2], Raffael Ernst[3], Matthew Fujita[4], Eli Greenbaum[5], Vaclav Gvozdik[6], Greg Jongsma[2], Adam Leaché[7], Patrick McLaughlin[8], Daniel Portik[9], Mark-Oliver Rödel[10], Bryan Stuart[11], Ange Ghislain Zassi-Boulou[12] and Rayna Bell[1]

[1]National Museum of Natural History, Smithsonian Institution, Washington, D.C., USA. [2]University of Florida, Gainesville, Florida, USA. [3]Senckenberg Natural History Collections, Dresden, Germany. [4]University of Texas at Arlington, Arlington, Texas, USA. [5]University of Texas at El Paso, El Paso, Texas, USA. [6]Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, Czech Republic. [7]University of Washington, Seattle, Washington, USA. [8]Drexel University, Philadelphia, Pennsylvania, USA. [9]University of Arizona, Tucson, Arizona, USA. [10]Museum für Naturkunde Berlin, Berlin, Germany. [11]North Carolina Museum of Natural Sciences, Raleigh, North Carolina, USA. [12]Institut National de Recherche en Sciences Exactes et Naturelles, Brazzaville, Congo

Diversification of Giant Treefrogs (Arthroleptidae: *Leptopelis*) in West and Central Africa

The Guineo-Congolian rainforests of West and Central Africa and the Gulf of Guinea Archipelago host immense biodiversity. Previous research has revealed important insights into the biogeography of this biodiversity hotspot; yet our incomplete understanding of phylogenetic relationships for most taxonomic groups in this region has hindered our understanding of the speciation mechanisms that fostered this diversity. The genus *Leptopelis* is a radiation of Afrobatrachian treefrogs that have a complicated taxonomic history and reputation for their elusive phylogeny. Three species of "giant" treefrogs in the genus form a species complex distributed across West (*L. macrotis*) and Central (*L. millsoni* and *L. rufus*) Africa, as well as on the land-bridge island Bioko (*L. rufus*). Here, we combine phylogeographic and morphological datasets to assess patterns of genetic structure and morphological divergence in the *Leptopelis* species complex across the Guineo-Congolian rainforests. To assess phylogeographic structure in the species complex we collected mitochondrial sequence (*16s*) and genome-wide SNP (ddRADseq) data from more than 160 specimens across 34 localities. To characterize morphological divergence among these closely related species, we collected 14 standardized measurements from over 90 museum specimens. We recovered pronounced genetic structure across the species complex corresponding to Upper Guinean, Lower Guinean, and Bioko Island lineages. Our morphological analyses revealed phenotypic divergence among these lineages, including differentiation in tympanum size. Our work resolves long-standing taxonomic issues in this group and sets the stage for future work investigating population divergence and speciation in this charismatic group of frogs.

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179 Herpetology Physiology, Highland C, Saturday 14 July 2018

Benjamin Johnson, Jeremy Searle and Jed Sparks

Cornell University, Ithaca, NY, USA

Morphological Drivers of Physiological Performance in Lungless Salamanders

Water balance is the dominant constraint on amphibian life histories. Understanding how amphibians resist water loss thus offers mechanistic insight into critical water balance adaptation. Water balance is highly constrained in the Plethodontidae, whose obligate cutaneous respiration mandates that the skin remain moist and permeable at all times to maintain gas exchange. In this group, water transport performance is driven by considerable variation in performance-related morphology: Cutaneous gas and water conductance is determined by diffusive surface area relative to body volume (determined by body size and shape) and barrier thickness (determined by cell size and arrangement within the dermis), each subject to selection independently. Here we examine how variation in these traits impacts physiological performance under different environmental conditions. We measured cutaneous respiration and water transport in nine species of *Plethodon* and *Eurycea* at four temperature x humidity treatments, coupled with morphological measurements for body mass, volume, genome size, cell size, and skin thickness. We used trait probability densities and a mixed modeling framework to assess the influence of whole-organism, integument, and cell-level morphology on individual and species-level physiological performance. Preliminary results indicate strong effects of body size on both respiration and water transport, with effects of genome size dependent on environmental conditions. These results demonstrate how different morphological means interact with environmental conditions to meet a common functional performance end.

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

Kendall Johnson[1], Chenhong Li[2], Luke Tornabene[3] and Frank Pezold[1]

[1]Texas A&M University - Corpus Christi, Corpus Christi, TX, USA. [2]Shanghai Ocean University, Shanghai, China. [3]University of Washington, Seattle, WA, USA

Finding Evolutionary Links and Genes in Adaptive Radiations of Reef Gobies (Gobiidae) by Targeted Gene Capture

Gobies (Gobiidae+Oxudercidae) are one of the most diverse and complicated groups of teleosts. Phylogenetic studies of gobies using traditional genetic markers or morphology have revealed a deep divide between saltwater, reef-dwelling gobies (Gobiidae) and freshwater or brackish gobies (Oxudercidae), but have not yet been able to resolve many intergeneric relationships within the Gobiidae. The lack of resolution is due to an early period of rapid diversification, which led to the evolution of a remarkable variety of ecologies and morphologies. This diversity makes them ideal subjects for the study of many topics of ecology and evolution, including the evolution of behavior and life history traits, ecological and morphological adaptation, and species diversification. The phylogenetic structure of the gobiids must be resolved to investigate the mechanisms behind such events, and a new gene-capture method can accomplish this. By examination of a suite of functional, protein-coding genes across a broad range of taxa both the evolutionary links among rapidly evolved taxa and the gene suites responsible for adaptations in gobiids will be determined. A high number of markers shall resolve the dense phylogenetic relationships, while the use of functional genes allows the investigation of signatures of selection in genes potentially associated with physiological and morphological adaptations. The ability to combine the identification of loci under selection with the resolution of difficult relationships via gene capture offers unprecedented opportunity understand of adaptive radiations and speciation in general.

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653 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Kiyomi Johnson, Marina Carbi and Edward Myers

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

Speciation and Phylogeography of *Anolis opalinus* on Jamaica

Anole lizards are common through the Caribbean and Neotropics and have been well studied because they represent a textbook case of adaptive radiation. However, even in well studied groups, like anoles, there are undescribed species. *Anolis opalinus* is widely distributed across the island of Jamaica and previous work on the systematics of the *grahami* series of *Anolis* lizards suggests that this species is non-monophyletic in a mtDNA gene tree. Here we generate a multi-locus phylogeographic data set for *A. opalinus* to test for cryptic speciation between these divergent mtDNA clades. With this multi-locus data set we also reassess the relationships of the Jamaican anole lizards and estimate divergence times among these species.

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118 Herpetology Morphology II, Highland D, Sunday 15 July 2018

Hugo Juarez and Domenic D'Amore

Daemen College, Amherst, NY, USA

Tooth morphology and function in the snake tribe Thamnophinii.

Although diet is well understood in numerous species of snakes, there have been very few studies that quantify snake tooth morphology to correlate with diet. Teeth from snakes belonging to the tribe Thamnophinii were surveyed from dry skeletons in the American Museum of Natural History. The goal of the study was to determine if tooth size and shape correlates with diet. 956 maxillary and dentary teeth from dry skeletons of 16 specimens were photographed from the labial perspective. The margins of the teeth were outlined using TpsDig2.6, and converted into equidistant semilandmarks. A generalized least squares Procrustes superimposition was carried out, and centroid size was calculated. Dietary data was taken from existing literature. Discriminant function showed maxillary teeth to be generally more distally curved than dentary, which may correlate to inertial feeding methods unique to snakes. Most snakes species had significantly different Procrustes shape distances from one another, with dentary teeth separating more than maxillary. Canonical variants showed the majority of shape variance represented how narrow/wide the tooth was. Several species, including *Clonophis kirtlandii* and *Regina alleni*, had smaller-sized, wide teeth, which may correlate to a diet relying heavily on aquatic crustaceans. *Storeria dekayi* and *Thamnophis melanogaster* prey preferentially on soft-bodied invertebrates, and have average-to-large sized, thin teeth that do not taper. This condition was shared with larger generalists such as *Thamnophis sirtalis* and *Natrix natrix*. Future work will investigate the degree of heterodonty in these species, as well as the influence of allometry on tooth form.

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

James Julian[1], Gavin Glenney[2] and Jerod Skebo[3]

[1]Pennsylvania State University, Altoona College, Julian, Pennsylvania, USA. [2]Northeast Fisheries Center, U.S. Fish and Wildlife Service, Lamar, Pennsylvania, USA. [3]Pennsylvania State University, State College, Pennsylvania, USA

Disease Outbreaks in Wood Frog (*Lithobates sylvaticus*) Populations and the use of

Environmental DNA to Detect Pathogens

High conservation value is often placed on diverse amphibian communities, but these assemblages can be at high risk for the occurrence of pathogens, and the outbreak of disease. Since 2014, we conducted amphibian inventories at breeding ponds in Stone Valley Forest (Petersberg, PA), as well as pathogen screenings using larval swab samples, larval tissue samples, and environmental DNA (eDNA) samples. Swab sampling suggests that each additional species within a pond nearly doubles the probability that wood frog (*Lithobates sylvaticus*) populations will be infected with the chytrid fungus *Batrachochytrium dendrobatidis* (*Bd*). Furthermore, the presence of green frogs (*Lithobates clamitans melanota*), red-spotted newts (*Notophthalamus viridescens viridescens*), and spring peepers (*Pseudacris crucifer*) were positively associated with *Bd* presence. In 2015, populations of wood frogs experienced mass mortality events associated with *Ranavirus* sp. outbreaks. These outbreaks were weakly associated with amphibian species richness, and outbreaks re-occurred at a subset of these ponds in 2017. In 2017, filtered water samples were taken from all wood frog populations to screen for the eDNA of pathogens. We will discuss pathogen screening results which compare investigator vs volunteer-collected eDNA samples, as well as *Ranavirus* detection before, concurrent with, and several weeks after the mortality events of 2017.

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

Allison Julien, Andrew Kouba, Scott Willard and Carrie Vance

Mississippi State University, Starkville, MS, USA

Efficacy of Administrating Luteinizing Hormone Releasing Hormone Analog (LHRHa) Nasally to Elicit Sperm Production in Fowler's Toads (*Anaxyrus fowleri)*

Declining amphibian populations around the world necessitate the need for artificial reproductive techniques, such as exogenous hormone therapy. Methods of hormone administration involve intraperitoneal injections, which can be considered invasive and potentially stressful. The purpose of this study was to determine the efficacy of administering a luteinizing hormone releasing hormone analog (LHRHa) intranasally to decrease potential stress yet maintain sperm production. Male *Anaxyrus fowleri* (n=15/trt) were nasally given 5 different hormone treatments (control, 1µg, 5µg, 10µg, and 20µg LHRHa) and subsequently assessed for sperm production. Spermic urine was collected from animals over an 8-hour period and evaluated for spermiation latency, sperm motility, and concentration. Nasal administration of LHRHa resulted in spermiation in 60%, 93%, and 80% of males in 5µg, 10µg, and 20µg treatments, respectively. Treatments of 1µg of LHRHa and the control did not elicit sperm production. On average, 5µg treatments of LHRHa resulted in spermiation within 2.3 hours, while 10µg and 20µg treatments of LHRHa resulted in spermiation within 2.8 hours and 1.5 hours, respectively. Sperm motilities averaged 70%, 63%, and 52% across the 5µg, 10µg, and 20µg treatment groups. The highest sperm motility resulted from the 5µg treatment. Moreover, males administered 10µg of LHRHa produced significantly higher sperm concentrations than males administered 5µg or 20µg of LHRHa. We found that nasal administration of small volumes of LHRHa provides a successful, minimally-invasive method for sperm production, which could be utilized by captive breeding programs for threatened species of anurans.

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

Carrie Vance[1], Kristen Counsell[1], Allison Julien[1], Andrew Kouba[1] and Ruth Marcec[2,1]

[1]Mississippi State University, Mississippi State, MS, USA. [2]Detroit Zoological Society, Royal Oak, MI, USA

ART in Action: F2 Embryos from an F1 Female Tiger Salamander (*Ambystoma tigrinum*) Produced by Cryopreserved Sperm and Hormone Therapy

Artificial Reproductive Technologies (ART) have been implemented in various amphibian species as a means to promote reproductive output and genetic diversity in efforts to stabilize captive and wild populations threatened with extinction. In caudates ART is well behind development of that in anurans, but successful efforts in model species such as the tiger salamander (*Ambystoma tigrinum*) have advanced recently and include hormone therapy, in-vitro fertilization (IVF) and sperm cryopreservation (Marcec, Ph.D. Dissertation, MSU). In 2015, male and female *A. tigrinum* were treated with human chorionic gonadotropin (hCG) and luteinizing hormone releasing hormone analog (LHRHa) for gamete development and release. Sperm from milt was frozen in 5% DMSO+0.05% BSA and thawed for IVF, yielding hatched F1 offspring (n=21). In 2018, a 3-year old F1 female, originally produced from frozen-thawed sperm, was analyzed using ultrasound (US) for oocyte development, and was treated with hormone therapy. Two males examined with US for testicular development were hormonally treated to obtain sperm. The F1 female produced viable eggs (n=45) upon manual expression which were subject to IVF (100µl 5.5×10^6 sperm/ml, 61% live sperm, 55% forward-motion). Fertilization, cleavage and early embryonic development of the F2 generation to blastula stage was achieved (n=8/45; 18%). Additionally, the F1 female laid 550 eggs overnight without a male present. The same sperm sample yielded blastula stage embryos (n=74/174; 42%) from an F0 female. We demonstrate that F1 generation females from frozen sperm can produce viable gametes for an F2 generation.

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

Michael Jungen[1], Shane Welch[1], John Holloway[2], Ernie Wiggers[3] and Jayme Waldron[1]

[1]Marshall University, Huntington, West Virginia, USA. [2]Marine Recruit Depot, Parris Island, South Carolina, USA. [3]Nemours Wildlife Foundation, Yemassee, South Carolina, USA

Long-distance Translocation of Eastern Diamondback Rattlesnakes (*Crotalus adamanteus*)

The eastern diamondback rattlesnake (*Crotalus adamanteus*; EDB) is a long-lived, large-bodied pit viper endemic to southeastern pine savannas and woodlands. The EDB is declining, and conservation efforts, including long-distance translocation, are being undertaken to aid in the species' recovery. Long-distance translocation to re-establish or supplement populations of viperids has yielded mixed results, with survival averaging less than 50%. We translocated

EDBs (N = 21) from a sea island population to a pine savanna restoration area located on private property in South Carolina, 2016-2017, and estimated post-translocation survival probability. We ran various known-fate models in MARK to analyze covariates affecting survival probability. Our top model had time since egress as the most important survival covariate, and survival averaged 48%. This study will further our understanding of the efficacy of translocation as a conservation tool for EDB restoration.

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67 Herpetology Morphology II, Highland D, Sunday 15 July 2018

Derek Jurestovsky and Henry Astley

University of Akron, Akron, OH, USA

Effects of the Zygosphene/Zygantrum Joint on the Range of Motion in Snake Vertebrae

Joint articulations can limit range of motion (ROM) and stabilize movement. Snakes have a relatively unique zygosphene/zygantrum joint in their vertebrae (either reduced or absent in all other vertebrates), but the role of this joint is poorly understood, with the majority of studies focusing on taxonomic identification within snakes. To experimentally determine the role of the zygosphene/zygrantrum in the range of motion in snake vertebrae, two sequential mid-body vertebrae of a corn snake (*Pantherophis guttatus*) were CT-scanned, segmented out, and 3D printed (14x size). Motion capture cameras were used to record the angular ROM in yaw (lateral bending), pitch (dorsoventral bending), and roll (axial torsion) as the joint was manually manipulated. Two copies of the posterior vertebrae were printed, one unaltered and one with the zygosphene digitally removed. Preliminary results show substantial differences in ROM in yaw and roll. Yaw ROM in the unaltered vertebra was +- 20 degrees vs +-30 degrees without the zygosphene, while dorsal pitch ROM was unaffected. In the unaltered vertebra, roll ROM was only 3 degrees for all combinations of pitch and yaw, whereas in the altered vertebra roll ROM was unconstrained at yaw angles where the pre- and post-zygapophyses were no longer articulated. The zygosphene limits vertebral ROM in snakes, particularly the vertebral roll ROM at high yaw angles. The zygosphene-zygantrum joint may allow snakes a greater range of motion without being constrained by the need to maintain pre- and postzygapophysal articulation.

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

Nancy Karraker[1], Mirza Kusrini[2], Ryan Healey[1] and Jessica Atutubo[1]

[1]*University of Rhode Island, Kingston, RI, USA.* [2]*Agricultural Institute of Bogor, Bogor, Indonesia*

Population Demography of Southeast Asian Box Turtles (*Cuora amboinensis*) in

Protected and Disturbed Habitats in Indonesia

The Southeast Asian box turtle (*Cuora amboinensis*) is considered the most heavily traded turtle in the world and is numerically the most important turtle exported from Indonesia. Targeted for food and traditional medicine trades largely in China and pet trade in the U.S. and Europe, as with many other turtles, delayed sexual maturity and small clutch sizes limit the capacity of populations to recover from impacts. Using mark-recapture methods, we compared abundance and demography of two protected populations (forested swamp and savanna ponds) inside a national park and two disturbed populations (fish aquaculture ponds and dam-created wetlands) outside the national park in Sulawesi, Indonesia. Turtle densities were >3x higher in forested swamp and >10x higher in savanna ponds in the national park than in the dam-influenced wetlands outside of the national park. No turtles were captured in the fish aquaculture ponds. Sex ratio (M:F) was close to 1:1 in savanna ponds in the national park, and was nearly 2:1 in forested swamp in the national park and in dam-influenced wetlands outside of the park. Juveniles made up about 40% of each population in the national park, and about 70% of the population outside of the park. Mean carapace length of adults was about 10% smaller in turtles outside of the park. Informal discussions with local fishermen suggest there is currently little harvesting of *C. amboinensis*, but land use change from forested swamp and savanna to rice paddy and other agricultural/aquacultural production appears to be impacting turtle populations.

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177 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Jerry Kattawar and Kyle Piller

Southeastern Louisiana University, Hammond, LA, USA

Comparative population genetics of the Relict Darter and Guardian Darter in western Kentucky.

The Relict Darter, *Etheostoma chienense*, is endemic to the Bayou du Chien drainage of western Kentucky. It is listed as a federally endangered species due to its limited distribution, and lack of suitable spawning habitat, as well as habitat fragmentation and historically poor land-use practices. A previous five year status review suggested that information on the levels of genetic exchange among populations within the basin was needed. Therefore, this study was undertaken to gather this relevant information. We obtained tissue samples from multiple populations of the Relict Darter from the Bayou du Chien drainage, as well as samples from another closely related congener, the Guardian Darter (*Etheostoma oophylax*) from the Clarks River. Examining genetic variation in a comparative context will give us insight on how to properly manage and protect this species. We amplified a fragment from the mitochrondrially encoded cytochrome b gene and developed haplotype networks to compare genetic diversity within each species. Results suggest that there is a greater amount of genetic variation (168 individuals, 10 haplotypes) in the Guardian Darter in comparison to the Relict Darter population (149 individuals, 3 haplotypes). The conservation implications of these results will be discussed.

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

Shannon Keating[1], Aaron Griffing[1], Stuart Nielsen[1], Daniel Scantlebury[2] and Tony Gamble[1]

[1]Marquette University, Milwaukee, Wisconsin, USA. [2]Washington, DC, USA

Identification of ZZ/ZW Sex Chromosomes in two *Aristelliger G*eckos.

Sex determination in vertebrates is accomplished by two different mechanisms: environmental sex determination where sex is determined by an environmental factor during embryogenesis, or genetic sex determination (GSD) in which the sex chromosome complement controls an organism's sex with either XX/XY or ZZ/ZW sex chromosomes. Squamates (lizards and snakes), and geckos in particular, exhibit all of these. Both forms of GSD, male heterogametic XY and female heterogametic ZW systems, have evolved multiple independent times in geckos. This makes geckos an ideal system to study sex chromosome evolution, and new studies often reveal novel GSD turnover events. *Aristelliger expectatus*, a sphaerodactylid gecko, has previously been shown to have ZZ/ZW sex chromosomes. Here, we examined the sex chromosome of two additional *Aristelliger* species, *A. lar* and *A. praesignis*, to test for sex chromosome conservation within the genus. RADseq was used to identify female-specific markers in *A. lar* and *A. praesignis,* confirming that all three studied *Aristelliger* species have a ZZ/ZW system. These new results suggest conservation of a ZZ/ZW sex chromosome system across the *Aristelliger* genus, which can further our understanding of sex chromosome evolution in geckos.

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158 Herpetology Morphology I, Highland D, Sunday 15 July 2018

Rachel Keeffe and David Blackburn

University of Florida, Gainesville, FL, USA

Comparative Morphology of the Forelimb and Pectoral Girdle in Forward-Burrowing Frogs

Anuran locomotor strategies are diverse and include saltation, swimming, walking, climbing, and burrowing. Burrowing has many benefits for frogs: predator avoidance, exploitation of novel food stores, and (especially for desert-dwelling frogs) access to a moist and cool environment. This behavioral strategy is widely convergent across the anuran tree—from basal groups like Rhinophrynidae to higher groups like Hemisotidae. Within burrowing frogs, there are two main burrowing strategies: head-first burrowing and feet-first burrowing. The majority (95%) of burrowing anurans dig feet-first, such as *Scaphiopus*, *Breviceps*, and *Pelobates*. While front-first burrowing is less common, it has evolved independently at least seven times across Anura. These forward-burrowers tend to be more specialized for life underground. Some of their adaptations include a reinforced rostrum, ossified sternum, enlarged forelimb retractor muscles, and robust forelimb and pectoral girdle bones. Using CT data generated through the oVert Thematic Collections Network, this project will (1) quantify shape variation in the humerus, coracoid, and scapula of burrowing taxa with 3D morphometrics, (2) measure the integration between these bone elements, and (3) identify potential front-first burrowing species based on their pectoral anatomy. This also provides a framework for predicting locomotor modes in taxa for which the natural history is poorly known.

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

Steven Kell[1], Ronald J. Brooks[2] and Jacqueline Litzgus[1]

[1]Laurentian University, Sudbury, Ontario, Canada. [2]University of Guelph, Guelph, Ontario, Canada

Nesting in Close Quarters: Causes and Benefits of High Density Nesting in Painted Turtles

Nesting is a costly time for female turtles, both energetically and from threat of predation. Although predation rates of eggs and juveniles are often high, ensuring maximum survival of offspring is crucial for population stability and individual fitness. Past observations from our long-term study site in Algonquin Park, Ontario indicate that female Painted Turtles (*Chrysemys picta*) may be nesting together, suggesting this clumping may have a benefit to themselves or offspring. Our goals were to determine if females are choosing to nest at high nest densities, what cues they use to locate nest sites, and what benefits the offspring might accrue from incubating at high nest densities. Using ArcGIS, we found that females nested in clusters, the location of clusters varied among years, and that nest site selection was not strongly determined by abiotic characteristics (overstory density, slope, soil temperature). Female turtle models were placed on the nesting embankment in three different densities and rotated among three locations, and we found that females nested most often with the highest density of models. In ~20% of cases, nests were so clustered that eggs were deposited directly into existing nests or directly beside existing nests. Survivorship of clustered nests (49%) was higher than solitary nests (39%). These lines of observational and experimental evidence strongly suggest that female Painted Turtles choose to nest in close proximity to conspecifics, and that this clustering results in a fitness benefit through increased nest survival.

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151 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: CONSERVATION & MANAGEMENT, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Steven Kell[1], Ronald J. Brooks[2] and Jacqueline Litzgus[1]

[1]Laurentian University, Sudbury, Ontario, Canada. [2]University of Guelph, Guelph, Ontario, Canada

Quantifying Road Effects on Painted and Snapping Turtle Population Demographics in Algonquin Park, Canada

Road mortality is a significant threat to turtle populations and has contributed to potentially deleterious changes in population demography. Road mortality can occur during annual nesting migrations of females, dispersal of juveniles, movements to escape unfavorable habitat conditions, or to find suitable habitat and mates. Although studies have investigated mortality

rates of turtles caused by vehicle collisions, our study is unique because it examines effects of road mortality on population characteristics that may cause population instability. We hypothesize that proximity to roads will decrease the health and fitness of turtle populations due to an increase in mortality from vehicle collisions, leading to changes in demography. We surveyed turtle populations in 8 impact sites (wetlands along the major highway corridor) and 8 non-impact sites (wetlands >4 km from roads) in Algonquin Park. We will compare body sizes and conditions, injury rates, population density, population age structure and sex ratio between impacted and non-impacted sites. We predict that non-impact sites will contain populations with larger body sizes, fewer injuries, older aged individuals, and an equal sex ratio. Snapping Turtles and Painted Turtles from wetlands will be captured in spring by canoe and dip net, and in late summer by trapping. From the 16 wetlands, 148 Painted Turtles and 94 Snapping Turtles were captured. Preliminary analyses indicate that non-impact sites have, on average, larger body sizes and more female-biased sex ratios. Roads cause direct mortality of turtles; our study will quantitatively determine whether roads negatively influence turtle populations in more subtle indirect ways.

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457 Herpetology Genetics I, Highland D, Sunday 15 July 2018

Audrey Kelly[1], Amanda Pierce[1,2] and Karin Pfennig[1]

[1]University of North Carolina, Chapel Hill, NC, USA. [2]US Environmental Protection Agency, Washington, DC, USA

Transfer via Hybridization of an Allele Associated with Rapid Development Time in Spadefoot Toads

Hybridization between species, and the gene flow (introgression) that can result, has been implicated in many aspects of evolution, including speciation, extinction, the generation of new traits, and the transfer of adaptations (termed adaptive introgression). In particular, the transfer of locally adapted alleles via hybridization may help the recipient species expand into novel environments. We investigated naturally hybridizing populations of the spadefoot toads *Spea bombifrons* and *S. multiplicata* and identified a microsatellite allele that shows evidence of having originated in *S. multiplicata* populations and was transferred to *S. bombifrons* via hybridization in the Texas panhandle. This allele subsequently spread into *S. bombifrons* populations in New Mexico and Arizona, following the same path as the species' range expansion into the area. Crucially, we discovered that this allele is associated with more rapid development times of *S. bombifrons* tadpoles, conferring a survival advantage in the rapidly drying ephemeral desert ponds where both species breed and develop. We also identified two genes positioned adjacent to this microsatellite in the *S. multiplicata* genome, and we are analyzing them for connections to development time and signatures of selection. This potential case of adaptive introgression facilitating range expansion has implications for how species might evolve in the face of changes to their environments brought about by climate change – hybridization may actually help species to adapt to their changing environments. This is particularly important because of the increased potential for hybridization that is also predicted to occur with continued climate change.

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348 Ichthyology Systematics II, Grand Lilac Ballroom South, Sunday 15 July 2018

Christopher Kenaley and Peter Jordan

Boston College, Chestnut Hill, Massachusetts, USA

Body-Size Evolution in Ray-finned Fishes (Actinopterygii): Tempo, Mode, and Ecological Correlates

Body size features prominently in nearly every aspect of an organism's biology, including several fitness-related parameters such as fecundity, mating success, energy budget, and life span. Thus, explorations of macroevolutionary trends associated with the tempo and mode of size-evolution are important in understanding the diversity of size in ray-finned fishes. Here we use body length data from 1,400 species of extant actinopterygians and the most current and expansive multi-locus phylogeny for the group to evaluate a multitude of models of log-transformed body-length evolution. We found that the tempo of size evolution in ray-finned fishes is explained best by an Ornstein-Uhlenbeck (OU) process, thereby suggesting that size evolves toward a phenotypic optimal value. In addition, to assess which ecological parameters may contribute to size diversity, we gathered distribution and habitat data for all of our included species. Using phylogenetic generalized least squares analysis under both OU and Brownian motion error models, we found that depth and ecoregion explain 60% of the variation in body length. Together, these results suggest that the evolution of body size is influenced by the ecophysiological constraints of habitat preference.

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

Ethan Kessler[1], John Crawford[2], Andrew Kuhns[1] and Christopher Phillips[1]

[1]Illinois Natural History Survey, Champaign, IL, USA. [2]National Great Rivers Research and Education Center, East Alton, IL, USA

Local and Landscape Drivers of Amphibian Community Composition across Illinois

Amphibian community composition is influenced by habitat at both local and landscape levels, making identification of factors driving amphibian diversity difficult. Additionally, the difficulties in collecting accurate community and habitat data and the inherent correlation within and among community and habitat factors complicates analyses and the interpretation of results. To determine the major drivers of amphibian assemblages in Illinois, our study utilized an occupancy and detectability sampling scheme for larval and adult amphibian presence at 252 ponds throughout the state to address primary local and landscape features driving amphibian communities across the state. For each pond, local habitat variables (e.g. presence of fish) were measured in situ and landscape scale variables (e.g. percent forest within a buffer) were determined using lidar derivatives and aerial photography (both from public sources). We used a multivariate approach to determine what factors had the greatest effect on amphibian community makeup and identify the species affected. After controlling for geographic location (latitude and longitude), the percentage of canopy cover within a buffer, the presence of fish, the number of ponds within a buffer, and slope of a wetland had the greatest effects on statewide amphibian communities. Ultimately, our results provide quantitative evidence of the factors shaping amphibian communities across the landscape and identified the species most affected.

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277 ASIH STOYE GENERAL ICHTHYOLOGY II, Grand Lilac Ballroom South, Thursday 12 July 2018

Daemin Kim[1], Bruce Bauer[2] and Thomas Near[1]

[1]*Yale University, New Haven, Connecticut, USA.* [2]*University of Tennessee, Knoxville, Tennessee, USA*

Species Delimitation and Phylogeography of the Longear Sunfish, *Lepomis megalotis* (Centrarchidae)

Lepomis megalotis, the Longear Sunfish, is a freshwater fish that inhabits various habitats across North America east of the Rocky Mountains. Species delineation within *Lepomis megalotis sensu lato* and its sister-group (*L. marginatus*) has been controversial for almost a century. Phylogenetic analyses derived from nuclear genomic (ddRAD-seq) data suggest that 1) *L. peltastes* makes *L. megalotis* paraphyletic, 2) there are several highly distinct lineages within *L. megalotis s.l.* and 3) these distinct lineages have geographic ranges that are consistent with several species in other groups of fishes (e.g., Cyprinidae and Percidae). Based on the multiple lines of evidence derived from molecular and morphological data, we propose the recognition of species that represent the distinct lineages identified within *L. megalotis s.l.*.

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

Saki Kimura and Yoshihiro Natsuhara

Nagoya University, Nagoya, Aichi, Japan

Influence of different farming methods on the trophic ecology of various tadpoles in paddy fields in Japan

Paddy fields provide not only rice production for food, but also diverse multiple functions and are increasingly considered as important surrogates for natural wetlands for conserving biodiversity. Many Japanese frog species have adapted to evolve in such habitats. In recent years, however, due to agricultural modernization, frog population declines and extinction have been reported in various regions in Japan. Frogs and their tadpoles occupy critical positions in the food webs as important prey and predators, and are thought to be crucial in maintaining biodiversity in water systems and in the surrounding ecosystems. Tadpoles often represent one of the largest animal biomass in Japanese paddy fields and are expected to play critical roles in these ecosystems, but we know very little about the potential effects of different farming methods on their trophic ecology. We combined gut content and stable carbon and nitrogen isotope analyses to examine the trophic ecology of the tadpoles of four Japanese frog species (*Hyla japonica, Fejervarya kawamurai, Rhacophorus schlegelii and Pelophylax nigromaculatus*) between conventional (with middle flesh) and organic paddy fields (without intermediate flesh, winter flooding) in Toyota city, Aichi. The four species overlap in their breeding seasons and their tadpoles can co-occur within the same habitat. We sampled tadpoles at different life stages

from mid-May to late July 2017. We predicted that the tadpoles would differ in their gut contents and isotope trophic spaces along ontogeny, between species and between habitats.

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

Katie King, Hayley Crowell, Heather Liwanag and Emily Taylor

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

The Metabolic Rates of *Crotalus oreganus* Determined via Respirometry

The metabolic rates of squamates are directly influenced by ambient environmental temperature. In a time when environmental temperatures are rising at unprecedented rates, it is imperative that we understand the possible physiological pressures these changes will exert on organisms. The Pacific rattlesnake (*Crotalus oreganus*) is the most common rattlesnake in Central California, and can be found in a variety of ecosystems encompassing a wide range of thermal habitats. However, the metabolic rates of this species have not been well studied and therefore little is known about the energy use and requirements of this particular species. Rattlesnakes from four study sites across central coastal California were collected, brought back to the laboratory, and metabolic rates were calculated using respirometry. We also used body temperature data from free-ranging snakes to estimate field resting metabolism. We will present findings comparing the metabolic rates and resting energy expenditure of snakes from mild, coastal populations to those of hot, inland populations. The preliminary results suggest that snakes from inland sites have a higher metabolic rate than coastal sites due to their larger body size. These data can be used to estimate the energetic requirements of various populations based on temperature, and to project possible changes in the amount of food needed to sustain life as climates continue to warm.

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

Lauren Kircher[1], Ariana Green[1], Matthew Bristol[1], Jessica Noble[1], Joy Young[2] and John Baldwin[1]

[1]Florida Atlantic University, Davie, FL, USA. [2]Florida Fish and Wildlife Conservation Commission, Tequesta, FL, USA

The Potential Impact of High Discharge Events on Snook Movement Patterns in the St. Lucie Estuary

Southern Florida’s water drainage has been altered from shallow, slow-moving sheets of water flowing south to channelized canals that flow east to Caloosahatchee estuary and west to St. Lucie estuary. Water managers use canals to prevent flooding, alleviate drought, and supply water for recreational, personal, and agricultural uses. Before a storm, water is flushed out to

the estuaries in a short period of time, forming a pulse of freshwater. These high discharge events can introduce osmoregulatory stress to the organisms and die-offs of seagrasses and oysters have occurred. This study utilizes Harbor Branch Oceanographic Institute's Indian River Lagoon Observatory Network of LOBO data loggers in St. Lucie to examine extent and duration of changes due to high discharge events and their potential impact on snook movement patterns. Fish movement can be cued by the environment. Although tolerant to a wide range of salinities, snook experience an osmoregulatory cost when moving through different salinities that may reduce fitness and success. We will compare changes in hydrologic parameters (salinity, flow, and temperature) surrounding high discharge events. Movement tracks will be plotted in ArcGIS from passive acoustic telemetry. Passive acoustic telemetry involves a transmitter implanted in the body cavity of the target organism and a stationary receiver in the environment that records unique ID codes as fish move. Understanding the effect of management on waterways, can enhance interpretation of animal responses to discharges. Future research will fully model the influences of hydrologic variables on movement to quantify their relationships and further inform management.

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

Sophie Kocheff[1], Adriana Jeckel[2], Taran Grant[2] and Ralph Saporito[1]

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Differences in palatability of various Central and South American dendrobatid poison frogs

Dendrobatid poison frogs are aposematic, sequester defensive alkaloids from dietary arthropods, and exhibit tremendous alkaloid variation by population, age, sex, size, and between species. Alkaloid variation in the dendrobatid frog *O. pumilio* has recently been correlated with differences in palatability to arthropods, which represent a group of natural predators upon frogs; however, differences in arthropod palatability among other poison frogs have yet to be examined. The goal of the present study was to compare how arthropods might respond to variable alkaloid defenses among different species of dendrobatid poison frogs in Central and South America. Alkaloid defenses were extracted from 54 individual frogs, representing seven species from nine different geographic locations throughout Central and South America. Alkaloid extracts were used in palatability assays using the fruit fly *Drosophila melanogaster* as a model arthropod. Our results demonstrate that fruit flies feed significantly less on solutions containing alkaloids as compared to controls, suggesting that all frog alkaloids are unpalatable. Furthermore, there are differences in palatability between species and among populations of the same species. Collectively, our results further suggest that alkaloid variation among dendrobatid poison frogs translate into differences in palatability, which could lead to differences in natural predation.

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

Matthew Kolmann[1], Karly Cohen[1], Kate Bemis[2], Patricia Hernandez[1] and Adam

Summers[3]

[1]George Washington University, Washington DC, District of Columbia, USA. [2]Virginia Institute of Marine Science, Gloucester, VA, USA. [3]Friday Harbor Laboratories, Friday Harbor, WA, USA

Tooth and consequences: heterodonty and tooth replacement in piranhas and pacus

Complex, heterodont dentitions are frequently associated with limited tooth replacement in amniotes, while non-amniotes are generally thought of as having homodont, continuously-replaced dentitions. These complex dentitions have been cited as key innovations, allowing mammals to process myriad prey or stubborn prey materials, by creating a division of labor among different teeth. Piranhas and pacus have curious dentitions for non-amniotes, as many species show some degree of heterodonty attributed to adaptations for either carnivorous or herbivorous diets, respectively. While tooth replacement mode in pacus is unknown, in piranhas all the teeth on one side of the head are lost as a unit and then replaced simultaneously. We used CT scanning and histological staining to examine tooth replacement and heterodonty in piranhas, and examine the evolution of these modalities using a published molecular phylogeny. While investigating tooth replacement across piranhas and pacus, we found that all serrasalmids are heterodonts. Most of these species are both monognathic and dignathic heterodonts, with teeth differing in shape between the upper and lower jaws, as well as within the jaws themselves. Additionally, all serrasalmids (with one notable exception) share a unilateral tooth replacement pattern, which casts doubt on whether this mode is an adaptation strictly for hypercarnivory. These patterns are found to be consistent over ontogeny in size series of *Pygocentrus* and *Metynnis*, using both histological and tomographic scanning methods. We propose that heterodonty begets simultaneous replacement, and ensures that division of labor among teeth is not interrupted, as might occur with polyphyodont dentitions.

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552 Lightning Talks II, Highland A, Saturday 14 July 2018

Michelle Koo[1], Carol Spencer[1], David Blackburn[2], David Cannatella[3], Alessandro Catenazzi[4], Ann Chang[1], Joyce Gross[5], Deanna Olson[6], Vance Vredenburg[7] and David Wake[1]

[1]Museum of Vertebrate Zoology, Berkeley, CA, USA. [2]Florida Museum of Natural History, University of Florida, Gainesville, FL, USA. [3]University of Texas at Austin, Austin, TX, USA. [4]Florida International University, Miami, FL, USA. [5]Berkeley Natural History Museums, Berkeley, CA, USA. [6]US Forest Service, Corvallis, OR, USA. [7]San Francisco State University, San Francisco, CA, USA

AmphibiaWeb Updates and Innovations to Address the Global Crisis in Amphibians

Amphibians comprise the most endangered group of vertebrates; about one-third of the world's amphibian species are under threat of extinction. Emerging infectious diseases such as chytridiomycosis are especially devastating. Many amphibian species are susceptible to disease caused by chytrid fungi (*Batrachochytrium dendrobatidis*, or Bd, and *Batrachochytrium salamandrivorans*, or Bsal). AmphibiaWeb was founded to directly address the urgent needs to facilitate research in amphibian biodiversity and emerging infectious disease. These include a central repository that provides primary information on amphibian biology, taxonomy, and

conservation by integrating data from VertNet, producing species accounts, tracking and mapping new species and more. By harnessing informatics tools and networks, we aim to facilitate collaborative efforts nationally and internationally. In collaboration with the US Forest Service in 2016, we launched the AmphibiaWeb disease portal which tracks Bd and Bsal data collected around the world (https://amphibiandisease.org). The portal enables users to visualize archived datasets in publications, as well as to easily download and reuse datasets from previous research in order to integrate multiple studies. Using this portal, researchers can coordinate and collaborate in efforts to understand disease impacts on amphibian biodiversity, including private data sharing for projects prior to publication.

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416 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: CONSERVATION & MANAGEMENT, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Cory Kozmik and Jacqueline D Litzgus

Laurentian University, Sudbury, Ontario, Canada

Using Spatial Ecology and Circuit Theory to Inform Age-class Appropriate Road Mortality Mitigation for Turtles

Habitat fragmentation, destruction, and degradation of wetland systems that provide Critical Habitat are key threats that contribute to declines in Species At Risk (SAR) reptile populations. Magnetawan First Nation (MFN) in Eastern Georgian Bay, Ontario is home to several SAR reptile species and fragmented by linear anthropogenic features consisting of two highways, including Trans-Canada Hwy 69 planned to expand within MFN and the surrounding area. This relatively pristine landscape includes contiguous wetland matrices consisting of upland habitat, marsh, swamp, fen, bog, and peatlands, many occur adjacent to Hwy 69, a documented mortality "hotspot" for reptiles. The general focus of road ecology studies has been adult turtles; however, alive and dead sub-adult and juvenile turtles have also been documented on the 6 km stretch of Hwy 69 throughout MFN. Knowledge gaps remain regarding dispersal patterns of younger age-classes in relation to highway infrastructure, and the impacts of highways on recruitment. Our goal is to predict the best locations for connectivity corridors allowing access to habitats adjacent to Hwy 69, and to ensure mitigations for future highway development are conducive to spatial movements of all age classes. We will use radio-telemetry, mark-recapture and road demographic data to quantify the spatial ecology of juvenile turtles around the highway. We will use circuit theory to model age-class connectivity patterns and requirements. Our research will fill knowledge gaps about impacts of anthropogenic linear features on vulnerable reptile communities and associated critical habitats, providing data to inform cost effective mitigation design in other locations.

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

Trevor Krabbenhoft[1] and Thomas Dowling[2]

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

Sex Determination in an Allotetraploid Fish (Cypriniformes: Catostomidae): On the Importance of Understanding Genetic and Epigenetic variation in Captive Breeding Programs

Genetic and environmental factors can play a role in sex determination, with significant variation in their relative importance across the tree of life. In some cases, epigenetic modifications can play an important role in developmental programming to allow organisms to respond appropriately to environmental variation. Here, we present the serendipitous discovery of previously unknown variation in mechanisms of sex determination in an allopolyploid fish. We identified two groups of males: those with and without a suite of male-specific genetic loci. We assess whether the two groups of males represent genetically- versus environmentally-determined sex, respectively. Preliminary evidence suggests that these two types of males have significantly different rates of reproductive success in a captive breeding program, underscoring the critical importance of understanding mechanisms of sex determination and epigenetic variation in such programs. We examine genetic and epigenetic (DNA methylation) variation within and between these two groups of male fish and explore possible mechanisms of sex determination in this allopolyploid species. To our knowledge, this is the first study describing potential mechanisms of sex determination in the Catostomidae. Our results demonstrate the value of understanding both genetic and epigenetic variation in captive breeding programs and in the wild.

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183 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Aaron Krolow and Kyle Piller

Southeastern Louisiana University, Hammond, Louisiana, USA

Environmental DNA (eDNA) Assessment of Fish Communities Occurring at or around Artificial Reefs along the Louisiana Coast

Worldwide, artificial reefs have been deployed to improve fisheries by providing hard substrate in an otherwise desolate environment. These structures allow for the colonization of a diverse invertebrate community that, in turn, attract an array of fish species. The success of artificial reefs in attracting fish has proven difficult, as sampling with traditional gear has been challenging. In addition, high turbidity has limited the effectiveness of remote operated vehicles (ROVs), and SCUBA to assess fish community structure on these reefs. Therefore, this study was undertaken to assess the fish community on artificial reefs using an alternative approach, environmental DNA (metabarcoding), a non-invasive monitoring technique. We gathered water samples, filtered, sequenced, and analyzed samples collected from multiple reef and control sites along the coast of Louisiana. Results, although preliminary, suggest that this is a viable approach that will allow us to monitor ray-finned fishes that utilize these reef structures. Preliminary results from our first season of sampling will be presented.

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83 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: CONSERVATION & MANAGEMENT, Empire Hall South – JF Rochester Riverside Convention Center,

Friday 13 July 2018

Brian Kron and Scott McRobert

St. Joseph's University, Philadelphia, PA, USA

The Effects of Salinity on Growth and Calcium Retention in Young Diamondback Terrapins

The diamondback terrapin (*Malaclemys terrapin*), is a species of turtle living in brackish water coastal environments ranging from Texas to Massachusetts. This species is listed as 'endangered' in Rhode Island, 'threatened' in Massachusetts, and 'near threatened' by the IUCN. Life in brackish water estuaries involves regular fluctuations in salinity, which could potentially affect young terrapins. In this study we compare growth and calcium retention in thirty-six terrapins, hatched from eggs collected at North Sedge Island, New Jersey in September 2017. One half of the turtles (18) were maintained in low saline water (LS=10ppt), and half (18) were maintained in higher salinity water (HS=25ppt). Between January and June 2018, each terrapin was measured weekly for weight, carapace and plastron length, and a marginal scute was removed from each terrapin at the beginning and end of the study to assess (by ACP-OES) calcium retention. Percent growth rate was determined for each growth measure. Mean weight for LS terrapins (60.14% +/- 6.83%) was not significantly different than mean weight for HS terrapins (59.75% +/- 4.54%). Mean carapace length was not significantly different between LS and HS terrapins (17.09% +/- 4.59%; 15.69% +/- 1.96%, respectively). Mean plastron length for LS terrapins (8.24% +/- 1.79%) approached significant difference from mean plastron length for HS terrapins (6.07% +/- 2.06%). In June, all terrapins will be released at the site of collection. We hope this work will add information on the effects of salinity on young terrapins and aid in conservation efforts for this species.

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263 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: CONSERVATION & MANAGEMENT, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Chelsea Kross and John D. Willson

University of Arkansas, Fayetteville, AR, USA

The Effects of Prescribed Fire on the Development of Larval Crawfish Frogs (*Lithobates areolatus*)

Prescribed fire is a common technique used in restored and managed prairies to reduce the abundance of non-native vegetation and prevent succession. Seasonal prairie wetlands can be affected by prescribed fire through a reduction in vegetative biomass, which serves as an important nutrient base, or through the deposition of ash from surrounding terrestrial habitat. Terrestrial amphibians have been shown to experience increased mortality due to the loss of habitat heterogeneity and cover as a result of prescribed fire. However, few studies have assessed the effects of reduced biomass or ash input on larval amphibians. We used a mesocosm approach to investigate the effects of prescribed fire on larval amphibian development. We had treatments representing three scenarios: (1) Control – unburned prairie vegetation, (2) Ash

Addition – unburned prairie vegetation, with added ash to simulate deposition from surrounding terrestrial habitat, and (3) Reduced Biomass – 50% of vegetation burned, with ash retained. We compared average time to metamorphosis, snout-vent-length, mass, and survival of larval *Lithobates areolatus* among treatments. Larval survival was lowest in the reduced biomass treatment, but other developmental metrics were similar among treatments. Our results suggest that prescribed fire has negligible effects on the development of aquatic amphibian larvae but might result in reduced survival if burning occurs prior to wetlands filling.

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

Ariel Kruger

Rutgers University, New Brunswick, NJ, USA

Pine Barrens Treefrog Skin Bacteria Inhibit Growth of the Chytrid Fungus, *Batrachochytrium dendrobatidis*

Probiotic therapy is currently being explored for ameliorating disease in wildlife. In the amphibian-chytrid fungus (*Batrachochytrium dendrobatidis*, hereafter *Bd*) system, identifying anti-*Bd* bacteria has been a promising avenue of conservation research. However, many studies searching for anti-*Bd* bacteria neglect the ecological interactions that may occur when *Bd* infects amphibian skin. In this study, I attempted to take a more holistic approach to determining whether individual amphibians may be protected from *Bd* based on their skin bacterial communities. I swabbed the skin of Pine Barrens Treefrogs (n=10) and grew bacterial communities on agar. After three days of growth, ten unique bacterial isolates were identified across all individuals, with an average of four isolates on each individual. To mimic natural interactions that may occur on frog skin, I set up co-culture assays where bacteria and *Bd* were grown together in liquid media in the community combinations found on each individual frog. After three days of growth, cell-free supernatants from co-cultures were used in inhibition assays to determine which bacterial isolates (singly and in naturally occurring combinations) successfully inhibited *Bd* growth. When grown together, all 10 frog's naturally occurring skin bacterial communities showed complete inhibition of *Bd*. However, when grown singly, only 5/10 bacterial isolates successfully inhibited *Bd* growth. These results suggest that probiotic therapy should be studied in a community context when assessing anti-*Bd* function. To my knowledge, this is the first study to take a community-level approach to determining individual amphibian susceptibility to *Bd* based on skin bacterial communities.

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

Kole Kubicek[1], Ralf Britz[2] and Kevin Conway[1]

[1]Texas A&M University, College Station, TX, USA. [2]Natural History Museum, London, United Kingdom

Developmental Osteology of the Channel Catfish, *Ictalurus punctatus* (Teleostei:Ictaluridae)

The skeleton of catfishes (Siluriformes) is characterized by several autapomorphies, including extreme modifications of certain elements (i.e. pectoral-fin spine) and the presence of several bones that are currently presumed to be the result of fusion (i.e. the parieto-supraoccipital). Despite the vast number of anatomical investigations of the adult skeleton in catfishes, comprehensive information on early development remains scarce. This is surprising given the number of species currently being reared for aquaculture or the aquarium trade. In order to further our understanding of the siluriform skeletal system, we document the development of the entire skeleton in the economically important Channel Catfish, *Ictalurus punctatus*. Our investigation is based on approximately 125 cleared and double stained individuals (8.1-36.2 mm NL/SL) and 50 specimens (8.6-21.2 mm NL/SL) cleared and stained with alizarin red S only. We examined and scored each individual for the presence/absence of 136 skeletal elements and generated a sequence of ossification for the entire skeleton. We compare the ossification sequence generated for *I. punctatus* to that of another ictalurid (*Noturus gyrinus*) and other otophysans (*Barbus holotaenia* and *Salminus brasiliensis*) to determine which heterochronic changes in skeletal development characterize siluriforms.

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

Bernie Kuhajda[1], Sarah Sweat[1], George Gavrielides[1], Anna George[1], Joe Powell[2], Mack Lunn[2] and Ryan Brown[2]

[1]Tennessee Aquarium Conservation Institute, Chattanooga, Tennessee, USA. [2]Tennessee Technological University iCube, Cookeville, Tennessee, USA

Freshwater Information Network (FIN): Merging Natural History and Living Museums to Reflect Fish Distributions in the Southeastern United States

The Southeastern United States is a global biodiversity hotspot for freshwater aquatic organisms. Unfortunately, the Southeast also harbors some of the most imperiled aquatic species in the world. Thus the need for collaborative conservation efforts for southeastern aquatic organisms is more important now than ever. However, distributional and status data for these organisms are stored in a variety of platforms, including spreadsheets, museum records and databases, unpublished reports, and field notes. This can be exceptionally problematic for endangered species where recent sightings cannot be vouchered and accessed by others. The Freshwater Information Network (FIN) aims to combine all of these data sources into a single user friendly “living” database containing georeferenced locations and voucher photographs. We collected museum, institutional, and field note data and georeferenced records. Currently FIN includes 402 species of fishes within the Tennessee, Mobile, and Cumberland river drainages. This interactive website allows users to submit new locality data and field photograph vouchers through a configurable application made with ArcGIS Solutions. Distribution maps, photo voucher galleries, a brief description of life history, and literature cited for each species will allow for a one stop webpage on information on all the species for both scientists and the public. Future additions to FIN will include other aquatic taxonomic groups in these drainages. With new addition of data from experts and citizen scientists, conservation efforts in the Southeast can become a focused collaborative effort.

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387 Lightning Talks II, Highland A, Saturday 14 July 2018

Arianna Kuhn[1,2], Sara Ruane[3], Chris Raxworthy[1] and Frank Burbrink[1]

[1]*American Museum of Natural History, New York, NY, USA.* [2]*City University of New York: Graduate Center, New York, NY, USA.* [3]*Department of Biological Sciences Rutgers-Newark, Newark, NJ, USA*

Spatially Explicit Historical Demography of Widespread Malagasy Gemsnakes

The accurate estimation of demographic and genetic population parameters often relies on the resistance or connectivity of landscape features. Although such dynamic population models are spatially explicit, population-level inferences frequently use aspatial models to estimate spatially-dependent parameters. We utilize an approach for investigating the diversification of Malagasy gemsnakes using species distribution models (SDMs) as estimates of historical landscape permeability and forest connectivity under various past-projection scenarios. Demographic parameters and SDM projections were used to simulate spatial population models to better understand how historical climatic change shaped structure and genetic diversity in widespread gemsnake populations, ultimately contributing to the elevated endemism seen across the island. This work will not only help resolve the controversy over Madagascar's historical landscape but also provide a platform for future investigations of the generation and maintenance of diversity in a shrinking and endangered global biodiversity hotspot.

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

Elizabeth Kull[1], James Titus-McQuillan[2], Edward L. Stanley[3], Matthew P. Heinicke[4], Aaron M. Bauer[5] and Juan D Daza[1]

[1]*Sam Houston State University, Huntsville, Texas, USA.* [2]*University of Texas at Arlington, Arlington, Texas, USA.* [3]*Florida Museum of Natural History, Gainesville, Florida, USA.* [4]*University of Michigan-Dearborn, Dearborn, Michigan, USA.* [5]*Villanova University, Villanova, Pennsylvania, USA*

Variation in the cranial osteology of the genus *Prosymna* (Lamprophiidae: Serpentes)

The Sub-Saharan lamprophiid genus *Prosymna* includes 16 recognized species of small sized snakes. Although external morphology of these snakes is similar, study of their skull has revealed tremendous phenotypic variation. We obtained high resolution computer tomographies for voucher specimens from eight species. We used a multigene phylogeny of 11 species as a molecular scaffold to map seven conspicuous variable cranial osteological features.

According to our results, the genus has undergone two independent losses of the postorbital bone. Although these snakes have a characteristic shovel-snout morphology, this trait is accentuated in a clade including *P. ruspoli*, *P. greigerti,* and*P. meleagris* which possess a bony premaxillary rostral shelf. In some *Prosymna* (*P. visseri*, *P. sundevalli*, *P. bivitatta* and *P. lineata*) there is a marked trend towards consolidation of the skull, fusion of parietals with the braincase (especially the supraoccipital). In some members of this clade (*P. sundevalli*, *P. bivitatta* and *P. lineata*) the premaxilla and the maxilla approach or contact each other, perhaps reinforcing the snout. Fusion of the skull is extreme in *P. visseri* in which not only the parietals and the braincase are fused, but the frontals and the nasals are integrated into a single continuous bony covering for their entire brain. *Prosymna visseri* also develops other adaptations in the skull, a diamond shaped prefrontal, and a hammer shaped maxilla. This species lives in cracks in rocky formations and is seem to be specialized on hard shelled gecko eggs, which may explain their divergent morphology.

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

Shannon L Kuznar, Jack M Craig and James S Albert

University of Louisiana at Lafayette, Lafayette, Louisiana, USA

Diversity of tooth morphology in the oral jaws of the Banded electric fishes *Gymnotus* (Gymnotidae: Gymnotiformes)

Tooth morphology is widely associated with trophic position and life history traits in fishes. Previous studies of dental morphology in *Gymnotus* have revealed characteristic features of subclades and species, including the presence and number of dentary and premaxillary teeth with conical, needle, or arrowhead shapes. For example, arrowhead-shaped teeth, anteroposteriorly compressed triangular teeth in the anterior portion of the dentary differ among species groups, ranging from 0-5 in members of the *G. carapo* group. Identifying dental traits among *Gymnotus* species contributes to understanding of the evolution of trophic position, as needle-shaped teeth are associated with insectivorous habits and arrowhead-shaped teeth with piscivorous habits. Here we use meristic and morphometric measurements of tooth shape along the dentary arcade to document diversity of oral teeth in *Gymnotus* species representing each of five major subclades, i.e. species groups. Species of the *G. carapo* group exhibit a common curve of tooth width to length ratios, in which anterior teeth are more anteroposteriorly compressed (all have a positive slope). Highly compressed anterior teeth can be achieved either by a lower y-intercept (all teeth more compressed) or a steeper slope (greater variance in tooth compression along dentary margin). Species also differ in total number of dentary teeth, irrespective of tooth shape. Species of the other species groups do not exhibit high variance in tooth compression along the dentary margin. These are the first results to quantify tooth shape within and among *Gymnotus* species, and demonstrate morphological specializations that are consistent with known interspecific trophic differences.

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

Brandon LaBumbard, Molly Bletz, Kelly Barnhart and Douglas Woodhams

University of Massachusetts Boston, Boston, MA, USA

Community Structure and Function of Amphibian Microbiomes Relating to Pathogen Defense

The skin microbial community plays a vital role in the defense against pathogens, yet it can vary temporally and between hosts. The amphibian skin microbiome can provide resistance to chytridiomycosis, caused by *Batrachochytrium dendrobatidis* (*Bd*). By determining which bacteria offer pathogen defense, when they are present, and relatively how abundant they are, we can better understand pathogen dynamics and develop more effective strategies for combating disease. We investigated the skin bacterial communities using 16S ribosomal RNA amplicon sequencing of the amphibian community in Colchester, VT to address seasonal and community patterns related to *Bd* presence or absence. We see that the overall composition appears to be stable over time but that the relative abundance shifts seasonally for two species of amphibian. We also used an amphibian skin bacteria database to determine the proportion of the sequenced microbiome with potentially *Bd*-inhibitory microbes to determine if protective function is maintained and if it differs among species.

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

Max Lambert

Yale University, New Haven, CT, USA

Sex reversal is widespread in wild green frogs

Sex in amphibians is typically believed to be strictly determined by genetics. Environmental effects on sexual development are therefore considered aberrant responses to anthropogenic contaminants or extreme temperatures. As such sex reversal, where tadpoles develop a phenotypic sex opposite their genotypic sex, is widely viewed as an unnatural process in wild frog populations. Using novel sex-linked genetic markers for the common and wide-ranging North American green frog (*Rana clamitans*), we show that sex reversal is common within and across populations, bidirectional, and independent of land use or contamination. Our work also illustrates that natural temperature variation experienced in the wild may be a dominant driver of sex reversal. Specifically, we found that cooler pond temperatures are associated with higher rates of female-to-male sex reversal and hotter temperatures are associated with higher rates of male-to-female sex reversal. Additionally, we also found intersex males (i.e., males with egg-like cells in their testes) in most populations and found no association between intersex and

either sex reversal frequencies or human land use. Combined, our results do not align with common perceptions of how sex is determined in amphibians and suggest a larger natural role for the environment in shaping the sexual fate of wild frogs. These findings suggest we begin to reconsider the relative natural and anthropogenic contributions to sexual development, sex reversal, and "sexual abnormalities" in amphibians.

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

Gabriel Langford, Triantofilos Iakovidis and Michael Politis

Florida Southern College, Lakeland, Florida, USA

Impact of Multiple Host Invasions on Native Parasite Assemblages: What Happens When Three Non-native Anurans Invade a Florida Frog Pond?

While much attention and resources have been given to the impact of free-living invasive species on native flora and fauna, few studies have focused on the impact invasive species have on native parasite assemblages. Florida is well-known for its invasive species, including an increasing number of anurans, many of which have already been surveyed for parasites. Our long-term survey of anurans from central Florida aims to compare a native parasite assemblage pre and post-invasion of 3 non-native anurans. We also aim to record any parasites introduced from the non-native species. From September 2010 – April 2018, we sampled adult anurans from a permanent, shallow wetland adjacent to the Florida Southern College campus. All anurans collected in 2010 – 2011 were species native to central Florida: *Anaxyrus terrestris, Acris gryllus, Hyla cineria, Rana grylio,* and *Rana utricularia*, which hosted diverse parasite assemblages that included native parasites, such as *Cosmocercella* sp., *Cosmocercoides* sp., *Rhabdias* spp., *Haematoloechus* spp., *Mesocoelium* sp., and *Lawrencarus* sp. Invasive anurans first appeared in our wetland in spring 2012 with non-native *Rana catesbiana*, which was followed by exotic *Rhinella marina* (spring 2013) and *Osteopilus septentrionalis* (fall 2016). Besides the introduction of these non-native anurans, no obvious changes occurred to the wetland environment. In 2018, the anuran community consists of 4 native and 3 non-native species, which varies markedly from the original community of 5 native host species. We found many native parasite species were still present in the wetland's anurans, however some parasite species have apparently become locally extirpated.

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

Tracy Langkilde[1], Thomas Adams[1], Julian Avery[1] and Robin Warne[2]

[1]Pennsylvania State University, University Park, PA, USA. [2]Southern Illinois University, Carbondale, IL, USA

Effects of anthropogenic noise on wood frog tadpoles

Anthropogenic noise permeates most of the world's habitats. There is increasing evidence that novel noise has effects on resident species, including on physiology and vocal communication. We have found that adult wood frogs (*Lithobates sylvaticus*) have difficulty locating calling males and exhibit elevated physiological signatures of stress in the presence of road noise. We wanted to test whether larval amphibians, which may be buffered by their aquatic habitat, are similarly affected by anthropogenic noise. We raised wood frogs from eggs to pre-metamorphic tadpoles in the presence or absence of noise from compressors associated with the transport of natural gas following extraction from the Marcellus Shale Play. We found that during the initial stages of development, noise and associated vibration reduced tadpole size and, when this stress was couple with physical disturbance, caused significant tadpole mortality. These effects of noise were not observed later in tadpole development after noise levels had been reduced, and there were also no associated significant effects on physiological stress (corticosterone) levels. Overall, our results suggest that anthropogenic noise may affect larval amphibians, and could be another factor affecting overall anuran decline, particularly when experienced with additional stressors.

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

Julia Laterza Barbosa and James Watling

John Carroll University, University Heights, OH, USA

Using Experimental Translocations of Reptiles and Amphibians to Evaluate Faunal Rescue in the Brazilian Amazon

Faunal rescue is a form of mitigation-driven animal translocation that is mandated by law in Brazil as part of the environmental licensing of large-scale construction projects, such as hydroelectric dams. Faunal rescue consists of moving animals from construction sites and releasing them in protected areas. This practice results in the translocation of thousands of animals from construction sites every year, most of which are reptiles and amphibians. Although commonly used as a mitigation measure, the monitoring in faunal rescues is insufficient to determine even the most basic measures of success, such as survival and settlement in release areas. Therefore, I conducted a field-based mark-recapture study to evaluate if leaf litter frogs and lizards settle in release sites, and if translocation influences density of animals in release areas. I found that lizards settled in release plots, although translocation did not increase densities significantly. Settlement of amphibians was not analyzed due to low recapture rates; densities were lower on the post-translocation phase but did not differ between control and release plots. These results suggest that lizards settle in release areas and amphibian settlement might be influenced by seasonality. Finally, I propose including mark-recapture methods in faunal-rescue monitoring transects and in release areas. This addition is a cost-effective way of improving evaluation of translocation success to determine if faunal rescue is an effective conservation tool for reptiles and amphibians.

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

Melissa Lech[1,2], Tracey Tuberville[2] and Melissa Pilgirm[1,2]

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Investigating Biomagnification of Hg and ^{137}Cs in *Nerodia floridana* using Stable Isotopes

Previous studies have shown that some contaminants bioaccumulate in organisms and biomagnify through food webs. Stable isotope techniques provide a non-lethal approach for evaluating trophic transfer of contaminants. In this study, we used the nitrogen isotopic composition (δ^{15}N) of 74 *Nerodia floridana* (Florida Green Watersnakes) collected from three former nuclear cooling reservoirs (i.e., Par Pond, Pond B and Pond 2) to examine potential biomagnification of two contaminants - mercury (Hg) and radiocesium (^{137}Cs). We found a significant positive relationship between δ^{15}N and Hg concentrations (r^2=0.29, df=73, p <0.001). We found a significant positive relationship between δ^{15}N and ^{137}Cs for individuals collected at Par Pond (r^2=0.85, df=9, p<0.001) but not for individuals collected at Pond B or Pond 2. In addition, δ ^{15}N values ranged from 5.6 to 9.3. Our results support that biomagnification of contaminants is occurring in our study systems.

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

Brenna Levine[1], Marlis Douglas[1], Julie Savidge[2], Bjorn Lardner[2], Robert Reed[3], Amy Yackel Adams[3] and Michael Douglas[1]

[1]University of Arkansas, Fayetteville, Arkansas, USA. [2]Colorado State University, Fort Collins, Colorado, USA. [3]United States Geological Survey, Fort Collins, Colorado, USA

Genomic Pedigree Reconstruction Provides Novel Insight into the Reproductive Ecology of the Invasive Brown Treesnake (*Boiga irregularis*) on Guam

Important to the control of an invasive species is an understanding of the manner by which its persistence is mediated by its reproductive ecology. Persistence of the highly invasive brown treesnake (*Boiga irregularis*; BTS) on Guam has been well documented since its introduction circa 1949. However, its mating and reproductive ecology are less well understood, and their relationships to population persistence over time have yet to be quantified. We examined the reproductive ecology of BTS by reconstructing a multigenerational pedigree for a closed population established on Guam in 2004 (N = 469). Pedigree reconstruction was accomplished by analyzing 506 independent, highly informative SNPs (= single nucleotide polymorphisms; minor allele frequency cutoff ≥ 0.25, H_e = 0.24) produced by filtering 6,180 loci derived from double-digest Restriction-site Associated DNA (ddRAD). Our preliminary pedigree analysis assigned 57 known males as the sires of 289 individuals in the population, and 67 known females as the dams of 179 individuals. Offspring per sire (μ = 5.1) exceeded that per dam (μ = 2.7), and relative variance in reproductive output among sires was significantly greater than

among dams (*F*-ratio test; $P < 0.05$). We also found evidence of multiple mating and promiscuity in both sexes. Our results provide novel insight into the cryptic mating and reproductive ecology of the invasive brown treesnake and have implications for population persistence over time. As such, these results have the potential to promote the development of effective invasive species control.

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

Peiwen Li, Rute Clemente-Carvalho, Peter van Coeverden de Groot and Stephen Lougheed

Queen's University, Kingston, ON, Canada

Comparing Methods for SNP Calling and Implications for Estimation of Population Parameters: An Empirical Study from a Tetraploid Arctic Fish

High-throughput DNA sequencing methods can facilitate population genomic analysis by providing access to panels of Single Nucleotide Polymorphism (SNP) from across the genome of nonmodel species. For such nonmodel species typically no reference genome is available, and SNP calling is usually accomplished *de novo*, or by aligning reads to a closely-related species' reference genome. However, empirical studies evaluating the effects of the two different SNP calling methods are still scarce, especially when confident SNP calling remains challenging for nonmodel, polyploid species as is the focus of our study. In this study, we use Double Digest Restriction Associated DNA sequencing (ddRADseq) to obtain millions of DNA reads for Arctic char (*Salvelinus alpinus*), a nonmodel, tetraploid arctic fish species for which no reference genome is yet available. We then perform SNP *de novo* calling using multiple pipelines, and also by aligning the genome to another salmonid species, the rainbow trout (*Oncorhynchus mykiss*). We compare the number of SNPs obtained using both approaches, plus pairwise F_{ST}, F_{IS}, and observed and expected heterozygosity. Preliminary results show that our *de novo* calling yielded about twice as many SNPs as the reference-based method, but we found no significant differences in pairwise F_{ST} values. Our study provides insights into the optimization of analytical design in population genomics for nonmodel, polyploid organisms, and presents a means for evaluating the impacts of different calling methods for analyses of population structure in wild species.

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

Russell Ligon

Cornell University, Ithaca, NY, USA. Arizona State University, Tempe, AZ, USA

Colorful language: Investigating the complex chromatic communication of chameleons

Sexual and social signals have long been thought to play an important role in speciation and diversity; hence, investigations of intraspecific communication may lead to novel insights regarding key processes of evolution. Communication, for example, can reduce the costs of conflict, and understanding how animals mediate conflict over different timescales can provide understanding of the factors guiding the evolution of contest strategies. To answer longstanding questions regarding how animals use dynamic signals to mediate conflict, I employed novel methods to measure the color changes used by male veiled chameleons *Chamaeleo calyptratus* during agonistic encounters. I discovered that rapid brightening serves as a signal of aggression and rapid darkening as a signal of submission. Interestingly, the honesty of these dynamic color signals of strategy appears to be maintained by social costs – dishonestly signaling chameleons receive more aggression than their honestly signaling counterparts. Among brightening chameleons, there is additional information encoded in particular elements of display coloration, for example the timing of maximum skin brightness is a strong predictor of maximum bite force. Together, these results indicated the utility of dynamic color signals which can communicate information about contest strategy, physiology, and physical performance.

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

Shi Lin

Museum of Vertebrate Zoology, Berkeley, CA, USA

Taxonomic Review of *Trachemys scripta troostii*: A Clarification of the *elegans-troostii* Problem

The Cumberland slider, *Trachemys scripta troostii* (Holbrook, 1836), is the most poorly studied subspecies of the pond slider (*Trachemys scripta*). This highland taxon has a long and nebulous taxonomic history. In early literature, the usage of the name "*troostii*" and "*elegans*" are confusing. The name *troostii* was initially used to describe melanistic male individuals while *elegans* are non-melanistic ones. Herein I addressed the complicated *elegans-troostii* problem, giving a summary of the taxonomic history and clarifying issues that overlooked by previous authors. Implications for future research are also discussed.

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243 Herpetology Physiology, Highland C, Saturday 14 July 2018

Craig Lind[1], Ignacio Moore[2] and Terence Farrell[3]

[1]*Stockton University, Galloway, NJ - New Jersey, USA.* [2]*Virginia Tech, Blacksburg, VA, USA.* [3]*Stetson University, DeLand, FL, USA*

Interactions between steroid hormones and snake fungal disease indicate potential sublethal effects on fitness in Pygmy Rattlesnakes, *Sistrurus miliarius.*

Snake fungal disease (SFD) has been identified as a proximate threat to snake biodiversity, however little is known regarding the physiological consequences of infection and their potential to impact populations. In cryptic species, direct effects of infection on fitness are not easily determined on timescales that facilitate timely conservation initiatives. In such contexts, physiological proxies for individual fitness are valuable in identifying the scope of the threat that SFD may represent to populations. The steroids testosterone and estradiol directly mediate reproductive investment in snakes, and adrenal glucocorticoids may play a role in mediating the tradeoff between immunocompetence and reproduction. To test the hypothesis that infection is associated with a physiological stress response that suppresses gonadal steroid production (i.e. the cort-fitness hypothesis), we estimated SFD severity by visual clinical signs and measured testosterone, estradiol, and corticosterone in a field-active population of Pygmy Rattlesnakes. We predicted a positive association between infection and corticosterone and a negative association between infection and testosterone (males) and estradiol (females), and that these relationships would be strongest during seasonal bouts of reproductive investment. Individuals with SFD exhibited increased corticosterone levels across seasons and sexes. Infected males had lower testosterone during summer spermatogenesis and during the fall mating season. Infected females were less likely to have elevated estradiol during the fall mating season and during spring vitellogenesis. Results are consistent with the cort-fitness hypothesis and suggest that seasonal energetic tradeoffs mediated by corticosterone may result in a decrease in reproductive success in afflicted individuals.

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316 SSAR SEIBERT CONSERVATION I, Highland B, Thursday 12 July 2018

Luke Linhoff[1], Francesca McGrath[2], William Symes[3] and Maureen Donnelly[1]

[1]Florida International University, Miami, Florida, USA. [2]University of Michigan, Ann Arbor, Michigan, USA. [3]National University of Singapore, Singapore, Singapore

Dramatic Increases in the Values of Traded U.S. Amphibians Indicates Higher Risk of Overexploitation

The collection of wild amphibians for human consumption and the pet trade may directly reduce populations through overexploitation. Additionally, human mediated movement of amphibians facilitates the spread of wildlife diseases and invasive species. Market fluctuations in the amphibian trade may directly impact conservation goals with potential global consequences. We examined changes in the market values of 52 species of amphibians in the United States in a 28-year time period by carrying out systematic surveys of U.S. based sellers of live amphibians. All but two species had increased in price dramatically during the study period. The mean percentage adjusted market price of U.S. amphibians rose 822%. The mean price for anuran species increased from US$4.26 to US$15.56 and caudates from US$5.32 to US$33.60. We found the market value is significantly higher for caudates with declining populations than other groups. We also found price increase to be positively correlated to range size from IUCN maps, indicating these maps may be insensitive to underlying range changes. Additionally, there was no influence on the prices of U.S. caudate species that were recently affected by a contentious 2016 emergency trade ban. The results provide valuable information on price trends of commonly traded North American amphibian species. We urge increased monitoring of amphibian market pressures and price dynamics to ensure the pet trade is sustainable.

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47 ASIH STOYE PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY, Highland D,

Friday 13 July 2018

Allison Litmer and Christopher Murray

Tennessee Technological University, Cookeville, TN, USA

Neutrophil: Lymphocyte Ratios as a Measure of Chronic Stress in Populations of the Hellbender (*Crypotbranchus alleganiensis*) Across a Habitat Quality Gradient

Amphibians are currently facing widespread population declines, primarily due to the introduction of anthropogenic stressors. Anthropogenic stressors have the potential to alter ecosystem dynamics and elicit long-term physiological responses that could hinder population viability. Current metrics of population viability rely heavily on demographics, population fluctuation, and degree of isolation. Physiological parameters, such as stress-response proxies, offer a new scale for population assessment, providing an explanation of the mechanism causing population declines. Implicating a method of assessing chronic stress, such as white blood cell counts, specifically neutrophil:lymphocyte (N:L) ratios, may provide a metric that can be rapidly assessed and related back to microhabitat characteristics for management purposes. As a long-lived, specialist facing population declines, the hellbender (*Cryptobranchus alleganiensis*) is a good candidate species for applying N:L ratios to assess population viability. This study used N:L ratios in relation to microhabitat variables to assess chronic stress among populations, determine environmental variables correlated with stress, and assess the implication of N:L ratios, among wild hellbender populations. Of the microhabitat variables assessed, low- dissolved oxygen and canopy cover, and high- pH and turbidity, correlated with elevated N:L ratios. Additionally, N:L ratios significantly differed among hellbender populations, suggesting that varying habitat condition and environmental stressors influencing population viability are reflected by N:L ratios. Specifically, N:L ratio indicated populations of management concern that traditional methods failed to suggest. Viability assessments incorporating physiological parameters provide evidence of declining viability earlier than traditional methods, and suggest specific variables contributing to stress, allowing for better management strategy.

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197 Ichthyology Systematics II, Grand Lilac Ballroom South, Sunday 15 July 2018

Juan Liu

SUNY University at Buffalo, Buffalo, NY, USA

You are how you look: body shape analysis of Eocene cypriniform fishes

The oldest skeleton-based fossil cypriniforms (Teleost: Ostariophysi: Cypriniformes) were recently recovered from Eocene sediments of North America and East and South Asia. These fossils belong to three families, Cyprinidae, Catostomidae, and Jianghanichthyidae, and represent the principal sources for understanding the early diversity and divergence of the Cypriniformes. However, low morphological disparity among Eocene cypriniforms is a major problem for confident taxonomic assignment even at the family level. To better understand the early morphological disparity of cypriniforms, I conducted geometric morphometric shape analysis on all available Eocene cypriniform specimens following a systematic taxonomic review. Complete and undeformed two-dimensional specimens preserved laterally on slabs were selected for image capture using a surface scanner. Fourteen homologous anatomical loci which represented body shape were digitized. A sample of 86 specimens from three families, four genera, and 9 species were studied, consisting of 54 individuals of catostomids, 29 jianghnaichthyids, and 3 cyprinids. Regressions of shape versus size suggest allometry plays an important role on the body shape changes through ontogeny and body shape variations among groups of Eocene cypriniforms. Moreover, discriminant function analysis on Eocene catostomids vs. cyprinids suggests significant difference between these two groups in body shape ($p<0.00001$). In addition, although only 3 observations are currently available from Cyprinidae, they are distinct from catostomids and jianhanichthyids in a body shape morphospace (PC1+2, 63% of variance). The next step of this research will be to collect more data from Eocene cyprinids and applying phylogenetic comparative methods to better understand evolutionary trajectory and patterns of Cypriniformes.

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490 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Tobit Liyandja[1,2] and Jonathan Armbruster[1]

[1]Auburn University, Auburn, Alabama, USA. [2]University of Kinshasa, Kinshasa, Kinshasa, Congo, the Democratic Republic of the

Geometric morphometric and molecular phylogeny provide new insights about convergent evolution, distribution and diversity within the African carp: *Labeo parvus*.

Labeo is the third most diverse African Cyprinoid genus and is widely distributed. *Labeo parvus*, a small species originally described from the Congo basin, seems to be the only species of the Reid's forskalii-group to be distributed in four different African ichthyo-provinces (Nilo-Sudan, Upper and Lower-Guinea, and the Congo). Several nominal species have been synonymized with *L. parvus* despite Reid's proposition to restrict the occurrence of that species to the Congo basin and the distinction between *L. parvus* and close relatives remains problematic. We used geometric morphometrics and molecular phylogenetics to assess the biological diversity within *L. parvus* and reevaluate its distribution. Our phylogenetic analysis strongly supports a non-sister relationship between the West Africa (Nilo-Sudan and Upper Guinea ichthyo-provinces) and the central Africa (Congo ichthyo-province) *Labeo parvus* lineages. Permutation tests for Procrustes and Mahalanobis distances, applied on the overall body shape dataset, reveal a significant difference (P-value < 0.0001, PD= 0.0267 and MD= 4.1437) between the West Africa and Congolese *L. parvus* lineages. Because phylogenetic reconstruction is corroborated by geometric morphometric analysis, we conclude that *L. parvus* is an endemic species of the Congo basin and does not occur in West Africa where it is replaced by *L. ogunensis* as suggested by Reid. Additionally, our analyses suggested that both *L. parvus* and *L. ogunensis* are species complexes. We discuss our findings in term of convergent evolution by mapping the phylogeny into the morphospace and testing for phylogenetic signal.

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

Oliver Ljustina

Southeastern Louisiana University, Hammond, LA, USA

Using Species Traits to Predict Habitat Partitioning in a Suburban Watersnake (Genus: *Nerodia*) Assemblage

Organisms which persist in urbanized areas often possess particular traits; for example, they tend to be generalist species with smaller body sizes. In this study, I used visual encounter surveys to examine a system of suburban drainage canals in southeastern Louisiana to determine if habitat use among watersnakes could be predicted by life history traits of individual species. I selected transects along three canal types (shallow/narrow, intermediate, deep/wide) which potentially exemplified habitat preferences of the four species of watersnake typically found in freshwater ecosystems in southeastern Louisiana. I hypothesized that 1.) generally piscivorous and more aquatic species (i.e. *Nerodia cyclopion* and *Nerodia rhombifer*) would be primarily found in deeper canals and would generally be the most abundant species, and 2.) that more terrestrial species which preferentially feed on anurans (i.e. *Nerodia erythrogaster* and *Nerodia fasciata*) would be restricted to shallower canals and be would be generally less abundant. Individuals of *Nerodia cyclopion* were found mostly in intermediate canals and were the most abundant snakes, while individuals of *Nerodia rhombifer* were found primarily in shallower canals and were the least abundant snakes. Individuals of *Nerodia erythrogaster* were found primarily in shallower canals and were the second most abundant snake. I encountered no individuals of *Nerodia fasciata*. Life history traits were effective in predicting habitat use in this system for some watersnake species, and less so for others. Urban systems provide the opportunity to examine factors influencing ecological community structure by stratifying habitat preferences among species.

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

Jeremy J Lomax[1] and Stephanie Crofts[2]

[1]*Brown University, Providence, RI, USA.* [2]*University of Illinois, Urbana-Champaign, Champaign, IL, USA*

Tooth Arrangement's Effect on Durophagous Predation

Durophagous organisms, like pacus and drums, consume hard prey items using teeth that are to some degree ‘molariform’ and arranged in semi-continuous crushing surface. This contrasts the tooth morphologies and arrangement of other organisms, who are either less specialized or specialized on prey without hard shells. Studies have made progress explaining this diversity in the context of a single tooth’s relative crushing performance, but understanding crushing ability is complicated by the interspecific variation seen in the arrangement of teeth. To understand the effects tooth pattern has on a predator’s crushing ability, we tested four tooth arrangement patterns roughly based on natural design, with teeth in: a) a single row; b) an off-set line; c) a square; d) a concentrated crushing surface. To test the interaction between tooth arrangement and tooth shape, we made milled aluminum tooth plate models reflecting our four patterns, and varying tooth morphologies, and used these to determine the force necessary to crush representative prey items using a material testing system. While preliminary data suggest a trend in linear arrangements requiring less force to fracture, these results were non-significant and potentially the result of highly variable testing material. Using 3D printed replicas of the intertidal snail *Nucella lamellosa* we created functionally identical prey items for testing, essentially reducing the effects of variation. We discuss here the relationship between crushing ability, tooth morphology, and general patterns of tooth arrangement focusing on tooth plates demonstrating a linear organization compared to those that coalesce teeth into a crushing surface.

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

John Loomis and Jennifer Deitloff

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

Comparison of Foot Morphology in *Plethodon ventralis* and *Plethodon websteri* using Geometric Morphometrics

Morphological features of species are often related to environmental conditions or resource use. *Plethodon websteri* and *P. ventralis* have overlapping ecological requirements, and the two species are very similar in appearance. When found in allopatric locations *P. ventralis* and *P. websteri* both show color polymorphism with the presence or absence of a red stripe along the dorsal side. When found in sympatry, they diverge in this characteristic with *P. ventralis* displaying the unstriped morph and *P. websteri* with the red striped morph. We hypothesized that foot shape would differ between species and would diverge in sympatry. We used geometric morphometrics with homologous landmarks on images of the front and hind feet to capture foot morphology. We used a multivariate analysis of variance (MANOVA) to assess the differences in feet shape, and a principle components analyses (PCA) to graphically demonstrate differences in foot morphology between the two species. We also used warp grids to show the divergence of each species from the overall average. We found support for our hypothesis that *P. ventralis* and *P. websteri* differed in front and hind foot morphology. Further research could be conducted to determine if foot shape is adaptive for each species in their natural environments.

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463 Herpetology Morphology I, Highland D, Sunday 15 July 2018

Jorge Alejandro Lopez Torres

LANGEBIO, Irapuato, Guanajuato, Mexico

Ecomorphology of Neotropical Salamanders

Ecomorphology is the branch of ecology study of the relationship between body shape and function of organisms, as well as the response of these to environmental pressures. In a phylogenetic context, ecomorphology can link the diversification of species with the use of environmental resources or microhabitat. In systems such as *Anolis* lizards, the combination of ecomorphological and phylogenetic studies has enriched our knowledge of the ecological and evolutionary factors that impacted the diversification and richness of species. The Neotropical plethodontid salamanders (tribe Bolitoglossini) include 40% of the global salamander species diversity and haves diversified into arboreal, cave, terrestrial and even fossorial microhabitats. Some cases of morphological homoplasy associated with the use of the same microhabitat have been identified, suggesting that there are different ecomorphs within the group. Previous studies of morphology of this lineage have focused on variation in size and shape or osteological analyses, but a formal analysis of ecomorphology has not yet been done. In this study, we use body measurements likely related to microhabitat use from preserved museum specimens and phylogeny, to identify convergent morphological regimes, and relate these morphological regimes to microhabitat use to test for the presence of ecomorphs within the Neotropical salamanders. Identifying convergent morphological regimes in Neotropical salamanders will contribute to a better understanding of the relationship between morphology and the microhabitat use, taking into account evolutionary processes that contributed to the diversification of this salamander lineage.

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132 Ichthyology Biogeography, Grand Lilac Ballroom South, Saturday 14 July 2018

Hernán López-Fernández[1], Stephanie Blain[2] and Viviana Astudillo-Clavijo[3]

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Increased phylogenomic resolution of Neotropical cichlids allows dating of Guiana Shield biogeographic events within the genus *Geophagus*

The genus *Geophagus* sensu stricto (ss., Cichlidae: Geophagini) is widespread in the Amazon, Orinoco and Guiana Shield basins but its diversity, phylogenetic relationships and biogeographic history remain poorly understood. *Geophagus* ss. is part of a monophyletic but unclearly resolved clade comprising *Gymnogeophagus* and the "*Geophagus*" *steindachneri* clade. We analyzed sequences from 742 exons using concatenated and summary coalescent methods to clarify relationships within the clade. Addition of "*G.*" *pellegrini* to the *steindachneri* clade unambiguously resolved relationships among the three genera. We used the newly resolved relationships, the Eocene fossil *Gymnogeophagus eocenicus* and a literature-based secondary root calibration to date the divergence of *Geophagus* ss. from throughout its range, with emphasis on Guiana Shield populations. Our analyses revealed complex relationships among Amazonian and Orinoco lineages, as well as a monophyletic clade of *Geophagus* comprised of a "Rio Negro clade" as sister to a "Guiana Shield clade" that included lineages from the Rio Branco and Rupununi basins, and a "Coastal Clade" of drainage-specific populations in each basin between the Essequibo and Marowijne river basins. Divergence between the Rio Negro lineage and the Guiana Shield clade appears to have occurred 4-10 Ma and the Coastal Clade was dated to 2.83-7.15 Ma (mean 5.1 Ma). The latter spans a late Miocene to a mid-Late Pliocene age that could be consistent with the breakup of the Proto-Berbice paleo drainage and the establishment of a connection between the greater Amazon basin and the coastal drainages of the Guiana Shield.

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

Stephen Lougheed

Queen's University, Kingston, Ontario, Canada

Using the Past to Explore the Future. Lessons from Landscape Genetics and Phylogeography of North America Herpetofauna

Predicting how organisms might be impacted by future climates and landscapes is fraught with challenges. Our research on phylogeography of frogs and snakes, including investigations of secondary contact zones, provides insights on how historical climate and habitat shifts shaped past species distributions and evolutionary trajectories, and thus how organisms might respond in the future. Our investigations of gene flow, across hierarchical spatial scales, help us to understand how landscape features modulate dispersal, and how human-induced environmental changes may affect this. Newer work on frog emergence and breeding time and variation in some mating system traits show how changing spring temperatures may affect phenology and fitness.

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

Robert Lovich[1] and Christopher Petersen[2]

[1]Naval Facilities Engineering Command Southwest, San Diego, CA, USA. [2]Naval Facilities Engineering Command Atlantic, Norfolk, VA, USA

Amphibians and Reptiles of United States Department of Defense Installations

The United States (U.S.) Department of Defense (DoD) occupies approximately 25 million acres of land within the U.S., spanning most ecosystems contained therein. To date, no comprehensive inventory or analysis of amphibian and reptile diversity has been conducted on military lands. This study updated and developed herpetofauna species lists for 415 DoD installations/sites within the continental U.S., and analyzed species diversity on DoD sites. The herpetofauna species confirmed present on DoD sites represent 63 percent of the total native herpetofauna species documented in the continental U.S. Of the Military Services, Army sites have the greatest number of confirmed species, followed by the Air Force, Navy, and Marine Corps, respectively. Those military installations with the greatest amphibian and reptile biodiversity are located in the southeastern U.S. DoD lands are home to many species of Federally-listed, State-listed, and at-risk herpetofauna. In general, the number of non-native and native transplant herpetofauna species/subspecies on DoD sites is relatively low. Lastly, our analysis has verified that that approximately half of the military sites evaluated in this study have at least one venomous snake species confirmed present. The results of this investigation directly assist in ongoing management and conservation of herpetofauna species on DoD lands.

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125 CHS: Effects of Climate Change Symposium, Grand Lilac Ballroom North,

Friday 13 July 2018

Leslie Anthony Lowcock[1] and Purnima Govindarajulu[2]

[1]N/A, Whistler, BC, Canada. [2]BC Ministry of Environment, Victoria, BC, Canada

Potential climate change effects on introduced and invasive herpetofauna in Canada: a review.

With the world's second-largest land area but relatively low herpetofaunal diversity, Canada seems an unlikely place for introduced reptiles and amphibians unadapted to northern climes to gain foothold, let alone become problematic. And yet, not only has this occurred, but it has involved both transplanted native and non-native forms. Warmer areas of the country such as southern British Columbia and southwestern Ontario—both of which are experiencing shorter winters and earlier springs—would be most vulnerable to alien species introduced from warmer climates, as the establishment/naturalization of exotic red-eared slider in both locations, and a burgeoning invasion of European wall lizard on Vancouver Island illustrate. Yet native species have also been successfully introduced to previously uninhabited areas of the country: Pacific chorus frog and red-legged frog in the Haida Gwaii archipelago; American bullfrog and northern green frog in the lower B.C. mainland and on Vancouver Island; mink frog on Anticosti Island in the Gulf of St. Lawrence; and American toad, mink frog, northern green frog, wood frog and Maritime gartersnake on Newfoundland. With invasive species second only to habitat loss as a force of extinction in the Anthropocene, we review successful introductions and current problems, using existing information for various introduced taxa from Canada and other jurisdictions to consider whether climate warming might catalyze further invasiveness of introduced herpetofauna in this country.

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188 ASIH STOYE GENERAL ICHTHYOLOGY I, Grand Lilac Ballroom South, Thursday 12 July 2018

William Ludt[1], Moises Bernal[2], Erica Kenworthy[1], Eva Salas[3] and Prosanta Chakrabarty[1]

[1]Louisiana State University, Baton Rouge, LA, USA. [2]King Abdullah University of Science and Technology, Thuwal, Saudi Arabia. [3]Cabrillo College, Aptos, CA, USA

Investigating species limits of surgeonfishes in the Eastern Pacific (Acanthuridae: *Prionurus*)

Many sister species can only be distinguished by slight color variation. However, coloration is a labile character that can be misleading, and molecular analyses have demonstrated that these patterns do not always accurately reflect the distinct evolutionary histories between closely related groups. In the present study, we analyze the evolutionary history of sister species of *Prionurus* in the Tropical Eastern Pacific (TEP), which are mainly distinguished by the presence or absence of dark spots on their body. We examined the species limits in this system using comparative specimen-based approaches, a mitochondrial gene (COI), more than 800 nuclear loci (Ultraconserved Elements), and abiotic niche comparisons. The results indicate there is a complete overlap of meristic counts and morphometric measurements between the two species, with only modal differences in pectoral and dorsal fin-rays. Further, we detected multiple individuals with intermediate spotting patterns suggesting that this trait is not diagnostic. Mitochondrial data recovered a single main haplotype shared between the species and all

locations resulting in a complete lack of structure ($\Phi_{ST} = 0$). Genomic analyses corroborate this lack of genetic differentiation ($F_{ST} = 0.013$), and no alternatively fixed SNPs were detected between the two species. Furthermore, niche comparisons could not reject niche equivalency or similarity between the species. Together, these results suggest that these two phenotypes are conspecific and widely distributed in the TEP. The underlying causes of this phenotypic plasticity are unknown. However, this system gives insight into general evolutionary dynamics within the TEP.

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

Marvin M. F. Lutnesky[1], Kenwyn R. Cradock[2] and James B. Reynolds[3]

[1]*Department of Science and Mathematics, Texas A&M University – San Antonio, San Antonio, TX, USA.* [2]*Department of Biology, Eastern New Mexico University, Portales, NM, USA.* [3]*College of Fisheries and Ocean Sciences, University of Alaska Fairbanks, Apache Junction, AZ, USA*

Estimation of Electroshock Immobilization Threshold and Effective Conductivity of Two Small Fishes

Electrofishing (EF) is commonly used for fish capture. The threshold power density (D_t, µW/cm^3) transferred from water to fish for immobilization is dependent on the conductivity of the water (σ_w) and the fish (σ_f). While EF is generally safe for fish, improper settings may cause injuries, including mortality, or more subtle damage to physiology, or delayed reproduction. EF is usually applied to a fish community, so we need to understand variation in σ_f to understand variation in D_t. Minimum threshold power density (D_m) is transferred to a fish when σ_w and σ_f are equal, i.e. in a matched condition. For unmatched conditions, more power density must be applied to the water to achieve the same transfer of power density as in the matched condition. At any water conductivity, D_t must be estimated by experimentation. Over a range of water conductivities, assuming the σ_f is bracketed, D_t as a function of σ_w will form a U-shaped curve and the nadir provides an estimate of D_m and σ_f. What we know about σ_f comes primarily from studies of game fishes. However, we estimated D_m and σ_f for a small cyprinid (*Cyprinella lutrensis*) and a poeciliid (*Gambusia affinis*). Using 73 *C. lutrensis*, and 23 *G. affinis*, we found D_m and σ_f values to be 120 µW/cm^3 and 23 µS/cm, and 142 µW/cm^3 and 23 µS/cm, respectively. These values of σ_f are less than half of previously known values, demonstrating the need to consider such variation in EF sampling.

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174 ASIH STOYE GENERAL ICHTHYOLOGY II, Grand Lilac Ballroom South, Thursday 12 July 2018

Daniel MacGuigan[1] and Thomas Near[1,2]

[1]Yale University, New Haven, CT, USA. [2]Peabody Museum of Natural History, New Haven, CT, USA

Genomic Data Clarify the Evolutionary History of Two Widespread Species of Darter, *Etheostoma nigrum*and and *E. olmstedi*

The prevalence of geographic isolation as a speciation mechanism is exemplified by darters, a clade of ~250 freshwater fishes. Nearly all darter sister species pairs are isolated in different river drainages, precluding the possibility of gene flow. One exception is *Etheostoma nigrum* and *E. olmstedi*, a widespread sister species pair with three separate areas of range overlap. These species have a complicated taxonomic history, fluctuating between one and four recognized species and between two and twelve recognized subspecies. To understand the evolutionary history of *E. nigrum* and *E. olmstedi*, we ask the following questions: 1) how many species are there within *E. nigrum* and *E. olmstedi*, 2) does genetic variation correspond to river basin arrangement or to geographic proximity, and 3) what is the nature of introgressive hybridization between *E. nigrum* and *E. olmstedi*? We used ddRADseq to collect thousands of SNPs for ~500 individuals from across the ranges of *E. olmstedi* and *E. nigrum*. Our data supported the recognition of two contested and highly localized species, *E. perlongum* and *E. susanae*, while also concluding that *E. olmstedi* consists of two species. We uncovered several surprising patterns of genetic variation, including two previously unrecognized peripheral and ancient evolutionary lineages within *E. nigrum*. Finally, our results revealed a complex history of introgression across two hybrid zones in New York and Virginia. Our study highlights the utility of genomic data for addressing complex taxonomic situations while simultaneously providing a window into the speciation process.

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

Andrew MacLaren[1], Paul Crump[1], Andy Royle[2] and Michael Forstner[1]

[1]Texas State University, San Marcos, Texas, USA. [2]USGS Patuxent Wildlife Research Center, Laurel, Maryland, USA

Observer free experimental evaluation of habitat and distance effects on the detection of anuran and bird vocalizations

For vocalizing animals, acoustic surveys are often used to determine density, distribution, and diversity. Surveys are traditionally performed by humans, but automated recording devices (ARD) are becoming increasingly popular. Sound attenuates as it travels, and habitat types may differentially increase attenuation further. These effects are unaccounted for in acoustic monitoring programs where equal detection among species and habitats is assumed. We evaluated 3 playback devices and 3 ARDs using vocalizations of 6 anurans, 6 birds, and 4 pure-tones. Using the optimal devices, we then broadcast and recorded vocalizations in five habitats along 1000m transects. We used generalized linear mixed models to test for effects of habitat, distance, species, environmental, and landscape variables. Finally, we predicted effective

detection distances (EDR; *p*=0.5) for all vocalizations. Among the devices tested, only one playback device simulated vocalizations consistently, and the most modern ARD outperformed its predecessors in sensitivity. We found differences in detectability between open and closed canopy habitats, and heterogeneity in EDR among species. Humidity positively influenced detectability, but where topography impeded sound transmission detectability decreased. Surprisingly, ~10% of the variability within the data occurs among sites, thus, optimizing survey designs to account for these issues may require pilot measurements. Our results refute the assumption of equal probability among species and habitats as distance increases, and suggest that researchers should model the effects of habitat and distance among species when calculating detection probabilities.

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30 SSAR SEIBERT CONSERVATION I, Highland B, Thursday 12 July 2018

Thomas Maigret[1], John Cox[2] and Jian Yang[2]

[1]University of Kentucky, Department of Biology, Lexington, KY, USA. [2]University of Kentucky, Department of Forestry and Natural Resources, Lexington, KY, USA

Persistent Geophysical Effects of Mining Threaten Ridgetop-Associated Herpetofauna of Appalachian Forests

Surface coal mining can permanently alter the rugged topography of Appalachia, which plays an important role in creating and maintaining the structure, composition, and diversity of the region's ecological communities. We used remote-sensing datasets to characterize the past and future topographic impacts of surface coal mining on the mixed-mesophytic forests of eastern Kentucky. To provide context, we examined the consequences of widespread topographic rearrangement for an imperiled ridgetop-associated predator, the timber rattlesnake (*Crotalus horridus*). We found that surface mining disproportionately impacts ridgetop habitats, causing large reductions in the suitable habitat for *C. horridus* and likely other ridgetop-dependent biota. Land permitted for surface mining is also concentrated in high topographic positions, thus patterns of habitat loss are likely to remain concentrated in these ecosystems into the future. These permanent topographic shifts complicate restoration of preexisting microhabitats, creating homogenized landscapes, threatening long-term ecosystem health, and charting a new course towards less diverse ecological communities.

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472 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Alex Maile and Matthew Davis

St. Cloud State University, St. Cloud, Minnesota, USA

Changes in Body Shape Across Habitat Transitions in Lizardfishes (Aulopiformes)

This study focuses on the morphologically diverse and species-rich (~282 species) marine lineage of lizardfishes (Aulopiformes). Aulopiform species possess a breadth of variation in body shape across their radiation, ranging from cigar-shaped to elongated. No study has ever

investigated the evolutionary pattern of body shape changes in this lineage of fishes, and we further compare the evolution of body shape to habitat distributions of lizardfishes. Evolutionary changes in the body shape of lizardfishes is quantified with a landmark-based geometric morphometric approach based on digitized specimens representing all of the major lineages of aulopiform fishes.

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

Zachary Marcou[1], Allison McElroy[1], Josh Pierce[2], Craig Rudolph[2] and Stephen Mullin[1]

[1]Stephen F. Austin State University, Nacogdoches, Texas, USA. [2]Southern Research Station, U.S. Forest Service, Nacogdoches, Texas, USA

Detecting Turtles (Emydidae: *Terrapene*) Using Wildlife Cameras

As expected for ectothermic species, the activity patterns of Box Turtles (*Terrapene carolina*) vary with changes in the temperature of their surroundings. In turn, changes in the turtles' levels of activity can affect the ability of researchers to detect individuals in the field. We used camera trap arrays to photograph turtles in the Angelina National Forest (eastern Texas) during two consecutive field seasons. Images were recorded every 30 sec at the intersection of 20 drift fence arrays and, for each turtle detected, we recorded the date, time, and temperature, and amount of precipitation. We examined whether or not turtle detections were influenced by these abiotic variables. Some turtles (~7 %) having a unique pattern of shell damage were positively identified as individuals moving through the same array on different days. We discuss our findings as they pertain to understanding the activity patterns of Box Turtles via remote detections.

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

Zachary Marcou[1], Josh Pierce[2], Craig Rudolph[2] and Stephen Mullin[1]

[1]Stephen F. Austin State Univ., Nacogdoches, Texas, USA. [2]Southern Research Station, U.S. Forest Service, Nacogdoches, Texas, USA

Remote Photography Reveals the Diel Activity Cycle of a New World Elapid

Knowledge of the activity patterns for a given species can be used to make predictions about its ecological role in the environment. Information reported about the diel activity cycles of snakes belonging to the genus *Micrurus* (Squamata: Elapidae) is predominantly based on anecdotal evidence. Reported observations of surface activity of *Micrurus* are not exclusive to any particular portion of a day, having occurred at any time within a 24–hr period. We used 20 remote photography arrays (RPA) to detect snakes during two consecutive activity seasons in the Angelina National Forest (eastern Texas). Cameras recorded images at 30–sec intervals, and automatically logged the date, time, and temperature for all images. RPA detected a total of 1094 individual snakes. Of these, we examined the data for the 174 images of *Micrurus tener* (Texas Coralsnakes) to determine if there were any temporal patterns for the activity of this species. In a given day, Texas Coralsnakes exhibited two peaks in activity that coincided with twilight. We interpret our findings as they relate anecdotal claims about the activity patterns of *M. tener*, the species' ecology, and the utility of RPA in future research that examines the natural histories of snake species that are challenging to detect in the field.

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615 Herpetology Physiology, Highland C, Saturday 14 July 2018

Jacob Marlay[1], Elizabeth Everman[2] and Paul Klawinski[1]

[1]Dept. of Biology, William Jewell College, Liberty, MO, USA. [2]Dept. of Molecular Biosciences, University of Kansas, Lawrence, KS, USA

Adaptation and Acclimation in an Introduced Gecko (*Hemidactylus turcicus*) Encountering Novel Thermal Environments during Range Expansion.

During a species' range expansion, range expansion may be limited to environments similar to the species' native range, but may include areas that pose novel environments. In this case, the species can cope with those new environments by either adapting to the new environments, relying on phenotypic plasticity, or a combination of both. We studied the thermal biology of the introduced gecko, *Hemidactylus turcicus*, in Galveston, TX, and Oklahoma City, OK, to examine how the species is coping with the colder environments it is encountering as it experiences a northward range expansion. We collected geckos during the winter of 2018 and the summer of 2017 and recorded field body temperatures and ambient temperatures as well as preferred temperatures of both populations. In addition, we raced geckos down a liner racetrack at 10 C, 15 C, 20 C, 25 C, 30 C, and 35 C after being lab acclimated at both seasons' field collected temperatures. Winter geckos in Oklahoma City were active on walls during the winter at temperatures significantly below their preferred temperatures but the same was not true for Galveston geckos. Both populations exhibited similar field body temperatures during the summer months demonstrating that Oklahoma City does pose a potential thermal challenge. Both winter and summer collected geckos were able to run at temperatures below their previously reported critical thermal minimum. Patterns of performance across temperatures indicated that this species may be coping with a novel, cooler environment through a combination of both adaptive response and acclimation.

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369 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY I, Highland D, Thursday 12 July 2018

Roberto Márquez[1], Tyler Linderoth[2], Daniel Mejía'Vargas[3], Pablo Palacios[3], Rasmus Nielsen[2], Adolfo Amézquita[3] and Marcus Kronforst[1]

[1]University of Chicago, Chicago, IL, USA. [2]University of California, Berkeley, CA, USA. [3]Universidad de los Andes, Bogotá, Colombia

Divergence, Gene Flow and Convergent Origins of Aposematic Phenotypes in *Phyllobates* Poison-dart Frogs

Understanding the evolutionary genetic processes that generate phenotypic diversity is among the main goals of evolutionary biology. Studying the spatial distribution of phenotypic and genotypic variation present within a lineage can provide valuable insight on the role that different evolutionary processes, (e.g. adaptation, isolation, gene flow) have played in shaping its phenotypic diversity. The genus *Phyllobates* is composed of five nominal species that have independently evolved aposematic coloration at least twice. Aiming to understand the evolutionary genetic processes underlying this case of convergent evolution, we study survey genetic and morphological, and colour-pattern variation in Colombian populations of this genus, where coloration has evolved rapidly. We focus on the upper/mid San Juan River drainage, where there is ample and seemingly continuous variation in coloration among geographically close populations. Based on phylogenetic, population genetic, and cline analyses we find 1. dynamic and correlated evolution of morphology, coloration, and toxin concentration and 2. evidence for gene flow and local adaptation as the forces shaping variation in aposematic phenotypes along the San Juan drainage.

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

Thomas Marshall[1,2], Thomas Jenkinson[3] and David Rodriguez[1]

[1]Texas State University, San Marcos, TX, USA. [2]University of Texas at Austin, Austin, TX, USA. [3]University of California at Berkeley, Berkeley, CA, USA

Population Genomics of Amphibian Chytrids in Texas: Understanding Pathogen Dynamics in Understudied Regions

Chytridiomycosis, an emerging infectious disease caused by the fungal pathogen *Batrachochytrium dendrobatidis* (*Bd*), has had a devastating impact on many amphibian populations worldwide over the last forty years. However, mortalities have not been distributed equally across species or geographic regions. Notable declines have occurred in Australia, the Neotropics, and the western United States, while populations in Asia and the eastern and central U.S. have been largely unscathed, despite the presence of *Bd* in these regions. There are still several geographic gaps in our knowledge of *Bd* genetics, and relatively few studies have focused on regions in which *Bd* exhibits low virulence, creating a bias in our current knowledge of the pathogen’s diversity. Here, we isolated, cultured, and used next-generation sequencing to characterize strains of *Bd* in central Texas, a region not known for major chytridiomycosis-associated declines. We then performed genetic clustering analyses with 28 Texas isolates and a panel of globally distributed strains from previous studies. Our results indicate that the isolates cultured here belong to the pervasive global panzootic lineage (GPL), and that they cluster with other strains from North America. We also found evidence of genetic structure within *Bd*-GPL across continents, as well as possible admixture between strains from different clusters. By turning our attention to understudied regions, we seek to gain a more complete evolutionary picture of *Bd* and a better understanding of the conditions that contribute to variable disease outcomes in different areas.

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196 SSAR SEIBERT CONSERVATION I, Highland B, Thursday 12 July 2018

Amanda Martin and Karen Root

Bowling Green State University, Bowling Green, Ohio, USA

Detecting Spatial Patterns of Herpetofauna Biodiversity in Northwest Ohio

The Oak Openings is a regional biodiversity hotspot with a multitude of endangered, threatened and potentially threatened species, including vulnerable herpetofauna. The bioregion has many protected areas that consist of oak forests and savannas, wet and dry prairies, and barrens that lie within a human-dominated landscape. Given the lack of holistic studies of herpetofauna diversity, this study fills in gaps in our knowledge of herpetofauna diversity, richness and abundance while providing a foundational spatial dataset. Herpetofauna were detected using visual encounter surveys within the Oak Openings Preserve, the largest protected area in the bioregion. Spatial patterns were examined using GPS coordinates for each individual detected. We observed 21 species encompassing 1345 individuals. Twelve expected species were not detected within the geographical area and amphibians accounted for 96% of our detections. We found that Caudata were widely distributed across the landscape, and all herpetofauna groups, except for squamates, had significant spatial clustering. Finally, we found that Anura and Caudata were found in forests significantly more than expected. Species distribution patterns vary over time and space and whether these changes occur from anthropogenic or natural factors, it is critical that we monitor changes to inform conservation efforts. Therefore, we have created a spatial representation of herpetofauna biodiversity to document current abundances and distributions. We developed a simple, reduced labor and cost-effective survey method for future monitoring. Furthermore, since Oak Openings Preserve is a representative park we would expect that herpetofauna diversity would follow similar patterns in other protected areas.

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189 ASIH STOYE GENERAL ICHTHYOLOGY II, Grand Lilac Ballroom South, Thursday 12 July 2018

Rene Martin

University of Kansas, Lawrence, KS, USA

The Role of Phylogeny in the Evolution of Body Shape of Lanternfishes (Myctophiformes)

Lanternfishes are an abundant and comparatively species-rich group of small mesopelagic fishes. The 257 species of myctophids share a relatively similar body plan, but many lineages show patterns of variation in their body shape. Some of this variation includes slimming of the caudal peduncle, body truncation, and body elongation. Little work has been done to explain the evolution of these observed patterns. To address questions of potential body shape convergence or adaptation across lineages, we use geometric morphometric methods to describe the body shape of over 700 lanternfish specimens including at least one representative of every genus of myctophiform. We examine patterns of body shape arrangement in a principal component-based morphospace and investigate the potential influence of phylogeny

on body shape using a recent phylogeny of lanternfishes.

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

Kristen Martinet, Leyna Stemle and Gabriel Langford

Florida Southern College, Lakeland, Florida, USA

A Comparative Analysis of the Commensal Diversity of Two Gopher Tortoise (*Gopherus polyphemus*) Populations in Central Florida

Gopher tortoises (*Gopherus polyphemus*) are extremely important to Florida's environments and have been called a keystone species because their burrows serve as shelter and foraging space for commensals. Burrow commensal diversity varies based on location and the age of the gopher tortoise community. However, no studies have accessed how commensal communities respond to gopher tortoise reintroductions. To determine the difference in commensal diversity between gopher tortoise populations, this study surveyed the commensals present in two Environmental Lands Program properties in central Florida: Circle B Bar Reserve (CBR), which has a relocated gopher tortoise population, and Lakeland Highland Scrubs (LHS), which has a natural, undisturbed population. Pit fall traps, motion-activated field cameras, and a burrow camera were used to survey the commensals that live among the gopher tortoises in both sites. Over 200 individual commensals spanning over 30 different species were found at each site during an eight-week sampling period. The distribution of these species at each site was analyzed using Shannon's Diversity Index. The two sites ultimately did not have statistically significantly different commensal diversity, even though their gopher tortoise populations were present in their environments for very different lengths of time. The similarity of commensal populations could be attributed to the similarity of plants around the burrows, as well as the existence of other burrow-dwelling species such as pocket gophers at CBR that allowed burrow commensals to live at CBR without gopher tortoises.

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

Wilfredo Matamoros[1], Sara Domínguez-Cisneros[1], Ernesto Velázquez-Velázquez[1] and Caleb McMahan[2]

[1]Universidad de Ciencias y Artes de Chiapas, Tuxtla Gutiérrez, Chiapas, Mexico. [2]The Field Museum of Natural History, Chicago, IL, USA

A New Species of Killifish of the Genus *Profundulus* (Cyprinodontiformes: Profundulidae) from the Mexican state of Oaxaca

The Middle American killifish genus *Profundulus* occurs in most Pacific and Atlantic drainages from the Mexican state of Guerrero to the Río Chamelecón in Honduras, with highest species

diversity in southeastern Mexico. In this study we document a new member of the genus from the Mexican state of Oaxaca. It is distinguished from closely related congeners by combinations of pigmentation patterns, meristic data, and osteological characters. Based on phylogenetic analysis of molecular sequence data, the new species is recovered as the sister taxon to *Profundulus balsanus*, recently re-elevated and re-described. The discovery of this new lineage in southeastern Mexico raises the number of species from this region to five and suggests that this area has been an important center for diversification within this clade of killifishes.

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

Laurie Mauger[1], Frank Mazzotti[2] and James Spotila[3]

[1]Southern Utah University, Cedar City, UT, USA. [2]University of Florida Fort Lauderdale Research and Education Center, Davie, FL, USA. [3]Drexel University, Philadelphia, PA, USA

Landscape Genetics of *Crocodylus acutus* in Pacific Costa Rica

The American crocodile, *Crocodylus acutus*, is a wide-ranging species that is endangered throughout much of its range. We investigated the influence of geographic features on gene flow between 11 *C. acutus* localities in Pacific Costa Rica. We utilized nine microsatellite loci to study the landscape genetics of 183 individuals. We identified three main population clusters using STRUCTURE, (1) Parque Marino Nacional (Las Baulas), (2) Parque Nacional Santa Rosa, Parque Nacional Palo Verde, and Rio Tarcoles and (3) Osa Conservation Area. Bayesian clustering analysis (Geneland) gave a somewhat different distribution, but rates of migration calculated by BayesAss+1.3 supported the results of STRUCTURE. Parque Marino Nacional (Las Baulas) was isolated from other populations with little migration occurring from or to this population. Parque Nacional Santa Rosa received a large number of migrants (approximately 30% of the population) from Parque Nacional Palo Verde, which contained a major source of crocodiles for the coast. There was no isolation by distance along streams with a cost distance analysis using GIS framework. These distances only explained up to 11% of the genetic differentiation observed between population pairs. The crocodile population in Las Baulas is of particular concern because of its isolation. A central management plan is needed including all Pacific Conservation Areas of Sistema Nacional de Areas de Conservacion (SINAC) to account for the effective dispersal observed between population clusters.

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471 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Zachary May and Matthew Davis

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

Evolution of Body Shape in the Deep-Sea Hatchetfishes (Sternoptychidae)

Stomiiformes (dragonfishes and their allies) are a species-rich order of fishes (~438 species) that are primarily found throughout the meso-bathypelagic zone of the world’s oceans. The bodies of stomiiforms are covered in an array of bioluminescent photophores that produce light in

their near-dark to dark environment. In contrast to the more elongated body plan of most stomiiforms, fishes of the family Sternoptychidae (hatchetfishes, ~79 species) have evolved a hatchet-like body shape. Few studies have investigated the evolution of body shape among stomiiform fishes, a lineage that has evolved exclusively in a pelagic deep-sea environment. In this study we use landmark-based geometric morphometrics to examine the differences in body morphology across Stomiiformes with a focus on the family Sternoptychidae. We also explore the evolution of body shape among hatchetfishes in the context of their evolutionary relationships inferred from a synthesis of genome-scale sequencing with ultraconserved elements (UCEs) and protein-coding gene fragments.

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288 General Herpetology III, Highland B, Sunday 15 July 2018

Jacob McCartney[1], Emma Bode[1], Josephine Reinhardt[1] and Nancy Stevens[2]

[1]SUNY College at Geneseo, Geneseo, NY, USA. [2]Ohio University, Athens, OH, USA

New fossils from the Oligocene of Tanzania reveal early origin of modern African snake fauna

The origins of modern snake faunas extend back to the Miocene with the sudden increase in importance of colubroid snakes following a period of low snake diversity. This evolutionary history is well documented in North America and Europe, but comparatively little is known about the appearance and evolution of snakes in the southern continents. Ongoing fieldwork in the late Oligocene Rukwa Rift Basin of southwest Tanzania has yielded new snake fossils that begin to address this faunal transition. Previously described material reveals that although two booid species occur, the fossils are majority colubroid, suggesting the timing of colubroid expansion may differ in Africa with respect to northern continents. Newly recovered material includes the earliest known definitive Lamprophiidae, extending their fossil record by more than 25 million years and providing the first fossil calibration point for the family. Using this new calibration point, we calibrated a molecular clock model using sequences of four mitochondrial loci from 104 species with mcmctree. Preliminary results suggest an origin for Lamprophiidae at about 50 million years ago, a date near the upper range of previously estimated origin times. The earlier divergence of Lamprophiidae indicates a nearly 25 million year gap in the fossil record, and demonstrates the importance of continued fieldwork in Africa and elsewhere. The extensive ghost lineage may be partly a result of the small size of the animals, and the lack of distinct morphologies in most species permitting differentiation of different snake families.

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

Sara McClelland and Sarah Woodley

Duquesne University, Pittsburgh, PA, USA

Ecologically Relevant Levels of an Organophosphorous Pesticide Causes Changes in Stress Levels and Brain Structures in Amphibians

The organophosphorous pesticide chlorpyrifos is the most applied insecticide in the United States. Like other pesticides, chlorpyrifos is found in surface waters throughout the US, most commonly at concentrations less than 10 ppb (though higher values have been reported). While chlorpyrifos has been shown to cause neurological and behavioral problems in vertebrates that are exposed to high doses, the effects of low dose exposures are still not well understood. This study aimed to better understand the effects of these low level exposures. We exposed a vertebrate model, the Northern Leopard Frog (*Lithobates pipiens*), to 0, 1, or 10 ppb chlorpyrifos during development in a controlled laboratory study. We measured levels of the stress hormone corticosterone and body and brain shape. Exposure to chlorpyrifos resulted in increased levels of corticosterone as well as changes in brain mass and alterations in brain shape. Specifically, tadpoles that were exposed to CPF during development had wider and longer telencephala and longer olfactory bulbs. This study provides evidence that exposure to low, ecologically relevant doses of organophosphorous pesticides causes neurological effects and increased stress levels. Our results indicate that amphibian physiology is being impacted by chlorpyrifos at the concentrations that are found contaminating natural habitats.

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

Eric McCluskey[1], H. Lisle Gibbs[2], Scott Martin[2] and Jennifer Moore[1]

[1]*Grand Valley State University, Allendale, Michigan, USA.* [2]*Ohio State University, Columbus, Ohio, USA*

Does habitat area influence genetic diversity? A case study with the Eastern Massasauga

The loss of genetic diversity in fragmented landscapes is a major concern for threatened and endangered species. Reductions in patch size and connectivity are expected to further erode genetic diversity for populations that do not receive immigrants. Most conservation efforts are focused on ameliorating the connectivity issue via corridor creation to promote gene flow. Addressing the potential loss of genetic diversity from a habitat perspective is less straightforward because the relationship between habitat area and genetic diversity has not been thoroughly investigated across taxa in the field of landscape genetics. We examined this relationship for a federally threatened species, Eastern Massasauga Rattlesnake (*Sistrurus catenatus*) that is largely restricted to isolated populations making loss of genetic diversity a pertinent management issue. We obtained genetic diversity data from populations across the range that varied in habitat amount and level of connectivity. We evaluated the relationship between these habitat attributes and genetic diversity using multiple habitat metrics. Our preliminary results indicate that genetic diversity does not appear to be directly related to habitat patch area when defined by patch borders delineated using aerial imagery. Variation in habitat type, microhabitat availability, and land use histories may also be important factors when considering the influence of habitat on genetic diversity.

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

Frank McCormick[1], Jackson Leonard[2] and Benerito Martinez[3]

[1]US Forest Service, Fort Collins, CO, USA. [2]US Forest Service, Flagstaff, AZ, USA. [3]US Forest Service, Durango, CO, USA

A risk assessment of aquatic resources based on fish assemblages in the upper Animas River, Colorado, USA.

In 2015, a bulkhead failure at the Gold King Mine spilled an estimated 3 million gallons (11M L) of mine drainage into Cement Creek, a tributary of the upper Animas River in Southwestern Colorado, USA. In 2017, USEPA designated the Bonita Peak Mining District, encompassing the upper Animas River basin and its tributaries as a Superfund site. The site is affected by surface and groundwater discharge from abandoned mine lands including 48 National Priority List sites. Remediation and restoration is complicated by the fact that the basin lies within the Silverton – San Juan caldera complex in the western San Juan Mountains. Hydrothermally altered bedrock naturally weathers to contribute significant loadings of iron, aluminum and other heavy and trace metals to surface and groundwater. We used historical records and recent collections to assess the structure and condition of the fish assemblage of the upper Animas River. Wherever possible, fish collections were linked with chemistry sampling that had been conducted either at the same time or in the same reach to develop associations between chemical stressor and biological response indicators. When fish were present, collections were dominated by non-native Brook Trout and other non-indigenous species. Native fish were either rare or absent. Where native species did occur, their abundance was low. Native fish presence was associated with lower metal concentrations.

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25 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Highland A, Thursday 12 July 2018

Ciera McCoy, Christopher Lupfer and Brian Greene

Missouri State University, Springfield, MO, USA

Survey of Arboviruses in Free-ranging Cottonmouths (*Agkistrodon piscivorus*) in Southern Missouri

Four arboviruses, Eastern equine encephalitis (EEEV), Western equine encephalitis (WEEV), Saint Louis equine encephalitis (SLEEV), and West Nile Virus (WNV), normally infect avian hosts but can be transmitted to various other organisms through mosquito vectors. Although infection risks are low, each virus is capable of causing significant central nervous system disease in humans, with mortality rates approaching 75%. Cottonmouths (*Agkistrodon piscivorus*) may serve as important EEEV reservoirs because of their high population densities and primary association with wetlands, where EEEV prevalence is highest. Because cottonmouths occur in a variety of aquatic systems, we hypothesized that the proportion of infected snakes may be population-specific and correlated with mosquito density. To determine if habitat type influences the likelihood of arbovirus infection, we examined arbovirus prevalence in free-ranging cottonmouths from contrasting habitats with different mosquito densities: an upland landscape and a lowland floodplain. We predicted that the

individuals sampled from the swampy habitat would have the highest prevalence of arboviruses. Blood samples were taken from free-ranging cottonmouths in the spring and fall and analyzed for all four arboviruses using qualitative PCR. Preliminary results indicate that cottonmouths from a lowland floodplain habitat exhibit higher levels of arboviruses when compared to cottonmouths from an upland landscape habitat.

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556 ASIH STOYE GENERAL ICHTHYOLOGY I, Grand Lilac Ballroom South, Thursday 12 July 2018

Tyler McCraney[1], Michael Alfaro[1], Janet Buckner[1], Brant Faircloth[2] and Christine Thacker[3]

[1]*University of California, Los Angeles, Los Angeles, CA, USA.* [2]*Louisiana State University, Baton Rouge, LA, USA.* [3]*Natural History Museum, Los Angeles, CA, USA*

Phylogenomic Systematics of Gobiiformes: Small Fishes Show Some Backbone

Gobiiformes comprise a global radiation of small, mostly marine fishes characterized by extraordinary species richness and ecological diversity. Molecular phylogenetics has been crucial to advancing gobiiform systematics, but classification remains unsettled due to disagreements on clade relationships and poor bootstrap support; especially along the backbone of the tree subtending lineages of goby families Gobionellidae and Gobiidae. Here we use a phylogenomic approach to infer gobiiform phylogeny from 851 ultraconserved element loci sequenced on a broadly sampled set of 50 taxa. Consistent with early mitochondrial work and recent phylogenomic studies, our results support successive sister group relationships of families Kurtidae, Apogonidae, Odontobutidae, Eleotridae, Butidae, Gobionellidae and Gobiidae. We also recover monophyly of all goby lineages sampled with complete bootstrap support. These results support the classification of Gobiiformes inclusive of Kurtiformes (Kurtidae and Apogonidae), provide improved resolution along the gobioid backbone, and advance systematics of goby lineages.

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

Michael McFadden[1,2], Deon Gilbert[3], Philip Byrne[2], Peter Harlow[1] and David Hunter[4]

[1]*Taronga Conservation Society Australia, Sydney, NSW, Australia.* [2]*University of Wollongong, Wollongong, NSW, Australia.* [3]*Zoos Victoria, Melbourne, Victoria, Australia.* [4]*NSW Office of Environment and Heritage, Albury, NSW, Australia*

Recovery Efforts for the Critically Endangered Southern Corroboree Frog (*Pseudophryne corroboree)*

The Southern Corroboree Frog (*Pseudophryne corroboree*) is a small myobatrachid frog restricted to Kosciuszko National Park, in south-eastern Australia, that has rapidly declined in recent decades largely due to disease, caused by infection with *Batrachochytrium dendrobatidis*.

Population numbers are critically low with the species now only occurring at translocation sites. Immediate management objectives for this species include establishing robust insurance colonies, maintaining populations in the wild via translocation, and developing efficient

captive breeding and translocation methods to increase the longer term capacity and resilience of the program. Ex-situ insurance colonies have now been established at Taronga Zoo, Zoos Victoria and the Amphibian Research Centre. The insurance population has a genetically-diverse founder base established from wild-collected eggs over many years. Despite initial difficulties, reliably high captive breeding results have been achieved in recent years permitting the use of offspring for reintroduction and research. Experimental translocations currently include the translocation of eggs into artificial pools at four natural sites, natural pools at two sites and artificial pools at three sites with reduced threat of the disease, due to the absence of suitable breeding habitat for a sympatric, reservoir host species. An additional management action currently being trialled involves releasing frogs into enclosures within their range that restrict vectors for the chytrid fungus.

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

Emily P. McFarland[1], Carole C. Baldwin[2] and Luke Tornabene[1]

[1]University of Washington, Seattle, WA, USA. [2]Smithsonian Institution, Washington, DC, USA

Trophic Structure of Deep-reef Fishes off Bonaire and Curaçao, Southern Caribbean

Tropical deep reefs (>50 m), which include mesophotic coral ecosystems, are too deep for SCUBA divers to explore for extended periods of time and too shallow for costly deep-diving submarines to study on their way down to the deep sea. These reefs, which contain both light-dependent and -independent species, are just recently beginning to be recognized for their importance and distinctiveness from shallow reefs. In particular, recent explorations of Caribbean deep-reef fishes have shown several taxonomically and ecologically distinct communities along the deep reef slope from 50-300 m. This study analyzed the distribution of trophic groups of deep-reef fishes across the deep-reef slope off the coast of two Caribbean islands, Bonaire and Curaçao, using data from manned submersible dives. Counts of species and their depth distributions were made from visual surveys and targeted collections (>10000 total observations) aboard the *Curasub* submersible, and the trophic guild of each species was determined from the literature. We then compared depth distributions for the different trophic guilds for both within- and between-site comparisons. The analysis showed significant differences between three different groups of trophic types: (i) strict carnivores, (ii) planktivores and planktivore/carnivores, and (iii) herbivores and omnivores. These results establish preliminary data that will serve as a robust foundation for making inferences about deep-reef ecology at Caribbean-wide or global scales.

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

Rhiannon McGlone, Jennifer Deitloff and David Savage

Lock Haven University, Lock Haven, Pennsylvania, USA

Territorial Behavior in *Plethodon cinereus* (Red-Backed Salamander) in Seven Populations from Pennsylvania

Species that have wide geographic ranges can diverge in characteristics such as morphology, resource use, or behavior due to adaptation to local environmental conditions. *Plethodon cinereus* is widely distributed throughout the northeastern United States. For many populations of *P. cinereus*, intraspecific competition for resources may occur, resulting in territorial behavior. However, some populations of *P. cinereus* do not display territorial behavior. Furthermore, the extent to which males and females display territoriality can differ among populations. We tested the hypothesis that populations and sexes of *P. cinereus* differ in territorial behavior by comparing behavioral responses among seven different populations across Pennsylvania. We found that populations differ in four of the behaviors that we recorded: all trunk raised, edging (walking along edge of experimental chamber), nose taps, and bites. Other behaviors, such as body flattening and touching between salamanders, do not differ among populations. None of these behaviors significantly differed between sexes. We concluded that differences in behavior among populations is due to variation in resource abundance at these different locations. The study of territorial behavior in *P. cinereus* could be extended to determine how territoriality differs throughout the entire geographic range. Furthermore, determining levels of resource availability for different populations is a key factor that can influence population size, habitat, and behavior.

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

Sarah McGrath, David McLeod and Morgan Steffen

James Madison University, Harrisonburg, VA, USA

Exploring the Microbiome: Diversity of the Microbial Community of Three Foam Nesting Frogs, Genus: *Polypedates*, Across a Developmental Gradient

Characterization of microbial biodiversity, including that of the amphibian skin-associated microbiome, is a burgeoning frontier of research recently made accessible through advances in sequencing technology. The interaction between microbe and host has been shown to have profound influences on host health across a wide range of macroscopic organisms. Amphibians are currently one of the fastest disappearing vertebrate groups on the planet, due in part to skin-associated diseases caused by pathogenic microbes. Therefore, it is particularly important to characterize the amphibian skin-associated microbiome and to delineate the host-microbe relationships that may influence host health. In determining the microbial community of amphibian skin, it is important to consider how microbial communities are established. One of the fundamental questions related to the microbiome of amphibians and other organisms is: To what extent are skin microbes being passed down from parent to offspring (vertical transmission) or obtained from the environment? This study will focus on characterizing the cutaneous microbial diversity of three species of Southeast Asian tree frogs (family Rhacophoridae) that reproduce via the specialized breeding strategy of building a foam nest. Microbes associated with reproducing adults, foam nests (a reproductive specialization), tadpoles, and the surrounding environment will be compared. Delineating these ecological relationships (between host, microbe, and environment) is important because it adds a missing piece to our knowledge of the natural world and can broadly inform conservation efforts for amphibians worldwide.

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

Sean Mchugh and Kelly Zamudio

Cornell University, Latham, NY, USA

Evolution of Body Size and Sexual Size Dimorphism in Tortoises

Sexual size dimorphism (SSD) varies in terrestrial vertebrates from male biased to female biased. In tortoises, SSD and body size vary widely across the family while following Rensch's rule, an allometric trend in which the intensity of male biased SSD increases and female biased SSD decreases as average body size increases. The ubiquitous male combat found within the family is theorized as driving a progressive male biased trend in SSD in the clade from a female biased ancestor. Using phylogenetic comparative methods, we found that while tortoises follow Rensch's rule, clades within the family do not. We found that South African tortoises followed isometry, and tortoises of the genera *Manouria* and *Gopherus* exhibited a qualitative pattern reverse of Rensch's rule. Furthermore, evolutionary rates for male and female body size varied from clade to clade. Males rates were higher in three clades, female rates were higher in one clade, and rates were the same for each sex in another clade. We also found that the evolution of body size followed a similar pattern in males and females and only diverged near the tips, with males becoming larger than females in some lineages. The evolution of male biased SSD was correlated with egg mass. Our results indicate that the evolution of SSD in tortoises is not uniform, and that current distribution of SSD biases is the result of recent divergences in body size driven by multiple selective mechanisms.

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

Joshua Mead and William Stark

Fort Hays State University, Hays, Kansas, USA

Spatial Ecology of the Western Massasauga (*Sistrurus tergeminus*) in a Large Interior Wetland

Insight into the spatial ecology of a population of animals provides information valuable to the management and conservation of a species. For cryptic taxa such as snakes, radio-telemetry allows for individuals to be reliably located on a consistent basis. We used radio-telemetry to investigate the spatial ecology of the Western Massasauga (*Sistrurus tergeminus*) at Cheyenne Bottoms in Barton County, Kansas. Eighteen individuals (12 male and 6 female) were implanted with VHF radio transmitters during 2016-2017 and tracked twice weekly throughout the active season. Data for 15 individuals (10 male and 5 female) with more than 30 unique locations each were used for our analysis. Home range estimates were calculated using 100% minimum convex polygon (MCP) and 95% kernel density estimators (KDE), along with 50% MCP and 50% KDE to give insight into core use areas. The average home range estimate using 100% MCP was 12.9 ha and the average estimate of core use area was 2.8 ha for 50% MCP. These results are similar to the 100% MPC estimates reported in Nebraska for *S. tergeminus*, but considerably smaller than those reported in Missouri. Male estimates were larger than female estimates across all estimators. We question the usefulness of the low KDE estimates in interpreting important aspects of natural history within our data.

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

Melissa Meadows

Saint Francis University, Loretto, PA, USA. University of Tübingen, Tübingen, Germany

Fish with Laser Vision and Other Fun Functions of Fluorescence

Why do fish sometimes exhibit striking patterns of red fluorescence? Red fluorescent pigments absorb **blue** light - the most plentiful component of the ambient spectrum in clear marine water deeper than about 20 m - and emit **red** light, which is highly attenuated at the same depths. In this talk, I will discuss the diversity of fish that are fluorescent and some ecological correlates hinting at diverse functions for red fluorescence in fish; for example, fluorescence appears to be used for camouflage against red fluorescent algae in scorpionfish and to be concentrated in the irides of small predatory fish with a proposed visual function. Within species, we discovered that several small fluorescent fish show brighter fluorescence irides when collected in deeper, bluer water, also consistent with a possible visual function. Lastly, I will focus on research on on small and inconspicuous Mediterranean predator, the triplefin *Trypterigion delaisi.* Several

lines of research are consistent with the hypothesis that *T. delaisi* uses its tunable red fluorescence in **active photolocation**, lighting up the reflective eyes of microcrustacean prey items with a red light contrasting with the blue background. *In vivo* measurements of iris and background radiance at depth shows that irisi red fluorescence contrasts with the visual background. In lab experiments, *T. delaisi* modulates fluorescence over the long term based on ambient brightness. It behaviorally controls an **ocular spark**, which can be turned bright fluorescent red, bluish-iridescent, or off when looking at prey. Fluorescent pigments in fish likely have many additional exciting and novel functions.

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

Madhava Meegaskumbura[1,2], Gayani Senevirathne[3], Kelum Manamedra-Arachchi[4], Rohan Pethiyagoda[5], James Hanken[6] and Christopher J. Schneider[7]

[1]*Guangxi University, Nanning, Guangxi, China.* [2]*University of Peradeniya, Peradeniya, Kandy, Sri Lanka.* [3]*University of Chicago, Chicago, IL, USA.* [4]*Postgraduate Institute of Archaeology, Colombo, Western Province, Sri Lanka.* [5]*Australian Museum, Sydney, NSW, Australia.* [6]*Harvard University, Cambridge, MA, USA.* [7]*Boston University, Boston, MA, USA*

Diversification of terrestrial direct-developing frogs across mountains on an island: radiation of *Pseudophilautus* (Anura, Rhacophoridae) on Sri Lanka

Both islands and montane regions act as pumps that generate high species diversity through similar evolutionary processes, especially in the tropics. Island diversifications, largely driven by ecological opportunity and/or taxon-specific key innovations, usually have an early burst phase and are often rapid. Here, using a time-calibrated and nearly complete phylogeny, we analyze the biogeography and tempo and mode of the species-rich radiation of Sri Lankan *Pseudophilautus,* which are characterized by terrestrial direct development (TDD). Lineage-through-time plots and dating estimates suggests a gradual diversification through Late Miocene and Pliocene periods (from 31 MYA), without an apparent early burst phase. Diversification was seeded by ancestral migrants from India followed by a long speciation phase on Sri Lanka, which culminated in a Late Miocene back migration to India (about 8.8 MYA); the clade representing Indian *Pseudophilautus* comprises only a few species. Different patterns of diversification between Sri Lanka and mainland India may be explained by ecological opportunity and the time available for diversification. Ancestral area reconstructions show sister species distributed on adjacent mountain ranges and also within a given geographic area (i.e., geographic and non-geographic speciation). We reconstruct the most recent common ancestor of *Pseudophilautus* as a cool-wet adapted form, whereas the back-migrating (to India) ancestor is reconstructed as a dry-adapted form, suggesting significantly different climatic conditions during these migrations. Point endemism facilitated by TDD across the cool-wet habitats of cloud forest refuges seems to have promoted speciation in this old radiation, albeit at a steady pace.

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166 General Herpetology III, Highland B, Sunday 15 July 2018

Jazmine Mejia Munoz

California State University, Bakersfield, Bakersfield, California, USA

Potential Use of Museum Samples for Tetrodotoxin Quantification

Each year many animals that are captured for research, and subsequently euthanized, are submitted to museums' collections of specimens. Some of the animals collected are known to harbor Tetrodotoxin (TTX). TTX is a powerful neurotoxin, primarily known for its ecological role as an antipredator defense mechanism. Current knowledge on the potential use of museum samples for Tetrodotoxin (TTX) quantification is lacking. Thus, the purpose of this research is to determine whether fluid preserved specimens of organisms with TTX, can be used for the accurate quantification of TTX levels. Fluid preserved specimens, such as museum samples, are fixed with formaldehyde, to stop autolysis, and then stored in ethanol (Waller and Simmons 2003). Tetrodotoxin levels were analyzed from skin samples of stored specimens following the standard preservation process, using a Competitive Inhibition Enzymatic Immunoassay (CIEIA). The results of this study will provide a clear understanding of the potential uses and accuracy of preserved TTX holding tissues, such as those from museum samples, in future TTX related projects that require accurate TTX quantification data.

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

Corie Mellinger[1], Dominique Didier[1], William Bemis[2], Catherine Boisvert[3] and Peter Currie[4]

[1]Millersville University, Millersville, PA, USA. [2]Cornell University, Ithaca, NY, USA. [3]Curtin University, Bentley, WA, Australia. [4]Monash University, Clayton, VIC, Australia

Morphological Analysis of Electroreceptive Organs in the elephantfish, *Callorhinchus milii* (Chondrichthyes; Chimaeriformes)

Among Chondrichthyes, the chimaeroid fishes are notable for their unique snout morphologies. In particular, the snout of the elephantfish, *Callorhinchus milii*, has a plow-like flap of tissue that extends anterior to the mouth. Ampullae are concentrated on the head and snout of *C. milli* with pores of varying sizes and regional differentiation in the location of different sized openings. The morphology of these ampullary organs appears to differ both externally and internally. To test this hypothesis we used traditional anatomical techniques to examine the ampullary organs in embryonic and adult *C. milii*. Comparisons were also made to *Hydrolagus colliei*, a species that lacks the plow-like snout. Gross anatomical examination of the location, number and size of pores was completed on both species. Internal anatomy was studied using LM and whole mount cleared and triple stained embryos and snouts. Ampullae

of Lorenzini with large pores and long canals are concentrated in specific regions on the dorsal and lateral sides of the head, while shallow, pit-like ampullae are found on the ventral surfaces of the snout. The anatomy and location of these shallow ampullae are consistent with the miniampullae described for other chondrichthyan fishes. The unique arrangement and morphology of ampullae in chimaeroid fishes suggests different electrical detection capabilities with possible differences in function specifically related to prey detection.

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452 ASIH STOYE GENERAL ICHTHYOLOGY II, Grand Lilac Ballroom South, Thursday 12 July 2018

Bruno Melo[1], Melanie Stiassny[2], Jairo Arroyave[3], Fábio Roxo[1], Ricardo Benine[1], Luz Ochoa[1], Brian Sidlauskas[4], Brant Faircloth[5], Michael Alfaro[6] and Claudio Oliveira[1]

[1]São Paulo State University, Botucatu, SP, Brazil. [2]American Museum of Natural History, New York, NY, USA. [3]Universidad Nacional Autónoma de México, Ciudad de México, Mexico. [4]Oregon State University, Corvallis, OR, USA. [5]Louisiana State University, Baton Rouge, LA, USA. [6]University of California, Los Angeles, CA, USA

Phylogenomics and the Timing of Diversification in Characiformes (Teleostei, Ostariophysi)

The order Characiformes includes more than 2,000 diverse species distributed throughout the freshwaters of tropical Africa and the Neotropics. Though several recent papers have hypothesized phylogenetic relationships among characiform families, incongruences and poorly supported clades remain and the timing of diversification remains uncertain. To address these issues, we used a genome-wide dataset of 1,288 ultraconserved elements (UCEs) spanning 310 species, 221 genera and 23 families to reconstruct phylogenetic relationships using concatenated likelihood and Bayesian analyses and a coalescent species-tree approach. Six characiform fossils time-calibrated these trees. Results indicate that the four large suborders originated during the early Cretaceous and 17 of the 23 characiform families originated during the Paleogene. Our phylogenomic tree supports the paraphyly of Characiformes due to the placement of most Neotropical characiforms as more closely related to Siluriformes than to the African suborder Citharinoidei. The newly proposed Crenuchoidei (only Crenuchidae) is resolved as the sister group of a clade containing two major suborders: Anostomoidei, composed by 11 families (Alestidae, Hepsetidae, Erythrinidae, Hemiodontidae, Cynodontidae, Serrasalmidae, Parodontidae and superfamily Anostomoidea) and the restricted Characoidei with nine families (Ctenoluciidae plus Lebiasinidae, Chalceidae, Bryconidae, Gasteropelecidae, Triportheidae, Iguanodectidae, Acestrorhynchidae, and the monophyletic Characidae). These results provide the temporal framework needed to understand the evolutionary history of one of the major groups of teleosts.

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

Joseph Mendelson

Zoo Atlanta, Atlanta, GA, USA

The remarkable career of Edmund D. Brodie, Jr.: if salamanders could speak

Here I present a summary of my data and personal observations from the Middle Brodiecene, based on extensive field work in Arlington, Texas, and Logan, Utah. Of especial interest are anecodotes of graduate-student terror, obsessively large data sets, and a pioneering pursuit of truly cross-dimensional programs of research.

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

Arianne Messerman and Manuel Leal

University of Missouri, Columbia, Missouri, USA

Latitudinal Desiccation Risk Among Juveniles of Five *Ambystoma* Salamander Species

Habitat suitability is determined by both the physiological tolerances of an organism, and the biotic and abiotic conditions acting on that organism. When conditions and an organism's physiology are misaligned, that individual may be unable to maintain minimum activity levels necessary for achieving energy balance (e.g., through sufficient foraging or movement to tolerable conditions). Energetic imbalances may affect growth, dispersal, reproduction, and increase the likelihood of mortality. Therefore, quantifying local conditions and identifying mechanisms by which organisms cope with stressors enable ecologists to better understand species distributions and population dynamics. Further, elucidating physiological responses to varying environmental conditions will improve predictions of habitat suitability and inform a growing body of conservation efforts in the face of global biodiversity losses. One diverse group of amphibians experiencing declines is the genus *Ambystoma*, which includes numerous pond-breeding salamanders. Terrestrial juvenile and adult ambystomatids require moist skin and are thermoconformers. Further, juveniles are both important for population viability and understudied. We therefore examined whether juveniles of five *Ambystoma* species differed in physiological rates of water loss across a latitudinal gradient of temperature and moisture in Missouri. We found that physiological water loss rates differed between individuals, species and populations. As there was not a strong latitude signature on physiological water loss, we characterized the abiotic microhabitat conditions across study sites. Insights into both the physiological tolerances of *Ambystoma* and the abiotic conditions experienced by juveniles of these species can inform efforts to protect a sensitive life stage among a diverse genus of amphibians.

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

Arianne Messerman, Manuel Leal and Raymond Semlitsch

University of Missouri, Columbia, Missouri, USA

Peering into a Black Box: Survival Among Terrestrial Juveniles of Three *Ambystoma* Salamander Species

To conserve declining populations, it is critical that researchers identify vital rates and life stages that importantly influence the population growth and persistence of target species. By doing so, environmental managers can optimize strategies for increasing population viability, particularly when the resources and threats experienced by differing life stages vary dramatically. Examples of such complex-lifecycle species are abundant among the diverse group of salamanders in the genus *Ambystoma*, with many species having aquatic larvae that develop into terrestrial juveniles and adults. Although we know relatively little about juvenile and non-breeding adult ambystomatids due to their fossorial nature, it is thought that amphibian population growth is most sensitive to changes in the vital rates of these terrestrial life stages. Using a mark-recapture approach in outdoor enclosures, we empirically estimated juvenile detection and survival rates for three species of *Ambystoma* over ten months. We designed the enclosures to approximate upland ambystomatid habitat and exclude predators. Recapture rates differed between species and over time, with temperature and precipitation explaining a majority of temporal variation in detectability for all species. Species-specific survival rates in the two-weeks between recapture occasions ranged from approximately 95-97%, and were constant through time. As such, the percentage of individuals of each species estimated to have survived over the ten-month study period was between 34-58% of those initially released. Subtle differences in terrestrial juvenile *Ambystoma* survival rates between species and populations may, therefore, dramatically impact annual adult recruitment, and thus the likelihood of population persistence among ambystomatids of conservation concern.

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532 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Vanessa Meza-Vargas[1,2], Bárbara Calegari[1,3] and Roberto Reis[1]

[1]Pontifícia Universidade Católica do Rio Grande do Sul (PUCRS), Porto Alegre, Rio Grande do Sul, Brazil. [2]Museo de Historia Natural (UNMSM), Lima, Lima, Peru. [3]Smithsonian Institution, Washington DC, Maryland, USA

A New Species of *Chaetostoma* (Siluriformes: Loricariidae) from Amazon Basin, Guiana Shield, Brazil

Chaetostoma is the second most diverse genus of Ancistrini, including 49 species, 22 of which are Cis-Andean. *Chaetostoma* are known as rubbernose armored catfishes because they lack plates and fleshy projections or tentacles on the anterior portion of the snout. Currently, the genus is distributed in Andean rivers in Peru, Ecuador, Colombia, Panama, Venezuela, and a single species in Brazil. Recent Expedition in the lower Amazon basin revealed a new species from the Maicuru River drainage, a north tributary of the Amazon River. The new species is recorded to the Guyana shield along with other two congeners, *C. jegui* and *C. vasquezi*, and represents the second species in Brazil. The new species is primarily diagnosed from most congeners by the modification on anal-fin morphology as well as color pattern of the head and trunk. Additionally, the new *Chaetostoma* is distinguished from both Guyana shield species (*C. jegui*, and *C. vasquezi*) by having the ventral surface of the premaxillary barbel dark brown and by shape of odontodes on the cheek plate. Also, the new species shows an unusual condition of the dermal keel on the parieto-supraoccipital, in which adults lack such keel that is present in juveniles.

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

Vanessa Meza-Vargas[1,2], Nathan Lujan[3] and Roberto Reis[1]

[1]Pontifícia Universidade Católica do Rio Grande do Sul (PUCRS), Porto Alegre, Rio Grande do Sul, Brazil. [2]Museo de Historia Natural (UNMSM), Lima, Lima, Peru. [3]University of Toronto Scarborough, Toronto, Ontario, Canada

How many genera are *Hemiancistrus* (Siluriformes: Loricariidae)?

The genus *Hemiancistrus* was erected by Bleeker, 1862, for the species *Ancistrus medians* Kner, 1854, from Suriname. Although molecular phylogenetic evidence consistently indicates that *Hemiancistrus medians* is monotypic, up to 44 nominal species have been historically placed in this genus. Recent taxonomic revisions have reduced the number of valid *Hemiancistrus* species to 12, yet more work is required to fully resolve the genus-level taxonomy of species assigned to this genus. Currently valid *Hemiancistrus* species are broadly distributed across both cis- (Orinoco, Amazon, Maroni, Uruguay) and trans-Andean (Guayas, Esmeraldas, San Juan) river basins and at least four different phylogenetic lineages. Thus, a genus-level taxonomic revision is needed to better reflect phylogenetic patterns and better highlight morphological and biogeographical diversification patterns within the Loricariidae. However, taxonomic revision of *Hemiancistrus* is hindered by poorly detailed original descriptions, missing type specimens and apparently homoplastic morphological characters. Currently, the genus lacks an exclusive morphological diagnosis. In this study, we review morphological evidence for breaking up *Hemiancistrus* species in the context of a phylogeny based on a 4,162 base pair alignment consisting of two mitochondrial (16S, Cyt*b*) and three nuclear loci (RAG1, RAG2, MyH6).

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

Aryeh Miller[1] and Graham Reynolds[1,2]

[1]University of North Carolina Asheville, Asheville, NC, USA. [2]Harvard University, Cambridge, MA, USA

Elucidating Cryptic Diversity in Burmese *Lygosoma* Skinks via Integrative Taxonomy

Supple skinks (Reptilia; *Lygosoma*), named for their attenuate limbs, like many other Indochinese herpetofaunal groups, have experienced particular taxonomic turbidity over the past few decades. With a widespread geographic breadth (spanning most of Africa to continental and insular Asia), the majority of species within this group are exceptionally poorly known. As is the case with so many understudied cryptic species groups, Southeast Asian Lygosomine species-complexes, such as *Lygosoma quadrupes*, require comprehensive molecular and morphological assessments to resolve the evolutionary relationships of these cluttered taxa. Here, using comparative morphological and novel multilocus phylogenetic data, we apply targeted species delimitation techniques to the *Lygosoma quadrupes* complex, focusing in particular on species from Myanmar. In so doing, we reveal multiple cryptic lineages and provide insight on the taxonomic status of this group, as well as additionally biogeographic discussion. Our dataset also provides opportunities to examine the evolution of body elongation and limb attenuation, which has happened independently in several Indochinese skink lineages.

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250 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Elizabeth Miller and John Wiens

University of Arizona, Tucson, AZ, USA

The Role of Sexual Selection in Generating Freshwater and Marine Biodiversity

The marine-terrestrial biodiversity gradient is the dramatic difference in species richness between marine and terrestrial environments. Species richness of actinopterygian fishes is comparable in freshwater and marine habitats, although less than 1% of Earth's habitable water is fresh. Traditionally, this pattern has been explained by greater opportunities for allopatric speciation in freshwater habitats, implying higher diversification rates in freshwater versus marine habitats. Our macroevolutionary analyses suggest freshwater fishes do have higher diversification rates on average than marine fishes. However, high diversification rates are not a

feature of freshwater clades in general. Instead, high rates are concentrated within a few freshwater clades that share a prevalence of sexual dichromatism. Here, we tested whether dichromatism evolves more readily in freshwater habitats, and whether dichromatism increases diversification relative to monochromatism across the Actinopterygii Tree of Life. We collected dichromatism data for over 6,000 species of actinopterygian fishes, a dataset of unprecedented size. Dichromatism is more prevalent in freshwater than marine habitats, and may be correlated with other ecological and life history characteristics. The tendency for sexual dichromatism to evolve in freshwater habitats and subsequently increase diversification rates is a novel explanation for the marine-terrestrial biodiversity gradient in fishes.

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248 ASIH STOYE GENERAL ICHTHYOLOGY I, Grand Lilac Ballroom South, Thursday 12 July 2018

Elizabeth Miller[1], Kenji Hayashi[2], Dongyuan Song[3] and John Wiens[1]

[1]University of Arizona, Tucson, AZ, USA. [2]Brown University, Providence, RI, USA. [3]Fudan University, Shanghai, China

Explaining the Ocean's Dominant Species Richness Gradient and Global Patterns of Marine Fish Diversity

The longitudinal diversity gradient is the dominant richness pattern across the marine tropics. Global marine richness peaks in the Central Indo-Pacific region and declines longitudinally, a striking pattern that remains poorly understood. A challenge to understanding this gradient is that the relative roles of diversification rates versus colonization history have not been disentangled among regions. Here, we collected distributional data for percomorph fishes, a group containing >75% of marine ray-finned fishes. We then analyzed biogeographic data using a phylogenetic framework to reveal how colonization and diversification have generated species richness differences among marine regions. We also compared the processes generating species richness in the tropics with those operating in cold marine habitats. The high diversity of the Central Indo-Pacific was explained by replicated colonizations of the region across the percomorph phylogeny during the Oligocene-Miocene. These relatively old colonization events allowed more time for species richness to accumulate compared to other warm marine regions. Surprisingly, net diversification rates were decoupled from marine richness patterns, and clades in low-richness cold marine habitats had the highest diversification rates. Therefore, the high richness of the Central Indo-Pacific is due to greater time-for-speciation, not higher diversification rates. By directly comparing colonization and macroevolutionary rates among regions, these results extend beyond the existing framework for understanding the longitudinal diversity gradient.

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

Eva Miller and Jennifer Deitloff

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

Comparing Population and Sex Differences in Head Shape for Two Populations of *Plethodon cinereus* (Red-backed Salamanders) in Pennsylvania.

Morphological variation within a species depends on many factors, including development, sex, genetics, and phenotypic plasticity. Morphology can correlate with ecological factors such as location, environment, and intensity of competition. *Plethodon cinereus* occupies a broad geographic area across the United States and exhibits variations in morphology dependent on their region. In addition to variation between populations, morphology can also vary between sexes. We tested the hypothesis that head morphology differs between populations and among sexes (males, gravid females, and nongravid females) of *Plethodon cinereus*. We investigated both lateral and ventral head-shape morphology of *P. cinereus* from two populations in Pennsylvania while also comparing shape among sexes. Photographs of both the ventral and lateral views of the head of each specimen were taken, and each specimen was assigned biologically homologous landmarks which were analyzed using geometric morphometric methods. We concluded that head morphology differed among populations, but the sexes did not differ. Each population likely experience different environmental factors because of their different geographic locations, which could be correlated with this difference in head-shape. Further research examining differences in environmental conditions or resource use could provide insight into why head morphology differs between these populations.

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

Kelsey Mitchell and Katherine Greenwald

Eastern Michigan University, Ypsilanti, Michigan, USA

Climate Change Effects on Body Size and Population Composition of Unisexual *Ambystoma S*alamanders

Climate change has been shown to drive changes in organisms' phenology, geographic ranges, and eco-morphology. Amphibians may show variable responses to climate change due to the diverse ecological, physiological, and genetic traits of these taxa. Unisexual (all female) *Ambystoma* salamanders reproduce via kleptogenesis, in which insemination by a sympatric sexual male is necessary to trigger egg development. The zygote can develop gynogenetically or via incorporation of the male's genome into the ovum, resulting in individuals that vary in

ploidy and genome composition. We will analyze genetic and morphological data of historic and modern-day unisexual and *A. laterale* specimens from the University of Michigan's E. S. George Reserve. Epidermal cell nuclei measurements will be used to establish ploidy levels of historic specimens (dating back to the 1960s) housed at the UM Museum of Zoology. Ploidy of current samples will be assessed using a panel of microsatellite loci. We predict that climate change (i.e. rising temperatures) will have driven population composition away from the more northern-distributed *A. laterale* and toward populations dominated by LLJ unisexuals. However, microclimate change (e.g. increased canopy cover) may mitigate the effects of these broader climatic shifts. We also predict that salamanders will show reductions in body size over the last half century. Changes in population composition and body size could inform our understanding of the susceptibility of amphibians to climate change, as well as whether adaptation can keep pace with rapid environmental change.

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

Shawna Mitchell and Bernie Kuhajda

Tennessee Aquarium Conservation Institute, Chattanooga, Tennessee, USA

Population Status and Life History of the Federally Endangered Laurel Dace, *Chrosomus saylori*

The Laurel Dace (*Chrosomus saylori*) is a federally endangered species endemic to the upper Tennessee River Basin in Tennessee. Their populations have suffered from heavy siltation and poor water quality from agriculture runoff. Laurel Dace historically occupied only eight streams on Walden Ridge of the Cumberland Plateau, however recent sampling indicates this species is only relatively common in two streams, Bumbee Creek and Youngs Creek. Previously, the northern population of Laurel Dace (Piney Creek system) appeared to be in relatively good shape, with high numbers of individuals in Bumbee and Moccasin creeks, but as of 2016 there have been no Laurel Dace found in Moccasin Creek. The abundance of Laurel Dace in Youngs Creek was low when it was last sampled in 2013; however in 2017 the site was visited twice, with the second survey capturing hundreds of young of the year Laurel Dace. Tennessee Dace (*Chrosomus tennesseensis*) are not listed in Tennessee and are a close relative to the Laurel Dace. They are found in Duskin Creek about 300 feet in elevation below Bumbee Creek and both creeks discharge into Piney Creek. We will be studying the life history of the Tennessee Dace in order to use it as a surrogate species for the life history of Laurel Dace. Studying the life history of the Tennessee Dace will allow us to make better informed decisions that will help determine what is needed for the recovery of the Laurel Dace.

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159 ASIH STOYE ECOLOGY & ETHOLOGY II, Highland C, Thursday 12 July 2018

Patrick D. Moldowan[1], Glenn J. Tattersall[2] and Njal Rollinson[1]

[1]*University of Toronto, Toronto, Ontario, Canada.* [2]*Brock University, St. Catharines, Ontario, Canada*

Population Ecology and Sensitivity to Environmental Change of the Spotted Salamander, *Ambystoma maculatum*

This presentation will highlight findings from one decade of a mark-recapture study and two decades of reproductive monitoring of Spotted Salamanders (*Ambystoma maculatum*) in Algonquin Provincial Park (APP), Ontario. Since 1992, the timing of breeding of APP salamanders has seemingly been advancing, and preliminary analyses demonstrate a negative correlation between reproductive effort and temperature during the pre-breeding period, suggesting that warmer spring temperatures discourage breeding activity. Relatedly, body condition and reproductive effort correlate negatively to previous summer temperatures, also suggesting that warmer temperatures curtail reproduction. Given changes in temperature, precipitation, and seasonality in APP in recent decades, we are interested in quantifying the relationship between changes in environmental conditions and changes in both individual-level (age-specific growth, body condition, reproductive effort) and population-level characteristics (breeding phenology, adult breeding abundance, age structure, timing of egg hatch and metamorphosis). We are studying what features of the life cycle are most sensitive to climate (change), and how the differential sensitivity of these features cumulatively impact population ecology and viability. We have recently established a comparative population sampling study involving minnow trap, cover board, and drift fence methodologies, and will be updating following our first field season of implementation. Continued research will address population demography via skeletochronology and the construction of an Integrated Population Model as a tool to jointly analyze data on population size and demographic data.

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329 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

Haley Moniz[1], Vicki Thill[1], Robert del Carlo[1], Jessica Reimche[1], Michael Hague[2], Edmund Brodie Jr.[3], Normand LeBlanc[1] and Chris Feldman[1]

[1]*University of Nevada, Reno, Reno, NV, USA.* [2]*University of Virginia, Charlottesville, VA, USA.* [3]*Utah State University, Logan, UT, USA*

Costs of Adaptation: Tradeoffs in Organismal Performance of Tetrodotoxin-Resistant Garter Snakes (*Thamnophis*)

Adaptive evolution of tetrodotoxin (TTX) resistance in certain garter snake populations (*Thamnophis*) has enabled a coevolutionary arms race between these snakes and their toxic, Pacific newt prey (*Taricha*). Resistance to TTX stems from mutations in the outer pore of voltage-gated sodium channels that are the molecular targets of TTX. Because these ion channels are essential for action potential propagation in excitable cells, any changes to the outer pore that reduce TTX ligation may also have adverse consequences on nerve and muscle function. Here we examine this potential tradeoff between TTX-resistance and physiological function in both muscle and whole-animal. We examine several aspects of muscle mechanics (phasic contraction, time to maximum force, etc.), as well as aspects of whole organism performance (sprint speed, endurance, etc.) in a range of TTX-resistant and TTX-sensitive snakes that express different sodium channel alleles. If tradeoffs at the molecular level scale-up to the whole-animal, then resistant snakes may be at a disadvantage under certain ecological conditions. Clarifying the nature and extent of these tradeoffs impacts our understanding of the coevolutionary dynamic between *Taricha* and TTX-resistant populations of *Thamnophis*.

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

Dillon Monroe and Robert Espinoza

California State University, Northridge, Northridge, CA, USA

A Comparison of Traditional and Citizen-Science Approaches to Inferring the Distribution of an Invasive House Gecko (*Hemidactylus turcicus*) in Texas

Citizen science has emerged as a practical, cost effective, and potentially prosperous means of collecting data. However, few studies have examined the extent to which decentralizing data collection introduces new sources of variance in patterns of spatial sampling. To assess this, we conducted a point-pattern analysis to compare traditional and citizen-science approaches to determining the invasive distribution of Mediterranean House Geckos (*Hemidactylus turcicus*; MHGs) in Texas. MHGs first arrived in Brownsville, Cameron County, Texas in 1950 and have since established populations in more than half of the 254 counties in Texas. Traditional data sources included museum/university collections (*n* = 59; 288 unique locations) and for the citizen-science databases we included HerpMapper and iNaturalist (1893 unique locations). Quadrate analysis was used to test whether the locations were non-random using variance-to-mean ratio and Poisson-distribution tests. To test whether the locations were clustered or dispersed, we used a nearest neighbor analysis. Our analyses support the notion that citizen-science data are comparable to traditional data sources for regional-scale inferences of species presences or absences. However, there were some differences in the location patterns that could pose problems when comparing small datasets. Overall, our results support the idea that citizen scientists can provide researchers with access to valuable data that would otherwise be challenging to acquire, particularly for human commensal species like house geckos.

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

Carmen Montaña[1], Christopher Schalk[2], Tiffany Schriever[3], T. M. S. D. G. Silva[1], David Hagyari[1], Jakob Wager[1], Lindsey Tiegs[1] and Cyrus Sadeghian[1]

[1]Sam Houston State University, Huntsville, Texas, USA. [2]Stephen F. Austin State University, Nacogdoches, Texas, USA. [3]Western Michigan University, Kalamazoo, Michigan, USA

Revisiting 'What do Tadpoles Really Eat?': A Ten-year Perspective

Tadpoles are diverse and abundant consumers and knowledge on their feeding ecology and trophic status is essential to understand their functional role within their aquatic habitats. Here we revisit Altig et al. (2007)'s paper that highlighted the knowledge gaps in tadpole feeding ecology and suggested application of modern techniques (stable isotope analysis, fatty acids, and ecological stoichiometry) to understand their trophic status in the context of species diversity and ecoregion. Our results highlight the importance of modern techniques for a better understanding of dominant food resources, food assimilation, and trophic position of tadpoles in aquatic ecosystems. Our findings indicate that most research on tadpole trophic ecology has been conducted in Neotropic and Neartic regions, and primarily on species from the families Ranidae, Bufonidae, and Hylidae. Tadpoles play important roles in food webs and ecosystem functions, therefore there is a sense of urgency for more studies in tropical regions like Africa and Asia, where species diversity and endemism is of great importance. Declines in amphibian abundance and diversity are occurring worldwide. A combination of modern techniques and more natural and manipulated experiments would offer a powerful approach for understanding of tadpoles' feeding ecology and trophic status and their consequences in food-web structure and ecosystem functions.

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201 Reptile Ecology II, Highland A, Sunday 15 July 2018

Jennifer Moore, Patrick Laarman and Joseph Altobelli

Grand Valley State University, Allendale, MI, USA

Ecology of Neonatal Box Turtles with Implications for Prescribed Burning

Eastern box turtle hatchlings are vulnerable to mortality incurred from various sources, including predation and management activities like prescribed burning, which is often used to promote fire dependent natural communities. Collecting data on neonatal turtles is challenging, thus the spatial ecology and mortality of young age classes of box turtles are not well understood. We investigated spatial ecology and survival of neonate eastern box turtles in the northern Lower Peninsula of Michigan. Our objectives were to document nesting, emergence, habitat use, dispersal rates, residency time of neonates in natal openings, and annual survival using radio telemetry. Nest emergence timing varied considerably in different years but no neonates dispersed more than 50 m beyond the boundary of their natal forest opening before onset of winter. Dispersal (distance from nest to overwintering site) was extremely limited in the first activity season, and by 1 June of their second activity season, all neonates were still present in or within 50 m of their natal opening, but all vacated openings by 1 July. Survival was 50% until overwintering, after which it dropped considerably, and no neonates survived beyond 335 days post hatching. Predation and exposure to suboptimal environmental conditions were the main sources of mortality. Our results have implications for turtle demography and habitat management, as prescribed burning, used to maintain open canopy habitats necessary for nesting, may negatively affect neonate survival.

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

Kevin Moore[1], Chris Brooks[1], Chuck Knapp[2] and Mark Welch[1]

[1]Mississippi State University, Starkville, MS, USA. [2]Shedd Aquarium, Chicago, IL, USA

Rock Iguanas and Their Ticks: Predicting The Infestation Bias of Nonspecific Herptophile Ticks in the Bahamas.

The faunal community of the Caribbean region is unique from most mainland communities in that the largest endemic vertebrates are reptiles, specifically rock iguanas: *Cyclura*. For this reason, the majority of locally adapted parasites specialize on reptilian and avian taxa instead of mammalian hosts. Parasite life history is concomitant with the ecology of potential hosts, and although *Cyclura* ecology is well studied, the prevalence of and susceptibility to parasitic infestation within and among populations has been a subject of little research. Ticks of the genus *Amblyomma* will infest any large-bodied reptile and are common in the Caribbean. Despite not being host-specific, ticks may infest species at biased rates. *Amblyomma* leave their hosts infrequently to oviposit and molt. I hypothesize that the territoriality and larger body size of *Cyclura* lead to ticks reinfesting their previous, or infest neighboring iguana hosts. Larval ticks would encounter a similar suite of hosts unless ticks disperse great distances to oviposit. I predict that these factors will result in an infestation bias of iguanids over any other reptilian host. To investigate these questions, I will simulate parasite load of three models of infestation bias: no biased infestation, iguana biased infestation, and biased infestation of non-iguanas. The empirical data of actual parasite load can then be fit to the best likelihood surface. The product of these simulations will contribute to our understanding of how parasites infest hosts; additionally, identify populations at risk of vector borne diseases, augmenting the conservation and management of a critically endangered reptile.

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54 ASIH STOYE GENERAL ICHTHYOLOGY IV, Highland E., Friday 13 July 2018

Thomas Morgan[1], Stuart Willis[2], Izeni Farias[3], Raphael Covain[4], Jan Mol[5], David Portnoy[6] and Hernán López-Fernández[7]

[1]*University of Toronto, Toronto, Ontario, Canada.* [2]*California Academy of Sciences, San Francisco, California, USA.* [3]*Federal University of Amazonas, Manaus, Brazil.* [4]*Natural History Museum of Geneva, Geneva, Switzerland.* [5]*Anton de Kom University of Suriname, Paramaribo, Suriname.* [6]*Texas A&M University at Corpus Christi, Corpus Christi, Texas, USA.* [7]*University of Michigan, Ann Arbor, Michigan, USA*

The Biogeography and Phylogenomics of *Geophagus* (Subfamily: Cichlinae) in the Guiana Shield.

The Guiana Shield region of South America is characterized by high levels of fish diversity and endemism. However, the processes that contributed to the formation of these unique fish assemblages have not been resolved. The modern fish diversity of the Guiana Shield likely originated from a combination of processes including invasion via river capture events and subsequent diversification, marine incursion, and the persistence of more ancient relictual species; however, how each of these processes has contributed to extant assemblages is not known. In order to elucidate drivers of endemism and patterns of diversity in the Guiana Shield fishes, we looked at 136 individuals from the genus *Geophagus* (subfamily: Cichlinae), collected from the Guiana Shield, Orinoco and Amazonian regions, representing 14 described species and several populations of unclear taxonomic identity. Using a ddRADseq approach we sequenced >15,000 loci to characterize *Geophagus* genetic diversity and phylogenetic relationships. Our results revealed monophyly of Guiana Shield endemics and phylogenetic relationships indicating that hydrological basins contain distinct and possibly isolated populations. Phylogenetic analyses identified 19 well resolved clades within *Geophagus* corresponding to described species as well as putatively undescribed taxa. Our results, as do previous unpublished analyses, also indicate that the currently distinct taxa *G. surinamensis* and *G. brokopondo* are likely one species. Broadly, phylogenetic patterns suggest a single evolutionary origin for endemic Guiana Shield *Geophagus*. These results suggest that diversification of Guiana Shield endemic *Geophagus* was likely *in situ*, and that this process has led to the high levels of observed endemism.

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534 Ichthyology Ecology and Ethology, Highland E, Sunday 15 July 2018

Nathan Morris[1,2], Janet Long[2] and Elizabeth Alter[1,2,3]

[1]*CUNY Graduate Center, New York, NY, USA.* [2]*York College, Jamaica, NY, USA.* [3]*Sackler Institute for Comparative Genomics at AMNH, New York, NY, USA*

"Characterization of the Gut Microbiome of Mummichog, *Fundulus heteroclitus*, Living in Polluted Urban Waterways"

Fish gut microbiome research, while still relatively new, has already begun to provide insights into the overall health, immune function, and digestive processes of host species. While the relationship between gut microbiome composition and physiology is not completely understood, it is known that gut microbiota are responsible for metabolizing foods that their

hosts could not otherwise digest, and for influencing immune functions. Fish guts are also likely inundated with microorganisms from the water and food in their immediate surroundings. It has been shown that habitat and diet affect gut microbiome composition, but the exact relationship has yet to be demonstrated. *Fundulus heteroclitus*, or the mummichog, is a species of fish known to live in diverse environments, feed on a wide variety of foods, and survive in severely polluted waters. The gut microbiome of mummichog living in polluted urban waterways has not been well explored. Here we present results characterizing the gut microbiomes of mummichog from various New York City waterways using 16S ribosomal RNA gene sequencing. Sampling sites include the Gowanus Canal (a superfund site), Jamaica Bay, and Long Island. Both the Gowanus Canal and Jamaica bay are known for their long history of pollution from industrial waste and combined sewer overflows. We examine alpha and beta diversity, and the taxonomic composition of the microbial communities found in fish gut. By characterizing the gut microbiome of the mummichog, we hope to contribute to further understanding of the mechanisms that enable this species to persist in such challenging environments.

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

Cherie Mosher[1], Brent Murray[1], Chris Johnson[1] and Stephen Spear[2]

[1]UNBC, Prince George, BC, Canada. [2]The Wilds, Cumberland, Ohio, USA

The Curious Case of the Coastal Tailed Frog: A Phylogeographic Study Using Multiple Methods

The coastal tailed frog (*Ascaphus truei*) is an indicator species for the health of its habitats in the Coastal and Cascade Mountains of the Pacific Northwest of North America. This ancient species, unique among and a sister species to all extant frogs, is associated with cool, fast-flowing, mountain streams. We compared the within region genetic diversity of populations near the northern extent of the coastal tailed frog's range (British Columbia, Canada) to four other regions (two in British Columbia, Canada and two in Washington, USA), moving towards the core of the range in Washington, USA. We used two genetic techniques – microsatellite (9 loci) and next-generation sequencing (4,249 loci) – to explore broad-scale genetic diversification. Sampled regions (N=5) separated into 4 genetic clusters with the two most northern regions clustering together, all marker systems being consistent. The allelic richness and heterozygosity reduced substantially as the latitude increased. Though northernmost populations are often characterized by lower genetic variability, we discovered an extreme case of reduction in a large portion of the coastal tailed frog range. This study showed a strong correlation between microsatellite and "big data" analyses. Additionally, our discovery of reduced diversity may have important conservation and management implications regarding population connectivity and response to climate change. This talk will detail our intriguing results and showcase insight into *A. truei*'s unique evolutionary lineage in British Columbia.

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380 ASIH STOYE ECOLOGY & ETHOLOGY II, Highland C, Thursday 12 July 2018

Jeanette B. Moss[1], Glenn P. Gerber[2], Aumbriel Schwirian[1], Anna C. Jackson[1] and Mark E. Welch[1]

[1]*Mississippi State University, Mississippi State, MS, USA.* [2]*San Diego Zoo Institute for Conservation Research, Escondido, CA, USA*

The sex life of a Caribbean lizard: sexual conflict, evolutionary constraint, and inbreeding avoidance in a small, insular population

In natural populations susceptible to inbreeding depression, behaviors such as female promiscuity and negative assortative mating may enhance the production of outbred progeny. However, the majority of empirical tests of such hypotheses have been undertaken in breeding systems where female choice is known to play a large role. We carried out pedigree reconstructions of 50 clutches of critically endangered *Cyclura nubila caymanensis* (Sauria: Iguanidae) to investigate the prevalence and efficacy of inbreeding avoidance behaviors. We found no evidence for negative assortative mating or female preference for outbred males, but successful sires were larger-than-average. We detected multiple-paternity in 36.2% of clutches, with reduced rates of 20% occurring in a human-modified habitat with high local densities compared to 40.5% for the remainder of the island. This finding implies that females paradoxically have fewer mates when more males are present. However, multiply sired clutches exhibited higher allelic diversity and lower rates of inbreeding than single sire clutches suggesting that there could be benefits to mating multiply. Our data imply that while female mating behaviors have the potential to confer adaptive benefits in this small population, the trajectory of mating system evolution may be largely constrained by sexual conflict.

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

Cy Mott[1] and Emily Croteau[2]

[1]*Eastern Kentucky University, Richmond, KY, USA.* [2]*University of Kentucky, Lexington, KY, USA*

Testing the abundant center distribution hypothesis in North American anurans using a citizen science program

The abundant center distribution hypothesis (ACH) predicts decreasing population densities as a species' geographic range edge is approached, a pattern that is considered to underlie spatial variation in ecological and evolutionary processes occurring in ecologically marginal habitats. However, the extent to which abundant center distributions represent a biogeographical rule is unclear, as such patterns occur in less than half of all species examined, and most ACH studies have focused on plants or endothermic vertebrates. Using call count data from a citizen science program, the North American Amphibian Monitoring Program, we examined range-wide abundance estimates for 13 anuran species across 16 transects spanning the eastern and central United States. Based on call-count density estimates for nearly 750 populations, we observed that 75% (12/16) of species-transects exhibited distributions fitting the ACH. In addition, ~88% (14/16) of species-transects exhibited decreases in abundance towards the range edge based on two other estimates of abundance. In contrast to previous studies of the ACH, our results indicate that anurans largely adhere to its predictions, potentially due to such factors as reduced vagility and increased sensitivity to local environmental conditions relative to other vertebrate groups. These results also speak to the value of citizen science programs in providing data that can address large-scale ecological and evolutionary questions, but that are difficult to address through traditional research methods.

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

Kevin P Mulder[1,2], André Lourenço[2], Rayna C. Bell[1], Ivan Gomez-Mestre[3] and Guillermo Velo-Antón[2]

[1]National Museum of Natural History, Smithsonian Institution, Washington, DC, USA. [2]CIBIO, Vairão, Porto, Portugal. [3]EBD-CSIC, Sevilla, Andalucia, Spain

RNAseq analyses across two independent transitions within *Salamandra salamandra* highlight candidate genes important in the shift from larviparity to viviparity

Shifts in reproductive mode occur across the tree of life and are key adaptations with profound effects on species' life histories and evolutionary trajectories. Understanding the proximate and ultimate causes of these shifts can be challenging due to concurrent neutral and adaptive changes that can arise alongside a shift in reproductive mode. *Salamandra salamandra* is an amphibian that exhibits intra-specific variation in reproductive mode allowing us to investigate both larviparity and viviparity in the same species. Although it yields fewer offspring, viviparity is an adaptive innovation that allows individuals to exploit ecological habitats with no available water bodies, and bypass the high predation pressure of the larval stage. *S. salamandra* is larviparous across the majority of its range but viviparity evolved during the Pleistocene within *S. s. bernardezi* populations of northern Spain and separately during the Holocene on the land-bridge islands of *S. s. gallaica* in northwestern Spain. We compared the gene expression profiles of the uterus and oviduct of pregnant females across both transition zones to detect candidate genes that are important in explaining the difference in reproductive mode. We identified differentially expressed genes specific to either transition zone as well as genes that appear important for both transition zones. We discuss the potential mechanisms that can explain the phenotypic differentiation based on what is known about the molecular function of the candidate genes.

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110 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: CONSERVATION & MANAGEMENT, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Damien Mullin[1], Rachel White[1], Andrew Lentini[2], Jory Mullen[1], Ronald Brooks[3] and Jacqueline Litzgus[1]

[1]Laurentian University, SUDBURY, Ontario, Canada. [2]Toronto Zoo, Toronto, Ontario, Canada. [3]University of Guelph, Guelph, Ontario, Canada

Evaluating Assumptions of Headstarting for Turtle Conservation

Headstarting is a conservation tool which assumes that raising turtles in captivity to a larger body size increases their survivorship compared to wild non-headstarted turtles. Our goal was to quantitatively test this fundamental assumption by comparing three groups of turtles with varying degrees of headstarting: (1) 15 turtles headstarted for 2-years (2yHS), (2) 15 turtles headstarted for 1-year (1yHS), and (3) 15 turtles hatched in captivity then released (i.e. no headstarting; 0yHS). We measured somatic growth rates of headstarted turtles while in captivity, and then all three cohorts of turtles were radio-tracked weekly during the active season and monthly during the winter to monitor behaviour, growth, and survivorship in the wild post-release. 2yHS and 1yHS were tracked for one year, from June 2016 until June 2017. 0yHS hatched in late July 2016, were released on 2 August 2016, and tracked for one month. All cohorts exhibited positive growth post-release from captivity. 0yHS had 73% confirmed survivorship one-month post-release, and three of these turtles were confirmed to have survived the winter. 2yHS had greater survivorship (73%) than 1yHS (40%) during the 12-months post-release (p=0.070). Our results support the fundamental assumption that bigger turtles have greater survivorship, and suggest that headstarting for 2 years increases post-release survival of turtles. Given the growing number of turtle headstarting projects globally, our study provides data that can aid in establishing best practices.

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

Damien Mullin[1], Rachel White[1], Andrew Lentini[2], Jory Mullen[1], Ronald Brooks[3] and Jacqueline Litzgus[1]

[1]Laurentian University, Sudbury, Ontario, Canada. [2]Toronto Zoo, Toronto, Ontario, Canada. [3]University of Guelph, Guelph, Ontario, Canada

Evaluating the Effectiveness of Headstarting for Wood Turtle (*Glyptemys insculpta*) Recovery from a Suspected Poaching Event

A population of endangered Wood Turtles (*Glyptemys insculpta*) was studied extensively beginning in 1988. By the mid-1990s, a suspected poaching event resulted in the removal of approximately 70% of the population. A population viability analysis determined that

extirpation was inevitable if no intervention was undertaken and so a headstarting project was initiated in 2003 and the first cohort was released in 2005. Our objective is to quantitatively assess the effectiveness of the 14-year headstarting program by modeling population demographic parameters to evaluate recovery efforts to date, and determine the next phase of recovery. To date, a total of 537 headstarted turtles have been released back into their maternal streams. At present, the population bears the hallmarks of a heavily managed system: headstarted turtles constitute a larger proportion of the population than non-headstarted wild turtles (149:25), and sexually immature juveniles outnumber sexually mature adults (139:35). The persistence of the population will likely require a demographic shift to a more natural situation in which the population is made up mostly of reproducing adults. Headstarted turtles from the first release groups are just now beginning to reproduce, indicating that the population may become self-sustaining. Modeling suggests population recovery has been slow, even with intensive management. Modeling population recovery scenarios with comprehensive long-term data is essential for evaluating the effectiveness of headstarting projects, while continuously improving recovery efforts.

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651 General Herpetology I, Highland B, Sunday 15 July 2018

Eric Munscher[1], Andrew Walde[2], Daren Riedle[3], Stephen Ross[4], Nicole Salvatico[5], Chris Collins[6], Mike Farris[7], Brian Butterfield[8], Brian Hauge[9] and Michael Skibsted[10]

[1]SWCA, Houston, Texas, USA. [2]Walde Research & Environmental Consulting, Atascadero, California, USA. [3]Kansas Department of Wildlife, Parks, and Tourism, Pratt, Kansas, USA. [4]Power Engineers, Inc., Houston, Texas, USA. [5]Florida Department of Health, Tavares, Florida, USA. [6]SWCA, San Antonio, Texas, USA. [7]NAFTRG, Houston, Texas, USA. [8]Freed-Hardeman University, Henderson, Tennessee, USA. [9]Peninsula College, Port Angeles, Washington, USA. [10]Aliso Creek Turtle Rescue, Ladera Ranch, California, USA

Lots of Turtles, Lots of Work: An Overview of the North American Freshwater Turtle Research Group's Research at Comal Springs

Comal Springs in New Braunfels, Texas, is the largest freshwater spring west of the Mississippi. The spring is within the Edwards Plateau Savanna Ecoregion of the Southeastern United States Turtle Priority Area (TPA). Because Comal Springs is in a TPA, it is ecologically important and may be impacted by recreational use; it is important to assess baseline population levels for the turtle community residing in this spring habitat. From February 2012 to February 2017, we captured nearly 5,000 turtles. Of these 5,000, we caught nearly 3,000 *Sternotherus odoratus*, 1,600 *Pseudemys texana*, 300 *Trachemys scripta*, and 20 *Chelydra serpentina serpentina.* The population of *Sternotherus* at Comal is one of the largest across the species range. Current estimates put the overall population at up to 14,000 individuals. The *Chelydra* at Comal all seem to be suffering from an unknown virus/disease that is causing ulcerations on the head and carapacial pitting. A unique aspect of the Comal Springs study is its incorporation of citizen scientists. Through this, the load of work accomplished is greatly enhanced. The data collected at Comal Springs can be used in future regulations on the spring concerning recreational use. The data collected also acts as a catalog of species that can be used in other studies looking at specific aspects of specific species. This talk will cover an overview of the project, providing data collected on species and the results of our work so far.

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

Matthew Murdoch[1], Lee Grismer[2], Perry Wood[3], Neang Thy[4], Nikolay Poyarkov[5], Ngo Van Tri[6], Roman Nazarov[5], Anchalee Aowphol[7], Olivier Pauwels[8] and Jesse Grismer[9]

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Six new species of *Cyrtodactylus* Gray (Squamata: Gekkonidae) *intermedius* complex from the Cardamom Mountains and associated highlands of Southeast Asia.

An integrative taxonomic analysis using color pattern, morphology, and 1449 base pairs of the ND2 mitochondrial gene and its five flanking tRNAs demonstrate that eight species-level lineages occur within the *Cyrtodactylus intermedius* complex (*Cyrtodactylus intermedius sensu stricto*, *C. phuquocensis* and related populations) of the Cardamom mountains and associated highlands of Cambodia, Thailand, and Vietnam that have a sequence divergence ranging 3.4-8.9%. Additionally, each lineage is discretely diagnosable from one another based on morphology and color pattern and most may be endemic to specific geographic regions (upland areas, karst formations or islands) that prevent or greatly restrict interpopulation gene flow. Six of these lineages were masquerading under the nomen *C. intermedius* and are described from the following locations: Phnom Aural, the highest mountain in Cambodia; Bokor Plateau; central Cardamom mountains; Phnom Dalai, the northernmost peak of the Cardamom mountains; Phnom Laang karst formation; and the Bå y Núi Hills of southwest Vietnam.

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

Henry Mushinsky, Earl McCoy, Adam Emerick, Brad Hauch and Nick Osman

University of South Florida, Tampa, FL, USA

Successful Translocation of the Florida Sand Skink

The Florida Sand Skink, *Plestiodon reynoldsi*, is precinctive to the high-elevation ridges of central Florida. Its preferred habitat has been, and continues to be subjected to numerous human

perturbations. Because of the immense pressure put on the skink by development, we used what we consider a last resort to protect the species. We translocated more than 500 individuals out of harm's way and monitored them for several years post-translocation. Our ultimate goal was to establish a viable population on land protected from future development and determine if translocation was an option for imperiled populations. We were interested in achieving two benchmarks: initial survival and reproduction and completion of the life cycle through subsequent recruitment of offspring. Individuals were released into enclosures at the recipient site in the same densities as found at the donor site. We modified the environments within enclosures to include specific conditions that we thought would promote survival and reproduction. We documented survival and reproduction of the individuals released into the enclosures, and the likely reproduction of individuals born in the enclosures. In spite of its small size and delicate appearance, the Florida Sand Skink is a resilient species that can survive and reproduce under apparently adverse conditions.

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

Edward Myers and Frank Burbrink

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

Population Genomics and Species Delimitation of *Coluber constrictor*

The North American racer (*Coluber constrictor*) is a wide-spread, phenotypically diverse taxon that has been shown to be composed of multiple divergent mtDNA lineages. While previous studies have suggested that species level diversity is under-represented, no process oriented species delimitation analyses have been conducted. Herein, we examine the phylogeographic history of the *C. constrictor* using 1,000's of loci, assessing population structure across North America while also estimating the timing of lineage divergence and quantifying gene flow among these lineages. Using coalescent species delimitation analyses, we explicitly test if these lineages represent species level diversity. Our results demonstrate that lineage divergence within *C. constrictor* is associated with several well-known biogeographic barriers in North America and that the taxonomy of this group is in need of revision.

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

Emily Nall, Brant Faircloth, William Ludt and Prosanta Chakrabarty

Louisiana State University, Baton Rouge, LA, USA

Is Peter Wainwright Right?

Maybe not? In Wainwright and Longo (2017) the success of Acanthomorpha is attributed to the development of eight characteristics: jaw protrusion, advanced fin-spines, pharyngognathy, endothermy, intramandibular joints, antifreeze proteins, air-breathing, and bioluminescence. Most of these characteristics are either also known outside of acanthomorphs or are only within a subset of the group. We think the success of this clade of 16,000 species

cannot be solely attributed to these features - even in combination. We hypothesize that features that were more likely to lead to the success of Acanthomorpha include a unique mix of bright coloration (including biofluorescence, bioluminescence, and conspicuous pigmentation) aided by sexual selection. We will map these characteristics on to the latest acanthomorph phylogeny to test our hypothesis.

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

Megan Napoli

Mohonk Preserve, New Paltz, NY, USA

Amphibian Phenological Shifts in Southeastern NY: Understanding the Local Effects of Climate Change through Analysis of a Unique Long-term Dataset

As springtime temperatures progressively become warmer earlier in the season, environmental time sensitive events such as amphibian over-wintering emergence and breeding have been shifting to occur at earlier dates than previously observed. By studying these phenological relationships valuable insight is gained to truly understand the local effects of climate change. This case study investigates the usefulness of a unique long-term dataset of vernal pool phenological activity from 1955 to 2018 on the Mohonk Preserve, NY. The goal for this study was to determine if calling and egg-laying dates in spring had shifted to earlier dates over time in a localized area due to increasing annual springtime temperatures and changes in precipitation levels. We analyzed anuran calling phenology in two species, wood frog (*Lithobates sylvaticus*) and northern spring peeper (*Pseudacris crucifer*), and egg-laying phenology in two species, wood frog and spotted salamander (*Ambystoma maculatum*). To perform time series analyses, calling/egg-laying dates were grouped into three time period categories of pre, during, and post-anthropogenic emergence. All records prior to 1989 were carefully digitized from notecard observations into a database containing the other subsequent phenological observations. As predicted, our preliminary results indicate a shift in both calling and egg-laying to earlier dates. Although these results show promise that our dataset can be valuable at determining local phenological changes, more robust analyses with other variables are necessary to fully understand complete impacts on regional phenological events. Next analyzation steps include correlating calling and egg-laying dates with average springtime temperatures and precipitation over time.

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

Thomas Near[1], Daniel MacGuigan[2] and Alex Dornburg[3]

[1]Yale University and Peabody Museum of Natural History, New Haven, CT, USA. [2]Yale University, New Haven, CT, USA. [3]North Carolina Museum of Natural Sciences, Raleigh, NC, USA

The Utility of RADseq for Resolving Cenozoic Adaptive Radiations: A Case Study of Antarctic Notothenioid Fishes (Percomorpha: Perciformes)

Notothenioids, a clade of ~120 marine species distributed in extreme south temperate near shore habitats and the Southern Ocean surrounding Antarctica. Over the past 25 years molecular and morphological approaches have redefined hypotheses of relationships among notothenioid lineages as well as their relationships within Percomorpha. These phylogenies provide a basis to investigate mechanisms of evolutionary diversification in the clade, including adaptive radiation. Despite extensive efforts there are many unresolved questions in the phylogenetics of notothenioids. In this study we deploy DNA sequences of ~100,000 loci obtained using ddRADseq to investigate the phylogenetic relationships of notothenioids and to assess the utility of RADseq loci for lineages that exhibit divergence times ranging from the early Cenozoic to the Quaternary. The notothenioid phylogenies inferred from the RADseq loci are well-resolved with strong node support for several key relationships including, 1) relationships among species of *Trematomus*, 2) resolution of *Indonototothenia cyanobrancha* as the sister lineage of *Trematomus*, 3) the deep paraphyly of Nototheniidae, 4) the paraphyly of *Lepidonotothen* s.l., 5) paraphyly of *Artedidraco*, and 6) the monophyly of the Bathydraconidae. Assessment of site rates demonstrates that RADseq loci are similar to mtDNA protein coding genes and RADseq loci exhibit peak phylogenetic informativeness at the time interval when the major Antarctic notothenioid lineages are hypothesized to have diversified. In addition to providing a well-resolved phylogenetic hypothesis for notothenioids, our analysis demonstrates the utility of RADseq loci for investigating phylogenetic relationships of lineages that diversified over the past 30 to 40 million years.

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

Lorin Neuman-Lee[1], Edmund Brodie, Jr.[2] and Susannah French[2]

[1]Arkansas State University, Jonesboro, AR, USA. [2]Utah State University, Logan, UT, USA

Examining the stress response in the gartersnake-newt-tetrodotoxin system

The gartersnake-newt-tetrodotoxin (TTX) system has provided us with a wealth of evolutionary and genetic information. This provides us with the ideal system to study complex endocrine relationships. We examined the hypothalamic-pituitary-adrenal (HPA) axis, which is associated with the stress response, by conducting two experiments. In our first experiment, we examined the HPA axis of the Rough-skinned newt (*Taricha granulosa*) in relation to antipredator behavior and toxicity by manipulating different hormones within the HPA axis. In our second experiment, we tested the effects of TTX exposure on the Common Gartersnake (*Thamnophis sirtalis*) by injecting increasing concentrations of TTX into male, female, and juvenile snakes. In both experiments, we tested the concentration of corticosterone (CORT), the primary hormone released by the HPA axis in reptiles and amphibians. In the first experiment, we found that TTX is not related to antipredator behavior or to CORT. However, CORT may play a role in mediating antipredator behavior, but the relationship is complex. In the second experiment, we found that female gartersnakes activated the HPA axis when exposed to TTX, but males and juveniles did not. Both of these experiments illustrate the potential for using this system for further untangling complex endocrine relationships.

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

Jennifer Neuwald[1] and Nicole Valenzuela[2]

[1]*Colorado State University, Fort Collins, CO, USA.* [2]*Iowa State University, Ames, IA, USA*

Increasing Thermal Variance due to Climate Change Alters the Sexual Development of Temperature-Dependent Sex Determined Turtles

Temperature-dependent sex determination (TSD) is a mechanism used by several reptilian lineages, including the majority of turtles. In an age when climate change is warming atmospheric temperatures and increasing thermal fluctuations globally, those species that rely on TSD may experience challenges to maintaining balanced sex ratios. Here, we examine how increased thermal variance around typical male-producing and female-producing temperatures in the painted turtle, *Chrysemys picta,* results in sex reversal and increased embryonic mortality – the combination of which can lead to biased sex ratios. These data are then considered in light of the genetic architecture underlying sex determination in *C. picta*. Specifically, we consider the degree of genetic variance in genes correlated to sexual development and discuss the potential for adaptive evolution in response to a changing environment.

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155 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION & BEHAVIOR, Empire Hall South – JF

Rochester Riverside Convention Center, Friday 13 July 2018

Thomas Nhu[1], Paul Maier[1], Gennesee Garcia[1], Sebastian Gonzales[1], Mallory Harmel[1], Miguel Jimenez[2], Katie King[1], John Thomas Nolan[1], James Whelan[1], Hayley Layne Crowell[1] and Emily Taylor[1]

[1]*California Polytechnic State University, San Luis Obispo, CA, USA.* [2]*Hancock College, Santa Maria, CA, USA*

Inglorious Baskers: Comparative Behavior of Pacific Rattlesnakes in Coastal and Inland Populations

The Pacific rattlesnake (*Crotalus oreganus*) is a moderate-sized, generalist pit viper species found throughout central California. These snakes live in a myriad of habitat types from coastal chaparral and rocky cliffs to the vast, inland plains of the Central Valley. Because this species is found over such a wide range of habitats, we hypothesized that different populations exhibit different thermoregulatory behavioral strategies in order to survive in their respective climates. The purpose of this study was to compare these behaviors of inland and coastal *C. oreganus*. To conduct this study, male rattlesnakes from two inland sites (Chimineas Ranch N = 5, Sedgwick Reserve N = 8) and two coastal sites (Vandenberg Air Force Base N = 7, Montaña de Oro State Park N = 8) were tracked throughout their active season (April-October). Environmental and behavioral data were recorded 4-5 times a week for individual snakes. Preliminary analysis showed that body temperatures of coastal and inland snakes were not significantly different. Inland sites had higher variability in air temperature than coastal sites, with higher midday temperatures. This suggests that inland and coastal snakes may have different behavioral activity throughout the day to maintain similar field-active body temperatures. We will present

data on the differences in their activity, posture, refugia type, and exposure time. These differences will indicate plasticity of behavior for maintenance of similar field-active body temperatures despite climate differences.

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206 General Herpetology I, Highland B, Sunday 15 July 2018

Max Nickerson and Joseph Mitchell

Florida Museum of Natural History, Gainesville, FL, USA

Turtle Communities for Remnant Wetland Restoration in the Upper Mississippi River Embayment

A century ago, almost half of the commercial harvest for freshwater turtles in the U.S. came from the forested wetlands of the Upper Mississippi Embayment (UME) region. Most of the habitat for freshwater turtles was eliminated, with only a few remnants remaining. Nearly 4,000,000 ha were destroyed 1955–1985. In 1983, we conducted a mark/recapture study of turtles in Allred Lake, Butler Co., MO, in one of those remnants now protected as Allred Lake State Park to ascertain which species remained and if the information could inform restoration efforts. The 6,154 trap-hour study in two sessions produced an assemblage of 359 turtles/ha and a standing crop biomass of 163 kg/ha. The two most abundant species were *Trachemys scripta elegans* (280 individuals/ha and 128.2 kg/ha) and *Sternotherus odoratus* (50 individuals/ha and 6.4 kg/ha). *Trachemys scripta* and *Chelydra serpentina* contributed the most biomass based on the techniques we used. The other turtles captured were, *Apalone spinifera*, *Chrysemys dorsalis*, and *Kinosternon subrubrum*. Two other species, *Deirochelys reticularia* and *Macrochelys temminckii*, were not captured but are known to occur in the UME. Comparisons with assemblages in a pond 96 km to the east and ponds in a U.S. Fish and Wildlife Service refuge 265 km to the southwest, both within the embayment, showed that at least 8 species occur throughout the UME. Focusing on the habitat needs and life histories of these species will guide construction and remediation efforts.

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

Stuart V. Nielsen[1], Jai L. Banks[1], Raul E. Diaz Jr.[2,3], Paul A. Trainor[4,5] and Tony Gamble[1,6,7]

[1]*Marquette University, Milwaukee, WI, USA.* [2]*Southeastern Louisiana University, Hammond, LA, USA.* [3]*Natural History Museum of Los Angeles County, Los Angeles, CA, USA.* [4]*Stowers Institute for Medical Research, Kansas City, MO, USA.* [5]*University of Kansas Medical Center, Kansas City, KS, USA.* [6]*Bell Museum of Natural History, Saint Paul, MN, USA.* [7]*Milwaukee Public Museum, Milwaukee, WI, USA*

Dynamic Sex Chromosomes in Old World Chameleons (Squamata: Chamaeleonidae)

Our current state of knowledge concerning sex chromosome evolution is based on a handful of ‘exceptional’ taxa with heteromorphic sex chromosomes. However, cataloging sex chromosome

systems of additional species lacking easily identifiable, heteromorphic sex chromosomes is indispensable if we wish to fully understand the evolutionary patterns and processes affecting the genesis, degeneration, and turnover of vertebrate sex chromosomes. Squamate reptiles are a potential model clade for studying sex chromosome evolution as they exhibit a suite of sex determining modes yet most species lack heteromorphic sex chromosomes. Only 3 (of 203) chameleon species have identified sex chromosome systems (all with female heterogamety, ZZ/ZW). This study uses a recently developed method to identify sex-specific genetic markers from restriction site-associated DNA sequence (RADseq) data, which enables the identification of sex chromosome systems in species lacking heteromorphic sex chromosomes. We used RADseq and subsequent PCR validation to identify an XX/XY sex chromosome system in the veiled chameleon (*Chamaeleo calyptratus*), revealing a novel transition in sex chromosome systems within the Chamaeleonidae. The sex-specific genetic markers identified here will be useful in embryology, particularly for studying the development of sexually dimorphic phenotypes, and further promotes *C. calyptratus'* utility as an emerging model organism.

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

Stuart V. Nielsen[1], Juan D. Daza[2], Brendan J. Pinto[1] and Tony Gamble[1,3,4]

[1]Marquette University, Milwaukee, WI, USA. [2]Sam Houston State University, Huntsville, TX, USA. [3]Bell Museum of Natural History, University of Minnesota, Saint Paul, MN, USA. [4]Milwaukee Public Museum, Milwaukee, WI, USA

Independently Derived ZZ/ZW Sex Chromosomes in the Puerto Rican Leaf-toed Gecko (*Phyllodactylus wirshingi*) are Homologous with the Avian Z

Investigating the evolutionary processes influencing the origin, evolution, and turnover of vertebrate sex chromosomes requires the classification of sex chromosome systems in a great diversity of species. Among amniotes, squamates – and geckos in particular – are worthy of additional study. Geckos possess all major vertebrate sex determining systems, as well as multiple transitions among them, yet we still lack data on the sex-determining systems for the vast majority of species. We here utilize restriction-site associated DNA sequencing (RADseq) to identify the sex chromosome system of the Puerto Rican endemic leaf-toed gecko (Phyllodactylidae: *Phyllodactylus wirshingi*), in order to confirm a ZZ/ZW sex chromosome system within the genus, as well as to better categorize the diversity within this poorly characterized family. RADseq has proven an effective alternative to cytogenetic methods for determining whether a species has an XX/XY or ZZ/ZW sex chromosome system – particularly in taxa with non-differentiated sex chromosomes – but can also be used to identify which chromosomes in the genome are the sex chromosomes. We here identify a ZZ/ZW sex chromosome system in *P. wirshingi*. Furthermore, we show that four of the female-specific markers contain fragments of genes found on the avian Z and discuss homology with *P. wirshingi* sex chromosomes.

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

Zachary Nikolakis and Brian Crother

Southeastern Louisiana University, Hammond, Louisiana, USA

Phylogenomics of the Eastern Pinesnake Complex (*Pituophis melanoleucus*)

The Eastern Pinesnake (*Pituophis melanoleucus*) is a polytypic wide ranging species comprised of three sub-specific taxa that occupy much of eastern North America with several disjunct populations. All three of these sub-specific taxa have distinguishing color patterns and are of taxonomic interest due to conservation concerns stemming from habitat degradation, fragmentation, and declining prey communities (e.g., Southeastern Pocket Gopher decline & longleaf pine degradation). Previous molecular phylogenetic studies have attempted to resolve evolutionary relationships within this complex utilizing single locus approaches. Here we use a sequence capture approach in the form of ultra-conserved elements (UCEs) to (1) infer the evolutionary relationships within this complex and determine if these molecular markers are viable for this type of study and (2) test the taxonomic validity of the current recognized nomenclature and describe any unrecognized diversity within the group. We also utilize population clustering analyses to determine levels of admixture across the range and quantify gene-flow across previously recognized southeastern biogeographic barriers.

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

Emmeleia Nix, Luis Burgos, Megan Corn, Averil E. Royal, Kiley A. Rucker, Sunny Vansdadia and Emily Taylor

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

Size Still Matters: Comparing Brain and Cloacal Heating Rates in the Western Fence Lizard (*Sceloporus occidentalis*)

A previous study from our laboratory found that larger individuals of Western Fence Lizards (*Sceloporus occidentalis*) had lower upper thermal tolerance limits (defined as critical thermal maximum, CTmax) than smaller individuals. When studying thermal tolerance, we measure cloacal temperature. However, brain temperature may be more germaine to CTmax than cloacal temperature, since high temperatures are thought to impact the central nervous system. Higher thermal inertia of larger lizards could mean that brain-cloaca temperature differentials are impacted by body size. To test whether the brain and cloaca heat at different rates, sixteen individuals were captured and tested. Lizards were anesthetized using isoflurane, and flexible thermocouples were inserted into both brain and cloaca. Brain and cloacal heating rates were measured as lizards were heated in a controlled environment at a constant rate until they surpassed their upper lethal temperature. We found that brain temperatures were consistently lower than cloacal temperatures. Smaller lizards had larger brain-cloaca temperature differences than larger lizards, potentially because cloacas of larger lizards heated more slowly than those of smaller lizards due to thermal inertia. The bodies were allowed to cool and we re-ran the heating trial on the dead lizards. Dead lizards had lower brain-cloaca temperature differences than live lizards, regardless of size, indicating that living lizards actively maintain lower brain temperatures via physiological regulation. Our data allow us to create an equation to calculate brain temperature from cloacal temperature for a lizard of a given size, so that we can examine the factors affecting CTmax more accurately.

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

José Luís Novaes[1], Danielle Peretti[2], Rodrigo Costa[1] and David Hoeinghaus[3]

[1]Federal University of Semiarid, Mossoro, RN, Brazil. [2]Rio Grande do Norte State University, Mossoro, RN, Brazil. [3]University of North Texas, Denton, TX, USA

Longitudinal Gradients in the Fish Assemblages of Small Reservoirs in Intermittent River Basins of the Brazilian Semiarid Region

Reservoirs are often characterized by fluvial, transition and lacustrine zones occurring from the upstream extent towards the dam, with concomitant structuring in biological assemblages. However, the aforementioned gradient in physical conditions is not persistent in reservoirs of intermittent river basins, which have flowing conditions during only part of the year. This study tested for longitudinal gradients in fish assemblage structure in reservoirs of the Brazilian semiarid region and for effects of season (i.e. flowing and non-flowing conditions) on fish assemblage structure. Field research was conducted quarterly from 2010 to 2014 in three differently-sized reservoirs in Northeast Brazil. Standardized gill-net sampling was conducted at multiple sites along the lacustrine-fluvial gradient in each reservoir. Species richness was calculated for each site and differences were evaluated using ANOVA for each reservoir in both seasons. Community structure (composition and relative abundances in CPUE) was summarized using nMDS. Differences were tested with PERMANOVA for each reservoir in both rainy and dry seasons. Species richness decreased from fluvial to lacustrine in both rainy and dry seasons in the larger Santa Cruz Reservoir ($p<0.05$), whereas the Pau dos Ferros and Umari Reservoirs did not present any longitudinal patterns in either rainy or dry seasons. Similarly, nMDS showed separation between fluvial sites and other sites in Santa Cruz Reservoir in both rainy and dry seasons ($p<0.05$). In this study, a longitudinal gradient in fish diversity and assemblage structure was observed only in the largest reservoir, Santa Cruz Reservoir, and that gradient was persistent between seasons.

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

Katherine O'Donnell[1], William Barichivich[1], Kurt Buhlmann[2], Jonathan Chandler[3], Kevin Enge[4], Anna Farmer[4], Thomas Gorman[5], Carola Haas[6], Pierson Hill[4], John Jensen[7], Mark Mandica[8], Jana Mott[9], John Palis[10], Lora Smith[11] and Susan Walls[1]

[1]U.S. Geological Survey, Gainesville, FL, USA. [2]Savannah River Ecology Laboratory, Aiken, GA, USA. [3]U.S. Fish and Wildlife Service, St. Marks, FL, USA. [4]Florida Fish and Wildlife Conservation Commission, Gainesville, FL, USA. [5]Washington Department of Natural Resources, Olympia, WA, USA. [6]Virginia Tech, Blacksburg, VA, USA. [7]Georgia Department of Natural Resources, Forsyth, GA, USA. [8]The Amphibian Foundation, Atlanta, GA, USA. [9]The Nature Conservancy, Bristol, FL, USA. [10]Palis Environmental Consulting, Jonesboro, IL, USA. [11]Joseph W. Jones Ecological Research Center, Newton, GA, USA

Range-wide Occupancy Status of Federally-listed Flatwoods Salamanders

Flatwoods salamanders (*Ambystoma cingulatum, A. bishopi*) are federally-listed pond-breeding salamanders native to the southeastern United States. Both species breed in wetlands embedded in pine-wiregrass ecosystems and have likely declined because of widespread habitat loss and degradation. It is critical to have a thorough understanding of remaining populations to inform recovery planning. In 2013, we initiated a multi-partner effort to survey known and potential flatwoods salamander ponds across the combined range of the two species. These species typically breed in late fall (October–December); surveys targeted larval salamanders approximately 2–3 months after breeding events (January–March). All partners incorporated repeated sampling into survey efforts, enabling us to analyze resulting data in an occupancy-based framework. We fit Bayesian models that account for nested sampling design (i.e., multiple wetlands within multiple geographically distinct survey areas; Miller & Grant 2015). Through this 4-year effort, we discovered several previously unknown breeding wetlands; however, we also failed to detect salamanders at many historical breeding sites. We surveyed over 500 unique wetlands; 19% of wetlands were occupied in at least one season. St Marks National Wildlife Refuge (FL) and Apalachicola National Forest (FL) contain the majority of active *A. cingulatum* ponds, whereas Eglin Air Force Base (FL) harbors the best population of *A. bishopi*. Populations in South Carolina, Georgia, and north-central Florida have been extirpated or are very small. Understanding the current status of these species provides the foundation for making key decisions about species recovery, including where to prioritize salvage efforts and potential reintroduction efforts.

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

Mizraim Olivares and Sean Rovito

LANGEBIO - CINVESTAV, Irapuato, Guanajuato, Mexico

The Role of Fungal Pathogens in Declines of an Obligate Cave-Dwelling Salamander from Eastern Mexico

Chiropterotriton magnipes is the only obligately cave-dwelling salamander known from the Neotropics and is known from a small region of the Sierra Madre Oriental of Mexico. This species was abundant in the decade following its description in 1965, but records decreased in subsequent years to the point where it disappeared from several localities where it was common and it is now classified as Critically Endangered. Its decline is coincident with that of other populations of Neotropical salamanders associated with the arrival of the fungal pathogen *Batrachochytrium dendrobatidis* (Bd). We hypothesized that the arrival of Bd played a key role in the declines of *C. magnipes*. We used a noninvasive sampling technique and qPCR assay to detect Bd in the skin of museum specimens of *C. magnipes* collected in from 1952 to 2012. We also examined the prevalence of the fungus in extant populations of *C. magnipes* and other sympatric species of amphibians. We obtain the earliest positive record of the fungus to date in Mexico, providing additional historical evidence for the “Bd epidemic wave" hypothesis. Our results provide an important historical baseline for actions to preserve the few known remaining populations of *Chiropterotriton magnipes*.

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301 Ichthyology Ecology and Ethology, Highland E, Sunday 15 July 2018

Daniel Oliveira[1] and Sarah Fitzpatrick[2]

[1]Clark University, Worcester, Massachusetts, USA. [2]Michigan State University, East Lansing, Michigan, USA

Phenotypic Differentiation matches Environmental Variation: a Potential Case for Local Adaptation in Rainbow Darters

Populations of species inhabiting different environments often display phenotypic differentiation associated with local conditions. Many well-known examples of local adaptation exist from freshwater fish populations occupying varying environments. However, population-level differentiation has rarely been documented in darters, one of the most species-rich groups of fish in North America. This study assessed fine-scale intraspecific variation in a suite of phenotypic traits across local populations of *Etheostoma caeruleum* (rainbow darters). Individuals were collected from five sites in Southwest Michigan, including from one of the few documented lake populations of rainbow darters. Variation in thermal tolerance and body shape was quantified per population, in addition to the collection of site-specific environmental variables (temperature and flow). Preliminary results indicate a positive trend between water temperature and thermal tolerance. Lake individuals differed significantly from stream populations across all traits, but some phenotypic differences were also found between stream populations. This is the first observation that we know of showing phenotypic differentiation among lake versus stream populations of darters. Next-generation sequencing data will identify intra and inter-population genetic diversity and patterns of gene flow in this landscape. Genomic information will provide an understanding of the contribution of gene flow to phenotypic variation as well as determining if underlying genetic variation correlates with phenotypic differentiation among populations.

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

Aaron Olsen and Elizabeth Brainerd

Brown University, Providence, RI, USA

An Ancient Throat Expansion Mechanism Functions as an 11-Bar Linkage in Channel Catfish

The throat expansion mechanism used by ray-finned fishes and chondrichthyans likely evolved at the origin of the jawed vertebrates. This ancient mechanism couples pectoral girdle retraction with hyoid depression and suspensorial abduction, enabling the axial (body) muscles to power throat expansion by simply pulling back on the shoulder. Previous studies have imaged the motion of this mechanism using lateral-view X-rays (two-dimensional kinematics) and concluded that the mechanism can be accurately modeled as a planar 4-bar linkage. However, it is clear from anatomy and live observation that the system is more complex than a 4-bar and likely exhibits significant non-planar motion. How this mechanism functions in three dimensions is unknown. To answer this question we collected 3D *in vivo* kinematics of six cranial skeletal elements in channel catfish (*Ictalurus punctatus*) during suction feeding using X-ray Reconstruction of Moving Morphology (XROMM). We then fit joint and linkage models of varying degrees of freedom (DoFs) to the *in vivo* motion. We find that the hyoid-pectoral girdle mechanism functions as an 11-bar linkage comprised of four bilaterally paired elements and

three unpaired elements. Despite having 11 bodies, the closed-chain nature of this linkage reduces the DoFs of motion to around six. In addition, only around four of these DoFs vary *in vivo*. Thus, in channel catfish a complex system with many parts actually functions and moves in a relatively simple manner, possibly a consequence of the coarse axial muscle control that powers this mechanism. Funding: NSF 1612230, 1655756.

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

Deanna Olson[1], Meryl Mims[2], Carmen Harjoe[3], Gisselle Xie[3], Andrew Blaustein[3], David Pilliod[4] and Jason Dunham[5]

[1]US Forest Service Pacific Northwest Research Station, Corvallis, OR, USA. [2]Virginia Tech, Blacksburg, VA, USA. [3]Oregon State University Department of Integrative Biology, Corvallis, OR, USA. [4]US Geological Survey, Boise, ID, USA. [5]US Geological Survey, Corvallis, OR, USA

Climate Niches and High-latitude Herpetofauna Risk: Multi-taxa Climate Sensitivity Modeling

Climate-smart management for species persistence includes consideration of species' climate sensitivity, exposure to changing conditions, and adaptive capacity. With all species potentially exposed to changing conditions, rapid multi-species systematic assessments are needed. Northern latitudes are particularly important for ectotherms relative to climate change because many species reach their northward extents here, and climate affects habitat suitability and aspects of physiological ecology. Three case studies illustrate different aspects of multi-taxa vulnerabilities to climate change. First, we evaluated the intrinsic risk to climate change for 114 reptiles, amphibians, and freshwater fishes in the US Pacific Northwest by combining geographic rarity and traits-based approaches. We found: 1) 17% of reptiles and 23% of amphibians had very high climate sensitivity; and 2) rarity and life history data provided complementary information on risk to climate change. Second, for northwestern-US reptiles, we examined climate niches and climate change projections. Both reduction and expansion of ranges were projected for different species, with reductions aiding identification of climate-smart refuges for land-management prioritization. Third, in addition to examining climate futures for herpetofauna, climate niches of species posing potential threats to amphibians and reptiles are important considerations. Using world data of amphibian chytrid fungal (*Batrachochytrium dendrobatidis, Bd*) infections, we projected the future *Bd* distribution with climate change scenarios. An expanded high-latitude range is expected. Initial sampling has detected *Bd* and a second pathogen, Ranavirus, in coastal Alaskan wetland ecosystems where a monitoring plan is under development to assess amphibians subject to changes in both climate and pathogen exposure.

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

Abiodun Onadeko

University of Lagos, Nigeria, Lagos, Lagos State, Nigeria

Tackling the Paucity of Information (Knowledge) of Anuran diversity and studies on Nigerian Landscapes: Platform for Research Collaboration.

Nigeria is rich in anuran diversity with biodiverse natural landscapes. As expected, being a tropical country, its climatic conditions and vegetation favour the thriving conditions of the anurans. The diversity of landscapes results in a corresponding diversity of anuran species. A few ecosystems where herpetological surveys have been carried out include; 1) high altitude plateau (Obudu Ranch), 2) lowland and montane rainforests (Cross River National Park) and 3) freshwater wetlands (Niger Delta). Prominent anuran species observed in these ecosystems were respectively: 1) *Cardioglossa pulchra, Leptopelis modestus, Phrynobatrachus werneri* and *Astylosterus montanus*; 2) *Scotobleps gabonicus, Amietophrynus tuberosus, Werneria mertensiana* and *Tichobatrachus robustus*; and 3) *Hylarana albolabris, Phlyctimantis boulengeri, Hymenochirus* sp and *Leptopelis boulengeri.* However appreciating the diversity of ecosystems, anurans have been understudied in Nigeria. Novel species, no doubt, do exist. Anuran decline compounded by emerging diseases (caused by the oomycete *Saprolegnia* and the fungus *Batrachochytrium*) needs to be studied and well documented. There is a paucity of information regarding the dynamics of anuran population on the various landscapes. Appreciating the importance of anurans in our environment and the fast and unprecedented rate of its decline, one cannot overemphasize the need for more research emphasis on anuran study. It is against this background which strongly suggests that there is need for international collaboration research work to harness more revelation on these beautiful jewels in Nigeria.

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

Xochitl Ortiz Ross[1], Michelle E. Thompson[2] and Maureen A. Donnelly[2]

[1]*College of the Atlantic, Bar Harbor, ME, USA.* [2]*Florida International University, Miami, FL, USA*

Oviposition Site Selection in Three Glass Frog Species

Oviposition site selection is an important behavior that can, directly and indirectly, affect hatching success and larval survivorship in oviparous organisms. Although we should expect strong selection pressure for the ability to recognize and select a favorable habitat, active selection for oviposition sites is not well supported for many species of anurans. We investigate oviposition site selection in three species of glass frogs—*Hyalinobatrachium valerioi, Espadarana prosoblepon* and *Teratohyla spinosa*—in northeastern Costa Rica. We conducted nocturnal visual encounter surveys to estimate glass frog egg mass abundance and characterize oviposition site features at nine different sites and across three different habitats (pasture, secondary growth forest, and old growth forest). We then characterized habitat availability with habitat surveys at the same sites. Our results show differential active oviposition site selection in all three species based both on stream and vegetation features, such as water velocity, leaf substrate type, and leaf size. *Espadarana prosoblepon* was the only species influenced by habitat type, preferring old growth forests. However, the large variation in egg mass abundance at different sites that is not explained by habitat type suggests that microhabitat features may play a larger role in oviposition site selection than habitat type. Therefore, pastures and other de-forested areas can still sustain glass frog populations so long as the appropriate riparian microhabitat is maintained. Our results offer new insights into the ecology, distribution and habitat use of glass frogs and have important implications for conservation practices and habitat restoration efforts.

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

Megan Osborne[1], Alyssa Sanchez[1], Thomas Dowling[2] and Thomas Turner[1]

[1]University of New Mexico, Albuquerque, New Mexico, USA. [2]Wayne State University, Detroit, Michigan, USA

Gender equality: large variance in reproductive success is driven by environmental factors not mating system in Bonytail.

Studying the reproductive ecology of aggregate broadcast spawning fishes is difficult because it generally is not feasible to sample all potential parents and unambiguously assign their offspring. We used molecular-based parentage analysis to gain insights into the reproductive ecology of the endangered Bonytail (*Gila elegans*) and to evaluate whether protected off-channel ponds could be used as an alternative to hatchery production. By genotyping adults and offspring stocked (n = 4130) into two experimental backwaters across three years, we determined that most adults (82-97%) contributed to progeny production across years and backwaters, with one exception. Both genders mated multiply and the number of mates and family size were positively correlated. There was also a positive correlation between adult size and metrics of reproductive success. Males and females made essentially equal contributions to the progeny pool within backwaters and years. There were strong interactions between sample years and backwaters suggesting that environmental factors are the primary driver of variance in reproductive success. Knowledge of mating systems and sources of variance in reproductive success is important for management of endangered fish because high variance in reproductive success leads to substantial losses of genetic variation when few individuals reproduce successfully. Although there was variation in reproductive success among Bonytail, high reproductive contribution of adults resulted in faithful transmission of genetic variation from parents to their progeny. These results suggest that use of predator-free but otherwise natural backwaters will be an important conservation tool for reintroducing Bonytail to its native habitat.

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579 Ichthyology Biogeography, Grand Lilac Ballroom South, Saturday 14 July 2018

Kenneth Oswald and Morgan Reich

Ohio Northern University, Ada, OH, USA

Population Genetics and Phylogeography Inform Conservation and Management of Rare Tonguetied Minnow (*Exoglossum laurae*)

Tonguetied minnow (*Exoglossum laurae*) is a rare species that maintains a fragmented distribution across a small geographic range, with individuals occurring only in the Upper Great Miami, Upper Allegheny, New, and Upper Genesee Rivers of the eastern United States. Populations currently face various anthropogenically-driven threats to persistence such as habitat destruction from alterations of native streams and interspecific hybridization resulting

from introductions of non-native cutlip minnow (*E. maxillingua*). DNA sequences from one mitochondrial locus and three single-copy nuclear DNA loci were used to estimate intraspecific genetic variation, ascertain phyletic affinities among drainages, and assess levels of interspecific hybridization. A coalescent-based model of evolution based on a Teays River ancestry for the species assessed demographic parameters, including effective population sizes (N_e) and times since divergence (t) among populations. Management recommendations will be given which aim to maximize the persistence of tonguetied minnow based on a holistic interpretation of these analyses.

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

Dustin Owen, David Ensminger, Michael Sheriff and Tracy Langkilde

Pennsylvania State University, University Park, PA, USA

Effects of Maternal Stress on Offspring of Lizards from High- and Low-stress Sites

While it is well established that maternal stress hormones, glucocorticoids, can induce transgenerational phenotypic plasticity, there is much debate over the adaptive significance of such effects. While many studies have examined how maternal stress influences traits of offspring, few have compared these effects across populations with different transgenerational histories. We tested the hypothesis that the effects of experimentally elevating corticosterone (CORT) in gravid female eastern fence lizards (*Sceloporus undulatus*) on offspring traits would differ for lizards from high-stress sites (those invaded by predator fire ants, *Solenopsis invicta*) versus low-stress (fire ant free) sites. Maternal CORT-treatment increased snout-vent length and tail length in offspring from high stress, fire ant invaded sites but decreased snout-vent length and tail length in offspring from low-stress, uninvaded sites when compared to controls. Larger offspring for high-stress sites could help mitigate the impact of some predators, such as envenomation by fire ants. Conversely, smaller size in offspring of females from uninvaded sites could facilitate avoidance of other predators, such as birds. There was no difference in glucose levels between offspring of females from invaded and unevaded sites. Maternal CORT could match the specific environmental stressor to the phenotypic change in the offspring, increasing the fitness of offspring within the environments into which they emerge. Future work should examine this possibility.

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605 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Highland A, Thursday 12 July 2018

Dustin Owen, Michael Sheriff and Tracy Langkilde

Pennsylvania State University, University Park, PA, USA

Effects of Maternal Stress on Lizard Heart Rate

Maternally-derived stress hormones, glucocorticoids, can induce phenotypic plasticity in many vertebrate taxa, and have consequences for resulting offspring. We tested the hypothesis that increased physiological stress of female eastern fence lizards (*Sceloporus undulatus*) while gravid will elevate heart rates of mothers and their offspring. Increased heart rates may facilitate energy allocation to deal with the environmental stressors, and can also speed development of offspring and decrease the amount of time in the vulnerable hatchling stage. Gravid females were dosed daily with topical corticosterone (CORT) until laying. Heart rate was measured five days after laying for mothers, and five days after hatching for hatchlings. We found that hatchlings of glucocorticoid-treated mothers had higher heart rates compared to hatchlings of control mothers. However, mothers from CORT-treated and control treatments had similar heart rates. Maternal stress appears to alter the physiology of offspring at five days of age, potentially speeding rates of development and resulting in earlier sexual maturity and larger body size, which could have important fitness benefits. Future work should investigate the adaptive significance of these maternal stress-effect to determine whether these offspring have increased fitness within high-stress environments.

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

Austin Owens[1], Renae Steinberger[1], Catherine Triplett[2], Howard Whiteman[2] and Cy Mott[1]

[1]Eastern Kentucky University, Richmond, KY, USA. [2]Murray State University, Murray, KY, USA

Trophic effects of intraspecific body size variation among exploitative and interference competitors

Despite the importance of intraspecific variation to population ecology studies, community ecologists have historically modelled predator-prey interactions with an assumption of functional equivalence among members of a single species. To more accurately predict the outcomes of ecological interactions, recent theoretical approaches have incorporated aspects of intraspecific trait variation into community ecology, disregarding mean trait values and instead focusing on the importance of variation around the mean. In larval salamanders, intraspecific body size variation is considerable and may impact predator-prey dynamics through associated risks of cannibalism at high levels of size variation. We manipulated body size variation around a standardized mean body size in two apex predators (larval *Ambystoma talpoideum* and *A. maculatum*) to determine the effects of size variation on intraspecific aggression, microhabitat partitioning, and attacks on/consumption of zooplankton prey. Despite broad differences in competitive strategy among larval *A. talpoideum* (interference competitor) and *A. maculatum* (exploitative competitor), intraspecific body size variation did not influence any of our response variables. However, interspecific differences independent of the influence of body size variation were observed for the number of attacks on zooplankton prey and the amount of zooplankton captured, with the exploitative competitor (*A. maculatum*) exhibiting higher totals for both. Our results indicate that increased size variation did not promote increased cannibalism among larval salamanders or associated release from predation for zooplankton prey, though the short-term nature of our study may have limited longer-term ecological consequences of intraspecific body size variation.

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

Hannah Owens and Edward Stanley

University of Florida, Gainesville, Florida, USA

Anatomy of Sexual Parasitism in Triplewart Sea-Devils (*Cryptosaras couesii*)

Ceratioid anglerfishes exhibit extreme sexual dimorphism; males are many times smaller than females, with enlarged nostrils and specialized jaw denticles to find and attach to females for mating. These attachments vary in permanence from facultative associations to putatively permanent obligate parasitism. In the case of obligate parasitism in the Triplewart Sea-Devil, epidermal and dermal tissues of the partners fuse. It is thought that males receive nutrients from mates via a merged circulatory system; however, investigation of the nature of these connections via traditional histological sections has been inconclusive. To elucidate the nature of sexual parasitism in the Triplewart Sea-Devil, we performed high-resolution microCT scans of two contrast-stained adult female Sea-Devils with attached males from the Florida Museum of Natural History. These scans allow unprecedented 3-dimensional digital models of the unusual anatomy of the Triplewart Sea-Devil, and provide important information regarding the nature of parasitic male attachment in this charismatic deep-sea fish.

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

Juan Pacheco and Christopher Beachy

Southeastern Louisiana University, Hammond, LA, USA

Effects of differential probiotic administration on *Ambystoma mexicanum's* response to a skin incision before and after metamorphosis

Amphibian populations all over the world are experiencing a decline, due to many environmental factors such as pollution and diseases; a lot of effort has been made to conserve species that may be endangered because of such factors and, many approaches have been taken to solve this problem. Diseases such as Chytridiomycosis, red leg disease and ranavirus are specially playing a role in the decline of amphibians. This investigation aims to test the effect of the administration of oral probiotics, identified from the gut of axolotls, in improving their response to a skin incision. The results of the study could provide an alternative choice for the prevention of the decline of amphibians threatened by skin diseases.

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

Robert Page[1], Claire Conarroe[2], Diana Quintanilla[1], Andriea Palomo[1], Joshua Solis[1] and

David Marsh[2]

[1]Texas A&M University--San Antonio, San Antonio, TX, USA. [2]Washington & Lee University, Lexington, VA, USA

Hybridization and Genetic Variation in the Range-restricted Peaks of Otter Salamander, *Plethodon hubrichti*

Climate change can alter the geographic ranges of species in ways that reshuffle the compositions of ecological communities, and one potential consequence of such reshuffling is increased hybridization between closely related species that were once reproductively isolated. Interspecific hybridization is recognized as a potential driver of extinction because it can lead to the production of less fit hybrids or the replacement of one or both species with hybrids. The Peaks of Otter Salamander (*Plethodon hubrichti*) is restricted to a ~ 19 km stretch of ridge in west-central Virginia. The area occupied by *P. hubrichti* is surrounded by the morphologically and ecologically similar Eastern Red-backed Salamander (*P. cinereus*). While hybridization among closely related plethodontids is well known, it is unclear whether *P. hubrichti* and *P. cinereus* are hybridizing. To assess this possibility, we used microsatellite markers to investigate whether there is evidence for admixture between *P. hubrichti* and *P. cinereus*. Preliminary results from our study suggest that hybridization between *P. hubrichti* and *P. cinereus* is rare. However, our results revealed that allelic richness and heterozygosity are substantially higher in *P. hubrichti* than they are in nearby *P. cinereus* populations. This suggests that *P. hubrichti* may have evolved *in situ* in this region for longer than *P. cinereus*, and that, despite its large geographic range, *P. cinereus* is a comparatively recent invader. We argue that additional work on the historical and contemporary demography of range-restricted plethodontids is needed in order to better understand their evolutionary histories and conservation statuses.

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

Daniel Paluh, Edward Stanley and David Blackburn

University of Florida, Gainesville, Florida, USA

Convergent Evolution and Function of Hyperossification in Frogs

Within fossil and extant anuran amphibians, a reoccurring trend in skull morphological diversity is hyperossification, i.e. the increased mineralization and excessive ossification of a skeletal element that results in dorsal sculpturing and pitted ornamentation of dermal bones. There is little research on the evolution of anuran skull hyperossification, but a survey of skeletal diversity indicates that it has persisted or independently evolved in at least 23 lineages and 14 families of frogs in taxa ranging in size from 16 to 245 mm snout–vent length. Three disparate hypotheses exist on the function of hyperossification—water balance enhancement in arid environments, protection against predators during phragmotic behavior, and increased skull biomechanic capabilities related to feeding biology—but there have been no explicit tests whether there is an association between hyperossified skull shape and these different functions. We utilized high-resolution micro-computed tomography, 3-D geometric morphometric analyses, and phylogenetic comparative methods to determine if there is a significant difference in shape between hyperossified and non-hyperossified skulls across all families of frogs. We

then further tested if a predicted relationship exists between skull shape, the habitation of arid environments, the use of phragmotic defensive behavior, and a carnivorous diet. Overall, we found that hyperossification has independently evolved in phylogenetically, morphologically, and ecologically diverse frog lineages. An association was found between hyperossification and large body size, carnivorous feeding biology, and predator defense behaviors. No relationship was found between skull shape and climate or microhabitat parameters.

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

Lynne Parenti[1], Diane Pitassy[1], Zeehan Jaafar[2,1], Kirill Vinnikov[3] and Kathleen Cole[3,1]

[1]*National Museum of Natural History, Smithsonian Institution, Washington, DC, USA.* [2]*National University of Singapore, Singapore, Singapore.* [3]*University of Hawaii, Honolulu, HI, USA*

The 2017 Smithsonian MarineGEO Assessment of the Fishes of Kaneohe Bay, Oahu, Hawaii

In 2017, we conducted a survey of the fishes of Kaneohe Bay, Oahu, Hawaii as part of a broader Smithsonian Institution MarineGEO Hawaii biodiversity assessment: *Ola I ke Kai*, or Life Comes from the Sea. Kaneohe Bay was chosen for intensive study because of the long history (ca. 1,000 years) of use of its land and sea resources by Hawaiian peoples living in and around the Bay. Our knowledge of the fishes of the Hawaiian Islands is broad compared to that of other subtropical and tropical islands of the central Pacific. Yet, there have been few attempts to compile a comprehensive systematic inventory and assessment of the fish species of Kaneohe Bay, an ultimate goal of MarineGEO Hawaii. We surveyed fishes throughout the Bay using a variety of sampling methods (dipnets, pushnets, hook and line, and spears) without chemicals. We collected about 100 species representing the larger, visible reef species as well as some cryptic species. We documented the occurrence of each species with an archived voucher specimen or a verified field observation, genome-quality tissue samples, and a color photograph of a freshly dead specimen. We sequenced DNA barcodes for each species to confirm identification and to test our hypothesis that Hawaiian populations of species broadly distributed throughout the Indo-Pacific may be genetically distinct. We consider the taxonomic implications of these findings and how they may affect our understanding of Hawaiian endemism.

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375 ASIH STOYE GENERAL ICHTHYOLOGY I, Grand Lilac Ballroom South, Thursday 12 July 2018

Elyse Parker[1], Alex Dornburg[2], Daniel J. MacGuigan[1], Edgar Benavides[1] and Thomas J. Near[1,3]

[1]*Yale University, New Haven, CT, USA.* [2]*North Carolina Museum of Natural Sciences, Raleigh, NC, USA.* [3]*Peabody Museum of Natural History, Yale University, New Haven, CT, USA*

Phylogenomic species delimitation and the reduction of species diversity in Antarctic Plunderfishes (Notothenioidei: Artedidraconidae)

Explaining the factors that underlie the uneven distribution of species-richness across the Tree of Life has been a core topic in evolutionary biology for over a century. However, the impact of taxonomic uncertainty on estimates of lineage origination and turnover is rarely considered in macroevolutionary studies. The notothenioids, a clade of percomorph fishes that dominates the ichthyofauna of the Antarctic continental shelf, provide an ideal case study for understanding the impact of taxonomic uncertainty on inferences of diversification patterns. Like many lineages of ray-finned fishes, notothenioid species diversity undergoes continuous revision based on morphological and molecular data. Uncertainty in species level diversity is especially evident in the Antarctic Plunderfish (Artedidraconidae) lineage *Pogonophryne.* This lineage comprises 29 valid species, 11 of which were described since 2000. Many of these species descriptions are based solely on variation in ornamentation of the mental barbel, a structure that is highly plastic within species, and are known only from holotype specimens. Extensive intraspecific variation in mental barbel morphology warrants renewed examination of species delimitation in the clade. Bayesian species delimitation approaches using both genome-wide SNP data and mtDNA data support a reduction in recognized diversity within *Pogonophryne* to no fewer than five species. This conclusion is supported by extensive overlap among *Pogonophryne* species in morphometric and meristic traits. Given that Artedidraconidae were previously hypothesized to exhibit an exceptionally high diversification rate relative to other notothenioid clades, we demonstrate how the dramatic reduction of species diversity within *Pogonophryne* necessitates a reinterpretation of adaptive radiation in notothenioids.

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

M. Rockwell Parker[1], Bryan G. Falk[2], Amy A. Yackel Adams[3] and Robert N. Reed[3]
[1]*James Madison University, Harrisonburg, VA, USA.* [2]*U.S. Geological Survey, Homestead, FL, USA.* [3]*U.S. Geological Survey, Ft. Collins, CO, USA*

A modified Judas approach for enhancing detection of Burmese pythons in Florida

The successful management of invasive species, especially vertebrates, depends on the development of techniques that increase detection and removal of individuals from the invasive range. Also, once an invasive species has become established, some tools maintain their utility in detecting early stage invasions/expansions of species into novel habitats. Burmese pythons (*Python bivittatus*) are an established invasive species that has contributed significantly to swift ecological changes in southern Florida. Detectability of pythons is a central problem for managers that necessitated the adaptation of existing tools as well as the evolution of new

approaches. Currently, we are integrating a standard technique in invasive vertebrate management, the Judas approach, with a novel technique, hormone manipulation. Sex steroid hormones are powerful regulators of pheromone production in snakes, and males can be feminized in their pheromone expression via estradiol treatment. We are using radiotelemetry to track male Burmese pythons (n=8) in Big Cypress National Preserve in southern Florida. Half of these males were given control surgery (SHAM), and half received silastic implants containing 17 β-estradiol, the latter of which we predict will be attractive to other males in the field. Blood samples will reveal male sex hormone concentrations during the breeding season in Florida and validate the estradiol implants. In June, we will extract the skin lipids from these snakes and identify compounds specifically upregulated in the skin as a result of estradiol treatment. If effective, our modified Judas approach may enhance existing detection probabilities for Burmese pythons in Florida.

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308 Herpetology Reproduction, Highland C, Sunday 15 July 2018

M. Rockwell Parker, Shannon A. Richard, Holly R. Rucker and Sydney E. Ashton

James Madison University, Harrisonburg, VA, USA

How to make a sexy snake, part deux: dose-specific feminization of males via estradiol

Many sexual signals in vertebrates are dynamically controlled by sex hormones, such as testosterone and estradiol. The sex-specific nature of these reproductive signals is also highly seasonal, with fluctuations in circulating steroids often matching the quality and complexity of the signals. In red-sided garter snakes (*Thamnophis sirtalis parietalis*), females elicit courtship from males by producing a potent sex pheromone, and the quality of this sex pheromone varies annually and maximized during the spring breeding season. Estradiol is the principle female sex steroid that activates pheromone production in garter snakes, and males can be stimulated to produce the pheromone via estradiol treatment. In this study, we gave males varying doses of estradiol and found that while all males became attractive, we saw a gradient of behavioral responses from wild males in the den. The lower the dose of estradiol, the less potent the male's pheromone was in bioassays as evidenced by the length of time wild males would court the manipulated male. We therefore propose that estradiol signaling manifests a gradient of phenotypic change via sex pheromones in garter snakes that can be assessed by males during the breeding season.

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

Larissa Patterson[1] and David Parichy[2]

[1]*Rhode Island College, Providence, RI, USA.* [2]*University of Virginia, Charlottesville, VA, USA*

Stripes, Spots, Bars and More: Pigment Pattern Development and Evolution in *Danio* Fishes

Teleost fishes boast colorful and dramatic pigment patterns. Adult pigment patterns of fishes in the genus *Danio* include horizontal stripes, spots, vertical bars and uniform patterns. The diversity of patterns within this genus, presents an opportunity to identify the genetic and cellular mechanisms underlying variation in a neural crest-derived trait. Armed with an understanding of stripe development in zebrafish, we can generate testable hypotheses about pattern evolution within this genus. In zebrafish, iridescent iridophores differentiate prior to other adult pigment cell types, establishing the location and orientation of adult stripes. In contrast, the barred pattern of *D. aesculapii* and the uniform pattern of *D. aff albolineatus*, are initiated by the differentiation of precocious xanthophores, not iridophores. In both species, widespread, early xanthophore development is associated with elevated expression of *colony-stimulating factor-1*. Csf1-signaling was experimentally manipulated in all three species to determine its effect on pattern formation. Together, these results provide insight into the cellular and molecular mechanisms underlying pattern diversification within this genus.

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

Mark Paulissen

Northeastern State University, Tahlequah, OK, USA

Does the Little Brown Skink, *Scincella lateralis*, Use Positional Cues for Spatial Learning?

Many small lizards escape from predators by rapidly running under a retreat. Lizards that have previously learned the location of such retreats through spatial learning should be better able to escape than lizards that run in a non-specific way in hopes of locating retreat before they are caught. Previous work has shown that LBSs learn to escape to retreats with vertical striped local cues significantly better than those with horizontal striped local cues. One hypothesis is that LBSs regard vertical stripes as positional cues to orient toward retreats (similar to orienting using tree trunks in nature). I tested this hypothesis with a series of trials in which LBSs were trained to escape to one of two retreats positioned on either side of a vertical positional cue. Fifteen trials were run on each LBS; those that escaped to the correct retreat in five consecutive trials were scored as having learned which of the two retreats was “correct” based on its position relative to the positional cue. Of the 16 LBSs tested, only 2 (12.5%) met the learning criterion, significantly fewer than had met the learning criterion in the earlier study using the vertical striped cue. This suggests that LBSs do not use positional cues for spatial learning of the location of escape retreats and that the reason they are better able to learn using a vertical striped local cue versus a horizontal striped one lies in some other aspect the sensory or cognitive biology of this species.

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

Gregory Pauly

Natural History Museum of Los Angeles County, Los Angeles, California, USA

The Nursery Trade as an Introduction Pathway for Nonnative Reptiles and Amphibians in California

The nursery trade is one of the primary pathways through which nonnative reptiles and amphibians are introduced around the globe. Here, I use a combination of citizen science approaches and traditional methodologies to document the arrival and spread of nonnative reptiles and amphibians in Southern California that are being transported via the nursery trade. These efforts have revealed four nonnative species now established in the state and another five species that are frequent hitchhikers on nursery shipments but are not yet established. Through a unique collaboration with a local wholesale nursery, we have documented one native frog species and seven nonnative frog and gecko species as hitchhikers on nursery shipments at just this one facility. More broadly throughout Southern California, Brown Anoles and Green Anoles are now established in and around multiple nurseries, and surveys suggest that both species are displacing native lizards in urban neighborhoods. These efforts are also documenting the rapid spread of Brahminy Blindsnakes in Southern California. Efforts to assess the role of the nursery trade, and other pathways, as sources of introductions are currently hampered by underreporting and failure to secure museum specimens and photo vouchers that document the transportation of hitchhikers. Citizen science databases can be an important tool in improving documentation of nonnative species transport.

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223 NIA BEST STUDENT PAPER, Highland E., Friday 13 July 2018

Holden Paz, Malorie Hayes and Jonathan Armbruster

Auburn University, Auburn, Alabama, USA

Phylogenetic Placement of a New Species of *Trichomycterus* from the Pakaraima Mountains in Guyana

Trichomycterus (Trichomycteridae: Siluriformes) is a genus of catfishes found throughout South American waters that is experiencing a growth in the number of described species. The genus has recently been shown to be paraphyletic with geography as a major factor determining relatedness. True *Trichomycterus* are believed to be those found in rivers draining to the Atlantic Ocean. Specimens of putative *T. guianensis* as well as undescribed species were collected from the upper Kuribrong, Potaro, and Ireng Rivers in Guyana. These rivers originate in the Pakaraima Mountains of the northwest Guiana Shield, and flow to the Atlantic Ocean, making

them members of true *Trichomycterus* according to a recent phylogenetic paper, although the species differ significantly in their interopercular and opercular odontode patterns from other *Trichomycterus*. The Pakaraima Mountains are a region of high endemism and have been the recent focus of biodiversity inventories. Using three mitochondrial (16S, COI, and cytb) and two nuclear markers (myh6 and RAG2), we determined the phylogenetic placement of these taxa within *Trichomycterus*. Our results suggest that there are multiple undescribed species of *Trichomycterus* in the highlands of Guyana, and we provide clarification of the identification of *T. guianensis* and *T. conradi*.

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425 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: CONSERVATION & MANAGEMENT, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Kenzie Pereira[1], Damien Wilburn[2] and Sarah Woodley[1]

[1]Duquesne University, Pittsburgh, PA, USA. [2]University of Washington, Seattle, WA, USA

Skin Peptides of Three-toed Amphiuma (*A. tridactylum*) Inhibit Growth of Chytrid Fungal Pathogens Linked to Worldwide Amphibian Decline

Amphibian skin is unique among vertebrate classes, containing a large number of multicellular exocrine glands. The secretions of these glands, particularly granular glands, vary among species and include a repertoire of bioactive compounds including a rich array of antimicrobial peptides (AMPs). AMPs are important for amphibian innate immune responses and may protect some species from chytridiomycosis, a lethal skin disease caused by the chytrid fungal pathogens, *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* (Bsal). Susceptibility to chytrid fungi is species-specific and related to AMP bioactivity. While AMP bioactivity against Bd has been measured for a number of amphibian taxa using in-vitro assays, similar studies are lacking for Bsal, a chytrid fungus which is especially pathogenic for salamanders. We studied the skin secretions of the fully aquatic salamander, Three-toed Amphiuma (*Amphiuma tridactylum*) to test for anti-chytrid properties. AMPs purified from the crude skin secretions of captive adult salamanders were analyzed by RP-HPLC and tested against the growth of Bd and Bsal using in-vitro assays. We found that secreted peptides were similar among male and female salamanders and inhibited the growth of Bd (minimum inhibitory concentration (MIC): 85.18 µg mL^{-1})) and Bsal (MIC: 147.5 µg mL^{-1}). Thus, AMPs that protect against Bd may also provide protection against Bsal.

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

John Peterson and Tyler Sternbach

University of Wisconsin-Platteville, Platteville, WI, USA

Environmental correlates and anuran abundance in a community including state-endangered Blanchard's Cricket Frogs.

The influence of environmental variables on the occurrence of amphibian vocalizations is species specific; however, few studies have observed the influence of environmental variables on relative abundance of amphibians. Automated recording devices were used to record frog vocalizations for one minute each hour during peak nightly calling across the breeding seasons of Gray Treefrogs (*Hyla versicolor*), Green Frogs (*Lithobates clamitans*), and state-endangered Blanchard's Cricket Frogs (*Acris balanchardi*) in Southwest Wisconsin. Relative abundance was determined using the standard amphibian calling index. Calling indices were assessed for each hour during peak calling and average nightly abundance was determined. Average nightly water and air temperature and relative humidity were determined via environmental data loggers. Similarly to previous studies of occurrence, relative abundance was influenced by environmental variables in a species specific fashion. Species responded to different variables depending on whether the early, middle, or late calling season was analyzed. Both *A. blanchardi* and *L. clamitans* were influenced more by date and water temperature, while *H. versicolor* was influenced more by air temperature and their relative abundances were more variable.

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465 Herpetology Morphology I, Highland D, Sunday 15 July 2018

Jackson Phillips and Kurt Schwenk

University of Connecticut, Storrs Mansfield, Connecticut, USA

The Mechanics of Air-Breathing in Tree Frog Tadpoles.

Air-breathing in tadpoles is a well-known, yet under-appreciated facet of anuran biology. The physiology of tadpole air-breathing has been well studied in a small number of well-known taxa, and previous authors have shown the physiological importance of air-breathing as a source of oxygen for larval frogs. However, the biomechanics of air-breathing has never been fully investigated in any species of tadpole, nor has the functional morphology of the organs associated with air-breathing. We use a combination of high-speed videography, gross dissection, and paraffin histology to describe the functional morphology and mechanics of air-breathing in gray tree frog (*Hyla versicolor*) tadpoles. We raised tadpoles in the lab until metamorphosis, and characterized the kinematics of air-breathing throughout ontogeny. During the course of these observations, we documented a novel form of air-breathing, previously undescribed in any other vertebrate, termed 'bubble-sucking'. During bubble-sucking, tadpoles attach their mouth parts to the under-surface of the water and pull the surface into the pharynx, creating a bubble. Most *H. versicolor* tadpoles perform a specialized 'double-suck', where the tadpole sucks in an initial bubble and empties the lungs, then after releasing the first bubble sucks in a second bubble. The second bubble is pinched off, compressed by the pharynx and forced into the lungs, with remaining air released from the mouth. Younger tadpoles, however, often use a single-suck behavior, which appears to be unrelated to lung ventilation. It is possible that some air-breathing behavior is related to ventilation of the gills rather than the lungs.

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

Josh Pierce[1], Craig Rudolph[1], Steve Reichling[2] and Emlyn Smith[3]

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Returning the Louisiana Pinesnake (*Pituophis ruthveni*) to Restored Habitat

Ongoing surveys suggest that populations of the Louisiana Pinesnake (*Pituophis ruthveni*) are limited to a few small blocks of degraded and highly fragmented habitat. Research indicates that the species requires frequently burned sites with a well-developed herbaceous understory capable of supporting populations of its primary prey, Baird's Pocket Gopher (*Geomys breviceps*). Recent changes in management practices on U. S. Forest Service lands have resulted in restoration of substantial blocks of suitable habitat, which are now available for reintroduction. A captive population consisting has been established from wild-caught snakes from Bienville Parish, LA. The reintroduction site is located on the Catahoula District of the Kisatchie National Forest. Ninety-one individuals have been released to date, and 3 snakes are currently being head-started to be released in April 2018. The current protocol is to release 50% of available animals as neonates immediately following post-natal shed, while the remaining snakes will be head-started and released the following April. Currently, automated pit tag readers and trapping are the primary monitoring techniques. To date, 20 snakes have been detected the year following release, or later. Five of those snakes have been detected 4 years following release. Louisiana Pinesnakes across 20+ zoos have been consolidated into 4 dedicated and successful facilities, which should increase the production of hatchlings in the future. Production of neonates and release of young will be repeated annually until a viable population is established or it is concluded that further releases are not likely to result in establishment of a population.

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

Todd Pierson[1], Benjamin Fitzpatrick[1], Kenneth Kozak[2] and Carlos Camp[3]

[1]University of Tennessee, Knoxville, TN, USA. [2]University of Minnesota, Saint Paul, MN, USA. [3]Piedmont College, Demorest, GA, USA

Historic hybridization and modern reproductive isolation in the two-lined salamander (*Eurycea bislineata*) species complex

Reticulate evolutionary histories provide useful systems for exploring the role of hybridization in evolution, and modern-day contact zones allow a closer examination of the mechanisms regulating gene flow. The biogeography of plethodontid salamanders is generally characterized by the allopatry of closely-related species, with aquatic and semi-aquatic species' distributions often explained by ancient and modern river drainage boundaries. One such example, distributed throughout the eastern United States, is the two-lined salamander (*Eurycea bislineata*) species complex. Here, we use low-coverage 3RAD data from 120 individuals representing all major mtDNA lineages of the *Eurycea bislineata* species complex and high-coverage RADcap data of a subset of these individuals to reconstruct the evolutionary history of the group. We use a suite of complementary methods to reveal instances of historical hybridization, and we demonstrate the bias these events have on the maximum likelihood phylogenetic inference, focusing in particular on putative hybridization events following major river drainage reorganization events. Next, to further explore mechanisms regulating gene flow at a modern-day contact zone, we sampled individuals from four replicate contact zones between two members of this species complex—*Eurycea cirrigera* and *Eurycea* cf. *wilderae*—in the foothills of the Appalachians. We generated RADcap data for 330 individuals and recovered no evidence for ongoing gene flow. Instead, we show a strong pattern of fine-scale segregation within an ecological mosaic, potentially driven by nest-site selection. Together, these studies highlight the importance of both large-scale, biogeographic factors and fine-scale, ecological factors in structuring gene flow across evolutionary time.

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

Kyle Piller[1], Elyse Parker[1,2], Alan Lemmon[3] and Emily Moriarty-Lemmon[3]

[1]*Southeastern Louisiana University, Hammond, LA, USA.* [2]*Yale University, New Haven, CT, USA.* [3]*Florida State University, Tallahassee, FL, USA*

Assessing relationships within the Goodeidae using Anchored Hybrid Phylogenomics

The Goodeidae (Cyprinodontiformes) has a limited distribution in the Great Basin of Southwestern United States and the Mesa Central of Mexico. The family consists of two subfamilies, the oviparous Empetrichthyinae and the viviparous Goodeinae. Despite much interest, previous attempts to investigate the evolutionary relationships among species in the family have been incongruent and primarily based on mitochondrial data. The lack of a comprehensive, multilocus nuclear DNA phylogeny for the entire family has hampered our ability to understand the evolutionary relationships. Therefore, we conducted the first phylogenomic study of the family to examine the relationships among taxa in the family using anchored hybrid enrichment, a targeted next generation sequencing approach. Sequence data were generated from more than 350 nuclear loci and nearly 75 goodeids from across the range.

Phylogenetic analyses were conducted using the concatenated data set and a locus partitioned RaxML analysis. The relationships among the species of goodeids within each of the Tribes were similar to previous studies, but the relationships among the Tribes differed, thereby challenging previous hypotheses. This study is the first phylogenomic study of the Goodeidae and provides an historical template that can be used to address a multitude of macroevolutionary questions focusing on the biogeography and the tempo and mode of diversification of the entire family.

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

Brendan Pinto[1], Juan Daza[2], James Titus-McQuillan[3] and Tony Gamble[1]

[1]Marquette University, Milwaukee, WI, USA. [2]Sam Houston State University, Huntsville, TX, USA. [3]University of Texas at Arlington, Arlington, TX, USA

The rapid evolution of post-zygotic isolating barriers and identification of the first stable hybrid zone in geckos

Investigating the processes that lead to the generation of new species, or speciation, is a cornerstone investigation in ecology and evolutionary biology. The process of speciation is mediated by the evolution of genetic incompatibilities that lead to reproductive isolation between divergent populations. We study and observe the speciation process in geographic regions where two species meet and interbreed, or hybrid zones. Gecko lizards are a species-rich group of vertebrate animals (>1,700 species), for which, hybridization is poorly represented in the literature, we characterize the first reported stable hybrid zone within geckos (infraorder Gekkota). Thirty-five years ago, *Sphaerodactylus* hybridization was reported between two Puerto Rican species, *Sphaerodactylus nicholsi* and *Sphaerodactylus townsendi*. We revisited this putative hybrid zone and confirmed its presence and geographic stability using modern molecular genetic methods and investigated the climatic disparity between these two species' niche breadths to determine that these two species may have been released from fierce competition by anthropogenically-mediated disturbances. This system provides us with the means to examine the iterative processes of reproductive isolation and speciation in gecko lizards for the first time.

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

Jessica Pita-Aquino, Christopher Thawley, Noah Gilbert and Jason Kolbe

University of Rhode Island, Kingston, Rhode Island, USA

The Effect of Substrate Diameter and Limb Morphology on Locomotor Performance in Brown Anoles (*Anolis sagrei*)

In lizards, locomotor performance is affected by both substrate diameter and limb morphology. For example, *Anolis* species with longer limbs run faster on broad substrates, whereas short-limbed species are more adept at moving on narrow diameters. For the brown anole (*A. sagrei*), previous studies have identified a positive relationship between perch diameter and hindlimb length across populations. This is consistent with natural selection favoring hindlimb lengths appropriate for different microhabitats. Also, limb kinematics studies have demonstrated a trade-off between speed and stability, which is mediated by substrate diameter. However, no study so far has measured the combined effects of substrate diameter and limb morphology on locomotor performance within an anole species. We examined the sprinting abilities of brown anoles from urban and natural habitats in southern Florida. We recorded lizard performance on six inclined racetracks of varying diameters (1.0–8.9 cm), and on a flat surface. We used Tracker® to measure maximum velocity for 10 cm and 25 cm distances as well as number of pauses, slips and falls during each run. To quantify effects of morphology on performance, we x-rayed lizards to measure limb lengths and counted the number of lamellae to measure toepad size. By generating performance curves, we will describe the relationships between maximal sprinting ability, locomotor stability, lizard morphology and surface diameter. Lizard sprint speed should decrease on narrower surfaces and with shorter limbs. We discuss our results in relation to within population morphological variation as well as differences between urban and natural habitats.

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

Sinlan Poo[1], Kristin Hinkson[1] and Maud Ferrari[2]

[1]*Memphis Zoo, Memphis, TN, USA.* [2]*University of Saskatchewan, Saskatoon, Saskatchewan, Canada*

Life-skills training: Antipredator behavior in captive-bred tadpoles

As one of the most endangered group of species, amphibians are threatened by rapid anthropogenic changes to their environment. In response to these threats, breeding programs have been established in many zoos to prevent extinctions by providing a safe harbor for amphibians, with the goal of releasing captive-bred individuals into wild. A key issue that determines the success of release programs, however, is whether captive-reared animals are able to exhibit ecologically-relevant behavior in response to dangers in their natural environment. The idea of training captive animals to survive in the wild is well-established in mammals, birds, and fishes, but has yet to be developed in amphibians. To fill this gap in scientific knowledge and conservation practice, we present the first attempt at increasing amphibian survival by "teaching" captive-bred tadpoles to recognize and respond to potential predators (life-skill training). For predator recognition training, we exposed *Anaxyrus fowleri* tadpoles to predator cues at two different stages (7 days of conditioning, starting at 3 or 13 days post hatching). We then assessed tadpole behavior at three different stages of development (10, 20, or 30 days post hatching). We found antipredator behavior increased with age, but did not differ between conditioned and non-conditioned tadpoles. Results indicated an innate ability of captive-bred tadpoles to respond to predator cues regardless of previous experience or exposure. These findings will help inform management of captive release programs and form the basis of future studies into the effects of captive breeding and rearing environments on predator recognition in amphibians.

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75 Herpetology Reproduction, Highland C, Sunday 15 July 2018

Sinlan Poo[1], Kristin Hinkson[1], Edward Stege[2] and Kimberly Terrell[3]

[1]Memphis Zoo, Memphis, TN, USA. [2]USFWS, Leadville, CO, USA. [3]Smithsonian Conservation Biology Institute, Washington, DC, USA

Sperm Output and Body Condition are Maintained Independent of Hibernation in an Endangered Temperate Amphibian

Hibernation is an integral part of the life history of species living in seasonal environments. However, our knowledge on the link between hibernation and reproductive success in amphibians is limited, and such information is critically needed to inform conservation efforts, as amphibians are disproportionately threatened with extinction. Therefore, we experimentally quantified the effects of *ex situ* hibernation on sperm quality, sperm quantity, and body condition in a federally-endangered anuran, the Wyoming toad (*Anaxyrus baxteri*). We tested the hypothesis that hibernation is essential for optimal reproductive output, but is detrimental to body condition. Captive-bred, male toads were exposed to 0, 30, or 60 days of low temperature, and sperm output (total number of cells, concentration, motility, and viability) and body condition were evaluated. Contrary to our hypotheses, no differences were observed in sperm metrics or in body condition across treatment groups. These unexpected findings suggest that hibernation is not an essential process for spermiation in *A. baxteri* and illustrates the potential of temperate amphibians to adapt to varying environmental conditions during winter months. Further research on reproductive behavior and possible multiyear effects of hibernation are needed to elucidate the overall significance of hibernation on the reproductive success in anurans.

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

Andrew Powers and Tim J. Karels

California State University, Northridge, Northridge, CA, USA

Habitat Fragmentation and Snakes in Southern California

Los Angeles is one of the largest urban areas in the world, and this rapid urban sprawl has created many scattered habitat fragments. These habitat fragments can have negative consequences on wildlife diversity and dispersal. Studies of habitat fragmentation have focused on lizards, mammals and birds, but rarely snakes. Many of these groups, such as lizards, have been chosen for their high visibility and conspicuous nature. Studies have shown that in areas of high fragmentation and urbanization, lizard diversity becomes lower than in unfragmented areas. However, this trend might not carry across all reptile groups. Snakes are an ecologically important group as primary predators on rodents and nesting birds in areas that other predators cannot reach. They are long-lived, habitat specific, and are vulnerable to human interference. I will explore the relationship between snake diversity and habitat fragmentation in Thousand Oaks, California. I will capture snakes, identify species, and will record mass, length and sex in order to quantify snake diversity and population composition in 25 large and small patches. I expect to find differences in snake composition between patch size

classes. Additionally, I expect large snake diversity and size will decrease as patch size decreases. I also hypothesize more recently fragmented patches will have higher diversity over older patches. My study will be the first to examine the indirect effects of habitat fragmentation on snake diversity in Southern California, and will help to better understand the challenges local wildlife are faced with through urbanization.

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

Worth Pugh and Phillip Harris

The University of Alabama, Tuscaloosa, AL, USA

Update on the Integration of the Geological Survey of Alabama and the University of Alabama Ichthyology Collections

Natural history collections have served as the foundation for the studies of ecology, evolutionary biology, systematics and conservation biology. Despite the importance of these collections many robust examples remain largely hidden due to lack of publicly available electronic data. The Geological Survey of Alabama Ichthyology Collection was created in the late 1970s as part of the enactment of the GSA's state-wide biological inventory assessments. In 2014, the GSA began to turn over their holdings to the University of Alabama Ichthyology Collection as part of an acquisition funded by the NSF Collections in Support of Biological Research program. Our goals are to incorporate this collection into the UAIC and then make all associated data available online (i.e., GBIF, VertNet, iDigBio). Thus far we have cataloged >13,000 lots from the GSA collection and estimate that we are only ~60% finished assimilating all lots. Preliminary results of the project show strong numbers of a variety of freshwater taxa from nearly every major tributary in the state of Alabama as well as some surrounding states with shared watersheds. While the sheer volume of specimens is astounding and likely fills many gaps in geographic distribution, the true significance of this collection lies in the data represented in the collection which were collected using standardized survey methods and includes environmental data across an extended spatial scale (1979-2010s). Future studies utilizing the GSA collection could examine many research topics related to shifts in fish species diversity in response to land-use change, water-quality, and climate change.

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

Worth Pugh[1], Gary Pandolfi[2] and Michael Gangloff[3]

[1]The University of Alabama, Tuscaloosa, AL, USA. [2]United State Fish and Wildlife Service, Austin, TX, USA. [3]Appalachian State University, Boone, NC, USA

Impacts of Land-Use, Catchment Size and In-Stream Habitat on Lotic Communities of the Upper New River Drainage in North Carolina

Land-use impacts local water quality by influencing hydroperiod, nutrient cycling, and substrate composition in freshwater systems. Deforestation and pollution generally have negative consequences on freshwater systems as well as animal communities that inhabit them. The New River originates in Watauga Co. NC and is home to several endemic aquatic fauna including several fishes, one crayfish and one snail. We examined how land-use and in-stream habitat parameters influence species diversity and distribution of sensitive aquatic taxa in the upper New River. Our data demonstrate negative relationships between forest cover and concentrations of fine sediments at the riparian and catchment scales. We also found that upstream forest cover shares a positive relationship with fish diversity and is an adequate predictor of New River Crayfish and hellbender salamander site occupancy. Moreover, our study finds that catchment size influences in-stream habitat which, in turn, impacts fish species diversity and community structure. Although reducing development while increasing reforestation within the entire catchment would be ideal, it may be more plausible to target catchments of headwater tributaries which would have positive cascading effects on main-stem tributaries. Future monitoring efforts in the New River are imperative to understand how further land conversion will affect these endemic communities as increases in urban development and water-use in headwater regions pose significant threats to sensitive stream fauna and water-quality.

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

Andrea Quattrini[1], Dominique Cheb Terrab[2] and Katriina Ilves[2,3]

[1]Harvey Mudd College, Claremont, CA, USA. [2]Pace University, New York, NY, USA. [3]Academy of Natural Sciences of Philadelphia, Philadelphia, PA, USA

Genetic and Morphometric Evidence for a New Species of Deep-Sea Anguilliform Eel (Congridae: *Conger*) from the Gulf of Mexico.

Biotic surveys in the deep-sea reveal there is still much biodiversity remaining to be discovered. Here we report evidence for a new species of anguilliform eel of the genus *Conger*, based on species tree analyses of mitochondrial and nuclear loci with additional support from morphometric characters. Five specimens were collected in the northern Gulf of Mexico from ~300 m depth using chevron traps deployed in deep-coral reef areas. Specimens were originally identified as *C. oceanicus*, yet are genetically distinct (e.g., >8% COI divergence) from putative conspecifics and other congenerics from the region. Morphometric analyses are ongoing. Comments are made on possible speciation scenarios in *Conger* and deep-sea fishes more generally. This study highlights the utility of using DNA barcoding as a starting point for biodiversity studies, particularly of deep-sea biota. Further, results emphasize the importance of

museum collections for housing not only tissue samples, but also voucher specimens and the expertise that accompanies these collections.

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

Aleta Quinn

University of Idaho, Moscow, ID, USA. National Museum of Natural History, Washington, DC, USA

Teaching philosophy of biology

I teach "environmental philosophy", "philosophy of biology" and related undergraduate courses. In this poster I reflect on what is/are the purpose(s) of teaching these courses, and in turn how I should teach. My goal is to collect feedback from individuals with broad backgrounds in molecular or organismal biology and wildlife management, both to improve my own class and to contribute to pedagogical literature. Challenges include students' belief that empirical studies will straightforwardly solve conceptual problems, colleagues' views about the relative value of different sub-fields of biology, and administrators' demand that pedagogy narrowly fit career objectives. Additionally, the things that interest me as a philosopher and a hobby herper differ from the things that would be of interest and value to my students. I recently argued successfully for my courses to earn credit towards biology degrees, and I expect to contribute to graduate students' research. What issues and skills, broadly considered "conceptual", do you wish that you and/or your students had an opportunity to study? My poster is an invitation to collaborate across disciplines to improve scientific literacy in the general population, but especially to help develop strong conceptual foundations for future biologists.

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

Aleta Quinn

University of Idaho, Moscow, ID, USA. National Museum of Natural History, Washington, DC, USA

When is a cladist not a cladist?

The term "cladist" has distinct meanings in distinct contexts. Communication between philosophers, historians, and biologists has been hindered by different understandings of the term in various contexts. In this paper I trace historical and conceptual connections between several broadly distinct senses of the term "cladist". I propose seven specific definitions that capture distinct contemporary uses. This serves to disambiguate some cases where the meaning is unclear, and will help resolve apparent disagreements that in fact result from conflicting understandings of the term.

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

Alison Davis Rabosky, Talia Moore, Erin Westeen, Joanna Larson and Ciara Sanchez Paredes

University of Michigan, Ann Arbor, MI, USA

Convergence or Divergence? 3-D Quantification and Characterization of Snake Anti-predator Behavior in the Peruvian Amazon

Coral snakes have bright color patterns and distinctive behavioral displays that honestly signal their venomous bite to potential predators. While the coloration of coral snakes and their many harmless mimics has been well studied, the behavioral repertoires that these snakes, and other cryptically colored species within the same ecological community, has not received the same level of attention. Tropical snake behavior is challenging to study due to changes in behavior in artificial settings, environmental hazards to electrical equipment, and difficulty capturing sufficient sample sizes with taxonomic breadth. By constructing wireless, waterproof, and portable data collection buckets with high definition video cameras, we captured the anti-predator behavior of snakes at the moment of collection from four sites in the Amazonian rainforests of Peru. We also constructed a pop-up kinematics lab to run a series of behavioral assays in semi-controlled conditions in the field. Over three month-long expeditions, we collected 1352 behavioral trials from 161 individuals across 51 species, including venomous models, harmless mimics, and non-mimicking snake species. We used qualitative analyses to characterize behavioral motifs and quantitative biomechanical analyses to characterize snake motions in three dimensional space. By placing these data in a phylogenetic context, we will test hypotheses regarding the evolution of behavioral mimicry, including quantifying the degree of mimetic convergence relative to sympatric cryptic species.

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

Andrea Racic[1], Catherine Tylan[2] and Tracy Langkilde

[1]*Pennsylvania State University, University Park, Pennsylvania, USA.* [2]*Pennsylvania State University, University Park, Pennsylvania, USA*

Temperature Effects on Corticosterone in the Eastern Fence Lizard, *Sceloporus undulatus*

The physiological stress response is frequently used as an indicator of an animal's interactions with its environment. However, activity of the hypothalamic-pituitary-adrenal axis, the primary regulator of the glucocorticoid stress response in vertebrates, may be affected by body temperature. In endotherms, this does not pose a serious issue since they maintain body temperature within a narrow range. In contrast, ectotherm body temperature is more strongly influenced by ambient temperature, which may affect our ability to measure and interpret physiological stress. We tested the effects of temperature on plasma corticosterone in the eastern fence lizard (*Sceloporus undulatus).* We assigned lizards to one of four temperature treatments within the range naturally experienced: 22ºC, 29ºC, 33ºC, or 36ºC. After four hours, body temperature was measured and blood taken to obtain baseline plasma corticosterone concentrations. The lizards were then exposed to a standardized stressor (placed in a cloth bag) and returned to their treatment temperature. After 30 minutes, we re-measured body temperature and obtained a second blood sample to measure stress-induced corticosterone. Both baseline and stress-induced corticosterone were elevated in lizards held at higher temperatures, indicating that the physiological activity of the hypothalamic-pituitary-adrenal axis is enhanced at higher temperatures. These results suggest environmental temperature can significantly affect plasma corticosterone concentrations by increasing body temperature in reptiles. Field biologists are encouraged to measure body temperature at time of sampling, as this could explain variation in their data. Similarly, investigators should consider the temperatures at which they run lab studies as this may affect their results.

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

Howard Rainey[1], Todd Pierson[2] and Jennifer Deitloff[1]

[1]Lock Haven University, Lock Haven, Pennsylvania, USA. [2]University of Tennessee, Knoxville, Tennessee, USA

Distinguishing Morphological Differences in the Head Shape of Male *Eurycea wilderae* (Blue-Ridge Two-Lined Salamander)

Morphology can be correlated with behaviors that impact a male's ability to obtain reproductive success when facing competition for mates. In addition, sexual selection can influence differences in morphological traits between males and females leading to sexual dimorphism. *Eurycea* salamanders display polymorphism in head shape among males as well as between the sexes. Males of *Eurycea wilderae* exhibit two different suites of correlated morphological traits often described as cirriferous and Morph A. Cirriferous males possess cirri that extend down from the nasolabial grooves, and they lack enlarged jaw musculature. Morph A males have enlarged jaw musculature resulting in broader heads than the cirriferous morphology, and they lack cirri, mental glands, and protruding premaxillary teeth. The ventral and lateral head morphology of *E. wilderae* was investigated in this study by using geometric morphometrics. We tested the hypothesis that males with and without cirri would be statistically different in overall head shape. We also tested the hypothesis that *E. wilderae* exhibit sexual dimorphism in head shape. We found support for the first hypothesis, and head shape of Morph A males were different than head shape of females. However, cirriferous males did not differ significantly from females in overall head shape even though the males possessed cirri and the females did not. Based on this and previous research, future studies should determine whether these two head morphologies of male *E. wilderae* (cirriferous and Morph A) demonstrate evolutionary adaptive characteristics that increase reproductive opportunities.

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

Muhammad Rais, Waseem Ahmed, Muhammad Saeed, Ayesha Akram, Imtiaz Ahmed Khan, Maqsood Anwar and Sidra Ikram

Department of Wildlife Management, Pir Mehr Ali Shah Arid Agriculture University Rawalpindi, Rawalpindi, Punjab, Pakistan

Occupancy and Detection Probability of Endemic Murree Hills Frog (*Nanorana vicina*) in Natural and Urban Areas of Murree, Pakistan

The modeling of species occupancy and determination of factors influencing its detection probability help formulate appropriate survey and monitoring programs. We studied if the occupancy of Murree Hills Frog (*Nanorana vicina*) differed in natural and urban areas and that certain survey covariates influenced its detection probability. The best fit model predicted occupancy (ψ) of the species as 48% while detection probability (p) as 25%. The best fit model predicted occupancy as a function of water velocity and salinity while habitat type (natural/ urban areas) did not contribute. None of the water quality and environmental variables measured from natural and urban areas during the study period differ significantly ($P > 0.05$). The species occupied sites occurring at an elevation above 900 m. The species was recorded from sub-tropical pine forest and moist temperate forest. The frog frequented fast flowing (> 10 m/s) natural freshwater springs/streams with associated pools of stagnant water having low water temperature.

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

Muhammad Rais[1], Imtiaz Ahmed khan[1], Aneeza Islam[2], Waseem Ahmed[1], Muhammad Saeed[1], Syeda Maria Ali[2] and Ayesha Akram[1]

[1]Wildlife Management, PMAS-Arid Agriculture University Rawalpindi, Rawalpindi, Punjab, Pakistan. [2]Department of Environmental Sciences, Faculty of Basic and Applied Studies, International Islamic University, Islamabad, ICT, Pakistan

Quantification of Herpetofauna Habitat and Assessment of Land Use Change in Rawalpindi and Islamabad Areas, Pakistan

The conversion of wildlife habitat into urban settings is a ubiquitous threat to herpetofauna globally. We assessed land use land cover change of District Rawalpindi and Islamabad area through satellite images for the year 2006, 2011 and 2016. We gathered presence only data of herpetofauna species using standard survey technique-visual encounter method (VES) from October, 2016 to June, 2017. We recorded ten amphibian and 25 reptilian species. We observed increase in urban/ built up area in Islamabad (20%); Rawalpindi (21%), Murree (46%), Kotli Sattian (33%), Kallar Syedan (25%), Gujar Khan (24%) and Kahuta (24%) tehils of District Rawalpindi. We recorded decrease in other habitats of areas of Islamabad (30% open space); Rawalpindi (17% open space), Murree (44% croplands), Kotli Sattian (47% croplands, 46% forest), Kallar Syedan (33% croplands), Gujar Khan (41% open space), Taxila (4% forest) and Kahuta (37% croplands) tehils, District Rawalpindi from 2006 to 2016. The increase in urban area could cause change in species composition favoring the spread of nuisance and invasive species as Indus Valley Toad (*Duttaphrynus stomaticus*), Bull Frog (*Hoplobatrachus tigerinus*), Indian Flapshell Turtle (*Lissemys punctata andersoni*), Common Tree Lizard (*Calotes versicolor*), Wall lizards (*Hemidactylus spp.*), Bengal Monitor Lizard (*Varanus bengalensis*) while reduction in wetlands, forest, open space and cropland areas may put threatened/ uncommon and endemic species such as Ballon Frog (*Uperdon systoma*), Burrowing Frog (*Sphaerotheca breviceps*), Murree Hills Frog (*Nanorana vicina*), Hazara Torrent Frog (*Allopaa hazarensis*), Indian Soft-shell Turtle (*Nilssonia gangetica*) and Indus Valley Spiny-tailed Lizard (*Saara hardwickii*) in danger.

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96 Herpetology Morphology I, Highland D, Sunday 15 July 2018

Deran Reddy, Cassidy Kuiper and Stephanie Schoeman

University of the Witwatersrand, Johannesburg, Gauteng, South Africa

A Light Microscopic Documentation of the Morphogenesis of the Lung of the Nile Crocodile (*Crocodylus niloticus niloticus*).

It is an established and well understood fact that the lung of the Nile crocodile is a heterogeneous organ. However, no documentation of the structural composition of the cells/tissues that create this unique architecture has been done. Understanding this is vital to understanding the crocodile's storage mechanism of air, its unidirectional air flow mechanism and lung compliance which all have an effect on progression of development and behaviour. For all age groups, it was found that the subdivision of the lung decreased in a cranio-caudal direction with all of the ventral regions of the lung being more subdivided than their dorsal counterparts. This level of heterogeneity became more marked with an increase in age of individuals. The younger age group crocodiles illustrated thinner septa (relative to older crocodiles) dividing the lumen into faveoli (terminal gas exchange units). In most instances the collagen fibre cores (septa) varied in thickness, elasticity (varying elastic fibre density), vascularity, levels of bifurcation and often eventually terminated in smooth muscle plates or knobs. Cilia was observed throughout the lung and decreased in density in a cranio-caudal direction. Also, the density of the cilia was higher in the younger crocodiles than the older ones. Similarly, the density of cartilage present in older individuals was higher with it being most prevalent in the ventral middle regions of the lung. By manipulation of these structural parameters individually or in combination, the respiratory cycle of the crocodile can be manipulated to suit its ontogenetic stage.

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

Jeanine Refsnider[1], Henry Streby[1], Song Qian[1], Sarah Carter[1], Ian Clifton[1], Gunnar Kramer[1], Adam Siefker[2] and Tyara Vazquez[1]

[1]*University of Toledo, Toledo, Ohio, USA.* [2]*University of Toledo, Toledo, Ohio, USA*

Does environmental heterogeneity predict degree of specialization? Testing the "jack-of-all-trades, master of none" hypothesis in a specialist lizard, *Phrynosoma hernandesi*

Niche width is often correlated with environmental heterogeneity, with generalists evolving in heterogeneous environments and specialists evolving in environments that vary less over space and time. Generalists are hypothesized to be better able to contend with rapid environmental change, and to persist longer in degraded habitat, than specialists. We used *Phrynosoma* horned lizards, a taxon considered to be highly specialized, to test the hypothesis that populations in a more heterogeneous environment were generalists compared to populations in a more homogeneous environment. We compared selection of prey items, microhabitat, light-environment, and spatial ecology between two populations that differed in elevation and environmental heterogeneity. Temperatures at the high-elevation site were more variable, and there was a greater diversity of microhabitats and associated light-environments at the high-elevation site, than at the low-elevation site. In contrast, available prey items were more diverse at the low-elevation site than the high-elevation site. Horned lizards selected for a wider range of prey items at the high-elevation site compared to the low-elevation site, and they showed similar selection for microhabitat types and had similar home ranges and daily travel distances at both sites. They showed specialization for light-environment use in opposing directions depending on elevation: low-elevation lizards spent more time buried underground and less time basking in full sun, while high-elevation lizards spent less time buried underground and more time basking in full sun. Our results demonstrate that environmental heterogeneity of a particular resource does not predict the degree to which organisms specialize on that resource.

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

Brendan Reid and Sarah Fitzpatrick

W. K. Kellogg Biological Station, Michigan State University, Hickory Corners, MI, USA

Don't fear the Rapture: efficient and inexpensive generation of genomic data for the Arkansas darter (*Etheostoma cragini*)

Next-generation sequencing approaches that combine restriction site-associated DNA (RAD) and sequence capture methods provide a highly efficient and inexpensive means of generating massive amounts of sequence data from a large number of targeted loci distributed throughout the genome. These approaches may be especially useful for resolving population processes at fine geographic scales using genetic data, for which large numbers of individuals and loci are both useful. We applied an existing hybrid RAD-capture approach (Rapture) to the Arkansas darter, (*Etheostoma cragini*), a species of conservation concern found in the Arkansas River and its tributaries. Using a pilot RAD dataset assembled to a draft genome for the orangethroat darter (*Etheostoma spectabile*), we first identified a set of 4,966 bait sequences targeting 2,121 loci distributed throughout the genome, including 29 loci potentially under selection. We then used dual-indexed RAD library preparation followed by bait capture to multiplex 384 individuals for sequencing in a single Illumina sequencing lane. Applying the Rapture method to our existing tissue collection (*n* > 2000 individuals) will enable us to estimate fine-scale population structure, levels of inbreeding, and contemporary population sizes throughout the range as well as provide evidence-based recommendations for management that take into account neutral genetic structure as well as potential adaptations to local environmental conditions.

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221 ASIH STOYE ECOLOGY & ETHOLOGY II, Highland C, Thursday 12 July 2018

Kelsey E. Reider and Maureen A. Donnelly

Florida International University, Miami, FL, USA

Survival at the Summits: Anuran Responses to Rapid Deglaciation in the High Andes of Southern Perú

Understanding biological responses to climate change is a top concern in conservation biology. Tropical high-elevation aquatic ecosystems are particularly sensitive to precipitation changes. Glaciers, which provide the only other water source, are rapidly disappearing. In the Cordillera Vilcanota in southern Perú, frogs including *Pleurodema marmoratum* and *Telmatobius marmoratus* have colonized new aquatic habitat inside the recently deglaciated zone. Their 150-200 meter upward shift represents one of the largest elevational range expansions observed for any vertebrate. We studied pond availability, water sources, and frog reproductive phenology over three hydrologic years at the upper limit of the biosphere. We used amphibian surveys and repeat photography to document occupancy, breeding activity, and pond hydroperiod variation. We determined d-excess and δ^{18}O values from the stable isotopes of water to distinguish amphibian breeding ponds fed by glacial runoff and ponds fed only by precipitation. Reproductive phenology in *Pleurodema marmoratum*, a terrestrial frog with aquatic larvae, was strongly linked to precipitation seasonality, whereas fully-aquatic *Telmatobius*

marmoratus tadpoles were present year-round but only in permanent ponds. Divergent strategies for dealing with variable and extreme conditions in high mountain environments leave each species vulnerable to different threats. El Niño caused a delay in the 2015 wet season and shortened the *P. marmoratum* breeding period in ephemeral ponds. *Telmatobius marmoratus* persistence is threatened by the loss of permanent ponds from ongoing glacial retreat. Our study shows that hydrologic alterations from the loss of glacial meltwater, changing precipitation patterns, and El Niño threaten some of the highest-known amphibians on Earth.

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

Jessica Reimche[1], Robert del Carlo[2], Amber Stokes[3], Erica Ely[4], Joshua Hallas[1], Edmund Brodie III[5], Michael Pfrender[6], Edmund Brodie Jr.[7], Normand Leblanc[1] and Chris Feldman[1]

[1]University of Nevada Reno, Reno, NV, USA. [2]University of Nevada, Reno, NV, USA. [3]California State University Bakersfield, Bakersfield, CA, USA. [4]California Academy of Sciences, San Francisco, CA, USA. [5]University of Virginia, Charlottesville, VA, USA. [6]University of Notre Dame, Notre Dame, IN, USA. [7]Utah State University, Logan, UT, USA

Is the Sierra Garter Snake the exception to the rule? TTX-resistance in *Thamnophis couchii* is not explained by molecular phenotype

The convergent evolution of tetrodotoxin (TTX) resistance in garter snakes (*Thamnophis*) has shown remarkable predictability. Patterns at both the phenotypic and genetic level have been consistent across multiple *Thamnophis* species, implying that there may be strong molecular constraints involved in this adaptive trait. TTX, a powerful neurotoxin found in Pacific newts (*Taricha*), binds to voltage-gated sodium channels in muscles ($\mathrm{Na_v}$1.4) and nerves ($\mathrm{Na_v}$1.6, 1.7), paralyzing these tissues and killing nearly all would-be predators. Despite this defense, three *Thamnophis* species have evolved similar structural changes in $\mathrm{Na_v}$1.4 that allow them to prey on sympatric newts. To further investigate the predictability of TTX-resistance, we examined geographic patterns of phenotypic resistance in the Sierra Garter Snake (*Thamnophis couchii*). We characterized both snake resistance and newt toxicity across their sympatric range. We then characterized functional genetic variation in three $\mathrm{Na_v}$ genes expressed in snake muscles and nerves, and measured expression levels of $\mathrm{Na_V}$1.4. We found that *T. couchii* demonstrate high geographic variation in TTX-resistance at the whole animal, and this variation correlates strongly with prey toxicity. However, *T. couchii* shows no variation in amino acid sequences in all three $\mathrm{Na_v}$ genes across its distribution and shows no significant changes in gene expression across populations. Thus, in *T. couchii*, resistance cannot be explained by a relationship between $\mathrm{Na_V}$ genotype and whole animal phenotype, suggesting that there are additional genetic mechanisms involved in TTX-resistance in *T. couchii*, and this feeding adaptation may not be as predictable as previously thought.

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

R. Graham Reynolds[1] and Alberto Puente-Rolon[2]

[1]*University of North Carolina Asheville, Asheville, NC, USA.* [2]*UPR Mayaguez, Mayaguez, Puerto Rico, Puerto Rico*

Ecology and Evolution of Boas in the West Indies

West Indian boid snakes in the genus *Chilabothrus* comprise an exclusively insular monophyletic lineage dating to a Miocene colonization of the proto-Antilles from South America. These nocturnal boas occupy habitats ranging from xeric scrub to montane rainforest and have maximum adult body sizes spanning a range from<1 m to nearly 4 m. As recently as 2013, only nine species were recognized, though substantial work in the last few years has revealed an additional four species. This includes the recognition of cryptic species such as the Virgin Islands Boa, the re-discovery of the Crooked-Acklins Boa, and the dramatic discovery of the Silver Boa, a new species found in 2015. Despite a modest number of species, this genus has undergone remarkable morphological evolution. Two morphotypes have been recognized: large-bodied generalists (five species) and small-bodied specialists (eight species). Both large and small species are distributed across the West Indies, though no single island has more than one large species, and small species frequently co-occur with large species (with the exception of the Bahamas banks). Further, this determinism in body size and ecological evolution has been arrived at via different evolutionary pathways, notably, via accelerated rates of head shape (trophic morphology) evolution as small-bodied species evolved from larger ancestors. I will discuss our current understanding of the ecology and evolution of these boas, including the application of multivariate morphological analysis, statistical historical biogeography, molecular phylogenetics, and phylogenetic comparative methods that have served to greatly increase our understanding of these lineages.

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

Shannon A. Richard[1], Sanjiv Jayamohan[1], Eric A. Tillman[2], Michael L. Avery[2] and M. Rockwell Parker[1]

[1]*James Madison University, Harrisonburg, VA, USA.* [2]*USDA National Wildlife Research Center, Gainesville, FL, USA*

Preliminary analysis of scent trailing behavior in Argentine tegus from Florida

Invasive species can accelerate ecological dysfunction, and a key, aggressive invasive reptile, the Argentine black and white tegu (*Tupinambis merianae*), has spread rapidly from west-central Florida into Everglades National Park and exacerbated local faunal declines. Because of their voracious, omnivorous diet and promiscuous occupation of burrows for habitat, tegus have

potential to be a significant, multiplicative invasion. The Argentine tegu produces large clutches and has established brumation sites throughout its invasive range indicating that the population has substantial potential to expand. Chemical signals are powerful cues used by conspecifics to locate potential mates in complex environments. For invasive species, mate searching is a key process that enables the reproduction and establishment of populations in novel habitats, and reptiles rely heavily on chemical signals for tracking mates. Our project is examining the trailing behaviors of male Argentine tegus (n=7) as they follow conspecific scent in a Y-maze. Males were tested in three scenarios: male trail only, female trail only, and male vs. female trails. We conducted these tests both within (April-May) and outside (August) the predicted mating season for Argentine tegus in central Florida. If males show sex-specific preferences and behaviors across these trial types and seasons, it will establish a foundation for future management research on this invasive predator.

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

Shannon A. Richard[1], Eric A. Tillman[2], Michael L. Avery[2] and M. Rockwell Parker[1]

[1]*James Madison University, Harrisonburg, VA, USA.* [2]*USDA National Wildlife Research Center, Gainesville, FL, USA*

Scent trailing behavior in male Burmese pythons

Invasive species impacts have been abated through reproduction-focused interventions. The Burmese python (*Python bivittatus*) is an invasive predator in southern Florida that is accelerating the decrease in native vertebrate abundance. To reproduce, snakes use chemical signals to facilitate mate identification and location, especially via scent trailing. Little is known about this aspect of Burmese python biology in its invasive range, and the goal of this research is to investigate chemical communication in pythons at the behavioral level. Scent trails created by female and male Burmese pythons were tested in a Y-maze with wild-caught male pythons (N=6 for female-only scent trials, N=5 for male-only and male vs. female scent trials). Males consistently followed female scent trails when presented alone but did not follow male trails. Surprisingly, males did not select female scent trails when presented simultaneously with those of males, and male performance was worse in this trial (more exploration of the non-target arm). Chemosensory sampling (tongue-flick rate) was higher in female-only trails compared to the others, indicating discriminatory ability. Males also showed an array of behaviors in the Y-maze that we analyzed independently and with an ethogram. In general, behaviors were more frequent and complex when female scent was present compared to male. Because males follow female scent trails efficiently in isolation but not when the trailing environment becomes complex, strategies using mixtures of conspecific odors could be implemented to aid in management of this invasive predator.

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

Eric Rittmeyer and Sara Ruane

Rutgers University - Newark, Newark, NJ, USA

Biodiversity of Northern Isolate Squamate Populations in the New Jersey Pine Barrens

The Pine Barrens of southern New Jersey is an unusual ecosystem, dominated by sandy-soiled pine and pine-oak forests, and acidic cedar swamps. These habitats have allowed numerous species distributed throughout the southeastern US to reach their northern distributional limit as isolated populations in this area. These include both habitat specialists and generalists, and species with diverse ecologies. We examine the degree of sandy habitat specialization in seven squamate species with this distribution by calculating the proportion of localities in sandy habitats and comparing this to a null distribution of availability for each species. We then use species distributional modeling to examine the potential distributions of each species and project these models onto paleoclimate layers to examine how distributions and connectivity may have changed over time. Finally, we also project these models onto future climate predictions to examine how distributions may have changed over time. We find that while all species were collected more frequently in sandy habitats, some species are found almost exclusively in these habitats, while others are found in sandy habitats no more frequently than random. Distributional models suggest species expanded rapidly northward over the past several thousand years, and that species are likely to continue expanding northward, but may retreat substantially in the southern portion of their range. These results emphasize the diversity of taxa that reach their northern limits in the Pine Barrens, as well as the need for increased conservation and monitoring to identify expanding populations in the north, and declining populations in the south.

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

Nelson Rivera[1] and Brian Folt[2]

[1]John Carroll University, University Heights, OH, USA. [2]Auburn University, Auburn, AL, USA

Community assembly of glass frogs (Centrolenidae) in a Neotropical wet forest: a test of the river zonation hypothesis

The river zonation hypothesis predicts that abiotic and biotic conditions along riparian gradients drive variation in animal communities. Glass frogs are a diverse group of Neotropical anurans that use riparian habitats exclusively for oviposition and larval development, but little is known about how glass frog communities are distributed across riparian gradients. Here, we measured glass frog community assembly across a gradient of riparian habitats from first- to fifth-order streams at La Selva Biological Station, Costa Rica. We performed repeated nocturnal frog calling surveys and built occupancy and *N*-mixture abundance models to test for varying

patterns of species occupancy, community assembly, species richness (α-diversity) and species turnover (ß-diversity). We observed significant differences in patterns of species occupancy and community assembly across a stream-order gradient: occupancy of two species increased with stream order (*Teratohyla pulverata*, *Hyalinobatrachium fleischmanni*), one species decreased (*Teratohyla spinosa*), and one species did not vary (*Espadarana prosoblepon*). We evaluated four a priori hypotheses describing how α- and ß-diversity of centrolenids are shaped across the riparian gradient; our data were most consistent with a pattern of nested assemblages and increasing species richness along the riparian gradient. Species-specific patterns of occupancy and abundance resulted in assemblage-level differences consistent with theoretical predictions for highly aquatic organisms along riparian gradients.

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

Pedro Rizzato[1], Flávio Bockmann[1] and Eric Hilton[2]

[1]Universidade de São Paulo/FFCLRP, Ribeirão Preto, SP, USA. [2]Virginia Institute of Marine Sciences, College of William & Mary, Gloucester Point, VA, USA

Development of bones associated with lateral-line canals in *Acipenser fulvescens* and *Polyodon spathula* (Actinopterygii: Chondrostei: Acipenseriformes)

In order to investigate the interrelationship between lateral-line canal and bone formation in Actinopterygii, we analyzed the development of bones associated with lateral line canals in representatives of the two extant families of Acipenseriformes (Actinopterygii: Chondrostei), the Lake Sturgeon, *Acipenser fulvescens* (Acipenseridae), and the North American Paddlefish, *Polyodon spathula* (Polyodontidae). Despite the morphological disparity between these families, we identified similarities in the characteristics of the lateral line and in the pattern of formation of bones associated with lateral-line canals. Both species share a high number of canal neuromasts and a very long infraorbital canal associated with the allometric elongation of the rostrum. We identified for the first time in *P. spathula* the lateral rostral canal bone, already known among sturgeons, hypothesized to be homologous to the antorbital of other actinopterygians. As in *A. fulvescens* and other acipenserids, the lateral rostral canal bone is among the first bones to form in the development of *Polyodon*. Finally, both species (especially *P. spathula*) are characterized by reduction of the skeleton, which is accompanied by a disassociation of the lateral-line canals from the dermal bones of the skull with which they are usually associated in actinopterygians. The condition of the lateral-line ossifications in acipenseriforms, therefore, provides support for the hypothesis of a two-component pattern of canal-bone morphogenesis in fishes.

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350 ASIH STORER ICHTHYOLOGY, Empire Hall South – JF Rochester Riverside Convention Center, Friday 13 July 2018

Pedro Rizzato[1], Eric Hilton[2] and Flávio Bockmann[1]

[1]Universidade de São Paulo/FFCLRP, Ribeirão Preto, SP, Brazil. [2]Virginia Institute of Marine Sciences, College of William & Mary, Gloucester Point, VA, USA

A review on the lateral-line system of polypterids (Actinopterygii: Cladistii: Polypteriformes)

The Polypteridae includes the African bichirs (*Polypterus* spp.) and the Ropefish (*Calamoichthys calabaricus*), fossils of the Upper Cretaceous of South America and Africa, and the Triassic 'scanilepiforms', recently interpreted as stem polypterids. The group is hypothesized to be the earliest diverging member of Actinopterygii, occupying a key phylogenetic position for understanding the evolution of bony fishes. A detailed and comprehensive understanding of their anatomy is, therefore, fundamental for the investigation of the anatomy and early evolutionary history of Osteichthyes. As part of a revisionary study of the anatomy of Polypteridae, we redescribe the laterosensory system of extant polypterids, including the number, distribution, and innervation of canal neuromasts (CNs) and lines of superficial neuromasts (SNs) in the head and trunk, the course of lateral-line canals, and the association of CNs with cranial bones. There are six lateral-line canals, identified according to their innervation by preotic and postotic lateral line nerves. The lateral line in the trunk is represented by three rows of lines of SNs innervated by branches of the posterior lateral-line nerve. The supraorbital line passes between the anterior and posterior nasal openings, a condition typical of non-teleostean actinopterygians, and there is a secondary connection with the infraorbital canal medial to the contralateral nares. The ethmoid commissure, another plesiomorphic feature of the lateral-line system of actinopterygians, is also present. The lateral line of polypterids is therefore characterized by the presence of many plesiomorphies and can be viewed as representative of a generalized ancestral condition of the lateral-line system of actinopterygians.

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20 Ichthyology Biogeography, Grand Lilac Ballroom South, Saturday 14 July 2018

D Ross Robertson

Smithsonian Tropical Research Institute, Panama, Panama

An Indo-Pacific damselfish in the Gulf of Mexico, 2018

We present an overview of what is currently known about the Regal Demoiselle, *Neopomacentrus cyanomos*, which was first recorded in the southwest Gulf of Mexico (GoM) in 2013, and which is only the second alien, Indo-Pacific reef-fish to have become successfully established in the tropical northwest Atlantic. This overview includes information on its origin, mode and location of introduction; its current known distribution and what is known of the tempo of its spread in the GoM, the potential for spread beyond the GoM; its habitat usage on GoM coral and artificial reefs; the potential for adverse interactions with ecologically similar

native reef-fishes; and adult and larval-biology characteristics that may have contributed to its success in arriving, establishing and spreading.

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

Elizabeth Rock, Jeffrey Bartman, Jamie Cornelius and Katherine Greenwald

Eastern Michigan University, Ann Arbor, MI, USA

Effect of urbanization on stress response in Eastern Garter Snakes (*Thamnophis sirtalis*)

Urbanization affects both abiotic and biotic components of the environment. Altering landscapes from natural states to urban states results in changes to microclimate, input of pollutants, and disruption of ecosystem function, all of which may increase stress on organisms persisting in these areas. Corticosterone (CORT) is a hormone produced in response to life history circumstances, daily demands, and stressful events. Chronic or long-term stress stimulus can alter the baseline status of CORT in the blood. This study will measure physiological stress response (CORT levels) and physical health metrics (body condition) in Eastern Garter Snakes (*Thamnophis sirtalis*) along an urban-rural gradient. *T. sirtalis* is a generalist species commonly found across the eastern United States in a variety of habitats, ranging from meadows to urban areas. We predict that snakes in urban areas will have increased CORT when compared to rural snakes through active seasons. We will also assess if the magnitude of this effect varies over time (e.g. decreased HPA axis sensitivity). We further predict that snakes in urban areas will have poorer body conditions than snakes in rural areas, as a reflection of this physiological response. Stress metrics of individual animals may be an indicator of how likely a population is to persist, which can inform our understanding of species living in urban environments.

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

Maria Roe[1], Jose Anadon[1] and Russell Burke[2]

[1]Queens College, Flushing, NY, USA. [2]Hofstra University, Hempstead, NY, USA

Estimates of Adult Survival for Female Diamondback Terrapins in Adjacent Jamaica Bay Populations

Jamaica Bay is inhabited by at least two populations of adult female Diamondback Terrapins (*Malaclemys terrapin*); one that nests at Ruler’s Bar Hassock and another at John F. Kennedy airport, only 4.5km apart. Monitoring programs have been in place for years, but population models are needed to support management programs. In addition, the effects of water quality, injuries, and climactic events like Hurricane Sandy (2012) need to be considered for this species which is vulnerable to urban development and climate change. We analyzed mark-recapture data using an age classified structure within the Cormack-Jolly-Seber model to account for transience. Apparent survival for resident females on Ruler's bar was high but declined from 0.951 to 0.869 over a 14-year period, while survival for JFK females was constant at an intermediate level. While the effect of water quality was not supported, the punctuated effect of Sandy showed support for a decline in survival in Ruler's Bar over a two-year period following the storm. Injuries were analyzed for Ruler's Bar using a multistratum approach to estimate survival and transition between minor and major injury states. Survival estimates for injury states were constant at 0.901 for individuals with minor injuries and 0.862 for major injuries. Results support a distinction in survival between the populations, and that individuals in Ruler's Bar exhibit lower survival after major injuries. Further investigation into environmental factors like marsh loss may be important in determining the cause of decline in survival in Ruler's Bar females and in promoting conservation measures.

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

Hilary B. Rollins and Michael F. Benard

Case Western Reserve University, Cleveland, OH, USA

Does shifting phenology early in ontogeny affect growth and development in subsequent stages?

As global climate change alters environmental cues, phenological shifts early in ontogeny may alter timing and circumstances for all subsequent life history events. However, if organisms are able to compensate, an early shift may not affect later events. The energy to compensate for phenological shifts might require trade-offs between growth and development. Wood frogs (*Rana sylvatica*) have shifted their breeding two weeks earlier, on average, over the past century. To examine the effects of phenological shifts early in developmental on subsequent life events, we manipulated aquatic temperature to create egg masses that hatched early or late. At hatching, we transferred the larvae to mesocosms where we manipulated food availability to test for the effects of resources on developmental trade-offs. Eggs in the cool treatment hatched 6.5 days before eggs in the warm treatment. At metamorphosis, that difference had decreased to 0.5 days. Therefore, larvae from cooled egg masses had accelerated their developmental rate to "catch up" to warm egg masses by metamorphosis. Mass at metamorphosis was significantly affected by the interaction of egg temperature and larval resources such that frogs raised in the warm egg treatment with added larval food had the highest metamorphic mass. Our results suggest that larval wood frogs are able to compensate for delayed hatching. However, the aquatic temperature they experience as eggs and larval resource availability interact to affect size at metamorphosis., Organisms may be able to compensate for climate change induced phenological shifts early in development but those shifts may alter growth.

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

Njal Rollinson[1], Melanie Massey[1], Jacqueline Litzgus[2] and Ronald Brooks[3]

[1]University of Toronto, Toronto, Ontario, Canada. [2]Laurentian University, Sudbury, Ontario, Canada. [3]University of Guelph, Guelph, Ontario, Canada

Rapid Warming has Increased Growth, Development Rate, and Survival in Populations of Freshwater Turtles Near Their Northern Range Limit

Southern Ontario is home to a diversity of Canada's turtle species. The region however is experiencing rapid warming, and few studies have investigated the long-term consequences of warming on turtle populations. Since the 1970s, we monitored populations of snapping turtles and painted turtles in Algonquin Park, Canada, near the northern range limit of each species. Our long-term data coupled with statistical models suggest advancement of spring reproductive phenology, faster rates of embryonic development in autumn, greater egg-hatching success, and faster juvenile growth rates. There have been no apparent changes in primary sex ratios, and no changes in the timing or duration of the thermosensitive period of embryonic development. Our data suggest that, so far, rapid warming has not had negative consequences on the turtles we studied, as growth and early-life survival have both increased in recent years.

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

Jonathan Rose, Michael Casazza, Glenn Wylie and Brian Halstead

USGS Western Ecological Research Center, Dixon, CA, USA

Focusing Research and Conservation Through Modeling: Building a Demographic Model for the Giant Gartersnake, *Thamnophis gigas*

Demographic population models are valuable tools for studying life-history and targeting conservation efforts to sensitive life stages. Demographic vital rates are often size-dependent in reptiles, so Integral Projection Models (IPM), which allow vital rates to be continuous functions of a state variable, are well-suited to modeling reptile populations. We developed an IPM for the threatened Giant Gartersnake (*Thamnophis gigas*) and used elasticity analysis to identify vital rates and life-stage transitions that have a large effect on the population growth rate. We used data on the growth, survival, and reproduction of Giant Gartersnakes collected from several populations over more than 20 years to estimate continuous functions that describe how snake size affects these vital rates. We found the growth rate of Giant Gartersnake populations was most influenced by the survival and growth of adult females, and the size at which one year old

snakes recruit to the modeled population. The probability of snakes surviving their first year remains an important unknown, but is less influential on population growth than the size of surviving one year olds. Despite their large size, the life-history of Giant Gartersnakes is similar to many other gartersnake species, with rapid growth, early maturity, and relatively low adult survival. Linkages between key vital rates and environmental factors are largely unknown, and identifying actions to improve population growth will be key to this species' persistence. The model-building process itself was valuable because it focused our research priorities and highlighted important knowledge gaps for this threatened snake.

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

Zachary Ross[1], Michael Jungen[1], John Holloway[2], Shane Welch[1] and Jayme Waldron[1]

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Maximizing the efficacy of eastern diamondback translocation to minimize human-snake interactions.

The eastern diamondback rattlesnake (*Crotalus adamanteus*; EDB) is a large-bodied, venomous reptile that suffers from large-scale habitat loss and fragmentation. For herpetofauna, movement through anthropogenic habitats is typically reduced as costs of movement become prohibitive. Human-rattlesnake interactions that occur as EDBs move through anthropogenic landscapes often result in the snake's death due to inflated risk perception and misconceptions about EDBs. Translocation is the primary tool used to manage human-snake interactions; however, it is often performed without regard to the snake's home range. The post-translocation behavior of snakes is characterized as erratic, often increasing exposure to anthropogenic environments. Research indicates that these erratic post-translocation movements can be largely attributed to homing instincts within a novel landscape. Here, we examine how distance affects the efficacy of translocation regarding human-snake interaction. Rattlesnake response to two different scales of intra-installation translocation, intra- and extra-home range, was assessed using radio telemetry. Previous studies indicate that extra-home range translocations will result in a higher potential for human-snake interactions than intra-home range translocations. The potential for human-snake interaction is determined using a modification of cost distance analysis. The post-translocation movement patterns of free-ranging telemetered snakes are cross-referenced with a landscape classified for human use. Habitats likely to represent higher risk of human-snake interactions such as roads and mowed areas are assigned higher cost scores than low-risk areas. This study will provide a greater understanding of EDB movement ecology following translocations, a critical component to EDB conservation and maximizing the efficacy of translocation techniques.

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

John Rowe, Chelsea Martin, William Mulligan and Tyler Goerge

Alma College, Alma, MI, USA

Spatial and Thermal Ecology of Snapping Turtles (*Chelydra serpentina*) in a Mid-Michigan Lake and its Associated Wetlands

Over a three year period, we studied the spatial ecology of Snapping Turtles (*Chelydra serpentina*) in a dystrophic lake with northern wetland margins in central Michigan. Thermally-sensitive radio-transmitters were implanted in the body cavities of four male and two female individuals although one female died early in the study. Turtles remained in the lake throughout the summer months where they established multiple core areas along the littoral shelf. Remotely monitored hourly body temperatures (T_b) cycled daily with the lowest values occurring during late morning (0900 – 1200 h) with a peak T_b during the evening (2000 – 2200 h). Turtles generally maintained their T_b throughout the day within a laboratory determined thermoregulatory set-point (21 – 26 °C). Operative temperatures measured by aluminum turtle replicas placed on the surrounding *Sphagnum* mat and by submerged thermal data loggers indicated that turtles likely remained mostly aquatic throughout the day, perhaps using warm surface water late in the day. Individual turtles showed strong fidelity to overwintering locations that were peripheral to the lake either in adjacent *Sphagnum* mounds or in a stream.

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

Ethan Royal[1], John Willson[1] and Jessica Homyack[2]

[1]University of Arkansas, Fayetteville, Arkansas, USA. [2]Weyerhaeuser Company, Tacoma, USA

Effects of forest management on habitat structure and upland pine-associated herpetofaunal communities

Longleaf pine (*Pinus palustris*) savannah once covered much of the southeastern Coastal Plain and was characterized by open canopy, diverse herbaceous vegetation, and high amounts of bare soil. The unique structural and vegetative conditions of this habitat type support many endemic species, including several reptiles and amphibians. Managed pine (*Pinus* spp.) stands now occur throughout the southeastern U.S. and have replaced much of the historic longleaf pine savannah. These managed stands have been shown to provide suitable habitat conditions for some open canopy-associated wildlife species if certain structural characteristics are maintained. However, little work has examined herpetofaunal communities. Using repeated, low intensity herpetofauna surveys and vegetation surveys, we assessed the ability of managed pine stands in sandy soil regions of Northwestern Louisiana to support open pine-associated herpetofauna. We selected 81 sites across 7 management regimes: mechanically managed young and thinned mid-age loblolly pine (*P. taeda*) stands, fire-maintained young, mid-age and mature longleaf stands, and fire-maintained mid-age and mature loblolly stands. We deployed

coverboards and performed repeated visual encounter surveys at each site over two field seasons. We also quantified vegetation characteristics including canopy cover, overstory, midstory, understory, and groundcover. Preliminary results suggest that young stands and some mid-age fire-maintained sites most closely resembled open-canopy, fire-maintained mature pine stands in vegetation characteristics and herpetofaunal community composition. Some closed-canopy mature sites supported the most diverse herpetofauna communities, but lacked upland pine associated species. Our results provide insight into how forest management practices affect herpetofaunal communities and will help guide management strategies.

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

Sara Ruane

Rutgers University-Newark, Newark, NJ, USA

Training YOUR Dog for Snake Detection!

Dogs are frequently used for a variety of tasks that rely on their superior sense of smell, including bomb, drug, and cadaver detection. Wildlife detection dogs have become popular in many biological study systems, being used primarily to find animal scat but also for tracking and finding live animals. Within herpetology, turtle detecting dogs are somewhat well known, and snake dogs are becoming more popular, especially for indicating the presence of endangered species (e.g., Indigo snakes). Here, I explain and discuss the how-to of training a dog for snake detection, based on my experiences training my own dogs.

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

Leah Rubin[1] and Elizabeth Sibert[2]

[1]College of the Atlantic, Bar Harbor, ME, USA. [2]Harvard Society of Fellows and Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA

Evidence for a Shark Extinction 20 Ma Using Morphometric Analysis of Dermal Denticles

Sharks are an important part of marine ecosystems but are increasingly at risk of extinction due to anthropogenic stressors of global climate change and overfishing. The abundance and diversity of sharks has changed over their nearly 400 million year history. Recent work has revealed a decline of elasmobranch denticles preserved in open ocean marine sediments at approximately 20 million years ago (Ma), going from ~20% of all vertebrate microfossils to <1%. However, the nature of this decline is poorly understood, and does not correlate with any known major climatic changes, nor other mass extinction events. We examine the morphological diversity of sharks before and after this significant decline using microfossil dermal denticles extracted from a sediment core from the South Pacific Gyre. We developed a novel character coding scheme with 20 categories to quantify the morphological disparity of 550 individual denticles within the sediments, ranging in age from 1.4 to 41.5 Ma. Additionally, 124 modern shark species' denticles were coded to create a modern catalog of shark denticle diversity. Groupings were made broadly into geometric and linear denticles and analysis displays a dramatic decrease in the geometric type. These results expose a possible selective extinction which has yet to be described and could be the result of changing ocean conditions and thus an increase in competition with other large migratory predators. Our analysis highlights 20 Ma as a potential tipping point in open ocean ecology, and demonstrates the utility of the microfossil record in elucidating changes in deep time.

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

Holly R. Rucker and M. Rockwell Parker

James Madison University, Harrisonburg, VA, USA

Decrypting female mimicry in red-sided garter snakes

Female sexual mimicry, the expression of female sexual signals by males, is a reproductive tactic that occurs in a wide range of species. Chemical cues, such as pheromones, are utilized by many species as sexual signals driving mate choice. There is only one example of chemical female mimicry in vertebrates: the red-sided garter snake, *Thamnophis sirtalis parietalis*. Female mimics in this species are males that produce female sex pheromones and are courted by other males. These female mimics have undetectable estradiol levels but elevated testosterone compared to normal males. Conversely, estradiol is necessary for females to produce the sex pheromone. Central to this is the link between estradiol and testosterone: testosterone is metabolized to estradiol via the enzyme aromatase. Female garter snake mimics are hypothesized to have higher expression of aromatase in their skin which would create estradiol locally to stimulate female pheromone production. Our project is the first empirical test of this hypothesis. Female mimics (n=20), males (n=20), and females (n=20) received injections of an aromatase inhibitor, fadrozole (FAD), or control injections (saline; SHAM) three times a week for three months. Skin lipids were extracted and fractionated from the shed skins of these snakes, and blood samples were collected to determine circulating hormone concentrations. We hypothesize that FAD treatment will prevent the production of female pheromone in the mimics and females, and if so will demonstrate that aromatase action is the key to female mimicry in garter snakes.

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

Lacy Rucker[1], Thomas Pauley[2], William Sutton[3] and Donald Brown[1,4]

[1]West Virginia University, Morgantown, WV, USA. [2]Marshall University, Huntington, WV, USA. [3]Tennessee State University, Nashville, TN, USA. [4]USFS Northern Research Station, Parsons, WV, USA

Occupancy Dynamics of Two Terrestrial Salamanders over 30 Years in Relation to Habitat Degradation and a Short Elevation Gradient

Amphibians are declining globally and while many factors are contributing to this decline, climate change and habitat loss and degradation are among the most critical. In the Appalachian region, plethodontid salamanders are thought to be particularly vulnerable to environmental changes due to their low vagility, and for many species, restriction to high elevations. Further, interspecific competition at high elevations could increase as the climate warms and becomes more suitable for lower elevation species. This is a concern in West Virginia, where competitive interactions between the federally-threatened Cheat Mountain Salamander (*Plethodon nettingi*; CMS) and the Eastern Red-backed Salamander (*Plethodon cinereus*; ERB) could increase at high elevations. We investigated spatial and temporal patterns in occupancy of CMS and ERB along a habitat degradation (i.e., forest clearing) and short elevational (i.e., 1193-1251 m) gradient using 30 years of population survey data (i.e., 1986-2016) at 43 survey plots. For each species, we used dynamic occupancy models to identify and model influential covariates for initial occupancy, colonization, and extinction at sites, and for survey detection probability. Preliminary results indicate that colonization and extinction was not strongly related to elevation for either species. However, habitat degradation was positively correlated with extinction for CMS and ERB, with stronger impacts on CMS. Our results indicate that forest clearing in CMS habitat can negatively impact their occurrence in adjacent forested habitat.

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

Ariana Rupp and Brad Moon

University of Louisiana Lafayette, Lafayette, LA, USA

Prey Handling and Feeding Mechanisms in Mud Snakes (*Farancia abacura*)

Feeding on elongate prey occurs in many vertebrates, including snakes. However, few publications have addressed the complexity of consuming elongate vertebrate prey. Some snakes can consume prey just as long, and sometimes longer, than themselves, although doing so takes considerable time and effort. Mud Snakes, *Farancia abacura*, are thought to be specialist feeders on elongate prey. This diet makes Mud Snakes a useful model for understanding how snakes consume elongate prey. Mud Snakes are widespread and abundant but secretive and difficult to find in large numbers for research, which has limited research on this species compared to other widespread snakes. We have recorded videos of Mud Snakes feeding on amphibians in order to describe and quantify the capture and consumption of elongate prey. From these video data, we have identified variation in prey handling in Mud Snakes of different

size classes and on different prey items. We have also studied retention of ingested prey to identify prey size limits for digestion. This research also includes the first quantitative data on feeding in hatchling Mud Snakes.

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

Ariana Rupp[1], Dustin Siegel[2], Stanley Trauth[3] and David Sever[4]

[1]University of Louisiana Lafayette, Lafayette, LA, USA. [2]Southeast Missouri State University, Cape Girardeau, MO, USA. [3]Arkansas State University, Jonesboro, AR, USA. [4]Southeastern Louisiana University, Hammond, LA, USA

Junk in the Trunk: Caudal Courtship Glands in Plethodontid Salamanders

Salamanders in the family Plethodontidae exhibit a unique tail-straddle walk during courtship that can include the use of sexually dimorphic mental glands and caudal courtship glands. Mental glands are found in the skin of the lower jaw and have been extensively studied and caudal courtship glands are found in the skin of the dorsal base of the tail in some male plethodontids and remain comparatively understudied. Both are thought to increase female receptivity during courtship, although there is only published evidence for this in mental glands. Prior to this research, only the male morph A specimens of *Eurycea wilderae* were known to have caudal courtship glands without the presence of mental glands. We conducted a histological analysis of museum specimens from several genera not previously studied for presence or absence of these caudal courtship glands. We present novel data on the presence of caudal courtship glands in *Hemidactylium*, *Gyrinophilus*, *Pseudotriton, Stereochilus*, *Hydromantes*, *Bolitoglossa*, and *Pseudoeurycea*. Notably, we have also examined the dorsal base of the tail in *Rhyacotriton*, and have not detected the presence of caudal courtship glands, which may indicate that the tail-straddling behavior evolved in *Rhyacotritonidae*, prior to the seemingly universal presence of these glands in Plethodontidae. These morphological data indicate the importance of caudal courtship glands in Plethodontidae and may be useful in understanding potential reproductive isolation via pheromone evolution that might have aided in a radiation of plethodontids.

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571 Lightning Talks II, Highland A, Saturday 14 July 2018

Trevor Ruppert and Robert Espinoza

California State University Northridge, Northridge, California, USA

Identifying the Physiological Limitations of Dispersal and Persistence of an Invasive Amphibian (*Xenopus laevis*) in Southern California

Invasive species are detrimental to native ecosystems and, once established, are challenging and costly to manage. Modeling approaches are widely used preventative management tools for identifying potential habitat in uninvaded regions. However, most such models are limited by their correlative approaches. Recently, mechanistic (physiological) approaches have emerged as more effective management tools for defining niches of invasives. In Southern California, releases of the African Clawed Frog (*Xenopus laevis*) threaten native frogs across their invasive range. Once imported for use in human pregnancy tests, the advent of chemical tests resulted in the release of thousands of these aquatic frogs in the 1960s, which quickly spread throughout Southern California. These pond dwellers eat any animal they can swallow, including conspecifics, and are resistant to traditional methods of extermination (poisoning, habitat drying, prolonged starvation). Yet despite characterization as “perfect” invasive species, *Xenopus* have not achieved their anticipated invasive potential in California. In fact, some populations have gone extinct, or where they persist, occur in low numbers. The aim of our project is to determine which aspects of the biology of invasive populations of *Xenopus* have allowed some to persist, while others failed. Using the strong inference approach, we will inductively ascertain the physiological factors that limit the persistence and dispersal of *Xenopus* in Southern California. We hypothesize that a specific suite of biotic and abiotic variables (hydroperiod, predators, distance between habitat) limits this species from invading and establishing at new sites, and that lab-based physiological tests will provide confirmation of our field-based correlations.

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

Allison Sacerdote-Velat[1], Mary Beth Manjerovic[2] and Rachel Santymire[3]

[1]*Chicago Academy of Sciences, Chicago, Illinois, USA.* [2]*Virginia Military Institute, Lexington, Virginia, USA.* [3]*Lincoln Park Zoo, Chicago, Illinois, USA*

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.

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

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

[1]*Southern Research Station, US Forest Service, Nacogdoches, Texas, USA.* [2]*Department of Wildlife and Fisheries, Texas A&M University, College Station, Texas, USA*

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.

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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 (Silurifomes: 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 *Dolichancintrus 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 loborhynchos*, 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.

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22 Herpetology Systematics, Highland B, Saturday 14 July 2018

Christopher Samuelson[1], Utpal Smart[1], Eric Smith[1], Mahmood Sasa Marin[2] and Alejandro Solorzano[3]

[1]University of Texas at Arlington, Arlington, Texas, USA. [2]Instituto Clodomiro Picardo, Universidad de Costa Rica, San Jose, San Jose, Costa Rica. [3]Sepentario Nacional & Museum of Zoology, Universidad de Costa Rica, San Jose, San Jose, Costa Rica

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.

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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.

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

Marcella Santos[1], Leandro Sousa[2] and Brice Noonan[1]

[1]*University of Mississippi, University, MS, USA.* [2]*Univesidade Federal do Pará, Altamira, PA, Brazil*

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.

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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.

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

Alan Savitzky[1] and Akira Mori[2]

[1]Utah State University, Logan, UT, USA. [2]Kyoto University, Kyoto, Kyoto Pref., Japan

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.

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

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

[1]Stephen F. Austin State University, Nacogdoches, Texas, USA. [2]USDA 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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48 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

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.

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

Jason Selwyn[1], John Johnson[1], Alan Downey-Wall[2], Adam Bynum[1], Rebecca Hamner[1], J. Derek Hogan[1] and Christopher Bird[1,3]

[1]Texas A&M University - Corpus Christi, Corpus Christi, TX, USA. [2]Northeastern University, Boston, MA, USA. [3]Hawai'i Institute of Marine Biology, Kane'ohe, HI, USA

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.

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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 *Phyllobates 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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420 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

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.

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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.

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

H. Bradley Shaffer[1], Erin Toffelmier[1] and Christopher Searecy[2]

[1]UCLA, Los Angeles, CA, USA. [2]University of Miami, Miami, FL, USA

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.

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

Brian Shamblin[1], Blair Witherington[2], Shigetomo Hirama[2], Robert Hardy[3] and Campbell Nairn[1]

[1]University of Georgia, Athens, GA, USA. [2]Fish and Wildlife Research Institute, Melbourne Beach, FL, USA. [3]Fish and Wildlife Research Institute, St. Petersburg, FL, USA

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: ≤ 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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521 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

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

Florida Museum of Natural History, Gainesville, FL, USA

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, crocodilians, 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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382 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018

Christopher Sheil[1], Arwen Mohr[2], Daniel Portik[3], Aaron Bauer[2], Sean Harrington[4] and Gregory Watkins-Colwell[5]

[1]John Carroll University, University Heights, OH, USA. [2]Villanova University, Villanova, PA, USA. [3]University of Arizona, Tucson, AZ, USA. [4]University of Hawai'i at Mãnoa, Honolulu, HI, USA. [5]Yale Peabody Museum of Natural History, New Haven, CT, USA

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 lizards 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.

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

Alexander Shepack[1], Dana Morin[2], Twan Leenders[3] and Alessandro Catenazzi[1]

[1]Florida International University, Miami, FL, USA. [2]Southern Illinois University, Carbondale, IL, USA. [3]Roger Tory Peterson Institute, Jamestown, NY, USA

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 Sarapiqui, 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 rufioculis)*, 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.

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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.

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11 Herpetology Reproduction, Highland C, Sunday 15 July 2018

Rick Shine[1], Thomas Madsen[2] and Greg Brown[1]

[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 hydrically-driven sex determination in a squamate reptile, and of the heterogametic genotype (ZW) developing as both sexes in a reptile.

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

Brian Sidlauskas[1,2], Casey Dillman[2,3], Kendra Hoekzema[1,4], Bruno Melo[5], Michael Alfaro[6], Michael Burns[1], Benjamin Frable[1,7], Claudio Oliveira[5], Mark Sabaj[8] and Brant Faircloth[9]

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

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

Barry Sinervo[1] and Donald Miles[2]

[1]University of California, Santa Cruz, CA, USA. [2]Ohio 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.

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

Randy Singer[1,2], Shari Ellis[2] and Lawrence Page[1,2]

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

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

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

[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.

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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 heterogenous rates corresponding to different ecomorphs. However, we find that different elements not only show different patterns of diversification, but also different rates. This patterns 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.

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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.

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

Leo Smith[1], Matthew Davis[2] and Michael Ghedotti[3]

[1]University of Kansas, Lawrence, KS, USA. [2]St. Cloud State University, St. Cloud, MN, USA. [3]Regis 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 "percoid" 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.

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

Margaret Smith[1], Jayme Waldron[1], Shane Welch[1] and Jeff Holmes[2]

[1]Marshall University, Huntington, WV, USA. [2]Amphibian 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.

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

Sierra Smith[1,2], Elyse Fritas[1,2], Jessa Watters[3] and Cameron Siler[1,4]

[1]*Herpetology Department, Sam Noble Museum, Norman, OK, USA.* [2]*Biology Department, University of Oklahoma, Norman, OK, USA.* [3]*Herpetology Department, Norman, OK, USA.* [4]*Biology 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.

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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 (µCT) 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, Anguidae and egerniine 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.

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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.

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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.

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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 m^2) 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.

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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.

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

Anne Stengle[1], Thomas Tyning[2] and Lou Perrotti[3]

[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 (*Crotulas 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.

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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.

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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, Odontaspididae, 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.

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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 bacteria 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.

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

Donald Stewart[1], Juliette Pouzadoux[2] and Christelle Tougard[2]

[1]SUNY Coll. Envir. Sci. & For., Syracuse, NY, USA. [2]ISEM, 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.

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

Amber Stokes[1], Brian Gall[2], Peter Ducey[3], Lorin Neuman-Lee[4], Susannah French[5], Charles Hanifin[6], Michael Pfrender[7], Edmund Brodie III[8] and Edmund Brodie, Jr.[5]

[1]California State University, Bakersfield, CA, USA. [2]Hanover College, Hanover, IN, USA. [3]The State University of New York, Cortland, NY, USA. [4]Arkansas State University, Jonesboro, AR, USA. [5]Utah State University, Logan, UT, USA. [6]Utah State University, Vernal, UT, USA. [7]University of Notre Dame, Notre Dame, IN, USA. [8]University of Virginia, Charlottesville, VA, USA

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.

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

Donella Strom[1], Nathan Bendik[2] and Jesse Meik[1]

[1]Tarleton State University, Stephenville, Texas, USA. [2]Watershed Protection Department, Austin, Texas, USA

Phenotypic variation and allometryin 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.

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

John P. Sullivan, Stacy Ciufo, 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.

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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 relaxed 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.

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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.

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

Alyssa Swinehart[1], Krista Larson[2] and Katherine Greenwald[1]

[1]Eastern Michigan University, Ypsilanti, Michigan, USA. [2]Minnesota Department of Natural Resources, Saint Paul, Minnesota, USA

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.

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

Milton Tan[1], Al Dove[2] and Timothy Read[3]

[1]George Washington University, Washington, DC, USA. [2]Georgia Aquarium, Atlanta, GA, USA. [3]Emory University, Atlanta, GA, USA

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.

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

Manette Tanelus[1,2], Guha Dharmarajan[2] and Melissa Pilgrim[1,2]

[1]USC Upstate, Spartanburg, SC, USA. [2]Savannah River Ecology Laboratory, Aiken, SC, USA

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.

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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.

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404 Herpetology Systematics, Highland B, Saturday 14 July 2018

Rory Telemeco[1], Brian Lavin[2] and Chris Feldman[3]

[1]California State University, Fresno, CA, USA. [2]Sonoma State University, Rohnert Park, CA, USA. [3]University 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.

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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.

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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.

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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 multicarinata* 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. multicarinata* 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.

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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.

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

Jessica Tingle[1], Brian Sherman[2] and Timothy Higham[1]

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

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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.

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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 the 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.

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

Erin Toffelmier[1], Adam Clause[2] and H. Bradley Shaffer[1]

[1]*Ecology and Evolutionary Biology, University of California Los Angeles, Los Angeles, CA,*

USA. [2]Warnell 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.

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

Luke Tornabene[1], Carole Baldwin[2] and D. Ross Robertson[3]

[1]University of Washington, Seattle, WA, USA. [2]National Museum of Natural History, Smithsonian Institution, Washington, DC, USA. [3]Smithsonian 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.

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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.

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

Claire Tracy[1,2], Kin Onn Chan[2] and Rafe Brown[2]

[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.

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

Scott Trageser[1], Paul Hamilton[1], Ross Maynard[1] and Juan Guayasamin[2]

[1]The Biodiversity Group, Tucson, Arizona, USA. [2]Universidad 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.

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

Scott Trageser[1], Shahriar Caesar Rahman[1] and Stephen Spear[2]

[1]Creative Conservation Alliance, Dhaka, Bangladesh. [2]The 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.

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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.

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

Karen Underkoffler[1], Luers Meagan[2], John Hyde[3] and Matthew Craig[3]

[1]NOAA National Marine Fisheries Service, Seattle, WA, USA. [2]NOAA National Marine Fisheries Service, Gloucester, MA, USA. [3]NOAA 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* (Brunnich 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.

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

Yasel Urgelles Alfonso[1], Leroy Nunez[1], Ansel Fong[2] and Javier Torres[3]

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

de Historia Natural "Tomas Romay", Santiago de Cuba, Cuba. ³Department 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 amaricana* between Cuba (eastern and western) and Bahamas provide deep split between them and may warrant recognition as a separate species, after further morphological study.

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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 Halophryininae have a subopercle with one or two spines, whereas in Porichthyinae and Thalassophryinae 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.

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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.

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

Matthew Venesy[1], Joseph DeMarchi[2], Rachel Marbach[1], Keva Pariyar[1], Cari-Ann Hickerson[2] and Carl Anthony[2]

[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.

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

Calvin Vick[1] and Kelly J. Irwin[2]

[1]Benton High School, Benton, Arkansas, USA. [2]Arkansas 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.

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

Richard C. Vogt[1] and Camila Ferrara[2]

[1]INPA, Manaus, Amazonas, Brazil. [2]WCS-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 bucal 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 seaturtles 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.

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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.

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

Rudolf von May[1], Edgar Lehr[2] and Daniel Rabosky[1]

[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.

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

Mitchell Vu[1], Sami R. Cherikh[1], Shai Meiri[2] and Peter Uetz[1]

[1]Virginia Commonwealth University, Richmond, VA, USA. [2]Tel 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.

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

Hardin Waddle[1], Jenny Keterlin[2] and Frank Mazzotti[3]

[1]*U.S. Geological Survey, Gainesville, FL, USA.* [2]*National Park Service, Homestead, FL, USA.* [3]*University 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 merianae*) 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.

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

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

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

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

Danielle Walkup[1], Wade Ryberg[2], Toby Hibbitts[3] and Lee Fitzgerald[1]

[1]Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas, USA. [2]Natural Resources Institute, Texas A&M University, College Station, Texas, USA. [3]Biodiversity Research and Teaching Collection, Texas A&M University, College Station, Texas, USA

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.

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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.

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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 vertebras 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 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.

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

Jessica Watson[1], Michelle Lawing[2] and Jesse Meik[1]

[1]Tarleton State University, Stephenville, Texas, USA. [2]Texas 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.

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

Jeffrey Weinell[1], Daniel Paluh[2] and Rafe Brown[1]

[1]University of Kansas and Biodiversity Institute, Lawrence, Kansas, USA. [2]Florida 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?

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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.

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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.

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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.

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

Sarah M Wenner[1], Jeanne M Robertson[1] and Katy Delaney[2]

[1]California State University, Northridge, Northridge, CA, USA. [2]National Park Service, Thousand Oaks, CA, USA

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.

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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-neurotoxiin (PLA_2) 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.

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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.

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

Michael Westphal[1,2] and Theodore Morgan[2]

[1]*US Bureau of Land Management, Marina, CA, USA.* [2]*Kansas 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.

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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.

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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.

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

Mary White[1] and Mark Merchant[2]

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

Expression of Immune System Genes in Alligators

Crocodilians 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 crocodilians 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.

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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.

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

Steven Whitfield[1], Frank Ridgley[1], Nicole Atteberry[1], Daniel Valle[2], Adrian Figueroa[2], Johnny Iglesias[2] and Brianna Chin[2]

[1]*Zoo Miami, Miami, FL, USA.* [2]*Florida 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.

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

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

[1]Wayne State University, Detroit, MI, USA. [2]University 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.

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

Mark Wildhaber[1], Lynsey Whitacre[2], Gary Johnson[2], Justin Downs[3], Tendai Mhlanga-Mutangadura[2], Vernon Tabor[4], Daniel Fenner[5] and Jared Decker[2]

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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.

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

Becky Williams[1], Jake Richardson[1] and Susan Durham[2]

[1]*Utah State University Uintah Basin, Vernal, UT, USA.* [2]*Utah 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 n 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.

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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.

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

Stuart C. Willis[1], Hudson T. Pinheiro[1], Carlos E. L. Ferreira[2], Ronaldo Francini-Filho[3], Paulo M. Affonso[4] and Luiz A. Rocha[1]

California Academy of Sciences, San Francisco, CA, USA. [2]Universidade Federal Fluminense, Rio de Janeiro, RJ, Brazil. [3]Universidade Federal da Paraiba, João Pessoa, Paraiba, 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 m^2) 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.

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

Stuart C. Willis[1], David E. Saenz[2], Gang Wang[3], Christopher M. Hollenbeck[4], Luiz A. Rocha[1], David S. Portnoy[4], James J. Cai[2] and Kirk O. Winemiller[2]

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

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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.

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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.

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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 Osbourn[2] and Lynn Siefferman[2]

[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.

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

Sean Wineland[1], Shane Welch[1], Thomas Pauley[1], Jeff Holmes[2], Joseph Apodaca[3] and Jayme Waldron[1]

[1]Marshall University, Huntington, WV, USA. [2]Amphibian and Reptile Conservancy, Nashville, TN, USA. [3]Tangled 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.

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

Whitney Wong[1], Luis Ceriaco[1], David Blackburn[2], Aaron Bauer[3] and Matthew Heinicke[1]

[1]University of Michigan-Dearborn, Dearborn, MI, USA. [2]University of Florida, Gainesville, FL, USA. [3]Villanova 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 damaresis*, is also much more widespread than originally believed. Evolutionary patterns are compared with *Sclerophrys*, another terrestrial anuran genus often found in sympatry with *Tomopterna*.

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

Vanessa Wuerthner[1], Obed Hernández-Gómez[2] and Jessica Hua[1]

[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.

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

Anne Yagi[1,2] and Glenn Tattersall[1]

[1]Brock University, St Catharines, ON, Canada. [2]8Trees Inc., Fonthill, ON, Canada

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.

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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

California State University, Northridge, Northridge, California, USA

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

Lauren Yetter[1], Carlos Rivera[2], Juan D. Daza[1] and Aaron M. Bauer[3]

[1]Sam Houston State University, Huntsville, Texas, USA. [2]Université de Genève, Geneva, Switzerland. [3]Villanova University, Villanova, Pennsylvania, USA

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 mabouia* (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* ontogenic 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.

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

Hu Yinan[1,2], John Majoris[3], Peter Buston[3] and Jacqueline Webb[2]

[1]Boston College, Chestnut Hill, MA, USA. [2]University of Rhode Island, Kingston, RI, USA. [3]Boston University, Boston, MA, USA

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 (utriculus, sacculus, 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.

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

Dara Yiu[1], Luke Tornabene[1] and Mark Erdmann[2]

[1]University of Washington, Seattle, WA, USA. [2]Conservation International, Arlington, VA, USA

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.

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

Gabriella Zagorski[1], James Trottier[2], Douglas Boreham[3] and Jacqueline Litzgus[1]

[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.

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

Gabriella Zagorski[1], James Trottier[2], Douglas Boreham[3] and Jacqueline Litzgus[4]

[1]Laurentian, Sudbury, ON, Canada. [2]Ministry of Natural Resources and Forestry, Blind River, ON, Canada. [3]Northern Ontario School of Medicine, Sudbury, ON, Canada. [4]Laurentian University, Sudbury, ON, Canada

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.

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

Christopher Zobek, Casey Dillman and Harry Greene

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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 syspila* 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.