

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

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

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

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

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

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

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

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

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

Hayden Davis, Aaron Bauer and Todd Jackman

*Villanova University, Villanova, PA, USA*

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

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

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

Matthew Davis

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

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

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

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

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

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<sup>4</sup>*University of Bristol, Bristol, United Kingdom.* <sup>5</sup>*Institut Català de Paleontologia Miquel Crusafont, Barcelona, Catalunya, Spain.* <sup>6</sup>*Harvard University, Museum of Comparative Zoology, Cambridge, Massachusetts, USA.* <sup>7</sup>*Washington University, Saint Louis, Missouri, USA*

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

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

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

Luiz Jardim de Queiroz<sup>1,2</sup> and Juan Montoya-Burgos<sup>1,3</sup>

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

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

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

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

Lesley de Souza<sup>1</sup>, Donald Taphorn<sup>2</sup> and Jonathan Armbruster<sup>3</sup>

<sup>1</sup>Field Museum, Chicago, IL, USA. <sup>2</sup>None, Belleville, IL, USA. <sup>3</sup>Auburn University Museum of Natural History, Auburn, AL, USA

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

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

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

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

Emily DeArmon and Matthew Davis

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

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

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

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

Jennifer Deitloff<sup>1</sup>, H. Nate Rainey<sup>1</sup>, Samantha P. Wesnak<sup>2,1</sup>, Jacob Fetterman<sup>3,1</sup>, Kelsey Young<sup>1</sup> and Todd Pierson<sup>4</sup>

<sup>1</sup>*Lock Haven University, Lock Haven, PA, USA.* <sup>2</sup>*Cornell University, Ithaca, NY, USA.*

<sup>3</sup>*Louisiana State University, Baton Rouge, LA, USA.* <sup>4</sup>*University of Tennessee, Knoxville, TN, USA*

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

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

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

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

<sup>1</sup>University of Nevada, Reno - School of Medicine, Reno, Nevada, USA. <sup>2</sup>University of Nevada, Reno, Reno, Nevada, USA. <sup>3</sup>University of Virginia, Charlottesville, Virginia, USA. <sup>4</sup>Utah State University, Logan, Utah, USA

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

The interaction between garter snakes (*Thamnophis*) and toxic newts (*Taricha*) is a model system of predator-prey coevolution. At the interface of this coevolutionary interaction are the snake voltage-gated sodium channels, Nav proteins, and the newt's sodium channel toxin, Tetrodotoxin (TTX). Nav proteins are responsible for the first electrical event initiating nerve impulses and fast muscular contractions. TTX ligation to the channel pore prevents sodium ion movement through the membrane, thereby abolishing excitability, and leading to numbness, paralysis, and eventually death by respiratory arrest. TTX has independently served as an agent of selection on several *Thamnophis* species that prey on sympatric *Taricha*. *Thamnophis atratus* and *T. sirtalis* have independently evolved adaptive mutations in the outer pore of the skeletal muscle channel, Nav1.4. The amino acid substitutions reduce the affinity of TTX to the pore, thereby providing physiological resistance to TTX. Here, we show that these same mutations actually reduce sodium channel performance, despite their adaptive value in reducing TTX

ligation to the pore. This channel hypofunction also appears to explain dramatic reductions in skeletal muscle performance (force and speed) in snakes that carry these naturally occurring channel mutants. We suggest that the proximate cause of these tissue performance deficits is reduced excitability imparted by reduced unitary sodium conductance and a shift in  $\text{Na}_v1.4$  steady-state kinetics. These findings may influence higher order phenomena such as the organism's capacity to evade predation, which in turn, may provide a traceable explanation for the geographic mosaic distribution of toxin resistance phenotypes across the landscape.

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

Naomi Delventhal<sup>1</sup> and Lynne Parenti<sup>2</sup>

<sup>1</sup>University of Manitoba, Winnipeg, MB, Canada. <sup>2</sup>National Museum of Natural History, Smithsonian Institution, Washington DC, USA

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

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

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

Joseph DeMarchi<sup>1</sup>, Carl Anthony<sup>1</sup>, Cari-Ann Hickerson<sup>1</sup> and Matthew Venesky<sup>2</sup>

<sup>1</sup>John Carroll University, University Heights, OH, USA. <sup>2</sup>Allegheny College, Meadville, PA, USA

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

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

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

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

*John Carroll University, University Heights, Ohio, USA*

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

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

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

Rob Denton and John Malone

*University of Connecticut, Storrs, Connecticut, USA*

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

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

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

Robert Denton<sup>1,2</sup>, Ariadna Morales<sup>2</sup> and Lisle Gibbs<sup>2</sup>

<sup>1</sup>*University of Connecticut, Storrs, CT, USA.* <sup>2</sup>*Ohio State University, Columbus, OH, USA*

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

Quantifying genetic introgression between sexual species and polyploid lineages traditionally thought to be asexual is an important step in understanding what factors drive the longevity of putatively asexual groups. However, the presence of multiple distinct subgenomes within a

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

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

Thomas DeWitt

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

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

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

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

Thomas DeWitt

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

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

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

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

Matthew Dickson<sup>1</sup>, Heather Liwanag<sup>2</sup>, Aaron Bauer<sup>3</sup> and Robert Espinoza<sup>1</sup>

<sup>1</sup>*California State University, Northridge, Northridge, CA, USA.* <sup>2</sup>*California Polytechnic University, San Luis Obispo, San Luis Obispo, CA, USA.* <sup>3</sup>*Villanova University, Villanova, PA, USA*

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

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

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

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

Devin DiGiacopo, George Meindl, Kirsten Prior and Jessica Hua

*Binghamton University, Binghamton, New York, USA*

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

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

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

Casey Dillman<sup>1</sup> and Eric Hilton<sup>2</sup>

<sup>1</sup>Cornell University, Ithaca, NY, USA. <sup>2</sup>Virginia Institute of Marine Science, Gloucester Point, VA, USA

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

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

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

David Dimitrie<sup>1</sup>, Michael Benard<sup>1</sup> and David Burke<sup>2</sup>

<sup>1</sup>Case Western Reserve University, Cleveland, Ohio, USA. <sup>2</sup>The Holden Arboretum, Kirtland, Ohio, USA

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

Anthropogenic activities can lead to acid deposition, resulting in the acidification of forest ecosystems. Applications of Hi-Ca lime to soil can be used to facilitate forest recovery from historic acidification. Although studies have examined how some organisms respond to these management strategies, few studies have addressed the effects on amphibians and their invertebrate prey. We assessed American toad (*Anaxyrus americanus*) survival and growth in northeast Ohio forests that have been treated for nine years with Hi-Ca lime to elevate soil pH. Field enclosures were constructed within both lime-treated forests (mean pH 6.0) and forests with untreated soil (mean pH 4.4), and four post-metamorphic toads were placed into each enclosure. We measured toad survival and growth after 25, 60, and 90 days. Invertebrates were sampled both before toads were placed into enclosures and after 90 days to assess prey

availability. We found no difference between the two soil treatments in toad survival or growth throughout the study. Invertebrate abundances also did not differ between soil treatments. Toad mass after 90 days was positively correlated with number of Collembola collected in invertebrate samples on day 90, regardless of soil treatment. Our study provides evidence that elevating soil pH via Hi-Ca lime does not have direct effects on post-metamorphic toad survival or indirect effects on growth mediated by prey availability. Understanding the implications of soil liming within acidic hardwood forests may provide managers with better insight into how this long-term treatment may affect not only anurans but other forest floor consumers as well.

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

Dawn Dittman

*USGS, Cortland, New York, USA*

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

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

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

Dawn Dittman, Marc Chalupnicki and Phyllis Randall

*USGS, Cortland, New York, USA*

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

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

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

Ken Dodd<sup>1</sup> and Corey Anderson<sup>2</sup>

<sup>1</sup>University of Florida, Gainesville, Florida, USA. <sup>2</sup>Valdosta State University, Valdosta, Georgia, USA

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

Temporary ponds are important breeding sites for many amphibians and may serve as refugia for species crossing unfavorable habitats while dispersing. In this study, we examined the immigration and emigration patterns of six amphibian species from October 1985 through September 1990 at an isolated temporary pond in a sandhills community in north central Florida, USA. Our results indicated that the circular distribution of amphibian captures around the pond was often non-uniform, especially when capture distributions were pooled over multiple years or multiple species. Species captured more frequently tended to be found at a wider range of directions moving into and out of the pond. Many species exhibited complex multimodal distributions, with potential shifts in modal directions from year to year. Interspecies variation in the frequency of dispersion at different angles into and out of the pond basin was common and likely reflected species-specific movement capabilities. Nonrandom

dispersal at our study site suggests that species may be moving to and from specific habitat types, such as nearby wetlands or terrestrial habitats used for foraging or refuge. The extensive interspecific variation in amphibian movement patterns seen at Breezeway Pond and observed in other studies, coupled with the potential for widespread and long-range dispersal, suggest that large areas of habitat should be protected to ensure the survival of amphibians breeding in temporary ponds from stochastic and long-term effects of climate change and isolation.

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

Terry Donaldson

*University of Guam Marine Laboratory, MANGILAO, Guam, USA*

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

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

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

Caroline Dong<sup>1,2</sup>, Claire McLean<sup>1,2</sup>, Adnan Moussalli<sup>2</sup> and Devi Stuart-Fox<sup>1</sup>

<sup>1</sup>*The University of Melbourne, Parkville, Victoria, Australia.* <sup>2</sup>*Museum Victoria, Carlton, Victoria, Australia*

### **Genomic and Phenotypic Patterns Across a Contact Zone of Colorful Agamids**

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

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

Erica Donlon and Marcelo Melo

*Instituto Oceanografico, Universidade de São Paulo, São Paulo, SP, Brazil*

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

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

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

Paul D'Ortona and Scott McRobert

*Saint Joseph's University, Philadelphia, PA, USA*

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

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

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

Dana Drake, Sean Giery and Mark Urban

*University of Connecticut, Storrs, CT, USA*

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

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

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

Peter Ducey

*SUNY Cortland, Cortland, NY, USA*

**Adaptation and Homology in Salamander Antipredator Behaviors and Tail Autotomy**

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

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

Thomas Duchak and Russell Burke

*Hofstra University, Hempstead, New York, USA*

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

In northern New Jersey, substrates of many turtle nesting areas are strewn with cobbles from past glaciations. Glacial till, along with vegetation, often hinders the ability of nesting wood turtles, *Glyptemys insculpta*, to excavate nests and consequently increases failed nesting attempts and time at nesting sites. Risk of predation and illegal collection are likely heightened in turtles that spend several days or even weeks attempting to nest unsuccessfully in exposed areas. Furthermore, gravid females that cannot find suitable nest sites may eventually jettison their eggs as captive turtles do when keepers fail to provide laying media. To facilitate nesting and inform management strategies during a multi-year wood turtle nesting study, we altered the grounds of a former stone quarry that attracts ≈30 nesting wood turtles annually. In 2013, we tilled the quarry to soften the ground and remove vegetation. Then, we delimited four

adjacent 80m<sup>2</sup> nesting plots and designated them as control and experimental plots in an alternating fashion. In the experimental plots, we excavated the original rocky sediment and replaced it with sand. In subsequent years, we tilled all plots to delay succession and keep soft sediments exposed. Besides annual tilling, the control plots were not manipulated. From 2013-2017, we monitored the quarry for nesting wood turtles. We found that more failed nesting attempts occurred in the control plots and more nests were successfully laid in the experimental plots. From these results, we conclude that nesting site management may be beneficial for turtle populations in areas with rocky soils.

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

Andrew M. Durso<sup>1,2</sup>, Isabelle Bolon<sup>3</sup> and Rafael Ruiz de Castañeda<sup>3</sup>

*<sup>1</sup>University of Geneva, Geneva, Geneva, Switzerland. <sup>2</sup>Max Planck Institute for Biogeochemistry, Jena, Thüringen, Germany. <sup>3</sup>Institute of Global Health, University of Geneva, Geneva, Geneva, Switzerland*

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

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

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

Andrew M. Durso<sup>1,2</sup>, Lorin A. Neuman-Lee<sup>3</sup>, Gareth R. Hopkins<sup>4</sup> and Edmund D. Brodie Jr.<sup>5</sup>

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

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

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

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

Julia Earl

Louisiana Tech University, Ruston, LA, USA

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

Natural populations are affected by many environmental variables that alter survival, growth, and developmental rates. Many observational studies and experiments have demonstrated the importance of competition, predation, resources, habitat, and chemical and thermal environments. However, the relative importance of these different variables remains unclear, as experiments typically examine only one or two mechanisms at a time. Here, I simultaneously examine the relative importance of all of these mechanisms for tadpole survival, growth, and development using a mesocosm experiment. Mesocosms were placed within forest and clearcuts, and plant litter input was manipulated. Mesocosms were naturally colonized by predators and competitors. I introduced tadpoles and assessed survival and time and size at metamorphosis using three species: wood frogs, American toads, and southern leopard frogs. I created seven models representing different mechanisms to examine which best predicted tadpole performance using AIC. For wood frog survival, water quality and thermal models

were competing for best model, showing a positive relationship between survival and tannin concentration and a negative relationship with pH and temperature. American toad survival was lower with higher dragonfly larval density. Wood frogs and American toads had longer body lengths with grass litter than leaf or no litter. Wood frog developmental time was longer in mesocosms with cooler temperatures. These results highlight the importance of water quality, temperature, and predation to tadpole survival, though the variable with the best predictive power varied by species. However, for size at metamorphosis, resource type was similarly important for two different tadpole species.

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

Diego J. Elias and Prosanta Chakrabarty

*Louisiana State University, Baton Rouge, LA, USA*

**Comparative Phylogeography of Freshwater Fishes in Northern Central America.**

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

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

Diego J. Elias<sup>1</sup>, Caleb D. McMahan<sup>2</sup> and Prosanta Chakrabarty<sup>1</sup>

<sup>1</sup>Louisiana State University, Baton Rouge, LA, USA. <sup>2</sup>The Field Museum of Natural History, Chicago, IL, USA

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

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

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**546 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: ECOLOGY, NATURAL HISTORY, DISTRIBUTION & BEHAVIOR, Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018 AND Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center; part of ASIH symposium: If Salamanders Could Speak, Saturday 14 July 2018**

Erica Ely<sup>1,2</sup> and Chris Feldman<sup>1</sup>

<sup>1</sup>University of Nevada Reno, Reno, Nevada, USA. <sup>2</sup>California Academy of Sciences, Herpetology, San Francisco, California, USA

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

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

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

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

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

*Pennsylvania State University, University Park, PA, USA*

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

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

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

James Erdmann

*Wyoming Game and Fish Department, Laramie, Wyoming, USA*

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

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

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

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

Taylor Eubank<sup>1</sup>, Juan Diego Daza<sup>1</sup> and Aaron M. Bauer<sup>2</sup>

<sup>1</sup>Sam Houston State University, Huntsville, Texas, USA. <sup>2</sup>Villanova University, Villanova, Pennsylvania, USA

**Alternative gaits in gekkotans explains femoral morphology**

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

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

Adriana Eugene<sup>1</sup>, Alexandra Kanonik<sup>2</sup> and Russell Burke<sup>1</sup>

<sup>1</sup>Hofstra University, Uniondale, NY, USA. <sup>2</sup>American Littoral Society, Highlands, NJ, USA

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

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

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

Allyson J. Evans<sup>1</sup>, Carlos David De Santana<sup>2</sup> and Casey B. Dillman<sup>1</sup>

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

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

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

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

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

Annette Evans<sup>1</sup>, Elizabeth Jockusch<sup>1</sup>, Mark C. Urban<sup>1</sup>, Brenna Forester<sup>2</sup>, Caitlin Fisher-Reid<sup>3</sup> and Bradley Cosentino<sup>4</sup>

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

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

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

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

Kory Evans<sup>1</sup>, Lesley Kim<sup>2</sup>, Brian Schubert<sup>2</sup> and James Albert<sup>2</sup>

<sup>1</sup>University of Minnesota, St. Paul, MN, USA. <sup>2</sup>University of Louisiana at Lafayette, Lafayette, LA, USA

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

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

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

Teah Evers and Jennifer Deitloff

*Lock Haven University, Lock Haven, PA, USA*

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

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

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

Vincent Farallo<sup>1</sup>, Martha Muñoz<sup>1</sup> and Donald Miles<sup>2</sup>

<sup>1</sup>Virginia Tech, Blacksburg, VA, USA. <sup>2</sup>Ohio University, Athens, OH, USA

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

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

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## 368 Herpetology Reproduction, Highland C, Sunday 15 July 2018

Terence Farrell<sup>1</sup>, Sarah Smiley<sup>1</sup>, Amber Clark<sup>1</sup> and Craig Lind<sup>2</sup>

<sup>1</sup>Stetson University, DeLand, FL, USA. <sup>2</sup>Stockton University, Galloway, NJ, USA

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

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

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

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

Dario Faustino-Fuster<sup>1,2</sup>, Rafael Angrizani<sup>1</sup> and Luiz Malabarba<sup>1</sup>

<sup>1</sup>Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil. <sup>2</sup>Museo de Historia Natural (UNMSM), Lima, Lima, Peru

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

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

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

Matthew Fedler, Coleman Sheehy and Kenneth Krysko

*University of Florida, Gainesville, Florida, USA*

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

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

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

Miranda Figueras<sup>1</sup>, Kent Hatch<sup>2</sup>, Beverly Roeder<sup>3</sup> and Russell Burke<sup>1</sup>

<sup>1</sup>Hofstra University, Hempstead, NY, USA. <sup>2</sup>LIU Post, Brookville, NY, USA. <sup>3</sup>Brigham Young University, Provo, UT, USA

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

Interspecific comparisons of physiological parameters, such as metabolic rates and temperature regulation, with ecological parameters such as activity patterns and thermoregulatory behavior,

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

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

João Pedro Fontenelle<sup>1</sup>, William Crampton<sup>2</sup> and Nathan Lovejoy<sup>1</sup>

<sup>1</sup>University of Toronto Scarborough, Toronto, ON, Canada. <sup>2</sup>University of Central Florida, Orlando, FL, USA

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

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

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

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

Cliff Fontenot<sup>1</sup>, Sydney Ferguson<sup>1</sup> and Helen Plylar<sup>2</sup>

<sup>1</sup>*Southeastern Louisiana University, Hammond, LA, USA.* <sup>2</sup>*Florida Institute of Technology, Melbourne, FL, USA*

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

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

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

Jessica Ford

*McGill University, Montreal, QC, Canada*

### **Methods for raising toad tadpoles in experimental mesocosms**

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

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

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

María J. Forzán<sup>1</sup>, Joe-Felix Bienentreu<sup>2</sup>, Danna M. Schock<sup>3</sup> and David Lesbarreres<sup>2</sup>

<sup>1</sup>Cornell University, Ithaca, NY, USA. <sup>2</sup>Laurentian University, Sudbury, ON, Canada. <sup>3</sup>Keyano College, Fort McMurray, AB, Canada

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

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

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

Claire Fox and William Bemis

Cornell University, Ithaca, NY, USA

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

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

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

Elyse Freitas<sup>1</sup>, Aniruddha Datta-Roy<sup>2</sup>, Praveen Karanth<sup>2</sup> and Cameron Siler<sup>1</sup>

<sup>1</sup>Sam Noble Museum, University of Oklahoma, Norman, Oklahoma, USA. <sup>2</sup>Centre for Ecological Sciences, Indian Institute of Science, Bangalore, India

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

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

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

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

Connor French and Jason Brown

*Southern Illinois University, Carbondale, IL, USA*

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

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

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

Aaron H Fronk, Maxwell J Bernt and James S Albert

*University of Louisiana at Lafayette, Lafayette, Louisiana, USA*

## **Ancestral Ranges and Geographic Range Evolution of Electric Ghost Knifefishes (Gymnotiformes: Apterontidae).**

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

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

César Fuentes

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

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

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

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

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**376 SSAR VICTOR HUTCHISON STUDENT POSTER AWARD: EVOLUTION, GENETICS, & SYSTEMATICS, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018**

Giovanni Fuentes<sup>1</sup>, Sean Harrington<sup>2</sup>, David Blackburn<sup>1</sup> and Daniel Paluh<sup>1</sup>

<sup>1</sup>University of Florida, Gainesville, Florida, USA. <sup>2</sup>University of Hawaii at Manoa, Honolulu, Hawaii, USA

**Comparative Morphology of Rattlesnake Cranial Diversity: Influence of Phylogeny, Ecology, and Modularity**

A fundamental goal of evolutionary biology is to classify patterns of diversity and identify the processes responsible for shaping those patterns. The vertebrate skull is often considered to be modular and partitioned into semi-independent blocks of traits, and these modules may be differentially influenced by historical constraints and selective pressures. We investigated the diversity of rattlesnake skulls (*Crotalus* and *Sistrurus*) using high-resolution x-ray micro-computed tomography. Our objectives were to characterize the morphology of individual cranial elements across species and determine 1) if overall skull shape is associated with habitat utilization or diet and 2) if certain elements or modules of the skull are more variable across lineages than others. Despite their similar overall body forms, rattlesnakes occupy a variety of habitats. The 47 taxa range from tropical savannahs, desert dunes, and high elevation rock outcrops to temperate deciduous forest. Diet is also variable across species, with some species specializing nearly exclusively on mammals while others include larger portions of lizards and other ectothermic prey in their diets. Preliminary results demonstrate that small-bodied, rock habitat specialists have repeatedly evolved relatively longer and narrower skulls than large-bodied species that occupy a diversity of environments. Structures associated with feeding (e.g., maxilla, pterygoid, dentary) appear to be more labile across species than the posterior region of the skull. Future research directions include quantifying morphological variation using 3D geometric morphometrics and testing how diets and habitats influence rates of evolution and phenotypic optima using phylogenetic comparative methods.

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

Rory Fuller and L. Michael Romero

Tufts University, Medford, MA, USA

## **Differences in the stress response of the painted turtle, *Chrysemys picta*, across sites of varying anthropogenic disturbance**

Urbanization and related anthropogenic stressors present an array of distinctive challenges for many extant species. However, many studies have shown conflicting information on how vertebrates respond to these stressors, necessitating further research into the reason for and nature of differing stress responses. As an initial step toward this goal, we sought to determine whether eastern painted turtles (*Chrysemys picta picta*) in eastern Massachusetts displayed substantial differences in their stress responses at three sites of greatly differing urbanization. Painted turtles represent an excellent subject for this study due to their long lives, high adult survivability, and relatively high site fidelity compared to more classical subjects of field stress physiology, such as birds. We trapped turtles at these locations for two summers, taking blood samples and behavioral data for comparison. Blood samples were used for analysis of glucocorticoid levels and various metabolic and immune function markers known to be related to stress physiology. Behavioral data consisted of observations and timing of escape behaviors post-handling. We discovered significant variation in glucocorticoid secretion patterns between sites, which were consistent between years. We also show potential signs of differences in immune system functionality between the sites, as well as in some escape behaviors. We conclude that the eastern painted turtle appears responsive to the presence of urbanization and therefore makes an excellent candidate for further investigations into differential responses to anthropogenic stressors.

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## **14 Ichthyology Genetics, Reproduction, and Development, Highland E., Friday 13 July 2018**

Emily Funk and Amy McCune

*Cornell University, Ithaca, NY, USA*

## **Gene expression patterns underlying gas bladder evolution in ray-finned fishes**

Study of the origin of evolutionary novelties, such as jaws and limbs, is central to understanding the history of life. With advancements in developmental genetics, we can investigate the genetic underpinning of evolutionary novelties, their origins and subsequent transformations. The gas bladder, derived from lungs of the bony vertebrate common ancestor, originated as a novelty within ray-finned fishes and is important for efficient buoyancy control. As homologous organs, the gas bladder and the lungs share many similarities; however, the defining difference between them is the location of budding from the anterior foregut; gas bladders bud dorsally and lungs bud ventrally. We are investigating whether the inversion of budding location is paralleled by a dorsoventral inversion of gene expression patterns. Bowfin (*Amia calva*) are ideal to study early evolution of the gas bladder because they are a deeply-branching lineage that diverged soon after gas bladder origination and possess a dorsal gas bladder. To capture transcriptome-wide expression during bowfin gas bladder development while maintaining dorsoventral spatial information, we used laser-capture microdissection to

isolate the dorsal and ventral foregut tissue from 3 developmental stages spanning bowfin gas bladder budding. We separately sequenced expression profiles for each tissue and identified genes differentially expressed between dorsal and ventral foregut. Subsequently, we characterized at what stage and tissue known lung-regulatory genes are expressed during bowfin gas bladder development and whether they are differentially expressed across the dorsoventral axis in the same or opposite (i.e. inverted) direction.

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### **364 ASIH STOYE GENETICS, DEVELOPMENT, & MORPHOLOGY III, Highland C, Friday 13 July 2018**

Nicole Fusco<sup>1</sup>, Ellen Pehek<sup>2</sup> and Jason Munshi-South<sup>1</sup>

<sup>1</sup>Fordham University, Bronx, New York, USA. <sup>2</sup>New York City Parks Department, New York City, New York, USA

### **Genetic Connectivity of Stream Salamander Populations within Stream Systems in the New York City Metropolitan Area**

The Northern two-lined salamander (*Eurycea bislineata*) plays an important ecological role in Northeastern forests yet they are incredibly susceptible to human disturbances due to a reliance on both terrestrial and aquatic habitats for survival, dispersal, and reproduction. Published results show that decreased canopy cover, a high presence of invasive predators, and alterations to water chemistry, can restrict movement and reduce the abundance of salamanders within stream systems. To understand if urbanization in and around New York City is affecting Northern two-lined salamander (*Eurycea bislineata*) populations, we investigated population structure, genetic diversity, and isolation-by-distance (IBD) within an urban, suburban, and rural stream habitat. Despite differing levels of urbanization within each habitat, results show fine-scale genetic structure within each stream network, suggesting that urban habitats may still play a role in maintaining some genetic connectivity. Yet there is significantly lower genetic diversity ( $H_o$  and  $p$ ) and greater genetic differentiation between streams within the urban watershed as compared to the suburban and rural sites. Additionally, IBD is governing the spatial patterns of populations to a greater degree in the urban habitat than in the suburban habitat. Whereas, IBD is not a significant factor contributing to population isolation in the rural watershed. These results demonstrate that urbanization affects gene flow in stream salamanders in highly urbanized stream networks. Overall, we need to maintain connectivity within and between branches of stream systems to sustain healthy salamander populations within freshwater aquatic ecosystems.

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

Brian Gall<sup>1</sup>, Yiyuan Li<sup>2</sup>, Michael Pfrender<sup>2</sup> and Edmund Brodie<sup>3</sup>

<sup>1</sup>Hanover College, Hanover, IN, USA. <sup>2</sup>University of Notre Dame, Notre Dame, IN, USA.

<sup>3</sup>Utah State University, Logan, UT, USA

## **Diffuse Coevolution? Tetrodotoxin and Insecticide Resistance in Egg Predators of the Rough-Skinned Newt (*Taricha granulosa*)**

Coevolution is typically viewed as shaping traits between pairs of closely interacting species. Yet, a single species may interact with dozens of others at each of several life-history stages, all of which could impose differing levels of selective pressure on a trait. Newts possess large quantities of Tetrodotoxin (TTX) in their skin and females deposit this toxin in their eggs. Caddisfly larvae (Order: Trichoptera) have been found to eat these toxic eggs. Here we present behavioral and genetic evidence that caddisflies sympatric with newts are resistant to TTX, as well as pyrethroid insecticides. We discuss the potential for these additional species to impose selective pressure on newts and the general implications for the coevolutionary interaction revolving around tetrodotoxin.

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

Gennese Garcia<sup>1</sup>, John Nolan<sup>2</sup>, Hayley Crowell<sup>2</sup> and Emily Taylor<sup>2</sup>

<sup>1</sup>Cal Poly San Luis Obispo, San Luis Obispo, California, USA. <sup>2</sup>Cal Poly San Luis Obispo, San Luis Obispo, California, USA

## **It's a Snake-Eat-Snake World: Quantifying Pacific Rattlesnake (*Crotalus oreganus*) Responses to Kingsnake (*Lampropeltis californiae*) Stimuli**

It is well known that kingsnakes (*Lampropeltis spp.*) often engage in ophiophagy and their presence can elicit extreme responses from possible prey species (primarily pit vipers). Rattlesnakes have been shown to utilize chemosensory cues to detect kingsnakes, but it is not known whether they can also do so using visual cues. Furthermore, small rattlesnakes respond more readily to kingsnake chemosensory cues than large rattlesnakes, perhaps because they are more easily predated. We observed the responses of rattlesnakes to various kingsnake stimuli and related them to the individual rattlesnakes' size to quantify the effect of kingsnake presence on rattlesnakes at various stages of their ontogeny. Pacific rattlesnakes (*Crotalus oreganus*) were presented with live kingsnakes, visual kingsnake models, or swabs of kingsnake scent, and behavioral responses were recorded in both field and laboratory settings, including body bridging, body jerks, body flips, expansion, head hiding, and fleeing. We will present preliminary data on how stimulus type (live kingsnake, kingsnake model, or kingsnake swab), setting (field or lab), and rattlesnake body size affect the snakes' behavioral responses. Smaller rattlesnakes are expected to display more frequent and pronounced behavioral responses to the kingsnake stimuli. Chemosensory stimuli are expected to have a greater impact on rattlesnake responses than visual stimuli. Determining when rattlesnakes are most vulnerable to kingsnake

predation can give researchers greater insight into predator-prey interactions and aid in determining which cues prey species use to assess threats in their surrounding environments.

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**440 ASIH STORER ICHTHYOLOGY, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018**

Jennifer Gardner and Luke Tornabene

*University of Washington, Seattle, WA, USA*

**Iodine-based contrast-enhancing staining methods for visualization of soft tissues of snailfishes (Family: Liparidae) through CT-Scanning**

The oVert Thematic Collections Network is an NSF funded endeavor to produce publicly available 3D scans across the vertebrate tree of life via X-ray computed tomography (CT). To date, CT scans of fishes typically capture dense structures such as bone, but diffusible iodine-based contrast enhanced CT (diceCT) can produce 3D scans of soft tissues. The majority of scans produced by oVert will be skeletons, but production of diceCT scans of select taxa are also an important component of this initiative. This method has been especially useful for projects focused on soft tissues, like looking at brain evolution across vertebrate lineages. While published works referencing diceCT from many different vertebrate taxa, including fishes, currently exist, published protocols or guidelines for iodine staining of fishes are lacking. The work presented here tests protocols for staining fishes, specifically snailfishes of the family Liparidae. Snailfishes from multiple genera (*Liparis* and *Careproctus*) were stained using different stain concentrations, formulations (aqueous versus in ethanol), and timings to determine the optimal protocol for a range of sizes of liparids. The methods developed here focus on the tradeoffs between optimizing visualization of tissues, minimizing degradation of specimens (including desiccation and long-term stain retention), and minimizing overall cost (including time required and chemicals used). From making specimen selection easier by detailing specimen condition before and after staining, to removing some of the guesswork around time of stain diffusion based on specimen size, this work aims to make future diceCT scanning of other fishes simpler, more efficient, and more repeatable.

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

Shana Geffeney<sup>1</sup>, Gabriela Toledo<sup>2</sup> and Charles Hanifin<sup>1</sup>

<sup>1</sup>*Utah State University Uintah Basin, Vernal, UT, USA.* <sup>2</sup>*University of Virginia, Charlottesville, VA, USA*

**Understanding evolution through natural experiments: Tetrodotoxin resistance in snakes**

A diverse array of species has evolved resistance to toxins that target proteins critical for nervous system function such as ion channels. Understanding the mode and tempo by which ion channels evolve resistance to toxins can inform our understanding of how proteins respond

to selection from multiple sources. Tetrodotoxin (TTX) is a well-studied example of a toxin that cripples nerve and muscle cell function by binding to and blocking the outer pore of voltage-gated sodium ion channels (VGSCs). Early work demonstrated that extreme TTX-resistance evolved in garter snakes by a few key changes in the TTX-binding site of VGSCs. These key changes are found in other species that have independently evolved resistance to TTX, including newts and octopuses. This convergence suggests common structural and functional constraints shape evolutionary change of VGSCs. Recent data gathered from a constructed native snake channel demonstrate that a single shared change in the outer pore causes the greatest increase TTX resistance and dramatically disrupts some aspects of channel function, voltage-dependence of activation and slow inactivation. This change, however, has minimal effects on other channel functions. Other shared changes are compensatory and recover functional disruptions without altering TTX resistance. These results suggest adaptive evolution of proteins is constrained by functional costs but that extreme phenotypes can evolve through combinations of progressive substitutions that increase resistance and compensatory substitutions that mitigate costs.

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### **531 Herpetology Biogeography I, Highland B, Saturday 14 July 2018**

Marcelo Gehara and Frank Burbrink

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

### **Comparative Historical Demography of Amphibians and Reptiles from Northeastern Brazil**

The northeast of Brazil is mostly covered by Seasonally Dry Tropical Forests, known as Caatinga, a xeric vegetation characterized by strong seasonality and unpredictable droughts. Palynological evidence suggests that the Caatinga experienced an increase in aridity during the Pleistocene. If this increase was important for the diversification of associated xeric-adapted species, simultaneous population expansions should be evident at the community level. Here we analyzed the demographic history of 7 reptiles and 4 amphibians associated with the Caatinga in a hierarchical approximate Bayesian computation (hABC) framework to test for simultaneous demographic expansion. We found a strong signal of synchronous population expansion in the Late Pleistocene, supporting the hypothesis of an increase in total area of the Caatinga during this time. This expansion likely enhanced the formation of communities adapted to high aridity and seasonality and caused regional extirpation of taxa adapted to mesic forest.

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### **40 Lightning Talks I, Grand Lilac Ballroom North, Thursday 12 July 2018**

Marina Gerson

*Stanislaus State University, Turlock, CA, USA*

**Homage to GE Hutchinson or Are there still so many kinds of animals? Long term studies needed.**

Long term studies are key to assessing changes in community structure. Data are lacking for most localities despite an urgent need for information in the light of rapid habitat degradation and loss related to human activity. The VertNet Database reports one amphibian record comprising a species of toad and 67 records of reptiles comprising 13 species from the Turtle Mountains desert region near Needles, San Bernardino County, California, USA. These records span a timeframe between 1910 and 1994. My preliminary survey data from June 2015, 2016, and 2017 documented continued presence of six of these species and one additional species, with two of these observed only in one survey year. Outside of designated survey times, I documented three additional species at the locality. These data support the notion that dedicated survey efforts are required to capture complete community data; annual June visits are planned into the foreseeable future. Only long term data sets can reveal ongoing changes to community structure. Despite the lack of short-term publication prospects, new assistant professors should consider targeting a locality for annual surveys in order to develop a longitudinal data set while traversing the path to tenure and promotion.

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

Michael Ghedotti<sup>1</sup>, Hannah DeKay<sup>1</sup>, Josephine Gruber<sup>1</sup>, W. Leo Smith<sup>2</sup> and Matthew Davis<sup>3</sup>

<sup>1</sup>Regis University, Denver, CO, USA. <sup>2</sup>University of Kansas, Lawrence, KS, USA. <sup>3</sup>St. Cloud State University, St. Cloud, MN, USA

### **Morphology of the luminous roughy bioluminescent organ (Teleostei: Trachichthyidae)**

Bioluminescence, the generation of light by living organisms, is widespread in fishes but light organs are often poorly known. The luminous roughies (genera *Aulotrachichthys* and *Paratrachichthys*) have a light organ in the region of the anus that houses bacteria in the genus *Photobacterium*. In this study we seek to determine the anatomic structure of the bioluminescent organ in two species *Aulotrachichthys prosthemi* and *Paratrachichthys fernandezianus* and shed light on its likely evolution. We used histological sectioning and gross dissection to explore the anatomy of the bioluminescent organs and we used a DNA sequence dataset to generate a phylogeny for the group. The bacterial bioluminescent organs in the luminous roughies are derived from pouching of the terminal intestine and the bacterial housing components are restricted to the region around the anus. This anatomy in the context of the phylogeny suggests that the bioluminescent organs of the luminous roughies arose via a single evolutionary transition along with a far more anterior position of the anus. Continuing work is needed to have a reasonably complete understanding of bioluminescence evolution in this group.

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### **578 Ichthyology Systematics II, Grand Lilac Ballroom South, Sunday 15 July 2018**

Ava Ghezelayagh<sup>1</sup>, Carole Baldwin<sup>2</sup>, Raymond Simpson<sup>1</sup> and Thomas Near<sup>1</sup>

<sup>1</sup>Yale University, New Haven, CT, USA. <sup>2</sup>National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

## **Revising Perciformes: Molecular Evidence of Non-monophyly in the Mail-cheeked Fishes (Scorpaeniformes) and the Sea Basses and Groupers (Perciformes: Serranidae)**

Positioned within the unresolved “bush at the top” of the teleost tree, Perciformes (the “perch-like” fishes) is a species-rich lineage of percomorph fishes. Discovered and delimited primarily through molecular phylogenetic analyses, there is no identified morphological synapomorphy for the clade. In the present study, we inferred Bayesian and maximum likelihood phylogenies for representatives of 71 perciform families and 238 genera utilizing sequences for 10 nuclear genes (*enc1*, *glyt*, *myh6*, *plag12*, *ptr*, *rag1*, *sh3px3*, *sreb2*, *tbr1* and *zic1*). Our newly-generated phylogenetic trees reaffirm most of the perciform relationships hypothesized in previous molecular studies and provides further support for the non-monophyly of Scorpaeniformes, as traditionally delimited, and the nesting of its taxa within Perciformes. This study also includes the broadest sampling to-date of Serranidae (sea basses and groupers), one of the most species-rich percomorph families that have long been hypothesized as paraphyletic. With representative species from all five hypothetical serranid subfamilies, our phylogenies reconfirm the paraphyly of Serranidae and provide strong support for six lineages containing serranids: 1.) Serraninae as previously delimited, 2.) Anthiinae (to the exclusion of *Acanthistius* and *Trachypoma*), 3.) Epinephelinae (to the exclusion of *Niphon*), 4.) *Niphon* as the sister lineage of Percidae, and 5.) *Hemilutjanus* that resolves outside of Perciformes and as sister lineage of Polyprionidae. Our results provide a foundation to incorporate morphological characters in a phylogenetic-based classification of perciform teleosts.

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

Sarah Gibson

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

## **The Evolutionary Relationships of the Order †Redfieldiiformes (Osteichthyes, Actinopterygii)**

Fishes of the order †Redfieldiiformes (~22 genera, 26 species) are an extinct group of stem ray-finned fishes found globally (e.g., Australia, Madagascar, Morocco, North America, South Africa) in geologic deposits from the Early Mesozoic. The order †Redfieldiiformes are one of a few stem actinopterygian lineages present in the Early Mesozoic, prior to the neopterygian radiation of the Late Triassic and Early Jurassic, and are often found in abundance in certain deposits after the extinction events of the Late Permian and Mid-to-Late Triassic.

Redfieldiiforms possessed a fusiform body shape, thick enameled (ganoid) scales covering the entire body, fixed maxillae and premaxillae, more upright jaw suspensoria, prominent and often tuberculated snouts, and reduction in the dorsal lobe of the caudal fin (hemiheterocercal). Some redfieldiiform fishes also possess unusual or novel patterns of pores along the sensory line canals of the skull. The evolutionary relationships within the †Redfieldiiformes were last examined over thirty years ago and have never been assessed via a quantitative phylogenetic analysis. Redfieldiiform fishes are reexamined in this study, with updates to the anatomical and morphological descriptions of certain taxa. Parsimony and maximum-likelihood analyses support a monophyletic †Redfieldiiformes with two families, †Brookvaliidae and

†Redfieldiidae. The order †Redfieldiiformes is closely related to the †Scanilepiformes, †Perleidiformes, and †Mesopoma. A new classification of the †Redfieldiiformes is presented.

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## **384 Reptile Ecology II, Highland A, Sunday 15 July 2018**

Sean Giery<sup>1</sup> and James Stroud<sup>2</sup>

<sup>1</sup>University of Connecticut, Storrs, CT, USA. <sup>2</sup>Washington University in St. Louis, St. Louis, MO, USA

### **Trophic Ecology of the Brown Anole (*Anolis sagrei*): Niche Compression in Species-Rich Communities**

Detailed assessment of the trophic ecology of *Anolis* lizards has fundamentally shaped our current understanding of how communities form, function, and evolve (e.g., partitioning, expansion, and complementarity). Despite these early advances and continued efforts to understand the trophic niche of anole lizards, a systematic review has yet to be performed. Similarly, thorough examination of intraspecific niche variation in any widespread anole species is lacking. Here, I assemble published and unpublished data on the dietary and structural niche of brown anole (*Anolis sagrei*) populations. These data, collected from populations spanning their huge geographic range (e.g., Florida, The Bahamas, Greater Antilles, Swan Islands, Bermuda, Taiwan, and Hawaii), reveal substantial interpopulation variation in trophic ecology. Intriguingly, our analysis reveals a clear pattern of increased Trophic Niche Width (TNW) where brown anoles coexist with congeners (e.g., *A. grahami*, *A. equestris*, *A. distichus*) and/or other members the diurnal insectivorous lizard guild (e.g., *Leiocephalus carinatus*). This positive relationship between TNW and guild richness is largely incongruent with expectations based on contemporary niche theory that suggests population resource use is more narrowly 'subsetting' as interspecific competition increases. However, our data are consistent with a little-used model of resource use that may deserve more attention - niche compression. In this talk I will share these results and discuss how niche compression might alter our understanding of the role of interspecific interaction in ecology and evolution.

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

Emilia A.R. Gildemeister and Aaron M. Sullivan

Houghton College, Houghton, NY, USA

### **Do Allegheny Mountain Dusky Salamanders (*Desmognathus ochrophaeus*) Learn to Associate Non-Predatory Smooth Greensnakes (*Opheodrys vernalis*) with Threat?**

Learning benefits organisms through increases in foraging success, reproductive output, and predator detection. The capacity to recognize and assess predators via chemical stimuli may be especially beneficial for amphibians, whose populations are declining globally due to a variety of environmental changes. With this study, we attempted to train Allegheny Mountain Dusky Salamanders (*Desmognathus ochrophaeus*) to associate non-predatory Smooth Greensnakes (*Opheodrys vernalis*) with stimuli from predation events by pairing conspecific damage-released cues with snake kairomones. Salamanders were collected from wooded areas of the campus of Houghton College and randomly assigned to one of six treatment groups: three controls (distilled water, damage-released cues, and aqueous rinses of *O. vernalis*) were used to establish baseline levels of locomotor and foraging activity, whereas three experimental groups varied the amount of time that salamanders were exposed to the paired chemical stimuli (48 h, 96 h, and 144 h) in an attempt to assess the effect of exposure duration on the learned response. The foraging of trained salamanders exposed to kairomones from *O. vernalis* was observed in the laboratory at night. Our results show no significant locomotor or foraging differences between the control and experimental treatments, suggesting a lack of learning by *D. ochrophaeus*. This may indicate the inability for associative learning by *D. ochrophaeus*, which is inconsistent with other studies of amphibian learning, or limitations on the types of associations that can be formed. Alternatively, the lack of pronounced behavioral responses to the damage-released stimuli could partially account for the results of this study.

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**287 ASIH STOYE GENERAL ICHTHYOLOGY I, Grand Lilac Ballroom South,  
Thursday 12 July 2018**

Matthew Girard

*University of Kansas, Lawrence, KS, USA*

### **Untangling threadfins: Relationships of Polynemidae using a total evidence approach**

Polynemids are best known for their numerous, elongated, thread-like lower pectoral-fin rays. Also known as the threadfin fishes, the Polynemidae consists of eight genera and 42 species that can be found in a diversity of habitats throughout the world's tropics. Despite substantive taxonomic work across the family or in particular geographic regions, our current knowledge of polynemid evolution is limited. Preliminary investigations and prior work on threadfin systematics have shown phylogenetic discrepancies in the family's sistergroup, with little work being done on the clade's intrarelationships. Fortunately, previous studies have depicted a wealth of external anatomical characters in the fins and scales, with a trend toward reduced eye size. In light of these features and their potential utility as a source of phylogenetically informative characters, an expanded survey of the variation in polynemid skeletal systems will be conducted. These data will be combined and analyzed with DNA sequence data to work toward a well-supported phylogeny of the Polynemidae.

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

Jessica Glass<sup>1,2</sup>, Richard Harrington<sup>1</sup>, Brant Faircloth<sup>3</sup> and Thomas Near<sup>1</sup>

<sup>1</sup>Yale University, New Haven, CT, USA. <sup>2</sup>South African Institute for Aquatic Biodiversity, Grahamstown, South Africa. <sup>3</sup>Louisiana State University, Baton Rouge, LA, USA

**Phylogenomics of carangiform evolution using ultraconserved elements**

Carangiformes is a clade of approximately 170 marine species that exhibit substantial morphological and ecological diversity, including species such as the jacks, scads, pompanos, billfishes, and remoras. Many carangiforms are large predators; ecologically significant for coral reef and coastal ecosystems; and economically important in recreational, commercial, and artisanal fisheries throughout the world. A number of molecular phylogenetic studies have brought into doubt the monophyly of several genera, as well as the relationships among major carangiform subclades, including monophyly of the most species-rich subclade, Carangidae. Previous molecular studies have either lacked sufficient taxonomic coverage or sampled too few loci to adequately resolve carangiform phylogeny. We sought to resolve taxonomic relationships within Carangiformes through genomic sequencing of ~1200 ultraconserved DNA elements (UCEs). Using this molecular dataset, which sampled 80% of the recognized carangiform species, we performed fossil-calibrated divergence dating in order to assess timing of carangiform diversification. The data strongly support the paraphyly of multiple traditional taxonomic groups, including Carangidae, *Alepes*, *Carangoides*, *Caranx*, and *Seriola*. A re-evaluation of morphological trait variation is needed to assess congruence with phylogenies inferred from molecular data. Our results provide new insight on the phylogenetic relationships of Carangiformes and the timing of carangiform evolution in the context of significant historical events such as the Cretaceous-Paleogene extinction. By mitigating taxonomic uncertainty in an important percomorph clade, we aim to more accurately characterize teleost biodiversity, a pressing issue in the face of increasing anthropogenic disturbances on marine ecosystems.

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**232 ASIH STORER ICHTHYOLOGY, Empire Hall South - JF Rochester Riverside  
Convention Center, Friday 13 July 2018**

Jessica Glass<sup>1,2</sup>, Scott Santos<sup>3</sup>, John Kauwe<sup>4</sup> and Thomas Near<sup>1</sup>

<sup>1</sup>Yale University, New Haven, CT, USA. <sup>2</sup>South African Institute for Aquatic Biodiversity, Grahamstown, South Africa. <sup>3</sup>Auburn University, Auburn, AL, USA. <sup>4</sup>Brigham Young University, Provo, UT, USA

**Long live the kingfish: phylogeography of an iconic sportfish, the Giant Trevally  
(*Caranx ignobilis*)**

The Giant Trevally (*Caranx ignobilis*), also called the Giant Kingfish, inhabits the Indo-West-Pacific and is a top predator associated with rocky and coral reefs. *Caranx ignobilis* is coveted by recreational fishermen and heavily targeted by small-scale and commercial fisheries throughout its range. We investigate the genetic structure of *C. ignobilis* across the full extent of its range using double digest restriction enzyme-associated DNA sequencing (ddRADseq). We sampled 140 individuals from multiple Indo-Pacific localities spanning Australia, Japan, South Africa and the Red Sea. Results indicate genetic admixture in the western Indian Ocean and genetically distinct populations in the western Pacific. The observed genetic homogeneity across the western Indian Ocean is interesting in light of recent acoustic tagging studies that indicate a high level of territoriality, which would presumably result in geographic structuring of genetic variation. Future research will incorporate samples from additional localities throughout the Indo-Pacific, with the objectives of identifying potential phylogeographic breaks, population bottleneck or expansion events, modeling the direction and magnitude of gene flow, and determining the functional roles of loci under selection. Understanding the population structure of *C. ignobilis* is essential for the sustainable management of this understudied species in the Indian and Pacific Oceans.

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### **374 Herpetology Systematics, Highland B, Saturday 14 July 2018**

Richard Glor

*University of Kansas, Lawrence, KS, USA*

#### **Speciation in the Hispaniolan Bark Anole (*Anolis distichus*)**

The Hispaniolan Bark Anole (*Anolis distichus*) is a widespread and highly polymorphic lizard with more than a dozen subspecies. My laboratory's prior research suggests that this species includes populations at various stages of the speciation process. These populations often exhibit some degree of ecological, phenotypic and genetic differentiation, but hybridize where they come into contact. Along hybrid zones, we have found evidence for reduced gene flow and intrinsic reproductive isolation. We have recently sequenced and assembled whole genome sequence data for this species, and are currently using this genome to identify the genomic basis for species differences and speciation. Our research suggests that geographic isolation and ecological specialization both contribute significantly to anole speciation, and that species divergence is restricted only to portions of the genome.

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### **279 Lightning Talks II, Highland A, Saturday 14 July 2018**

Brad M. Glorioso<sup>1</sup> and J. Hardin Waddle<sup>2</sup>

<sup>1</sup>*U.S. Geological Survey, Wetland and Aquatic Research Center, Lafayette, LA, USA.* <sup>2</sup>*U.S. Geological Survey, Wetland and Aquatic Research Center, Gainesville, FL, USA*

## **A Decade of Turtle Capture-Mark-Recapture in a Small Urban Pond Complex**

Turtles are among the longest-lived vertebrates, and as such, it is important that studies examining survival be conducted for as long as possible. We have conducted an ongoing 10-year capture-mark-recapture study of the aquatic turtle assemblage in an urban landscape in Lafayette, Louisiana, USA. The manmade pond complex, built in the 1990s, lies within meters of a busy four-lane divided road on the University of Louisiana at Lafayette's Research Park. From 2009–2018, we captured aquatic turtles using two methods (deep-water crawfish nets and standard three-ring hoop nets) using a robust design, where we had five consecutive sampling days (secondary periods) each year in May (primary periods). We have captured over 100 individual Red-eared Sliders, 20 Eastern Musk Turtles, and just a few individuals of several other species. We captured more female Red-eared Sliders than males, but this was not significantly different from equality. We have recaptured nearly 50% of individual Red-eared Sliders in subsequent years after initial capture. Deep-water crawfish nets were much more effective, compared to hoop nets, at capturing turtles in our study. Continued investigation into this urban turtle population will enable us to refine our estimates of survival and compare them to populations studied in more natural habitats.

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

Christopher Goatley and Stephen Wroe

*University of New England, Armidale, NSW, Australia*

## **Micro-CT Scanning Techniques to Study the Ecology of Small Vertebrates**

In recent years, micro-computed tomography (micro-CT) scanning has become more accessible for use in biological studies. It now offers relatively quick, cost-effective and non-destructive opportunities to visualise internal morphological structures of specimens. Where micro-CT data is beginning to prove exceptionally useful for studying the anatomy and taxonomy of specimens, it has, until recently, been largely overlooked by ecomorphological studies. With this poster I aim to show how this innovative technique can be applied to better understand the functional ecology of small vertebrates in a broad, comparative framework. I will present a brief description of how micro-CT scanning works, and some considerations that must be taken into account during basic scanning. I will then introduce the advantages of diffusible iodine contrast enhanced CT (DiceCT) techniques, to visualise soft tissue structures. Finally, using small fishes as a model system, I will showcase how micro-CT scanning can be used to directly identify the functional roles of fishes through dietary analyses, and indirectly assess functional capabilities through the application of morphological techniques including biomechanical modelling. This poster will provide a detailed background on the potential application of increasingly available micro-CT data, with the goal of increasing the uptake of this technique among researchers in different fields of vertebrate ecology.

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

Christopher Goatley<sup>1</sup>, Simon Brandl<sup>2</sup>, David Bellwood<sup>3</sup> and Luke Tornabene<sup>4</sup>

<sup>1</sup>University of New England, Armidale, NSW, Australia. <sup>2</sup>Simon Fraser University, Vancouver, BC, Canada. <sup>3</sup>James Cook University, Townsville, QLD, Australia. <sup>4</sup>University of Washington, Seattle, WA, USA

### **Cryptic Biodiversity: Community Composition of Cryptobenthic Reef Fish Faunas**

Cryptobenthic reef fishes have typically been defined as fishes under 50mm long that have cryptic colouration or behaviour, and are associated with the benthos. Wherever they have been studied, these fishes numerically dominate coral reef fish communities in terms of both their abundance and diversity. Yet, despite this prevalence, these fishes are both poorly defined and, due to the difficulty of sampling them, the number of places that cryptobenthic reef fishes have actually been censused remains remarkably small. In this presentation, I will focus on the potential treasure-trove of biodiversity represented by cryptobenthic reef fishes. I will begin by highlighting the trends in rates of descriptions of fishes which gives us a broad introduction to how many species may be left to describe. I will then move on to discuss the findings of a recent field trip to one of the best studied reef systems in the world, and one of the few places that cryptobenthic reef fishes have been studied: Lizard Island on the Great Barrier Reef.

Remarkably, and somewhat worryingly, in just 10 days sampling we found that many of the current identifications of common taxa are incorrect. Even more compelling, was that on this short field trip we found numerous taxa never reported from this location, and even entirely new species. This presentation will provide a broad overview of a poorly known reservoir of biodiversity and introduce techniques which can be employed to explore new communities in new locations around the world.

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

Cody Godwin<sup>1</sup>, Chris Murray<sup>1</sup>, J. Sean Doody<sup>2</sup>, Simon Clulow<sup>3</sup> and Dave Rhind<sup>4</sup>

<sup>1</sup>Tennessee Technological University, Cookeville, Tennessee, USA. <sup>2</sup>University of South Florida Saint Petersburg, Saint Petersburg, Florida, USA. <sup>3</sup>University of Newcastle, Newcastle, New South Wales, Australia. <sup>4</sup>Monash University, Clayton, Victoria, Australia

### **Observation on Australia's Largest Lizard, The Perentie (*Varanus giganteus*)**

Australia is home to the world's third largest lizard, the perentie (*Varanus giganteus*). While the species is an icon of the outback and an important apex predator, very little is known about their life history in the interior. Here, I present observations on an interior population including

movement patterns and habitat preference after a six-week preliminary field season. The study was performed in the Northern Territory of Australia in mid summer. Baited camera traps and baited live traps were deployed to identify preferred sites and areas to focus search efforts. Perentie were detected via driving and hiking surveys and captured with noose poles. Perentie of appropriate size were radio tagged and tracked daily. Cameras were placed at active burrows to assess haul in and haul out times. A total of 13 perentie were detected with five captures, two observations and six individuals discovered on camera traps. All size groups were discovered during the survey from hatchlings to large adults. Of the five perentie captured, three were large enough to be outfitted with a radio telemetry tags. Perentie do not create their own burrows and use rock crevices and rabbit warrens for refuge. Movement appears to be crepuscular with burrows used to escape the heat of the day. Perentie exhibits site recidivism and will use specific rock crevices repeatedly. Future work will include boosting the sample size, tracking during different seasons and comparing sex specific movement patterns.

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## 554 Herpetology Genetics I, Highland D, Sunday 15 July 2018

Caren Goldberg

*Washington State University, Pullman, WA, USA*

### **Ten Years of Environmental DNA Detection of Amphibians and Reptiles: Toward a Synthetic Framework**

A decade ago, the first paper documenting detection of amphibians through analysis of DNA shed into water was published. After a brief lull of skepticism and hope, the field of environmental DNA (eDNA) detection of vertebrates began to grow exponentially, with over 200 papers published by the end of 2017. I used empirical results of eDNA detection studies conducted by my research group for 28 amphibians and 4 reptiles in lotic and lentic systems across western North America, in Florida, and internationally to create a synthetic framework for understanding eDNA detection of amphibians and reptiles. Informative examples include studies of Arizona treefrogs (*Hyla wrightorum*), California tiger salamanders (*Ambystoma californiense*), Columbia spotted frogs (*R. luteiventris*), flatwoods salamanders (*A. bishopi*), narrowheaded gartersnakes (*Thamnophis rufipunctatus*), northwestern pond turtles (*Actinemys marmorata*), western toads (*Anaxyrus boreas*), and yellow-legged frogs (*Rana sierrae* and *R. boylei*). Main findings include: 1) contrary to early expectations, eDNA of vertebrates is not uniformly distributed even in small wetlands (<0.1 ha) and declines quickly with distance from source in streams; 2) eDNA detection probability increases with temperature as ectothermic animals become more active and decreases as temperatures reach degradative conditions (~25°C); 3) eDNA signal can disappear quickly when animals leave lotic systems to bask; 4) some species are more difficult to detect than others, even within taxonomic groups; and 5) eDNA production among and within individuals is highly variable. This framework can be used to inform design of eDNA detection studies for amphibians and aquatic reptiles across systems.

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

Alexandra Gonzalez and Jennifer Dever

*University of San Francisco, San Francisco, California, USA*

**Seeing Red: Analyzing IUCN Red List Data of Amphibians in Southeast Asia**

In the midst of the current sixth mass extinction event which is now underway, it appears that amphibians are one of the most impacted vertebrates. Over 7,500 amphibian species are listed on the IUCN Red List of Threatened Species (an assessment tool which provides species' conservation status, perceived threats, and distribution range). While it is well-known that populations under multiple stressors are more likely to undergo significant declines, there are limited resources available for visualizing how these threats may work synergistically and interact within a species' range. This is especially the case for Southeast Asian amphibians, which much less attention has been paid as compared to other parts of the globe. Additionally, the IUCN Red List provides a description of threats affecting species and categorizes species into Red List Categories. However, this data is not easily accessible for wide-scale analyses. The aims of this project were as follows: (1) utilize bioinformatics to increase accessibility to IUCN Red List data and (2) analyze the IUCN data repository to identify trends in amphibians of Southeast Asia.

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**631 Lightning Talks III, Highland B, Sunday 15 July 2018**

Alexandra Gonzalez and Jennifer Dever

*University of San Francisco, San Francisco, California, USA*

**Visualizing Threats of Amphibians in Southeast Asia**

In the midst of the current sixth mass extinction event which is currently underway, it appears that amphibians are one of the most impacted vertebrates. Over 7,500 amphibian species are listed on the IUCN Red List (an assessment tool which provides species' conservation status, perceived threats, and distribution range). The primary threats amphibians face include habitat loss, disease, invasive species, pollution, climate change, overexploitation, natural disasters and human disturbance. While it is well-known that populations under multiple stressors are more likely to undergo significant declines, there are limited resources available for visualizing how these threats may work synergistically and interact within a species' range. This is especially the case for Southeast Asian amphibians, which much less attention has been paid as compared to other parts of the globe. Using code previously developed to increase the accessibility of IUCN threat data, various threats affecting amphibians of Southeast Asia are plotted by species range.

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

Sebastian Gonzales, Hayley Crowell and Emily Taylor

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

**A Comparative Study of Home Range and Movement Patterns Between Coastal and Inland Pacific Rattlesnakes**

Few studies have compared home range size among different populations of snake within a given species. In this study, we compared the home ranges and movement patterns of coastal and inland populations of adult, male Pacific rattlesnakes (*Crotalus oreganus*). Using radio telemetry, we tracked 28 male snakes (n/coastal=15, n/inland=13) from April to October of 2017 in four study sites throughout central California. Our four field sites included one inland and one coastal northern site in San Luis Obispo County as well as an inland and coastal site in Santa Barbara County to examine possible differences in movement patterns between each location based on climate. Individuals were tracked 4-5 times per week at random times throughout the day, and location was recorded via handheld GPS. We will present data on the home range sizes as well as timing and length of movement bouts. Increased movements typically occur during the mating season, while male snakes are searching for mates. Apart from the mating season, the snakes stay in small home ranges, with short infrequent movements. This is particularly true during the cool winter months while many *C. oreganus* over-winter underground. We will present data about the relationship between spatial ecology and climate in these four populations.

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**572 ASIH STORER ICHTHYOLOGY, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018**

Alex Gourlay, Kurvin Li, Daniela Brouwer and Robert Drew

*University of Massachusetts Dartmouth, North Dartmouth, MA, USA*

**Skin Mucous Proteome of the Clark's anemonefish (*Amphiprion clarkii*) while Interacting with Different Sea Anemone Species**

When an anemonefish (clownfish) encounters a host sea anemone, they often engage in a behavior called "acclimation," in which they gradually increase physical contact with a potential host. The purpose of this acclimation behavior is unclear, given that naïve anemonefish are usually protected from host anemone species, even if the fish have never before encountered sea anemones. We hypothesized that anemonefish use acclimation to regulate the mucous proteome to suit diverse host species that differ widely in toxicity and adhesiveness. To test this hypothesis, we used LC-MS/MS to compare the mucous proteomes of naïve Clark's anemonefish (*Amphiprion clarkii*) to fish associating with one of two natural hosts: the bubbletip sea anemone (*Entacmaea quadricolor*, Family Actiniidae) or the more venomous

carpet anemone (*Stichodactyla* sp., Family Stichodactylidae). There were no significant differences in peptide content or quantity between naïve and associating anemonefish, or between fish associating with different species. There were also no differences in the post-translational modifications detected by this technique which included oxidation, acetylation, and deamidation of glutamine. Preliminary comparisons with the mucous proteomes of non-symbiotic fish species also did not reveal any obvious differences associated with symbiosis with sea anemones. We therefore conclude that this symbiosis does not depend upon changes in the quantities of peptides in the mucus, but instead likely involves some other aspects of the anemonefish's mucus.

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### **396 Reptile Ecology II, Highland A, Sunday 15 July 2018**

Sean Graham and Crystal Graham

*Sul Ross State University, Alpine, Texas, USA*

#### **Amphibians and Reptiles as Prey of the Loggerhead Shrike in West Texas**

While the ecological impacts of apex predators are well known, the trophic effect of secondary consumers (“mesopredators”) is less well known and more difficult to quantify. Loggerhead shrikes are small predatory birds that are common secondary consumers in open habitats throughout the United States. Loggerhead shrikes are generalist predators on arthropods and small vertebrates and important selective agents on these animals. However, the net impact of their predation on small animals has not been quantified. We surveyed an active shrike larder (a barbed wire fence) in West Texas once per month during 2014-2017 to quantify the seasonal abundance and identity of shrike prey. We also studied prey turnover time weekly during 2017 to estimate the total number of prey captured at this location. 1061 individual prey items were collected during 34 surveys. Shrikes preyed upon 13 taxa of arthropods and 13 species of amphibians and reptiles, and several unidentified species of small mammals and birds. Incidence and diversity of impaled prey was highest during October-December. Orthopterans (mostly grasshoppers) were the most abundant impaled prey, followed by Coleopterans and lizards. Our estimates of predation rates suggest impaled prey turnover time at this larder is rapid, so that our monthly collections are indicative of about one week of predation by the local population of shrikes. In addition, shrikes often consume prey immediately and only impale a small subset of their prey. Therefore, the number of prey killed by shrikes is considerably higher than the total numbers reported here.

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

Sean Graham<sup>1</sup>, Richard Kline<sup>2</sup>, David Steen<sup>3</sup> and Crystal Kelehear<sup>4</sup>

<sup>1</sup>*Sul Ross State University, Alpine, Texas, USA.* <sup>2</sup>*University of Texas Rio Grande Valley, Brownsville, Texas, USA.* <sup>3</sup>*Georgia Sea Turtle Center, Jekyll Island, Georgia, USA.*

<sup>4</sup>*Smithsonian Tropical Research Institute, Ancon, Panama*

**Description of an extant Salamander from the Gulf Coastal Plain of North America: the Reticulated Siren, *Siren reticulata*.**

The Sirenidae family contains a number of eel-like salamanders currently restricted to North America. Despite their apparent abundance throughout the southern United States and their status as some of the world's largest amphibians, the biology, ecology, and phylogeography of this group is poorly-known. In this study we use morphological and genetic evidence to describe a long-suspected species from southern Alabama and the Florida panhandle; a species we name the Reticulated Siren, *Siren reticulata*. Future studies will enable more precise phylogenetic information about *S. reticulata* and will almost surely reveal additional undescribed species within the family.

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

Alejandro Grajal-Puche, Christopher Murray, Donald Walker and Tania Datta

*Tennessee Tech University, Cookeville, TN, USA*

**The Structure and Function of Microbial Communities within Alligator Nesting Ecosystems: A Comparative Approach Across Ecological Scales**

Recent publications have highlighted the ecological significance of both the endo- and exogenous microbiome. Thus, the characterization of microbial assemblages, across focal scales, and elucidation of environmental drivers behind microbial communities can further scientific understanding of pattern-driven ecological phenomena. Many questions remain regarding the formation and functional role of a host's microbiome, especially within understudied taxonomic classes, such as Reptilia. Crocodylians are keystone reptiles, which are crucial to the resiliency of the ecosystems they inhabit. Utilizing high-throughput DNA sequencing, I have categorized the microbiome of wild American alligator (*Alligator mississippiensis*) nests, the alligator eggshell surface, and surrounding nest habitat. In addition, I have identified which environmental variables influence the associated alligator-nest microbial assemblage and predicted the functional role of core microbial members. These results reflect a single sampling season and location. We will be expanding our sampling effort to an additional five sample sites to determine spatiotemporal microbial variations. With these findings, I address ecological scaled-based questions, add to the scientific understanding of ecosystem dynamics, and establish baseline modeling predictions of microbial community shifts due to altered environmental variables.

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## **466 Herpetology Conservation II, Highland C, Sunday 15 July 2018**

Brian Gratwicke<sup>1</sup>, Anna E Savage<sup>1,2</sup>, Matthew H Becker<sup>1,3</sup>, Blake Klocke<sup>1,4</sup> and Robert C Fleischer<sup>1</sup>

<sup>1</sup>Smithsonian Conservation Biology Institute, Washington, DC, USA. <sup>2</sup>University of Central Florida, Orlando, FL, USA. <sup>3</sup>Liberty University, Lynchburg, VA, USA. <sup>4</sup>George Mason University, Fairfax, VA, USA

### **Panama Amphibian Rescue and Conservation Project**

The Panama Amphibian Rescue and Conservation Project cares for a living collection of 12 amphibian species at risk of extinction from the amphibian chytrid fungus in Panama. The collection is cared for by 11 fulltime staff in a 450 square meter facility at the Smithsonian Tropical Research Institute. The purpose of this and similar Amphibian Ark projects around the world is to buy us time to figure out how to mitigate the disease threat. Our initial research focused on understanding the microbiome of amphibian skin and how the microbiome of highly susceptible species might be modified to confer protection from disease. We even tried genetically modified core skin microbes to produce known antifungal metabolites. In addition to a probiotic approach to disease mitigation, we sought to understand the genetic mechanisms underlying differential disease outcomes in partially susceptible species. We have not yet identified any specific mitigation approaches likely to improve the host's ability to survive a Bd infection, but the captive breeding program is now producing surplus animals allowing us the start release trials. These trials will help us to observe disease dynamics in the released frogs and the native amphibian community, and understand how climatic variables might influence persistence. One potential release strategy could be to identify potential climatic refugia where animals will have a higher probability of persistence. An adaptive management approach to these experimental release trails will also help us to improve release-trial efficacy with non-disease-related questions.

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

David Green

*McGill University, Montreal, QC, Canada*

### **Cold Comfort: Amphibians in winter.**

Northern amphibians are dormant for most of the year while weather conditions are too cold for surface activity. To survive a long period of winter dormancy, the animals must physiologically "stop the clock" and reside where it is just cold enough to minimize metabolic rate but not cold enough to kill them. They need to seek refuge sites with sufficient humidity and available oxygen for them to maintain a metabolism low enough to allow them to live for

an extended period of time entirely off stored fat reserves. They should, therefore, alter their active season behaviour as winter approaches to seek out favourable overwintering sites where they are unlikely to be disturbed or die. As spring approaches, though, they have to be able to respond to indications of the return of warmer conditions on the surface. Although the cues triggering the onset of winter dormancy and the animals' behaviour during winter dormancy remain largely a mystery, the conditions associated with the animals' breaking their winter dormancy and re-emerging onto the surface in spring are becoming increasingly better understood. Re-emergence is tied, first, to changes in subsurface conditions and, then, by the re-appearance of springtime atmospheric conditions that allow for the resumption of surface activity.

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## **78 SSAR SEIBERT PHYSIOLOGY & MORPHOLOGY, Highland A, Thursday 12 July 2018**

Aaron Griffing<sup>1</sup>, Sanger Thomas<sup>2</sup>, Daza Juan<sup>3</sup>, Stuart Nielsen<sup>1</sup>, Edward Stanley<sup>4</sup> and Tony Gamble<sup>1,5,6</sup>

<sup>1</sup>Marquette University, Milwaukee, Wisconsin, USA. <sup>2</sup>Loyola University in Chicago, Chicago, Illinois, USA. <sup>3</sup>Sam Houston State University, Huntsville, Texas, USA. <sup>4</sup>Florida Museum of Natural History, Gainesville, Florida, USA. <sup>5</sup>Bell Museum of Natural History, Saint Paul, Minnesota, USA. <sup>6</sup>Milwaukee Public Museum, Milwaukee, Wisconsin, USA

### **Embryonic development of a parthenogenetic gecko (*Lepidodactylus lugubris*) with special reference to adhesive toepads**

One goal of evolutionary developmental biology (evo-devo) is to understand the role of development in the origin of phenotypic novelty and convergent evolution. Squamates are an ideal clade to study this topic as they are species-rich and exhibit a suite of diverse morphologies – many of which have evolved independently multiple times. In particular, geckos are extraordinary models for squamate evo-devo due to their phylogenetic position as the sister clade to most other squamates. Therefore, by including geckos in comparative evo-devo studies, one can encompass nearly all squamate diversity. Here we characterize the embryonic development of a gecko with adhesive toepads, *Lepidodactylus lugubris*, with a non-gecko squamate exhibiting an independent evolution of adhesive toepads, *Anolis sagrei*. *Lepidodactylus lugubris* is an ideal evo-devo model because it is parthenogenetic, easily kept in a laboratory setting, and there is a suite of resources being developed. We harvested 170 embryos of *L. lugubris* throughout embryonic development, characterized developmental events, and compared the timing and pattern of toepad development with that of *A. sagrei*. We find broadly similar patterns of toepad development between the two species, suggesting remarkable convergence in the developmental pathways underlying toepad development. This embryonic staging table will serve as a foundational tool to study convergent evolution of adhesive toepads and other questions concerning squamate evolution and development.

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

Michael Grundler

*University of Michigan, Ann Arbor, MI, USA*

**Patterns of ecological specialization in colubrid snake diets**

I use data on snake feeding observations gathered from dissections of museum specimens and the published literature to address two hypotheses regarding the evolution of ecological specialization in colubrid snake diets along a temperate to tropical gradient. More than 8000 predator-prey observations from 350 colubrid snake species reveal substantial variation in snake diets but do not indicate that rates of ecological specialization are higher in tropical snakes than in temperate snakes or that more specialized feeding ecologies are less evolutionary labile than more generalized feeding ecologies.

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

Anna Gruszkiewicz and Kyle Piller

*Southeastern Louisiana University, Hammond, Louisiana, USA*

**Analysis of Body Size Evolution and Diversification Rates in the Family Poeciliidae (Cyprinodontiformes)**

From the guppy to the whale shark, one of the most interesting characteristics of animal diversity is the wide range of body sizes. Body size can play a vital role in the ecology, life history, physiology, and niche partitioning of a species. Previous studies have found that many freshwater fish species exhibit a phyletic shift toward smaller body size over evolutionary time potentially due to the invasion of small streams and subsequent isolation. This body size trend raises interesting questions about the potential correlation between diversification rates and the rate of body size evolution. This study examines this relationship within Poeciliidae. Poeciliidae is a highly speciose (> 250 species) group of live bearing New World fishes ranging from the southern US to southern regions of South America and the Antilles. Within the family, species richness as well as average standard length (SL) vary widely among genera. For this study, ultra-conserved elements (UCEs) were used to produce a new phylogeny for Poeciliidae including 82 species that represent 24/29 total genera. Diversification rates and body size evolution were inferred using multiple phylogenetic comparative analyses. It was predicted that poeciliid species would exhibit a correlation between body size evolution and diversification rates and a general shift toward smaller body size over evolutionary time. The results from this study will be presented.

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

Wilson Guillory<sup>1</sup>, Jason Brown<sup>1</sup>, Connor French<sup>1</sup>, German Chavez<sup>2</sup>, Rudolf von May<sup>3</sup>, Jennifer Serrano-Rojas<sup>4</sup>, Ignacio De la Riva<sup>5</sup>, Jose Padial<sup>5</sup>, Andrew Whitworth<sup>6</sup>, Migeul Trefaut Rodrigues<sup>7</sup>, Stefan Lötters<sup>8</sup>, Steffen Reichle<sup>9</sup>, Ivan Prates<sup>10</sup> and Evan Twomey<sup>11</sup>

<sup>1</sup>*Southern Illinois University, Carbondale, IL, USA.* <sup>2</sup>*CORBIDI, Lima, Peru.* <sup>3</sup>*University of Michigan, Ann Arbor, Michigan, USA.* <sup>4</sup>*Universidad Nacional San Antonio Abad del Cusco, Cusco, Peru.* <sup>5</sup>*Museo Nacional de Ciencias Naturales, Madrid, Spain.* <sup>6</sup>*University of Glasgow, Glasgow, United Kingdom.* <sup>7</sup>*University of Sao Paulo, Sao Paulo, Brazil.* <sup>8</sup>*Universitat Trier, Trier, Germany.* <sup>9</sup>*Museo de Charupus, Santiago de Chiquitos, Bolivia, Plurinational State of.* <sup>10</sup>*Smithsonian National Museum of Natural History, Washington, DC, USA.* <sup>11</sup>*Vrije Universiteit Brussel, Brussel, Belgium*

**Resolving species relationships in the Amazonian Poison frog genus *Ameerega* using ultraconserved elements**

*Ameerega* is a relatively large (~32 species) genus of poison frog in the family Dendrobatidae, ranging throughout the Amazon but with especially high diversity in the eastern foothills of the Peruvian Andes. Despite high interest in dendrobatids, the taxonomy and systematics of *Ameerega* are still in flux. Several phylogenies of the genus have been produced, but with a highly divergent array of topologies, leading to systematic inconsistencies and uncertainty as to the monophyly of several species. Previous trees have also generally been produced using only a few mitochondrial genes, thus not accounting for potential gene/species tree discordance. To resolve these issues, we produced a comprehensive species tree of *Ameerega* using subgenomic data derived from sequence capture of ultraconserved elements (UCEs).

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

Jennifer Gumm

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

**Evolution and Function of Coloration in Darters (genus *Etheostoma*)**

Darters of the genus *Etheostoma* are a group of colorful freshwater fishes that occur in the Southeastern US. Herein, I highlight several integrative studies aiming to uncover the causes and consequences of elaborate coloration in this group. First, behavioral studies have shown that color is used by females and males for mate choice. Work in this group provides evidence for a link between sexual selection and behavioral isolation, and by extension for a role of sexual selection in speciation. Combining reflectance spectrophotometry with comparative phylogenetic methods shows that coloration has high evolutionary lability, suggesting that color may be influenced by ecological factors that are not phylogenetically conserved. Interpreting visual signals also relies on the corresponding visual system. Using physiological tools to describe the spectral sensitivity of fish visual systems, shows differences in peak

absorbance of visual pigments among species and individuals within a species. Additionally, intraspecific variation may have implications for visually based behaviors such as female and male preferences for color, which may contribute to reproductive isolation between species.

Using molecular genetics to examine visual pigment genes (opsins) provides strong evidence that structural genetic changes (i.e. changes in amino acid sequences) and regulatory genetic changes (i.e. gene expression) both underlie variation in darter visual systems. Examining the signal, the receiver, and the function of coloration provides a comprehensive understanding to the sensory ecology of these fishes and demonstrates how evolutionary processes acting on genes, mediated by physiological systems and behavioral interactions, can lead to an increase in biological diversity.

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

Joe Gunn<sup>1</sup>, Leah Berkman<sup>2</sup> and Lori Eggert<sup>1</sup>

<sup>1</sup>University of Missouri, Columbia, MO, USA. <sup>2</sup>The Missouri Department of Conservation, Columbia, MO, USA

### **Validating the Taxonomic and Distributional Status of the Neosho Smallmouth Bass (*Micropterus dolomieu velox*)**

Smallmouth Bass (*Micropterus dolomieu*) are economically important as a sportfish, accounting for a multi-billion-dollar angling industry in the United States alone. Thus, stocking has become increasingly common. The taxonomic status of *M. dolomieu* is controversial. Two subspecies are currently recognized: the Northern Smallmouth Bass (*M. d. dolomieu*), whose native range extends north and east of the Mississippi River, and the Neosho Smallmouth Bass (*M. d. velox*), which is restricted to the Arkansas River Basin. Although they are allopatric, their distinction is based primarily on a few morphological traits, such as the number of soft dorsal fin rays, predorsal contour, and body size. The taxonomic relationship between these subspecies has not been adequately resolved on a molecular level. Because mixing of genetically unique populations can lead to hybridization or, in extreme cases, loss of species-wide diversity, it is vital to consider genetic distinctions within *M. dolomieu* when restocking fisheries. To investigate the taxonomic and distributional status of *M. d. velox* in Missouri, Arkansas, and Oklahoma, we measured levels of genetic differentiation at 14 microsatellite loci among samples collected from the putative native ranges of both subspecies. With these results as a guide, we identified 95 samples representing relatively high genetic divergence and evaluated genome-wide differentiation between subspecies using double-digest RAD sequencing (ddRAD-seq). Our genomic analysis lays the groundwork for an assessment of population structure at thousands of single nucleotide polymorphisms (SNPs), which will allow us to evaluate the taxonomic and distributional statuses of the *M. dolomieu* subspecies.

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

Jacquelyn Guzy<sup>1</sup>, Kelly Halloran<sup>1</sup>, Jessica Homyack<sup>2</sup> and John D. Willson<sup>1</sup>

<sup>1</sup>University of Arkansas, Fayetteville, AR, USA. <sup>2</sup>Weyerhaeuser Company, Centralia, WA, USA  
**Population biology of Ouachita Dusky Salamanders (*Desmognathus brimleyorum*) in a managed forest landscape.**

Salamander populations can play a key role in the function and diversity of temperate forest ecosystems. However, the population parameters of salamanders residing in forests managed for timber production are generally unknown. We conducted a capture-mark-recapture (CMR) study at three streams within intensely managed pine forests in the Ouachita Mountain region of Arkansas from March 2015-October 2016. Specifically, we used robust design CMR models to explore the effects of seasonal, site, and age-class variation on the capture probability, recapture probability, temporary emigration, abundance, and apparent survival of a stream salamander, *Desmognathus brimleyorum*. We found evidence of significant seasonal variation in temporary emigration rates, which were lowest in late spring and highest in the winter months. Our estimates of mean salamander density (1.31 individuals/m<sup>2</sup>, adjusted to account for temporary emigration and conditional capture probability) and apparent survival (46%) were comparable to those of other *Desmognathus* species. This suggests that streams in forests managed for even-aged timber production can support viable, dense populations of salamanders comparable to those in protected forests. Understanding the dynamics of such populations may help inform future assessment, monitoring, and conservation of stream-associated salamanders.

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

Michael Hague<sup>1</sup>, Chris Feldman<sup>2</sup>, Edmund Brodie, Jr.<sup>3</sup> and Edmund Brodie III<sup>1</sup>

<sup>1</sup>University of Virginia, Charlottesville, VA, USA. <sup>2</sup>University of Nevada, Reno, NV, USA.

<sup>3</sup>Utah State University, Logan, UT, USA

**Convergent adaptation to dangerous prey proceeds through the same first-step mutation in the garter snake *Thamnophis sirtalis***

Convergent phenotypes often result from similar underlying genetics, but recent work suggests convergence may also occur in the historical order of substitutions en route to an adaptive outcome. We characterized convergence in the mutational steps to two independent outcomes of tetrodotoxin (TTX) resistance in separate geographic lineages of the common garter snake (*Thamnophis sirtalis*) that coevolved with toxic newts. Resistance is largely conferred by amino acid changes in the skeletal muscle sodium channel (Nav1.4) that interfere with TTX-binding.

We sampled variation in Nav1.4 throughout western North America and found clear evidence that TTX-resistant changes in both lineages began with the same isoleucine-valine mutation (I1561V) within the outer pore of Nav1.4. Other point mutations in the pore, shown to confer much greater resistance, accumulate later in the evolutionary progression and always occur together with the initial I1561V change. A

gene tree of Nav1.4 suggests the I1561V mutations in each lineage are not identical-by-decent, but rather they arose independently. Convergence in the evolution of channel resistance is likely the result of shared biases in the two lineages of *T. sirtalis* – only a few mutational routes can confer TTX resistance while maintaining the conserved function of voltage-gated sodium channels.

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**340 ASIH STORER HERPETOLOGY, Poster Session I, Empire Hall South - JF Rochester Riverside Convention Center, Friday 13 July 2018 AND Poster Session II, Empire Hall South - JF Rochester Riverside Convention Center; part of ASIH symposium: If Salamanders Could Speak, Saturday 14 July 2018**

Joshua M. Hallas<sup>1</sup>, Chris R. Feldman<sup>1</sup>, Edmund D. Brodie III<sup>2</sup>, Michael E. Pfrender<sup>3</sup>, Edmund D. Brodie Jr<sup>4</sup> and Thomas L. Parchman<sup>1</sup>

<sup>1</sup>University of Nevada, Reno, Nevada, USA. <sup>2</sup>University of Virginia, Charlottesville, Virginia, USA. <sup>3</sup>University of Notre Dame, Notre Dame, Indiana, USA. <sup>4</sup>Utah State University, Logan, Utah, USA

**Adaptive variation in the Sierra garter snake (*Thamnophis couchii*): The influence of biogeography and genetic structure on patterns of TTX-resistance**

Most species consist of multiple, genetically differentiated populations that may also experience different abiotic conditions and community interactions. Despite the importance of a population genetic perspective for understanding geographic variation in coevolution, few studies have thoroughly examined the role of population genetic structure underlying geographic mosaics of coevolution. Here, we quantified phenotypic variation and population genetic structure in the Sierra garter snake (*Thamnophis couchii*) using over 26,000 genome-wide single nucleotide polymorphisms. Our goal was to understand the geographic scale at which gene flow might be reduced among populations, and allow for independent local adaptation in response to variation in the tetrodotoxin (TTX) defense of their Pacific newt (*Taricha*) prey. We documented pronounced geographic variation in TTX-resistance, with snakes from the southern regions of the Sierra Nevada displaying higher TTX-resistant phenotypes than those in the north. In addition, phylogenomic analyses recovered relationships among clades strongly associated with geographic and phenotypically distinct regions. Even though we recovered fine scale population genetic differentiation at the level of neighboring watersheds, explanation of genetic distances among populations is confounded by the influences from both geography and phenotype. This does, however, give evidence that the geographic scale in which adaptive phenotypic variation can arise and persist is likely narrow.

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## 186 Amphibian Ecology II, Highland A, Sunday 15 July 2018

Brian Halstead<sup>1</sup>, Patrick Kleeman<sup>2</sup> and Jonathan Rose<sup>1</sup>

<sup>1</sup>USGS WERC, Dixon, CA, USA. <sup>2</sup>USGS WERC, Point Reyes, CA, USA

### **Time-to-detection Occupancy Modeling: An Efficient Method for Analyzing the Occurrence of Amphibians and Reptiles**

Occupancy models provide a reliable measure of species distributions while accounting for imperfect detectability. The cost of accounting for false absences is that occupancy surveys typically require repeated visits to a site or multiple-observer techniques. More efficient methods of estimating detection probabilities would allow more sites to be surveyed, resulting in greater information about the ecological processes leading to occupancy. Time-to-detection surveys allow the estimation of detection probability based on a single site visit by one observer, and therefore might be an efficient technique for herpetological occupancy studies. We evaluated the use of time-to-detection surveys to estimate the occupancy of pond-breeding amphibians at Point Reyes National Seashore, California, USA, including variables that affected detection rates and the probability of occurrence. We found that detection times were short enough to reliably estimate the probability of occurrence of four of five pond-breeding amphibians at Point Reyes National Seashore, and that survey and site conditions had species-specific effects on detection rates. In particular, larger sites resulted in reduced detection rates for Sierran Treefrogs (*Pseudacris sierra*) and Rough-skinned Newts (*Taricha granulosa*). Probability of occurrence was negatively related to the presence of fish for these species, and positively related to grazing within the watershed for California Red-legged Frogs (*Rana draytonii*). Pond area also negatively affected Sierran Treefrog occurrence. Time-to-detection surveys can provide an efficient method of estimating detection probabilities and accounting for false absences in occupancy studies of reptiles and amphibians, allowing researchers to study a wider area for the same cost.

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

Gregor Hamilton<sup>1</sup>, Alex Cameron<sup>1</sup> and Randy Jennings<sup>2</sup>

<sup>1</sup>University of New Mexico, Albuquerque, NM, USA. <sup>2</sup>Western New Mexico University, Silver City, NM, USA

### **Identification of whiptail lizards (*Aspidoscelis*) using multivariate analysis of a morphometric dataset.**

Whiptail lizards of the genus *Aspidoscelis* can be difficult to identify, especially for museum specimens where color is often leached and formalin fixation makes genotyping difficult. The ranges of the three parthenogenetic species of *Aspidocelis* intersect in an ecotone along the Gila River in Southwest New Mexico: *A. sonorae* (Sonoran Spotted Whiptail), *A. flagellicauda* (Gila Spotted Whiptail), and *A. exsanguis* (Chihuahan Spotted Whiptail). Typically, these unisexual species can be distinguished as adults using the following morphological attributes: *A. exsanguis* is heavily spotted on dorsal stripes, on the base of the tail, and on the dorsal surface of the thighs, *A. flagellicauda* has 2 pre-anal scales as well as spots touching dorsal stripes, and

*A. sonora* has three pre-anals with spots seldom touching dorsal stripes. However, intraspecific variation in these diagnostic characters makes identification of variant individuals challenging and is further compounded by specimen preservation. The Gila Natural History Collection at Western New Mexico University in Silver City, NM, possesses many specimens of these three species that could not be identified confidently and catalogued. To address this, we collected a morphometric dataset of 14 continuous and 7 binary characters, including scale counts, spot counts, and spot and stripe presence/absence data (n=337). We then implemented a multivariate approach to identify characteristics that enabled the assignment of unknown individuals (n=207) to species using a training data set (n=72) generated from catalogued specimens of each species.

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

Kathryn Hamilton<sup>1</sup>, Shannon O'Leary<sup>1</sup>, Kyle Piller<sup>2</sup>, Kevin Conway<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>Southeastern Louisiana University, Hammond, LA, USA. <sup>3</sup>Texas A&M University, College Station, TX, USA

**Phylogenetic relationships within the genus *Erimyzon* (Family: Catostomidae) based on mitochondrial and nuclear loci**

*Erimyzon* is a genus in the family Catostomidae, currently consisting of four described species: *E. oblongus* (Eastern creek chubsucker), *E. claviformis* (Western creek chubsucker), *E. sucetta* (lake chucksucker), and *E. tenuis* (sharpfin chubsucker), all native to North America. Most studies of catostomid phylogenetics focus on resolving relationships among genera and higher taxonomic groups. Due in part to the fact that catostomids are polyploid, previous studies have relied mainly on mitochondrial markers and inconsistencies between various studies are likely due to a combination of the loci used and limited taxon sampling. While the genus *Erimyzon* is consistently recovered as monophyletic, in a recent study, *E. oblongus* was not monophyletic; a result that could be due to misidentification, presence of cryptic lineages, incomplete lineage sorting, and/or hybridization/introgression. Because the genus *Erimyzon* has not been thoroughly examined genetically, and there may be unrecovered lineages in the genus, we amplified mitochondrial and nuclear markers in multiple individuals of each of the four currently recognized species to reconstruct phylogenetic relationships among them. This research is an important first step towards a better understanding of evolutionary relationships in the genus *Erimyzon*.

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## **443 Lightning Talks III, Highland B, Sunday 15 July 2018**

Paul Hampton

*Colorado Mesa University, Grand Junction, CO, USA*

### **Is Foraging Ecology an Overlooked Influence on Organ Position in Snakes?**

Sea snakes have relaxed selection on cardiovascular function because low gravitational forces and water pressure in the marine environment place little stress on blood pressure homeostasis. Relative heart position in sea snakes is quite variable among species considering that the environmental influence on cardiovascular function should be similar. Sea snakes are diverse with respect to foraging ecology, which may be driving morphological diversification. I measured the position of the heart, liver and small intestine in sea snakes both by linear measurements on specimens and axial position (vertebral counts) determined from radiographs. The relative position of the organs was compared between species that forage for prey in either open habitats or burrows. Results will be discussed.

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

Paul Hampton<sup>1</sup> and Jesse Meik<sup>2</sup>

<sup>1</sup>*Colorado Mesa University, Grand Junction, CO, USA.* <sup>2</sup>*Tarleton State University, Stephenville, TX, USA*

### **Trophic Morphology and Prey Shape in Snakes**

As gape-limited predators, head morphology in snakes should be strongly correlated with prey shape. In particular, specialization on elongate versus robust prey should result in divergent head morphologies, because under these circumstances the jaw would be subject to opposing functional demands. We compiled detailed dietary data for 70 species of snakes from 8 families, and evaluated head morphology and integumentary distension (through dorsal scale counts) for each of these species in order to characterize morphological differences between robust and elongate prey specialists. In addition, we evaluated whether shifts in diet were associated with shifts in speciation rate. Principal components analysis demonstrated that dietary specialists are positioned at the extremes of head morphospace, and moreover that integumentary distension was correlated with prey specialization. While results of this study support the general agreement that robust prey consumers have relatively large gapes and increased skin distension, we also find that elongate prey specialists possess unique adaptations to preferred prey shape.

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

Charles Hanifin and Shana Geffeney  
*Utah State University, Vernal, UT, USA*

**Toxicity, Resistance, and Protein Evolution: What Can We Learn from Newts and Snakes?**

Natural product toxins provide powerful empirical systems to explore biological processes on multiple levels including large-scale ecological interactions, micro evolutionary processes and organismal physiology. Newts of the genus *Taricha* and their snake predators (Genus: *Thamnophis*) are engaged in a coevolutionary arms race in which reciprocal evolution drives increased TTX toxicity in newts and increased TTX resistance in snakes. To use TTX as a defense, *Taricha* newts must concentrate TTX in their tissues and also be resistant to the toxin. Here we will report results associated with the adaptive evolution of TTX-resistance in both snakes and newts. Our results show that TTX-resistance is ancient and ubiquitous in the modern-newt clade and that the molecular basis of TTX resistance in snakes and newts is strikingly convergent. In both groups, TTX-resistance results from similar substitutions in their VGSCs. This convergence likely results from shared constraints on channel function. Empirical manipulations of snake channels demonstrate that a single shared change in the outer pore of highly resistant snakes and all modern newts causes the greatest increase TTX resistance. Furthermore the first change along the path to resistance is shared in both newts and snakes but may occur in response to selection on organismal performance rather than resistance to TTX. Lastly, the identification of single “super-resistant” mutation in snakes indicates that snakes may have a simple path to resistance and explain why snakes appear to be the only winners in their arms races with newts.

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

James Hanken, Stephen Turney and Linda Ford  
*Harvard University, Cambridge, MA, USA*

**Unlocking the Vault: Mass Digitization and Imaging of Historical Slide Collections for use in Comparative Biology**

Natural history museums hold vast collections of glass microscope slides amassed from a variety of sources over the last 100 or more years. These slides were prepared in association with a variety of botanical and zoological studies but were especially important for studies of fishes, amphibians and reptiles. While such collections represent a unique and irreplaceable resource for studies of integrative and comparative biology, most are fragile or otherwise difficult to access and work with. Hence, they are largely ignored by contemporary researchers. We have developed a cost-effective, high-throughput and semi-automated workflow for digitally scanning and displaying slides of many different sizes characteristic of the collections of the Harvard Museum of Comparative Zoology, which is

applicable to like collections at other institutions. The resulting high-resolution digital images, each depicting the contents of an entire slide, may be accessed via a customized web application that allows a variety of kinds of image analysis and data capture. Ready access to these historically and scientifically rich data sources will enable fruitful and timely collaborations between natural history museums and other branches of biology, such as neuroscience, physiology, developmental biology, functional morphology and ecology, and complements the growing number of digital-image repositories available via the Internet.

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## **328 Ichthyology Conservation, Grand Lilac Ballroom South, Saturday 14 July 2018**

Jadziah Hannon-Moonstone

*University of Massachusetts, Amherst, Massachusetts, USA*

### **Growth-At-Age of Blueback Herring in the Connecticut River**

Blueback Herring (*Alosa aestivalis*) is an anadromous fish that has experienced extreme declines in abundance in the Connecticut River beginning in the mid 1990's. The Atlantic States Marine Fisheries Commission coastwide stock assessment in 2017 determined this species severely depleted. Beginning in 2013, a large-scale US Fish and Wildlife Service (USFWS) data monitoring project was started in the Connecticut River to address data deficiencies for the species. This project will use fish sampled by the USFWS from 2013-2017 to look at Blueback Herring age and growth determined using otoliths. Back calculations of size-at-age will be conducted using measurements of annual growth increments for male and female blueback herring collected from five sites throughout the Connecticut River. Otolith measurements will be used to create a von Bertalanffy growth function for the population. This work will help inform more complex fisheries models that assist state and federal agencies in the management of blueback herring in the Connecticut River. This data could also be used to explore possible factors that influence of at-sea growth of blueback herring.

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

Maggie Hantak<sup>1</sup>, Robert Page<sup>2</sup>, Paul Converse<sup>1</sup>, Carl Anthony<sup>3</sup> and Shawn Kuchta<sup>1</sup>

<sup>1</sup>Ohio University, Athens, OH, USA. <sup>2</sup>Texas A&M University-San Antonio, San Antonio, TX, USA. <sup>3</sup>John Carroll University, University Heights, OH, USA

### **The Relationship Between the Genetic Structure, Landscape Ecology, and Color Polymorphism in the Eastern Red-backed Salamander (*Plethodon cinereus*)**

An underexplored question in color polymorphic species pertains to how phenotypes are maintained among populations. Mechanisms that maintain polymorphisms include negative

frequency dependent selection, spatiotemporal variation in selection, and gene flow among populations. Investigating these mechanisms in multiple populations provides insight into the processes influencing geographic variation in genetic structure and color morph frequency. The Eastern Red-backed Salamander (*Plethodon cinereus*) is widely distributed in northeastern North America and contains two common color morphs (striped and unstriped). Currently, the evolutionary processes that maintain the polymorphism are not well understood. Using microsatellite loci, we investigated whether patterns of morph frequency variation conformed with patterns of population structure in Ohio. In addition, we examined whether genetic distance, landscape variables, or geographic distance had a stronger relationship with morph frequency variation. Our results demonstrate clear population structure with three genetic clusters, one of which is monomorphic for the striped morph. There was no relationship between genetic differentiation and morph frequency variation. Instead, we found that genetic distance was most correlated with ecological and landscape features, and morph frequency variation was most correlated with geographic distance and waterway barriers. Gene flow alone does not appear to maintain the polymorphism in *P. cinereus*, rather a balance between gene flow and selection likely maintains the two color morphs. Overall, our study provides critical information on the role of gene flow and natural selection in the evolution and maintenance of this color polymorphism, and links patterns of genetic differentiation with an understanding of the ecology of *P. cinereus*.

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## 26 Herpetology Physiology, Highland C, Saturday 14 July 2018

Rebecca Hardman<sup>1</sup>, Kendall Oziminski<sup>1</sup>, Laura Reinert<sup>2</sup>, Louise Rollins-Smith<sup>2</sup>, Kelly Irwin<sup>3</sup> and Debra Miller<sup>1</sup>

<sup>1</sup>University of Tennessee, Knoxville, Tennessee, USA. <sup>2</sup>Vanderbilt University, Nashville, Tennessee, USA. <sup>3</sup>Arkansas Game and Fish Commission, Little Rock, Arkansas, USA

### **Hellbender skin antimicrobial peptides show variable inhibition against chytrid fungus (*Batrachochytrium dendrobatidis*)**

Hellbenders (*Cryptobranchus alleganiensis*) are large aquatic salamanders from the eastern USA and have experienced considerable population declines in both Ozark and Eastern subspecies, *C. a. bishopi* and *C. a. alleganiensis*, respectively. *Batrachochytrium dendrobatidis* (*Bd*) is a fungal skin pathogen of concern as it is present in wild hellbender populations and is known to cause mortality in captivity during times of stress. Furthermore, ulcerative non-healing lesions have been frequently observed in *C. a. bishopi* adults alongside high prevalence of *Bd*. Antimicrobial peptides (AMPs) secreted on the skin are an important component of amphibian innate immunity and may be a factor in manifestation of observed lesions. For instance, frog AMPs have demonstrated growth inhibition of *Bd* in vitro and, in some species, have been linked to variable resistance. Our objective was to determine if hellbender AMPs exhibited anti-*Bd* activity and if inhibition correlated to subspecies. We challenged *Bd* zoospores against serial concentrations of field collected Hellbender AMPs and found significantly higher *Bd*-inhibition from *C. a. alleganiensis* compared to *C. a. bishopi* with an MIC<sub>50</sub> of 250 and 2500 ug/mL,

respectively. Although we were unable to evaluate effects of *Bd* infection status on AMP activity, AMPs from ranavirus negative animals had significantly higher inhibition than those from ranavirus positive animals within *C. a. alleganiensis* populations (MIC<sub>50</sub> 75 and 400 ug/mL, respectively). Our study is the first to report hellbender AMPs with inhibition against *Bd* and that factors such as infection status and subspecies can affect peptide quality and risk for chytridiomycosis.

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## **291 ASIH STOYE ECOLOGY & ETHOLOGY I, Highland C, Thursday 12 July 2018**

Mallory Harmel, Hayley Crowell and Emily Taylor

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

### **50 Shades of Clay: Rattlesnake Coloration Affects Detection by Predators**

Crypsis, or the ability of an animal to avoid detection by other animals, is strongly related to the organism's coloration. Southern Pacific Rattlesnakes (*Crotalus oreganus helleri*) vary in coloration within and among populations, suggesting selection on coloration within specific habitats and environments. The purpose of this study was to investigate the effect of coloration on likelihood of being attacked by a predator, on latency to attack, and to observe where on the snake body predators tend to attack. Clay snake models representing four commonly observed color morphs of rattlesnakes (light, dark, intermediate color with white pattern, intermediate color with dark cream pattern) were placed in grassy and wooded habitats at a reserve in central coastal California, and marks made on the models by predators' teeth, beaks, and claws were quantified. We found that model type was a significant predictor of the overall number of attack marks, with dark colored snakes being attacked significantly more often than light-colored snakes. The latency to attack did not differ significantly among model types. Model type was related to where on the models the marks were made although the location of the marks on the models was not significantly different. Our data show that coloration can play a large role in crypsis, and suggest that dark-colored rattlesnakes, which have the most contrast with the golden-colored grasses and therefore have the lowest crypsis, are most at risk from predation.

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## **504 Ichthyology Systematics I, Grand Lilac Ballroom South, Saturday 14 July 2018**

Richard Harrington<sup>1</sup>, Thomas Near<sup>1</sup>, Brant Faircloth<sup>2</sup> and Matt Friedman<sup>3</sup>

<sup>1</sup>*Yale University, New Haven, CT, USA.* <sup>2</sup>*Louisiana State University, Baton Rouge, LA, USA.*

<sup>3</sup>*University of Michigan, Ann Arbor, MI, USA*

### **Swimming in Data: Addressing Pelagaria Relationships with Phylogenomic Datasets**

Pelagaria is a clade of fishes that was discovered on the basis of molecular phylogenetic analyses. This group represents a largely pelagic, marine radiation of approximately 270 species classified in 16 families that previously had been hypothesized to belong to multiple percomorph suborders. Its members include the scombroids (e.g., tunas and mackerels,) and stromateoids (e.g., butterfishes and driftfishes), as well as Icosteidae (Ragfish), Chiasmodontidae (swallowers), Bramidae (pomfrets) and Caristiidae (manefishes). Pre-molecular, morphology-based hypotheses of intra- and inter-relationships of Pelagiaria groups were by no means settled, and increasingly larger and taxonomically more inclusive molecular datasets have yet to converge on well-supported topologies, with the exception of strong support for monophyly of the crown group. We gathered sequence data for more than 1,000 ultraconserved DNA elements (UCEs) in order to assess molecular support for relationships among the Pelagaria subclades, and to incorporate fossil information into a phylogenetic framework for analyses of diversification and patterns of morphological evolution. As in previous molecular phylogenetic analyses, we find support for an early, rapid radiation of major Pelagaria clades. Our analyses of UCE loci show strong support for some previous morphological hypotheses of relationships, but also reveal strong support for new relationships among major subclades, and some areas in the phylogeny that are characterized by high levels of incongruence among loci. These results provide directions for future efforts to investigate morphological and molecular data in order to resolve relationships among the subclades of Pelagaria.

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## 264 Herpetology Systematics, Highland B, Saturday 14 July 2018

Sean Harrington<sup>1</sup>, Jordyn de Haan<sup>2</sup>, Lindsey Shapiro<sup>3</sup> and Sara Ruane<sup>4</sup>

<sup>1</sup>University of Hawaii, Honolulu, HI, USA. <sup>2</sup>LSU, Baton Rouge, LA, USA. <sup>3</sup>Briarcliff High School, Briarcliff Manor, NY, USA. <sup>4</sup>Rutgers University, Newark, NJ, USA

### **Habits and characteristics of arboreal snakes worldwide: arboreality constrains body size and has complex effects on lineage diversification**

Arboreal lifestyles represent common and major habitat shifts among snakes. Major habitat shifts are often facilitated by particular traits that confer advantages in the new environment. Although studies have examined the habits and characteristics of arboreal snakes at the level of individual species or small clades, a broad survey has never been performed across all snakes. We surveyed the literature to identify all known arboreal snakes and summarize their general characteristics. We then tested for associations between diversification rates and arboreal habits and reconstructed ancestral states using the HiSSE approach. Finally, we tested for an association between body size and arboreality by fitting multi-peak OU models. We found that generally, arboreal snakes are most frequently nocturnal, oviparous, reptile eating, brown/banded/patterned snakes inhabiting the Neotropics (assessing each trait individually, not jointly). The effect that arboreality has on diversification depends on how data are coded, but when comparing primarily arboreal snakes to all others, we identified an increase in diversification rates associated with arboreality, consistent with previous findings. Our OU

models showed that arboreal snakes tend to be larger than non-arboreal snakes, that rates of body size evolution are generally slower in arboreal snakes, and arboreal body sizes are pulled more strongly toward their optimum than in non-arboreal snakes. These results suggest that arboreal snake lineages may diversify more rapidly than non-arboreal lineages, even though morphological evolution is more constrained.

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

Pamela Hart-Burress<sup>1</sup>, Matthew Niemiller<sup>2</sup> and Prosanta Chakrabarty

<sup>1</sup>Louisiana State University, Baton Rouge, LA, USA. <sup>2</sup>University of Alabama in Huntsville, Huntsville, AL, USA

**Phylogenomics of the Amblyopsidae (Percopsiformes)**

Cave-obligate organisms long have captured the imagination and interest of scientists and the general public, yet their evolutionary histories and modes of subterranean adaptation are still poorly understood. The endemic North American Amblyopsidae fishes are one of very few families across the fish Tree of Life to contain both surface- and cave-dwelling members; thus, this group is ideal for comparative studies of cave adaptation. Morphological and molecular datasets have presented conflicting evolutionary relationships within the Amblyopsidae, particularly with respect to the placement of eyed species in relation to the blind, cave-obligate taxa. Molecular phylogenies indicate a possible subterranean ancestor for one eyed genus, suggesting the regeneration of eyes and re-invasion of surface habitat. Morphological topologies recover a continuum of forms, progressing from surface to cave without re-evolution. To further elucidate phylogenetic relationships within the Amblyopsidae, we collected genomic data from over 700 ultraconserved element (UCE) loci from 119 samples representing all described taxa as well as additional undescribed lineages. Each of the three states of troglomorphy (surface, cave-utilizing, and cave-obligate forms) was sampled for this study. This work will provide insight into the patterns and modes of cave adaptation.

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

Jordan Hartley and Dustin Siegel

*Southeast Missouri State University, Cape Girardeau, MO, USA*

**Comparison of pelvic and genital kidney glomeruli in *Eurycea longicauda***

Salamanders possess kidneys with two distinct regions: a caudal pelvic part and cranial genital part. Nephrons of the pelvic region are only responsible for urine formation and transport. Nephrons of the genital region transport sperm from the testes to the Wolffian ducts. However, they possess all the same functional regions found in pelvic kidney nephrons that are involved with urine formation and transport; i.e., renal corpuscles, proximal tubules, distal tubules, and collecting ducts. Thus, past researchers hypothesized that nephrons of the genital kidneys possess dual function: sperm transport and urine formation/transport. However, this hypothesis has never been tested. Considering size of glomeruli is directly related to the total amount of blood plasma filtered into the Bowman's space, we tested the hypothesis that nephrons of the genital kidneys have reduced urine formation function by comparing glomeruli size between nephrons of the pelvic and genital kidney regions in *Eurycea longicauda* with general histological techniques. Glomeruli of the pelvic kidneys were significantly larger than those measured from the genital kidneys. Greatest cross sectional surface area of pelvic kidney glomeruli averaged 7,822.83 mm. Genital kidney glomeruli averaged 1,669.35 mm. In conclusion, although structurally similar at the histological level, it appears that nephrons of the genital kidneys have decreased urine formation function based on glomerular size comparison between pelvic and genital kidneys.

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

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**A New Genus of Minnow in West Africa (Cypriniformes, Cyprinidae, Smiliogastrini)**

The monophyletic *Enteromius jae* species group (*E. jae*, *E. condei*, *E. nounensis*, and *E. parajae*) is a group of African small barbs that represents a new genus that we will describe as *Baka*. *Baka* occurs in coastal rivers of Cameroon and Gabon as well as the Dja River (Congo River tributary). *Baka* can be separated from all other African small barbs based on the following combination of characters; from *Barboides* by having a pigmented pseudotympanum (vs. not pigmented with fat globules); from *Clypeobarbus* by lacking a cleithral mark and having lateral-line scales the same height as all other scales (vs. dark line present along the posterior edge of the pectoral girdle and a midlateral row of enlarged, pigmented scales); from *Enteromius* by having an incomplete lateral line, possessing a pseudotympanum, having reduced numbers circumorbital bones (vs. an often complete lateral line, no pseudotympanum, and a complete series of circumorbital bones); from *Pseudobarbus* by having eight dorsal fin rays (vs. seven dorsal fin rays); and from the cave barbs (*Caecobarbus* and *Barbopsis*) by fully developed eyes and pigment (vs. no eyes and lacking pigmentation). A molecular phylogeny is also presented demonstrating the placement of *Baka* in the context of *Enteromius* and other African taxa.

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