



# JOINT MEETING OF ICHTHYOLOGISTS AND HERPETOLOGISTS

JULY 11-15, 2018

ROCHESTER, NY - JOSEPH A. FLOREANO ROCHESTER RIVERSIDE CONVENTION CENTER &  
ROCHESTER RIVERSIDE HOTEL



## ABSTRACTS

# Abney - Cutler

## 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 preference ( $T_{set}$ ) 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<sup>1</sup>, Craig Lind<sup>2</sup> and Terence Farrell<sup>3</sup>

*Fairleigh Dickinson University, Madison, NJ, USA.* <sup>2</sup>*Stockton University, Galloway, NJ, USA.*  
<sup>3</sup>*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 *Ophiomyces ophioidiicola* 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<sub>2</sub> 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. ophioidiicola* 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<sup>1</sup>, Aryn Wilder<sup>2</sup> and Nina Therkildsen<sup>1</sup>

<sup>1</sup>Cornell University, Ithaca, NY, USA. <sup>2</sup>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<sup>1</sup>, Sarah Baker<sup>2</sup>, Megan Britton<sup>1</sup> and Angela Kent<sup>1</sup>

<sup>1</sup>*University of Illinois, Urbana, IL, USA.* <sup>2</sup>*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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## **478 General Ichthyology II, Grand Lilac Ballroom South, Sunday 15 July 2018**

Elizabeth Alter<sup>1,2</sup>, Matthew Aardesma<sup>3,2</sup> and Melanie Stia<sup>2</sup>

<sup>1</sup>York College/CUNY, Jamaica, NY, USA. <sup>2</sup>AMNH, New York, NY, USA. <sup>3</sup>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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## **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<sup>1</sup>, Colleen McDonough<sup>1</sup>, Namrata Bhandari<sup>1</sup>, Gregory Lee<sup>2</sup> and J. Mitchell Lockhardt<sup>1</sup>

<sup>1</sup>Valdosta State University, Valdosta, GA, USA. <sup>2</sup>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<sup>1</sup>, Brittany Ousterhous<sup>2</sup>, Dana Drake<sup>3</sup>, Jacob Burkart<sup>4</sup>, Freya Rowland<sup>4</sup>, William Peterman<sup>5</sup> and Jon Davenport<sup>1</sup>

<sup>1</sup>*Southeast Missouri State University, Cape Girardeau, MO, USA.* <sup>2</sup>*National Great Rivers Research and Education Center, Alton, IL, USA.* <sup>3</sup>*University of Connecticut, Storrs, CT, USA.* <sup>4</sup>*University of Missouri, Columbia, MO, USA.* <sup>5</sup>*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<sup>1</sup>, Brittany Ousterhout<sup>2</sup>, Freya Rowland<sup>3</sup>, Jacob Burkart<sup>3</sup>, Dana Drake<sup>4</sup> and William Peterman<sup>5</sup>

<sup>1</sup>*Southeast Missouri State University, Cape Girardeau, MO, USA.* <sup>2</sup>*National Great Rivers Research and Education Center, Alton, IL, USA.* <sup>3</sup>*University of Missouri, Columbia, MO, USA.* <sup>4</sup>*University of Connecticut, Storrs, CT, USA.* <sup>5</sup>*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 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<sup>1,2</sup> and Lee Fitzgerald<sup>2</sup>

<sup>1</sup>*Auburn University, Auburn, Alabama, USA.* <sup>2</sup>*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<sup>1,2</sup>, Conor McGowan<sup>3</sup> and Anna Tucker<sup>1</sup>

<sup>1</sup>Auburn University, Auburn, AL, USA. <sup>2</sup>Alabama Cooperative Fish and Wildlife Research Unit, Au, AL, USA. <sup>3</sup>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 plethodontid 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<sup>1</sup>, Julian Glos<sup>2</sup>, Djoko Iskandar<sup>3</sup> and Alexander Haas<sup>1</sup>

<sup>1</sup>*Centrum für Naturkunde-Zoologisches Museum, Universität Hamburg, Hamburg, Germany.*

<sup>2</sup>*Biozentrum Grindel-Tierökologie & Naturschutz, Fachbereich Biologie, Fakultät für Mathematik, Informatik und Naturwissenschaften, Universität Hamburg, Hamburg, Germany.*

<sup>3</sup>*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 be 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<sup>1,2</sup>, Tobias Mankis<sup>1</sup> and Hernán López-Fernández<sup>3</sup>

<sup>1</sup>University of Toronto, Toronto, Ontario, Canada. <sup>2</sup>Royal Ontario Museum, Toronto, Onta, Canada. <sup>3</sup>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 patterns 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<sup>1,2</sup>, Darren Coker<sup>1</sup>, Tane Sinclair-Taylor<sup>1</sup>, Joseph Dibattista<sup>1</sup>, Alexander Kattan<sup>1</sup>, Alison Monroe<sup>1</sup> and Michael Berumen<sup>1</sup>

<sup>1</sup>Red Sea Research Center, Division of Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia. <sup>2</sup>School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA

**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<sup>2</sup>), 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<sup>1</sup>, Davit Vasilyan<sup>2,3</sup> and Madelaine Böhme<sup>1,4</sup>

<sup>1</sup>University Tübingen, Tübingen, Germany. <sup>2</sup>JURASSICA Museum, Porrentruy, Switzerland. <sup>3</sup>Université de Fribourg, Fribourg, Switzerland. <sup>4</sup>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 these 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<sup>1,2</sup> and David Beamer<sup>2</sup>

<sup>1</sup>East Carolina University, Greenville, NC, USA. <sup>2</sup>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 [ $\psi$   $\diamond$   $\diamond$  = 0.737) and exhibited variable abundance, from <250 to >1000 N·ha<sup>-2</sup>, associated with increased soil moisture and reduced solar exposure due to slope face. While more ubiquitously distributed ( $\psi$   $\diamond$   $\diamond$  = 0.95), *P. kentucki* abundance varied from <400 to >1000 N·ha<sup>-2</sup> 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<sup>1</sup>, Michael Fraker<sup>1</sup>, Robert Denver<sup>2</sup>, Barney Luttbeg<sup>3</sup> and Stuart Ludsin<sup>1</sup>

<sup>1</sup>The Ohio State University, Columbus, Ohio, USA. <sup>2</sup>University of Michigan, Ann Arbor, Michigan, USA. <sup>3</sup>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<sup>1</sup>, Teresa Baird<sup>1</sup> and Richard Shine<sup>2</sup>

<sup>1</sup>University of Central Oklahoma, Edmond, Oklahoma, USA. <sup>2</sup>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<sup>1</sup>, Jake Daane<sup>2</sup>, Matthew Harris<sup>3</sup> and Nathan Lovejoy<sup>1</sup>

<sup>1</sup>University of Toronto, Scarborough, Canada. <sup>2</sup>Harvard, Boston, MA, USA. <sup>3</sup>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<sup>1</sup>, Luke Tornabene<sup>2</sup> and D. Ross Robertson<sup>3</sup>

<sup>1</sup>National Museum of Natural History, Smithsonian Institution, Washington, DC, USA.

<sup>2</sup>University of Washington, Seattle, WA, USA. <sup>3</sup>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<sup>1,2</sup>, Aaron Bauer<sup>1</sup>, Luis Ceriaco<sup>3</sup>, Mariana Marques<sup>3</sup> and David Blackburn<sup>4</sup>

<sup>1</sup>Villanova University, Villanova, PA, USA. <sup>2</sup>Instituto Nacional da Biodiversidade e Areas de Conservacao, Luanda, Angola. <sup>3</sup>Museu de Natural e da Ciencia de Lisboa, Lisboa, Portugal.

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

<sup>1</sup>U.S. Geological Survey, Gainesville, FL, USA. <sup>2</sup>St. Marks National Wildlife Refuge, St. Marks, FL, USA. <sup>3</sup>Florida Fish and Wildlife Conservation Commission, Gainesville, FL, USA. <sup>4</sup>Virginia Tech, Blacksburg, VA, USA. <sup>5</sup>Washington State Department of Natural Resources, Chehalis, WA, USA. <sup>6</sup>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<sup>1</sup>, Bryan Frazier<sup>2</sup>, Douglas Adams<sup>3</sup> and David Portnoy<sup>1</sup>

<sup>1</sup>Texas A&M University-Corpus Christi, Corpus Christi, TX, USA. <sup>2</sup>South Carolina Department of Natural Resources, Marine Resources Research Institute, Charleston, SC, USA.

<sup>3</sup>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<sup>1</sup>, Brad Moon<sup>1</sup> and David Penning<sup>2</sup>

<sup>1</sup>University of Louisiana at Lafayette, Lafayette, Louisiana, USA. <sup>2</sup>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 Ceriaco

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 multilocus 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<sup>1</sup>, Travis Glenn<sup>1</sup>, Manuel Uribe-Alcocer<sup>2</sup> and Píndaro Díaz-Jaimes<sup>2</sup>

<sup>1</sup>Department of Environmental Health Science, University of Georgia, Athens, GA, USA.

<sup>2</sup>Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma 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 Strait 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 July 14 2018**

Matthew Bealor<sup>1</sup>, Victoria Kuhnel<sup>2</sup>, Victoria Brady<sup>1</sup> and Kelsey Revicki<sup>1</sup>

<sup>1</sup>Rowan University, Glassboro, New Jersey, USA. <sup>2</sup>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<sup>2</sup> vs. 25 cm<sup>2</sup> 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<sup>2</sup>), 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 extrasosseously. 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 extrasosseously, although large fangs are rotated extrasosseously in snakes. We compare this mode of tooth replacement to the intrasosseous 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<sup>1</sup>, David McLeod<sup>2</sup>, William Flint<sup>2</sup>, Oliver Hyman<sup>2</sup>, Gregory Steffenson<sup>2</sup>, Cerrie Mendoza<sup>3</sup>, Rayna Bell<sup>4</sup>, Daniel Mulcahy<sup>4,5</sup>, Roy McDiarmid<sup>4,6</sup> and Steve Gotte<sup>4,6</sup>

<sup>1</sup>*Wilson College, Chambersburg, PA, USA.* <sup>2</sup>*James Madison University, Harrisonburg, VA, USA.* <sup>3</sup>*Eastern Mennonite University, Harrisonburg, VA, USA.* <sup>4</sup>*Smithsonian Institution, National Museum of Natural History, Washington, DC, USA.* <sup>5</sup>*Global Genome Initiative, Washington, DC, USA.* <sup>6</sup>*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<sup>1</sup>, Callie Crawford<sup>2</sup>, Sara Ruane<sup>1</sup> and Brooke Flammang<sup>2</sup>

<sup>1</sup>*Rutgers University-Newark, Newark, New Jersey, USA.* <sup>2</sup>*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<sup>1</sup>, Victor Tagliacollo<sup>2</sup>, Aaron Fronk<sup>1</sup> and James Albert<sup>1</sup>

<sup>1</sup>University of Louisiana at Lafayette, Lafayette, Louisiana, USA. <sup>2</sup>Universidade Federal de Tocantins, Palmas, Brazil

### **Diversification of the Ghost Knifefishes (Gymnotiformes: Apterontidae)**

The Apterontidae is the most species-rich and morphologically-disparate family of electric knifefishes (Gymnotiformes), with roughly 100 species in 15 genera. Apterontids 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 apterontid evolution. Our results suggest apterontids 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 *Apterontus*, 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 Apterontidae, 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<sup>1</sup>, Matthew Chatfield<sup>2</sup> and Cheryl Frederick<sup>2</sup>

<sup>1</sup>Colby College, Waterville, Maine, USA. <sup>2</sup>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<sup>1</sup>, Samantha Grant<sup>2</sup>, Danna M. Schock<sup>3</sup>, Christopher Kyle<sup>2</sup>, Craig Brunetti<sup>2</sup> and David Lesbarrères<sup>1</sup>

<sup>1</sup>Laurentian University, Sudbury, Ontario, Canada. <sup>2</sup>Trent University, Peterborough, Ontario, Canada. <sup>3</sup>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<sup>1</sup>, Christopher Austin<sup>2</sup>, William Bemis<sup>3</sup>, David Cannatella<sup>4</sup>, Kevin Conway<sup>5</sup>, Alison Davis Rabosky<sup>6</sup>, Casey Dillman<sup>3</sup>, Benjamin Frable<sup>7</sup>, Richard Glor<sup>8</sup>, James Hanken<sup>9</sup>, Philip Hastings<sup>7</sup>, Dean Hendrickson<sup>4</sup>, Eric Hilton<sup>10</sup>, Sarah Huber<sup>10</sup>,

Michelle Koo<sup>11</sup>, Travis LaDuc<sup>4</sup>, Katherine Maslenikov<sup>12</sup>, Amy McCune<sup>3</sup>, Heather Prestridge<sup>5</sup>, Daniel Rabosky<sup>6</sup>, Zachary Randall<sup>1</sup>, Alan Resetar<sup>13</sup>, Luiz Rocha<sup>14</sup>, Mark Sabaj<sup>15</sup>, Carol Spencer<sup>11</sup>, Adam Summers<sup>16</sup>, Luke Tornabene<sup>12</sup>, Gregory Watkins-Colwell<sup>17</sup>, Luke Welton<sup>8</sup> and Edward Stanley<sup>1</sup>

<sup>1</sup>University of Florida, Gainesville, FL, USA. <sup>2</sup>Louisiana State University, Baton Rouge, LA, USA. <sup>3</sup>Cornell University, Ithaca, NY, USA. <sup>4</sup>University of Texas, Austin, TX, USA. <sup>5</sup>Texas A&M University, College Station, TX, USA. <sup>6</sup>University of Michigan, Ann Arbor, MI, USA. <sup>7</sup>University of California, San Diego, San Diego, CA, USA. <sup>8</sup>University of Kansas, Lawrence, KS, USA. <sup>9</sup>Harvard University, Cambridge, MA, USA. <sup>10</sup>Virginia Institute of Marine Science, Gloucester Point, VA, USA. <sup>11</sup>University of California, Berkeley, Berkeley, CA, USA. <sup>12</sup>University of Washington, Seattle, WA, USA. <sup>13</sup>Field Museum of Natural History, Chicago, IL, USA. <sup>14</sup>California Academy of Sciences, San Francisco, CA, USA. <sup>15</sup>Academy of Natural Sciences, Philadelphia, PA, USA. <sup>16</sup>Friday Harbor Laboratory, Friday Harbor, WA, USA. <sup>17</sup>Yale University, New Haven, CT, USA

## **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<sup>1</sup> and Christopher Murray<sup>2</sup>

<sup>1</sup>The University of Central Missouri, Savannah, TN, USA. <sup>2</sup>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<sup>1</sup>, Michael Burns<sup>2</sup> and Tiffany Schriever<sup>1</sup>

<sup>1</sup>Western Michigan University, Kalamazoo, MI, USA. <sup>2</sup>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<sup>1</sup>, Eduardo Pineda<sup>2</sup>, Jorge Galindo-González<sup>1</sup>, Antonio Muñoz-Alonso<sup>3</sup> and Francisco Díaz-Fleischer<sup>1</sup>

<sup>1</sup>INBIOTECA/ Universidad Veracruzana, Xalapa, Veracruz, Mexico. <sup>2</sup>Instituto de Ecología AC, Xalapa, Veracruz, Mexico. <sup>3</sup>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<sup>1</sup>, Justin Lawrence<sup>1</sup>, Richard Buchholz<sup>1</sup>, Guarino Colli<sup>2</sup>, Jessica Heppard<sup>1</sup> and Brice Noonan<sup>1</sup>

<sup>1</sup>University of Mississippi, Oxford, MS, USA. <sup>2</sup>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<sup>1</sup>, Luis Ceriaco<sup>1</sup>, Edward Stanley<sup>2</sup>, David Blackburn<sup>2</sup>, Mariana Marques<sup>3</sup>, Suzana Bandeira<sup>4</sup>, Aaron Bauer<sup>4</sup> and Matthew Heinicke<sup>1</sup>

<sup>1</sup>University of Michigan-Dearborn, Dearborn, MI, USA. <sup>2</sup>University of Florida, Gainesville, FL, USA. <sup>3</sup>CIBIO Research Center in Biodiversity and Genetic Resources, Vairão, Portugal.

<sup>4</sup>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, Eugongylineae, 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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**CANCELED 342 Ichthyology Ecology and Ethology, Highland E, Sunday 15 July 2018**

Simon Brandl

*Simon Fraser University, Burnaby, BC, Canada*

**Exploring Cryptoland: of small fishes, functions, and fairytales**

Every tenth vertebrate species on Earth is a coral reef fish. However, approximately 50% of coral reef fishes generally go unnoticed due to their small size and hidden lifestyle: cryptobenthic reef fishes. But what exactly are cryptobenthic reef fishes? What do they do? And why should we care? This talk provides some answers to these questions. Specifically, I will demonstrate a striking dichotomy in body size distributions that allows us to delineate cryptobenthic reef fish families from their large, conspicuous counterparts and examine the ecological challenges and solutions that define life in Cryptoland. Using empirical data from the Caribbean, French Polynesia, and Australia, gathered with a mix of molecular, behavioral, and

physiological approaches, I will then highlight the role of ecological niche partitioning in supporting the extreme diversity of cryptobenthic reef fishes. Finally, I will integrate cryptobenthic reef fish communities into the trophic structure of coral reef ecosystems to explore their functional roles on reefs.

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

Laurel Brandsmeier<sup>1</sup> and Richard Mayden<sup>2</sup>

<sup>1</sup>HudsonAlpha Institute of Biotechnology, Huntsville, Alabama, USA. <sup>2</sup>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<sup>2</sup>) than in intact (0.82 arthropods/20m<sup>2</sup>) 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) than 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<sub>2</sub> 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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**CANCELED 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<sup>1</sup>, Jennifer Smith<sup>1</sup>, Emmanuel Frimpong<sup>1</sup>, Thomas Gorman<sup>1,2</sup>, Houston Chandler<sup>1,3</sup> and Carola Haas<sup>1</sup>

<sup>1</sup>Virginia Tech, Blacksburg, VA, USA. <sup>2</sup>Washington State Department of Natural Resources, Castle Rock, WA, USA. <sup>3</sup>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<sup>1</sup>, Jennifer Smith<sup>1</sup>, Thomas Gorman<sup>1,2</sup> and Carola Haas<sup>1</sup>

<sup>1</sup>Virginia Tech, Blacksburg, VA, USA. <sup>2</sup>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 allochthonous 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<sup>1,2</sup>, Petra Wood<sup>3</sup>, Yong-Lak Park<sup>1</sup>, Sara Crayton<sup>1</sup>, Lenza Paul<sup>4</sup> and Alice Millikin<sup>1</sup>

<sup>1</sup>West Virginia University, Morgantown, West Virginia, USA. <sup>2</sup>U.S. Forest Service, Northern Research Station, Parsons, West Virginia, USA. <sup>3</sup>U.S. Geological Survey, West Virginia Cooperative Wildlife Research Unit, Morgantown, West Virginia, USA. <sup>4</sup>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<sup>1</sup> and Ana Carnaval<sup>2</sup>

<sup>1</sup>*Southern Illinois University, Carbondale, IL, USA.* <sup>2</sup>*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<sup>1</sup>, Dan Hill<sup>2</sup>, Alan Haywood<sup>2</sup> and Ana Carnaval<sup>3</sup>

<sup>1</sup>*Southern Illinois University, Carbondale, IL, USA.* <sup>2</sup>*Leeds University, Leeds, United Kingdom.*

<sup>3</sup>*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<sup>1</sup> and Matthew G. Simon<sup>2</sup>

<sup>1</sup>*Skidmore College, Saratoga Springs, NY, USA.* <sup>2</sup>*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  $5.8 \pm 3.5$  (0–16) yr, and at their final recapture their ages were  $27.3 \pm 6.3$  (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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**127 Poster Session II, Empire Hall South – JF Rochester Riverside Convention Center, Saturday 14 July 2018**

Bryant Brumbill, Cari-Ann M. Hickerson and Carl D. Anthony

*John Carroll University, Cleveland heights, OH, USA*

**Effects of Invasive Asian Earthworms on Water Balance Maintenance of Eastern Red-backed Salamanders, *Plethodon cinereus***

Historically, glacial denudation excluded native earthworms from northern forests covered by the Laurentide ice sheet. Earthworm species have relatively slow dispersal rates resulting in northern forests evolving in the absence of native worm species. Lack of earthworms and slower fragmentation/decomposition of leaf litter by other detritivores allowed for accumulation of a thick organic horizon of decomposing plant matter on the forest floor. Invasive Asian pheretimoid earthworms are rapidly expanding their range into previously glaciated forests. These largely surface dwelling worms consume and remove the organic horizon which is vital to many forest fauna, and in its place create a layer of loose worm castings. Terrestrial plethodontid salamanders lack lungs and conduct all gas exchange cutaneously making these taxa especially vulnerable to desiccation and heavily reliant upon humid microhabitat for facilitating respiration. Like other plethodontids, Eastern Red-backed Salamanders (*Plethodon cinereus*), rely on the leaf litter layer as a buffer from thermal and hydric extremes. Modification of microhabitat humidity caused by pheretimoid worms may influence foraging range and dependence on cover-objects by *P. cinereus*. Historically it has been proposed that amphibians exhibit negligible resistance to cutaneous water loss, making their skin essentially a free water surface. Models made from many different substances have been used in previous studies to approximate cutaneous water loss in amphibians. Our research addresses the effects of earthworm mediated loss of leaf litter on the ability of *P. cinereus* to maintain water balance by deploying biologically validated plaster of Paris analogs in pheretimoid invaded and non-invaded localities.

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

Matthew Buehler<sup>1</sup>, Todd Jackman<sup>1</sup>, Jamie Oaks<sup>2</sup>, Stacie Hathaway<sup>3</sup>, Robert Fisher<sup>3</sup> and Aaron Bauer<sup>1</sup>

<sup>1</sup>*Villanova University, Villanova, Pennsylvania, USA.* <sup>2</sup>*Auburn University, Auburn, Alabama, USA.* <sup>3</sup>*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<sup>1</sup>, Karina Cervantes<sup>2</sup> and Emily Taylor<sup>1</sup>

<sup>1</sup>*California State Polytechnic University, San Luis Obispo, San Luis Obispo, CA, USA.* <sup>2</sup>*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<sup>1</sup>, Beverly Clendening<sup>1</sup> and Alexandra Kanonik<sup>2</sup>

<sup>1</sup>Hofstra University, Hempstead, NY, USA. <sup>2</sup>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**

Thaddeus Buser<sup>1</sup>, Brian Sidlauskas<sup>1</sup> and Adam Summers<sup>2</sup>

<sup>1</sup>Oregon State University, Corvallis, OR, USA. <sup>2</sup>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**

Thaddeus Buser<sup>1</sup>, Brian Sidlauskas<sup>1</sup> and Adam Summers<sup>2</sup>

<sup>1</sup>Oregon State University, Corvallis, OR, USA. <sup>2</sup>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 multilocus 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<sup>1</sup>, Adia Sovie<sup>2</sup>, Cathryn Greenberg<sup>3</sup> and James Austin<sup>2</sup>

<sup>1</sup>Virginia Tech, Blacksburg, VA, USA. <sup>2</sup>University of Florida, Gainesville, FL, USA. <sup>3</sup>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 relictata relictata*) 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<sup>1</sup>, Stuart Wells<sup>1</sup>, Joseph Incandela<sup>1</sup>, Jennifer Lamb<sup>1</sup> and Christopher Beachy<sup>2</sup>

<sup>1</sup>*Southeastern Louisiana University, Hammond, LA, USA.* <sup>2</sup>*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<sup>1,2</sup>, Melissa Lech<sup>1,3</sup>, Kyle Brown<sup>1,2</sup>, J. Christopher Leaphart<sup>2</sup>, Melissa Pilgrim<sup>1,2</sup> and Tracey Tuberville<sup>2</sup>

<sup>1</sup>*USC Upstate, Spartanburg, SC, USA.* <sup>2</sup>*Savannah River Ecology Laboratory, Aiken, SC, USA.* <sup>3</sup>*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 ( $0.87 \pm 0.08$ ), followed by kidney ( $0.49 \pm 0.04$ ), liver ( $0.47 \pm 0.04$ ), scale clip ( $0.24 \pm 0.06$ ), and tail tip ( $0.25 \pm 0.06$ ). 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<sup>1</sup>, David Camak<sup>1</sup>, Tyler Pilger<sup>2</sup>, David Propst<sup>1</sup> and Thomas Turner<sup>1</sup>

<sup>1</sup>*University of New Mexico, Albuquerque, New Mexico, USA.* <sup>2</sup>*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-continental 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<sup>1</sup>, A.J. Belden<sup>1</sup>, Joseph Pich<sup>1</sup> and Sasha Tetzlaff<sup>2</sup>

<sup>1</sup>Wabash College, Crawfordsville, IN, USA. <sup>2</sup>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<sup>1</sup>, Christina Staudhammer<sup>2</sup> and Leslie Rissler<sup>3</sup>

<sup>1</sup>Virginia Polytechnic Institute and State University College of Natural Resources, Blacksburg, VA, USA. <sup>2</sup>University of Alabama, Tuscaloosa, AL, USA. <sup>3</sup>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<sup>1</sup> and Barbara Calegari<sup>2</sup>

<sup>1</sup>Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil. <sup>2</sup>Pontifícia Universidade Católica do Rio Grande do Sul, Porto Alegre, RS, Brazil

#### **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 punctatus*) 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<sup>1</sup>, Thomas F. Duda, Jr.<sup>1,2</sup> and Alison Davis Rabosky<sup>1</sup>

<sup>1</sup>*University of Michigan, Ann Arbor, Michigan, USA.* <sup>2</sup>*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 Ceriáco<sup>1,2,3</sup>, Mariana Marques<sup>4,3</sup>, Suzana Bandeira<sup>2,5</sup>, Mathew Heinicke<sup>1</sup>, Carly Boye<sup>1</sup>, Edward Stanley<sup>6</sup>, David Blackburn<sup>6</sup> and Aaron Bauer<sup>2</sup>

<sup>1</sup>*Department of Natural Sciences, University of Michigan-Dearborn, Dearborn, Michigan, USA.* <sup>2</sup>*Department of Biology, Villanova University, Villanova, Pennsylvania, USA.* <sup>3</sup>*Museu Nacional de História Natural e da Ciência, Universidade de Lisboa, Lisboa, Portugal.* <sup>4</sup>*Research Center in Biodiversity and Genetic Resources (CIBIO), InBIO, University of Porto, Vairão, Portugal.* <sup>5</sup>*Instituto Nacional da Biodiversidade e Áreas de Conservação, Kilamba-Kiaxi, Luanda, Angola.* <sup>6</sup>*Department of Natural History, Florida Museum of Natural History, University of Florida, Gainesville, Florida, USA*

### **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 19<sup>th</sup> 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**

Luis Ceriaco<sup>3,2</sup>, Suzana Bandeira<sup>3,4</sup>, Ishan Agarwal<sup>5</sup>, Nuno Ferrand de Almeida<sup>6</sup> and Aaron Bauer<sup>5</sup>

<sup>2</sup>*Museu Nacional de História Natural e da Ciência, Lisboa, Portugal.*

<sup>3</sup>*Department of Biology, Villanova University, Villanova, Pennsylvania, USA.* <sup>4</sup>*Instituto Nacional da Biodiversidade e Áreas de Conservação, Ministério do Ambiente de Angola, Kilamba-Kiaxi, Angola.* <sup>5</sup>*Department of Biology, Villanova University, Villanova, Pennsylvania, Portugal.* <sup>6</sup>*Research Center in Biodiversity and Genetic Resources (CIBIO), InBIO, University of Porto, Porto, Vairão, Portugal*

**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<sup>2</sup>) 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<sup>1</sup>, Sebastian Kirchhof<sup>2</sup> and Aaron Bauer<sup>3</sup>

<sup>1</sup>Museum of Vertebrate Zoology, UC Berkeley, Berkeley, CA, USA. <sup>2</sup>Museum für Naturkunde, Berlin, Germany. <sup>3</sup>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<sup>1,2</sup>, John Waldman<sup>3</sup> and Elizabeth Alter<sup>1</sup>

<sup>1</sup>York College, New York, NY, USA. <sup>2</sup>CUNY Graduate Center, New York, NY, USA. <sup>3</sup>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<sup>1</sup>, Ryan McCleary<sup>2</sup>, R. Manjunatha Kini<sup>3</sup> and Devadasan Velmurugan<sup>1</sup>

<sup>1</sup>University of Madras, Guindy Campus, Chennai, India. <sup>2</sup>Stetson University, DeLand, FL, USA. <sup>3</sup>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<sup>1</sup> and Te-En Lin<sup>2</sup>

<sup>1</sup>Texas A&M University, College Station, Texas, USA. <sup>2</sup>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<sup>1</sup>, Robert Denton<sup>1</sup>, Michael Zasloff<sup>2</sup> and John Malone<sup>1</sup>

<sup>1</sup>University of Connecticut, Storrs, Connecticut, USA. <sup>2</sup>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 taumantellic 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. betsileo* 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<sup>1</sup>, Maria Akopyan<sup>2,1</sup>, Gideon Bradburd<sup>3</sup>, Andres Vega<sup>4</sup> and Jeanne Robertson<sup>1</sup>

<sup>1</sup>California State University, Northridge, Northridge, CA, USA. <sup>2</sup>Cornell University, Ithaca, NY, USA. <sup>3</sup>Michigan State University, East Lansing, MI, USA. <sup>4</sup>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<sup>1</sup>, Juan Daza<sup>1</sup>, Ian Brennan<sup>2</sup>, Mark Hutchinson<sup>3</sup> and Aaron Bauer<sup>4</sup>

<sup>1</sup>Sam Houston State University, Huntsville, Texas, USA. <sup>2</sup>The Australian National University, Canberra, Australia. <sup>3</sup>University of Adelaide, Adelaide, Australia. <sup>4</sup>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 parabasisphenoid rostrum, with no support of the pterygoids due to a reduction of the epipterygoids. 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<sup>1</sup>, George Bakken<sup>2</sup> and Hannes Schraft<sup>1</sup>

<sup>1</sup>San Diego State University, San Diego, CA, USA. <sup>2</sup>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 COI, we found four distinct genetic clusters, two for *C. sardinella*, one for *C. clupearformis* and one for *C. autumnalis*. Pairwise p-distances showed the following ranges: 0-0.9% within *C. sardinella*, 1.1-1.5% between *C. clupearformis* and *C. sardinella*, 1.7-2% between *C. clupearformis* 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<sup>1</sup>, Robert Espinoza<sup>1</sup>, L. Lee Grismer<sup>2</sup>, Shahrul Anuar<sup>3</sup> and Evan Quah<sup>3</sup>

<sup>1</sup>*California State University Northridge, Northridge, CA, USA.* <sup>2</sup>*La Sierra University, Riverside, CA, USA.* <sup>3</sup>*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<sup>1</sup> and Roberto Alonso Bosch<sup>2</sup>

<sup>1</sup>University of Kansas, Lawrence, Kansas, USA. <sup>2</sup>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 Hernandez

*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 of 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<sup>1</sup>, L. Patricia Hernandez<sup>1</sup>, Callie H. Crawford<sup>2</sup> and Brooke E. Flammang<sup>2</sup>

<sup>1</sup>The George Washington University, Washington, DC, USA. <sup>2</sup>New Jersey Institute of Technology, Newark, NJ, USA

#### **Modeling silver carp filtration using $\mu$ CT 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  $\mu\text{m}$ , 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 10 $\mu\text{m}$  and 28 $\mu\text{m}$   $\mu\text{CT}$  scans of adult Silver carp and its sister species Bighead carp) were placed in a recirculating flow tank. Neutrally-buoyant 50 $\mu\text{m}$  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<sup>1</sup> and Lynne Parenti<sup>2</sup>

<sup>1</sup>University of Hawaii at Manoa, Honolulu, HI, USA. <sup>2</sup>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 Gobioidae 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 Gobioidae. 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<sup>1</sup> and Katherine E Bemis<sup>2</sup>

<sup>1</sup>Smithsonian Institution, Washington, D.C., USA. <sup>2</sup>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 South - JF Rochester Riverside Convention Center, Saturday 14 July 2018**

Kevin Conway<sup>1</sup> and Dustin Siegel<sup>2</sup>

<sup>1</sup>Texas A&M University, College Station, TX, USA. <sup>2</sup>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<sup>1</sup>, Jen-Chieh Shiao<sup>2</sup>, Todd Pierson<sup>1</sup>, Jie Zhang<sup>3</sup> and Benjamin Fitzpatrick<sup>1</sup>

<sup>1</sup>University of Tennessee, Knoxville, TN, USA. <sup>2</sup>National Taiwan University, Taipei, Taiwan.

<sup>3</sup>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 hopfish (*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<sup>1</sup> and Wm. Leo Smith<sup>2</sup>

<sup>1</sup>NOAA National Marine Fisheries Service, La Jolla, CA, USA. <sup>2</sup>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<sup>1</sup>, Zachary Randall<sup>2</sup> and Brooke Flammang<sup>1</sup>

<sup>1</sup>New Jersey Institute of Technology, Newark, NJ, USA. <sup>2</sup>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, *Cryptотора*. Previous work found that the cave loach, *Cryptотора 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 *Cryptотора 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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## **536 Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center, Saturday 14 July 2018**

James Creed<sup>1</sup>, Kimberly Bernotas<sup>2</sup>, Elizabeth Alter<sup>1,2</sup> and Melanie Stiassny<sup>2</sup>

<sup>1</sup>York College/CUNY, Jamaica, NY, USA. <sup>2</sup>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 *Teleogramma* 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<sup>1</sup>, Brian Sidlauskas<sup>2</sup>, Hans Mipounga<sup>3</sup> and Jean Herve Mve Beh<sup>3</sup>

<sup>1</sup>UC Santa Cruz, Santa Cruz, CA, USA. <sup>2</sup>OSU, Corvallis, OR, USA. <sup>3</sup>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.

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