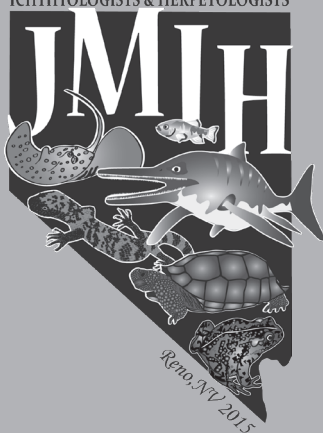




Abstract Book

JMIH 2015

JOINT MEETING of
ICHTHYOLOGISTS & HERPETOLOGISTS



**Abstracts for the 2015
Joint Meeting of Ichthyologists and Herpetologists**

**AES - American Elasmobranch Society
ASIH - American Society of Ichthyologists and
Herpetologists
HL - Herpetologists' League**

**Reno, Nevada
16-19 July 2015**

**Edited by
Martha L. Crump
1 May 2015**

0381 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Connor Adams¹, Brandon Bowers¹, Brad Wolaver², Heather Prestridge¹, Toby Hibbitts¹, Wade Ryberg¹

¹Texas A&M University, College Station, USA, ²University of Texas, Austin, TX, USA

Distribution and Population Status of the Western Chicken Turtle (*Deirochelys reticularia miaria*) in Texas

The Western Chicken Turtle (*Deirochelys reticularia miaria*) is thought to be rare and declining throughout its range. As a result, the U.S. Fish and Wildlife Service (FWS) issued a 90-day finding (FWS 2011) that states listing the species as threatened or endangered may be warranted. In this 90-day finding, FWS requested information on current and future threats to *D. r. miaria* populations and habitat throughout its range. Current information on the distribution and population status of *D. r. miaria* in Texas is lacking, and development of a comprehensive conservation and management plan at either the state or federal level is not possible. To address this problem, we initiated a state-wide survey of suitable *D. r. miaria* habitat. Survey locations were selected from suitable habitat areas based on access and proximity to public roadways where access was denied. When access was granted, turtles were captured using a combination of aquatic traps and nets (e.g., hoop nets, crayfish traps). When access was not granted, wetlands near public roadways were surveyed with binoculars and spotting scopes. Here, we present preliminary results from this survey effort and discuss the implications of our findings for conservation of *D. r. miaria* populations and habitat in Texas and distribution wide.

0387 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Cory Adams, Daniel Saenz

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

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

The Rio Grande Chirping Frog (*Eleutherodactylus cystignathoides*) is a small direct developing frog species in the family Leptodactylidae. Their native range extends from northeastern Mexico to extreme southern Texas; however, it has been rapidly expanding into other parts of Texas presumably by way of accidental human transport, primarily the potted plant trade. Very little information is known about this anuran across most of its introduced range. The purpose of this study is to determine the calling habits of the introduced Rio Grande Chirping Frog. We surveyed for calling Rio Grande Chirping Frogs at three study sites using automated recording devices set to record for the first minute of every hour, each day. We detected frogs calling at all three of our survey sites. Rio Grande Chirping frogs can call any month, with calling mainly occurring during the warmer months. Frogs called primarily during dark hours but did occasionally call

during the day. The mild climate of eastern Texas appears to be suitable to support an established population of Rio Grande Chirping Frogs.

0576 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Joseph Agugliaro

Fairleigh Dickinson University, Madison, NJ, USA

Absence of Metabolic Acclimation during Artificial Hibernation in Rubber Boas (*Charina bottae*)

Defining reptilian hibernation, as either an intrinsic physiological or purely behavioral phenomenon, has long been problematic. In part, this uncertainty has been due to the diversity of metabolic responses exhibited by reptiles during cold acclimation. Among snakes, the few species for which appropriate measurements are available have variously exhibited decreases, increases, or no change in metabolic rate during the winter season. At present, sampling is insufficient to distinguish among differences in phylogenetic position, geographic origin, and/or experimental methodology as potential sources of this apparent physiological diversity. To improve our understanding of snake metabolic responses to hibernation, I measured the effects of seasonal laboratory acclimation, acute temperature, and body mass on resting metabolic rate (CO₂ production) in the Rubber Boa (*Charina bottae*), an ercine snake with a wide latitudinal distribution in western North America. Metabolic rates of 10 *C. bottae* from southeastern Idaho were measured as a function of acute temperature (5, 9, 13, 17°C) during the simulated late active season and during artificial hibernation. Repeated-measures ANCOVA revealed significant effects of acute temperature and body mass, but no effects of acclimation treatment or the interaction between treatment and temperature, on resting metabolic rate. Despite the absence of any downregulation in metabolic rate during artificial hibernation, metabolic rates of *C. bottae* are still quite low relative to other snake species for which similar data are available. Clearly, before attempting to explain the diversity of snake acclimation responses, more rigorous studies of the effects of hibernation on snake metabolism are needed.

0392 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Matthew Ajemian¹, Philip Jose¹, John Froeschke², Gregory Stunz¹

¹Harte Research Institute for Gulf of Mexico Studies, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA, ²Gulf of Mexico Fishery Management Council, Tampa, FL, USA

Trends and Characterization of the Land-based Recreational Shark Fishery off Texas

Most analyses of shark population trends use seasonally-limited fishery-independent data that generally neglect important nearshore coastal habitats (i.e., <20m bottom depth). The Texas coast supports one of the largest year-round, land-based recreational shark fisheries in the United States. However, no studies have characterized the catch composition and overall trends in this fishery despite its beginnings several decades ago. We used fishery-dependent data from two distinct periods (historic = 1973-1986, and modern = 2008-2014) to assess the status of the nearshore shark community off Texas. Monthly catch records from both data sets were examined using multivariate techniques to examine seasonality in shark assemblages as well as potential shifts in catch composition over time. These fishery-dependent data revealed relatively distinct assemblages by season (ANOSIM Global R = 0.159; P = 0.0001) and period (ANOSIM Global R = 0.222; P = 0.0001). Similarity Percentage analysis showed a general shift in shark community assemblage from larger to smaller species. Most notably, Bull Shark (*Carcharhinus leucas*) dominance decreased over time while Blacktip Shark (*Carcharhinus limbatus*) contribution increased. Our analyses also identified a large decrease in mean total length (TL) of Bull Sharks from 232.8 cm to 175.1 cm and a modest increase in Blacktip Shark size from 125.1 cm to 127.9 cm TL. These findings document a significant change in the size and composition of Texas' nearshore shark community potentially driven by overfishing and removal of large (>2 m) sharks. Future management decisions should account for these removals as stocks are rebuilt to historical levels.

0371 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Matthew Ajemian, Gregory Stunz

Harte Research Institute for Gulf of Mexico Studies, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA

Migratory Behavior and Habitat Use of Large Sharks in the Western Gulf of Mexico

Large sharks serve as critical apex predators in many marine ecosystems around the world, yet the habitat requirements and migration patterns of these species remain poorly understood throughout much of their ranges. The growing demand for shark habitat use information has supported a proliferation of satellite biotelemetry studies. Despite the multitude of anthropogenic pressures in the region, few data exist on large shark movement patterns in the western Gulf of Mexico. In summer of 2014, four large

sharks (2 Scalloped Hammerhead, *Sphyrna lewini*; 2 Tigers, *Galeocerdo cuvier*) were tagged and released near an offshore production platform and tracked with Smart Position or Temperature transmitters. Sharks were tracked for thousands of miles, and demonstrated some important ecosystem connections between nearshore locales and open waters of the Gulf of Mexico. While Scalloped Hammerheads provided more frequent reports and fidelity to the Texas continental shelf, Tiger Sharks exhibited larger dispersal patterns, including a cross-basin venture towards the Campeche escarpment (Mexico) as shelf waters cooled in December and a subsequent return to the Texas shelf. Tiger Sharks also demonstrated use of NOAA-designated Habitats Areas of Particular Concern such as the south Texas hard banks and the Flower Gardens National Marine Sanctuary. Our work highlights the connected nature of many seemingly disparate habitats within the Gulf of Mexico by large sharks and the importance of establishing satellite tagging programs for conservation and management purposes. Continued tagging efforts in 2015 will assess potential year-to-year variability in the movement and habitat use patterns observed to date.

0432 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Linda Allison¹, Ann McLuckie²

¹U.S. Fish and Wildlife Service, Reno, NV, USA, ²Utah Division of Wildlife Resources, Hurricane, UT, USA

SWPARC Trends in Mojave Desert Tortoise Densities

Populations of the Mojave desert tortoise (*Gopherus agassizii*) experienced severe declines in abundance in the decades leading up to 1990, when the current species was listed as threatened under the United States Endangered Species Act. We report regional population trends of desert tortoises and evaluate whether interim population trajectories are on track to meet the specific recovery plan criterion of increasing densities in each recovery unit after 25 years. We used distance sampling from line transects to estimate annual adult densities since 1999 in Utah and since 2004 elsewhere in the range of Mojave desert tortoises. We applied mixed model regression to log-transformed adult tortoise densities to estimate annual percent change through 2014 in each of 17 Tortoise Conservation Areas (TCAs) in the 5 recovery units. We report annual proportional increases in density of adults only in the Northeastern Mojave Recovery Unit, but declines in the other 4 recovery units. Adjusting these density trends for the area of potential habitat in each recovery unit, we estimate that in 2004 there were 336,569 adult tortoises (standard error [SE] = 51,596), with an overall loss of 124,396 adult tortoises (SE = 36,162) by 2014. We used the proportion of juveniles in our surveys to estimate trends among juveniles relative to adult tortoises in each recovery unit. The proportion of juveniles differed between recovery units and has been decreasing in all 5 recovery units since 2007.

0039 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Abdulaziz Alqahtani

University of Bisha, Bisha, Saudi Arabia

Geographical Distribution and Ecological Studies of the Arabian Toad (*Bufo arabicus*) in the Asir Region South of The Kingdom of Saudi Arabia

Bufo arabicus is an endemic species in the Arabian Peninsula, a medium-sized to reach a length of 78 mm in length, with a lean structure, parts of the dorsal gray color in general and sometimes speckled small dark spots. Head with an average size, the parties slender and fairly long. Arabian toad is sexually variant, since males are identified by internal voice bag that are noticed through the laryngeal membranes. Tadpole of the Arabian toad is fairly large, up to 50 mm in length. Arabian toad is one of the most prevalent types of amphibians in the study area in the Arabian Peninsula. About 85 locations were recorded, that extend from far south of the study area at Alkhoba south Jazan to the north of Mecca area. Moreover, 60 new locations were recorded recently in Tehama, Sarwat mountain chain and even in hilly and interior regions such as Najran area. Arabian toad is active in natural environments at night, and disappears during the day in crevices and burrows to avoid the sun's heat, rarely active during the day in the temperate zones of water and shadow areas. *Bufo arabicus* breeding were recorded in two seasons, one in summer while the other is in autumn.

0394 AES Reproduction, Carson 2, Friday 17 July 2015

Brenda Anderson¹, Carolyn Belcher², JoAnn Slack³, James Gelsleichter¹

¹*University of North Florida, Jacksonville, FL, USA*, ²*Georgia Department of Natural Resources, Brunswick, GA, USA*, ³*University of Pennsylvania School of Veterinary Medicine, Kennett Square, PA, USA*

The Use of Ultrasonic Imaging to Detect Reproductive Activity in Female Bonnetheads (*Sphyrna tiburo*)

Ultrasonography has become a widely used diagnostic tool in the veterinary field, following its introduction to obstetrics in humans in the 1960s. Traditional methods for investigating shark reproduction include euthanasia and dissection, which is not conducive to studying large or endangered sharks and are usually fatal to embryos. Ultrasound machines have not been widely used in shark research due to the machine's fragile construction. The purpose of this study was to determine reproductive activity in female bonnetheads (*Sphyrna tiburo*) using a field-ready ultrasound machine and to compare the "gold standard" dissection method to ultrasound methods by determining their level of agreement. Female sharks (n = 71) were collected, euthanized, externally examined via ultrasound, and uteri dissected to determine reproductive activity. Presence and number of eggs and/or embryos were recorded using 8 MHz linear and 5 MHz curvilinear transducers. Contents of the uteri were dissected and counted. Kappa

statistic was used to compare the level of agreement between the different methods: dissection to curvilinear transducer, dissection to linear transducer, and linear to curvilinear transducers. Dissection versus curvilinear transducer methods resulted in 88.9% agreement (Kappa coefficient = 0.7798). Dissection versus linear transducer methods resulted in 61.3% agreement (Kappa coefficient = 0.4192). Linear versus curvilinear transducer methods resulted in 97.3% agreement (Kappa coefficient = 0.9510). Overall, the ultrasound was a good indicator of presence of eggs/embryos in the bonnethead. Limitations of ultrasonography include image quality, gut content interference, and stacking of pups in utero.

0609 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

James Anderson¹, Kim Holland²

¹University of Hawaii, Honolulu, HI, USA, ²Hawaii Institute of Marine Biology, Kaneohe, HI, USA

Holy Grail, Needle in a Haystack, or Wild-Goose Chase: Searching for a Shark Magnetoreceptor

The physical basis of magnetic field perception in both vertebrates and invertebrates has been the subject of debate for some time, with three hypotheses prevailing above others. The elasmobranch fishes (sharks, skates and rays) are the only class hypothesized to use their electrosensory capability in the perception of geo-magnetic stimuli. Other taxa argued to orient to or via the geomagnetic field have been hypothesized or demonstrated to use alternative mechanism. One such theory is the magnetite hypothesis, whereby intracellular crystals of the iron oxide magnetite (Fe₃O₄) are coupled to mechanosensitive channels that give rise to neuronal activity in specialized sensory cells. Efforts to find these primary sensory structures have failed to convincingly describe receptor locations, illustrating the need to develop new methods to test the magnetite hypothesis of magnetoreception. Here we describe an ongoing study that aims to identify and describe suitable candidate sensory cells in both the olfactory and vestibular organs of the Scalloped Hammerhead shark (*Sphryna lewini*). We report upon the efficacy of a novel approach to identify candidate cells, and in turn report efforts to both quantify and qualify cells with magnetic properties that could function in the perception of magnetic stimuli.

0503 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Krystal Anderson, Erika Nowak

Northern Arizona University, Flagstaff, AZ, USA

SWPARC: Wildfire Effects on *Thamnophis rufipunctatus*

A key issue in conservation biology is to better understand how wildfires can directly and indirectly have a detrimental effect on riparian species and their habitat. The narrow-headed gartersnake (*Thamnophis rufipunctatus*) is a highly aquatic species endemic to Arizona and New Mexico streams which was recently listed as 'Threatened' under the Endangered Species Act. Factors that are thought to cause decline include habitat loss, loss of native fish prey due to invasive species, post-wildfire flooding effects, and water quality. There are few studies done that examine wildfire effects on streams and riparian habitats, specifically on aquatic reptiles. This case study explores wildfires that have occurred in riparian areas inhabited by narrow-headed gartersnakes and assesses some of the factors that may be contributing to the species decline. We conducted gartersnake surveys and abiotic stream transects pre-and post-flooding after the Slide Fire in Oak Creek to determine silt depth, water depth, habitat, rock embeddedness, and average rock size. Long-term project goals are to compare previous surveys and stream transects where wildfires have occurred across the range of *T. rufipunctatus* to determine the severity of wildfire impacts on narrow-headed gartersnakes. Although thus far, we have not detected effects on gartersnakes within the Slide Fire area, Northern Arizona University is working with state and federal agencies to track long-term effects and implement proactive management to prevent further species decline.

0288 General Herpetology, Carson 1, Friday 17 July 2015

Rachel Anderson, Sharon Lawler

UC Davis, Davis, CA, USA

Rapid Evolution of Adaptive Response to an Introduced Predator

The American Bullfrog (*Lithobates (Rana) catesbeianus*) is a voracious global invader implicated in the decline of native amphibian species, including the threatened California Red-legged Frog (*Rana draytonii*). Our previous work demonstrated that tadpoles from populations of native *R. draytonii* that had co-occurred with bullfrogs for many generations showed potentially adaptive behavioral responses to bullfrog scent. Here, we examined whether co-evolved *R. draytonii* larvae would perform better with bullfrogs than allopatric populations. We conducted mesocosm experiments with *R. draytonii* tadpoles that were sympatric and allopatric to bullfrogs, and observed their survival and growth when exposed to overwintered bullfrog larvae. We found that co-evolved *R. draytonii* raised with bullfrogs did not experience the same decrease in body condition relative to bullfrog-free controls that the allopatric populations did.

Additionally, the two groups experienced opposite morphological changes in the presence of bullfrogs, with proportionally longer tails in the experienced group and shorter tails in the naïve group. This work shows that adaptive changes have occurred in populations of *R. draytonii* exposed to invasive bullfrogs.

0511 Herp Ecology, Carson 4, Saturday 18 July 2015

Roger Anderson

Western Washington University, Bellingham, WA, USA

Effects of Climate Variation Compared for Three Syntopic Lizard Species Across a Decade in the Northern Great Basin

Because syntopic species of desert lizards may vary considerably in a) modes of food acquisition, b) prey types, c) activity patterns, d) predation threat, e) daily patterns of body temperature, f) life-history traits, and g) trophic levels, it is difficult to predict the relative effects of among-year variation in means and extremes of temperature and precipitation across the seasons on the different lizard species. A first approach to investigating climate effects was performed with a decade-long observational-descriptive-comparative study of very different lizard species: 1) the western whiptail lizard, *Aspidoscelis tigris*, which is a wide foraging insectivore, 2) the desert horned lizard, *Phrynosoma platyrhinos*, a trap-line and ambush predator of ants and 3) the long-nosed leopard lizard, *Gambelia wislizenii*, which preys mostly on grasshoppers and lizards. The annual patterns of population density, juvenile recruitment, adult body condition and fecal production were analyzed with respect to inter-annual variation in climate and availability of prey. Some of the expected correlates of climate with prey and predator productivity were revealed, but there were intriguing species-specific differences in the responses to these indirect abiotic and direct biotic variables.

0121 AES Ichthyology, Carson 2, Thursday 16 July 2015

Allen Andrews¹, Michelle Passerotti², Lisa Kerr³, Lisa Natanson⁴, Sabine Wintner⁵

¹NOAA Fisheries – PIFSC, HI, USA, ²NOAA Fisheries – SEFSC, FL, USA, ³Gulf of Maine Research Institute, ME, USA, ⁴NOAA Fisheries – NEFSC, RI, USA, ⁵KwaZulu-Natal Sharks Board, Durban, South Africa

Maximum Age and Missing Time in Shark Vertebrae: The Limits and Validity of Age Estimates Using Bomb Radiocarbon Dating

Bomb radiocarbon dating has become a common tool in determining valid measures of age for large shark species. In most cases, estimates of age were made by counting growth-band pairs in vertebrae and usually in the *corpus calcareum* of vertebral cross-

sections. These estimates of age have been either supported or refuted using measured radiocarbon values (reported as $\Delta^{14}\text{C}$) that are equated to a year-of-formation, and subsequently compared to an appropriate $\Delta^{14}\text{C}$ reference record. While the approach seems straightforward, the application is not and an effective ageing project may require some significant assumptions that are sometimes overlooked. Two of the most important considerations are the sources of carbon available to the vertebrae and the use of a valid $\Delta^{14}\text{C}$ reference to provide validated age estimates. Recent findings for some species indicate the vertebrae cease growth and as a consequence ages have been underestimated by decades (i.e. sand tiger shark, *Carcharias taurus*). However, proper alignment of the $\Delta^{14}\text{C}$ measurements from vertebral samples to the $\Delta^{14}\text{C}$ reference record does not always provide well-defined ages and many are still considered estimates that require some assumptions (i.e. white shark, *Carcharodon carcharias*). The aim of this presentation is to provide an overview of how bomb radiocarbon dating can work for shark vertebrae with some insight on how the method can fall short of expectations.

0138 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Jennifer Andrews

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

Review of the Pygmy Sleepers (Teleostei: Butidae: *Kribia*) of West Africa

Kribia is a genus of sleepers in the family Butidae endemic to freshwater habitats of West and Central Africa. Currently, there are four recognized species: *Kribia kribensis*, *K. uellensis*, *K. leonensis*, and *K. nana*, of which there are 5 subspecies, *K. nana nana*, *K. nana chevalieri*, *K. nana katangae*, *K. nana elongata*, and *K. nana itimberiensis*. The species and subspecies are poorly distinguished in existing keys by small differences in variable features with overlapping ranges in character state. Recent molecular work in our lab suggests that there are at least 7 species in Guinea alone. Thus, there are more species than currently described and some are cryptic species not easily distinguished with the naked eye. A combination of pigmentary, meristic, and morphological features, including cutaneous cephalic papillae is being developed to diagnose the cryptic species of *Kribia*.

0343 Herp Conservation II, Carson 1, Saturday 18 July 2015

Whitney Anthonymsamy¹, Michael Dreslik², Marlis Douglas¹, Dan Thompson³, George Klut⁴, Andrew Kuhns², David Mauger⁵, Gary Glowacki⁶, Christopher Phillips²

¹University of Arkansas, Fayetteville, AR, USA, ²IL Natural History Survey, Champaign, IL, USA, ³Forest Preserve District of DuPage County, Wheaton, IL, USA, ⁴Forest Preserve District of Cook County, River Forest, IL, USA, ⁵Forest Preserve District of Will County, Joliet, IL, USA, ⁶Lake County Forest Preserves, Libertyville, IL, USA

Genetic Patterns Among Rare and Common Turtle Species

Population genetic studies that incorporate life history information are important for informing management and conservation actions that seek to maintain biodiversity and preserve multiple species. The goal of this study was to use a comparative approach to evaluate population genetic patterns among rare (*Emydoidea blandingii*, *Clemmys guttata*) and common (*Chrysemys picta*, *Chelydra serpentina*) freshwater turtle species persisting in highly modified habitats across northeastern Illinois. These species differ in traits expected to modulate genetic structure across heterogeneous landscapes. Here, we employed microsatellite DNA analysis to investigate patterns of genetic structure and project future loss of genetic diversity for each species. Rare species exhibited more genetic divergence among populations compared to common species. However, a past bottleneck was only detected in *C. guttata*. Further, simulations showed that long-term loss of genetic diversity is inevitable in all four turtle species, but particularly imminent in *E. blandingii* and *C. guttata*. Differences in genetic patterns are likely attributed to a variety of factors including population size, dispersal capacity, habitat specialization, generation time, reproductive strategies, and historical processes. Lack of gene flow and genetic drift within species is potentially masked by long-generation times and relatively recent landscape modification. In addition to protection of habitats, long-term management should focus on maintaining gene flow, potentially considering actions such as translocation or head-start programs.

0123 Fish Morphology & Histology, Crystal 1 & 2, Saturday 18 July 2015

Mariangeles Arce H., Maureen O'Leary

Department of Anatomical Sciences, Stony Brook University, Stony Brook, NY, USA

Reinvestigating the Phylogeny of Ictaluridae, a Study Done Using MorphoBank

In this talk we present phylogenetic findings for the family Ictaluridae and we use this family as an exemplar taxon for the methodology of collecting morphological data using the NSF AVAToL Phenomics tools as linked to MorphoBank. The catfish family Ictaluridae is a group of North American freshwater fishes comprising eight genera (1

extinct) and 68 species - 52 living (12 with fossil records) and 16 extinct. The family originated at least by Late Paleocene and diversified during the Cenozoic on the dynamic paleogeographic stage of North America. Their relatively good fossil record, combined with a partly resolved phylogenetic framework, has provided insights on historical biogeography, minimum ages of origin for many ictalurid subclades, evolutionary novelties, and estimates of evolutionary rates. We used the NSF AVAToL Phenomic tools linked to the well-established web application and database, MorphoBank, to curate and illustrate morphological characters from previous morphological studies and gather molecular data available in Genbank to produce a total evidence, species-level phylogeny of living and fossil species of the Ictaluridae. Morphobank is a web application and database that allows users to build matrices linked to comparative phenomic data through a web browser interface. Within MorphoBank, users can label and score media in phylogenetic matrices, specify relationships among characters, and download matrices for analysis.

0044 Herp Ecology, Carson 4, Saturday 18 July 2015

James Archie

California State University Long Beach, Long Beach, CA, USA

Demographic Collapse (and Recovery) of Sky-island Populations of *Sceloporus occidentalis* in the Mojave Desert

Climatic fluctuations in the Mojave Desert of California include extended drought periods which have resulted in the collapse of populations of the western fence lizard (*Sceloporus occidentalis*). Over a 6 year period (2010-2015), which coincided with a severe 3-year drought, we carried out a mark-recapture study of two lizard populations (1450m and 1850m). The high elevation population was up to four times more dense than the low elevation population, which is at the lower elevation limit of the species. Both populations experienced a demographic collapse during the 2012 and 2013 seasons due to the lack of juvenile recruitment. The frequency of first-year lizards dropped from 55-83% of all lizards captured per hectare during the 2010-2012 sampling periods down to 0% in 2013 as no (i.e., zero) first-year lizards were found either on the sampling grids or anywhere on the mountain (10 sampling days and 225 person-hours of searching). Population densities declined by 50% (1850m) and 30% (1450m) over this period. In both localities, inter-annual adult recapture frequency (survivorship) *increased* following the severest drought year (2012-2013). During summer 2013, adult mid-summer dispersal activity occurred that was triggered by monsoonal rains. The lack of monsoonal events in 2012 resulted in higher *apparent* adult survivorship due to lack of monsoon-triggered dispersal. Although the drought in southern California continues, sporadic monsoonal and winter rains since summer 2013 have resulted in annual and perennial plant blooms and successful juvenile recruitment to the populations such that both populations are growing.

0556 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Csilla Ari^{1,2,3}, Dominic D`Agostino¹

¹University of South Florida, FL, USA, ²Foundation for Oceans of the Future, Budapest, Hungary, ³Manta Pacific Research Foundation, HI, USA

Sensory and Cognitive Experiments on Giant Manta Rays

Large, complex and highly foliated brain of Mobulid species suggest good sensory abilities and complex social behavior. The largest brain of all fish species is possessed by manta rays with exceptionally large optic tectum and telencephalon among elasmobranchs. Visual accuracy and wavelength sensitivity were tested on two captive giant manta rays and evidence for visual threshold and wavelength discrimination abilities were found. Self-recognition is one of the more advanced cognitive skills, which has never been proven in any fish species so far. Manta rays have high encephalization quotient similarly to those species that passed the mirror self recognition test, therefore mirror exposure experiments were conducted on two captive giant manta rays to document their response to their mirror image. The present studies show contingency checking and self-directed behavior of manta rays when exposed to a mirror, implying higher order brain function, sophisticated cognitive and social skills.

0557 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Csilla Ari^{1,2,3}, Dominic D`Agostino¹

¹University of South Florida, FL, USA, ²Foundation for Oceans of the Future, Budapest, Hungary, ³Manta Pacific Research Foundation, HI, USA

Melanosome Aggregations Might Cause Manta Ray Skin Change Color

Natural body coloration and spot markings of giant manta rays are used to identify individuals and to distinguish species. However, recent observations revealed rapid and long-term coloration changes of giant manta rays, suggesting that their body pigmentation is not permanent over their lifespan as assumed before. The rapid coloration changes happened within a few minutes, while such rapid changes were not described in other elasmobranch species yet. In order to reveal the mechanism of these changes, histological studies were performed on giant manta ray skin. The results suggest that changes of the degree of melanophore and melanosome aggregations might contribute to coloration changes in the manta ray skin. Further studies are needed to determine what regulates the changes in melanosome aggregations and to understand the role of such changes in giant manta rays.

0417 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Jonathan Armbruster, Milton Tan, Malorie Hayes, Carla Stout

Auburn University, Auburn, AL, USA

The Cypriniform African Invasion

Cypriniformes are relative newcomers to Africa. Approximately 20 MYA, the Afro-Arabian plate connected to Eurasia allowing an exchange of fauna between the continents. At least seven different groups of Cypriniformes entered into Africa: loaches, chedrins, *Barbus*, *Labeobarbus*, *Enteromius*, *Garra*, and *Labeo*. Two loach species of *Afronemacheilus* are known, but diversity of the other groups can be quite large with *Enteromius* likely being the largest genus of vertebrates (over 300 species). The diversity of African Cypriniformes will be discussed, and we will date the movement of the cyprinids into Africa. The oldest cyprinid fossils on the Afro-Arabian plate are from 18 MYA in Saudi Arabia, and the oldest known fossils of *Labeobarbus*-like fishes are from 10-12 MYA in Kenya. Drying of the Arabian Peninsula and the Sahara occurred ~5-7 MYA, and migration into Africa probably could not have occurred after desertification. Our preliminary estimates of ages of movement into Africa vary widely. Based on a strict clock on a cytochrome b dataset, *Enteromius* is ~27 MY old. On the other hand, estimates from chronos (ape package in R) on a phylogeny inferred using nuclear and mitochondrial genes, and a calibration point from gonorrhynchiforms, the other cyprinids are from 250K - 1.7 MY old. These preliminary estimates are either too old or too young, and more sophisticated analyses will be presented to examine the cyprinid invasion of Africa.

0329 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Lauren M. Armstrong, Christopher R. Tracy

California State University, Fullerton, Fullerton, CA, USA

Thermoregulatory Behaviors of the Insular Giant Chuckwalla, *Sauromalus varius*

Thermoregulatory behaviors of the insular giant chuckwalla (*Sauromalus varius*) have been poorly studied to date. This descriptive study aims to determine the preferred temperature range of *S. varius* in an enclosed thermal gradient, and use this as the basis for studying thermoregulatory behaviors in a semi-natural outdoor enclosure. iButton temperature dataloggers were attached to six giant chuckwallas using a gaffer tape vest. The lizards were individually placed within the thermal gradient and observed for twelve hours. Individuals selected temperatures from 33.7 °C to 40.4 °C in the thermal gradient, with an average selected temperature of 35.6 °C ± 2.14. Temperatures in the outdoor enclosure were measured using iButton vests on the lizards, and iButtons secured inside seven copper models placed at the areas identified to have the hottest and

coldest temperatures throughout the day. Preliminary data from the outdoor enclosure in mid-summer show that the lizards only reach their preferred temperature for an average of 1.4 hours per day. The copper models show that they have the capability to reach their preferred temperature for about 8.5 hours per day. This suggests that thermoregulation to their preferred temperature is not the highest priority in the summer, when suitable temperatures and food would have limited availability in their native habitat. The identification of a species' preferred temperature is crucial for understanding thermoregulatory patterns in the field. It can also provide useful information toward conservation efforts and potentially reveal how this endemic island species copes with rising temperatures in a rapidly-changing world.

0109 Fish Systematics II, Carson 3, Sunday 19 July 2015

Jairo Arroyave, John SS Denton, Melanie LJ Stiasny

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

Pattern and Timing of Diversification in the African Freshwater Fish Genus *Distichodus* (Characiformes: Distichodontidae)

Distichodus, the type genus of the African-endemic characiform family Distichodontidae, is a tropical freshwater fish clade that comprises 23 valid species and whose geographic distribution includes the Nile River basin and most Sub-Saharan drainages. This study investigates the phylogenetic relationships, timing and rates of diversification, and biogeographic history of *Distichodus* from a taxonomically comprehensive (~90% of species-level diversity) multilocus dataset (8 loci, including both nc- and mt-DNA markers) analyzed using Maximum Likelihood and Bayesian methods of phylogenetic inference (including multispecies coalescent), divergence time estimation, biogeographic reconstruction, and detection temporal shifts in diversification rates. The resulting fully resolved and robust phylogeny reveals the existence of two major clades of similar species-level diversity and provides support for the monophyletic status of most sampled species. Preliminary results indicate that the origins of the genus date back to the late Eocene/early Oligocene and the current distribution patterns are the result of a complex biogeographic history involving vicariance, dispersal, and range expansion scenarios, likely promoted by palaeohydrological fluctuations and landscape evolution processes occurring in Sub-Saharan Africa throughout the mid-Cenozoic to recent. Likewise, preliminary results suggest a near constant rate of lineage accumulation throughout this time period despite changing environmental conditions.

0012 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Roy Averill-Murray¹, Brian Henen², Terry Christopher³

¹U.S. Fish and Wildlife Service, Reno, NV, USA, ²Marine Corps Air Ground Combat Center, Twentynine Palms, CA, USA, ³Great Basin Institute, Reno, NV, USA

Reproductive Ecology of Female Sonoran Desert Tortoises (*Gopherus morafkai*)

We studied reproductive patterns in female Sonoran Desert Tortoises (*Gopherus morafkai*) for 10 years to evaluate reproductive variation and environmental factors that influence reproduction. Vitellogenesis occurred during the spring after emergence from hibernation, but was highly variable among individuals; egg production also varied considerably among individuals. Many individuals stopped vitellogenesis and failed to produce eggs each year, while many other females rapidly developed follicles and shelled eggs during a short period in the same spring. The smallest egg-producing female had a carapace length of 220mm, and no female produced more than one clutch per year. Compared to small females, large females were more likely to reproduce in a given year and produced larger eggs than did small females, but body size did not affect clutch size (3.8 to 5.8 eggs per year). More females reproduced following wetter than drier winters, and the earlier that females emerged from hibernation, the more likely they were to produce eggs. Early-emerging females also produced larger eggs than did females that emerged later. These reproductive traits contribute toward a life history that resembles an income-breeder more than the more capital-breeding strategy of the closely-related Mohave Desert Tortoise (*Gopherus agassizii*). These differences in life history may hold different implications for each species in the face of climate change.

0025 General Herpetology, Carson 1, Friday 17 July 2015

Agnes Awharitoma, Confidence Okoh, Augustus Ehiorobo, Omoyemwen Edo-Taiwo, Martins Aisien, Edema Imalele

University of Benin, Benin City, Edo State, Nigeria

Parasitofauna of Reptiles from Southern Nigeria

This study is part of an ongoing study of herps in Southern Nigeria to investigate the role of diseases and parasitism among factors responsible for herp population declines and range reductions. Reptiles examined: include *Osteolaemus tetraspis* (Africa dwarf crocodile), *Varanus ornatus* (Ornate Nile monitor), snakes belonging to families Pythonidae, Viperidae and Colubridae and *Hemidactylus brookii angulatus* (wall gecko). Snout-Vent Lengths [SVLs] were measured and the reptiles euthanized. Gastrointestinal tract and other organs of the viscera were examined for parasites. Isolated trematodes and cestodes were flattened and fixed with 10% formol-saline under cover slip pressure on a microscope slide and later stained with acetocarmine. Nematodes were fixed in hot 70% alcohol while pentastomids were preserved in 70% alcohol-saline. The study

yielded the following parasites: cestoda: *Duthiersia fimbriata*, unidentified pseudophyllidean (from *V. ornatus*), *Oochoristica* sp (from *H. brookii angulatus*) and *Ophiotaenia* sp. (from snakes); Trematoda: *Pseudoneodiplostomum thomasi* (from *O. tetraspis*), unidentified trematode (from *V. ornatus*) and *Paradistomoides gregarinum* (from *H. brookii angulatus*); Pentastomida: *Sebekia* sp. (from *O. tetraspis* and *V. ornatus*), *Raillietiella frenatus* (from *H. brookii angulatus*); Nematoda: *Dujardinascaris* sp., *Camallanus* larva (from *O. tetraspis*), *Tanqua tiara*, *Cosmocerca ornata*, *Oswaldocruzia hoepplii* (from *V. ornatus*), *Thelandros scleratus* (from *H. brookii angulatus*), *Kalicephalus* sp. and *Ophidascaris* sp. (from snakes). *Pseudoneodiplostomum thomasi* and *Duthiersia fimbriata* are new locality records in Nigeria. Noteworthy is the zoonotic importance of some of these parasites since the studied reptiles are either consumed or closely associated with human habitation.

0356 Fish Systematics II, Carson 3, Sunday 19 July 2015

Carole Baldwin, Victor Springer

Smithsonian Institution, Washington, DC, USA

Resolving *Ecsenius* (Blenniiformes: Blenniidae) Species Issues in the Middle East: It Takes an International Village

Research for a master's degree by an Iranian student at the Chabahar Maritime University has prompted another look at species issues surrounding *Ecsenius pulcher* (Murray 1887). *Ecsenius anomalus* (Regan 1905) was relegated to the synonymy of *E. pulcher* by Chapman & Schultz (1972), who believed that the banded pigment pattern characteristic of *E. pulcher* and the non-banded pattern characteristic of *E. anomalus* were male and female, respectively, patterns of a single species. Springer (1971) accepted this synonymy but noted that the two color patterns are not sex linked: he found that both sexes exhibit both patterns. Recent collections of banded and non-banded specimens from Iran provided the first tissue samples for genetic analysis, which revealed species-level divergence in COI between the two color forms, suggesting that *E. anomalus* should be resurrected as a valid species. Recent collections and genetic analyses of *Ecsenius* from Oman and Socotra by German colleagues, however, have complicated the taxonomic picture by introducing a new color pattern (spotted) from Socotra that is genetically the same as the Iranian non-banded "*E. anomalus*." To further complicate the taxonomic situation, there are non-banded *anomalus*-like individuals from Oman and Iran that are genetically the same as banded individuals from Oman and Iran. Currently there appear to be two genetically distinct species in the complex, *E. pulcher* and a new species, both of which have at least two color patterns that are not sex linked. Future genetic analyses to investigate the ostensible color polymorphisms are planned.

0115 Fish Morphology & Histology, Crystal 1 & 2, Saturday 18 July 2015

Vikram Baliga, Rita Mehta

University of California Santa Cruz, Santa Cruz, CA, USA

Kinematics of Picking Behavior in Wrasses

Cleaner fishes remove ectoparasites from other organisms. Observers have described the mouth movements of cleaner fishes as "picking" ectoparasites precisely and repetitively off clients. The term "picking" has also been described in the kinematic literature as "forceps-like" movements of the upper and lower jaws by cyprinodontiform taxa to selectively grasp specific food items from the water column. Whether the functional morphology of picking in cleaner fishes is similar to that of picking in cyprinodontiforms has yet to be systematically studied, and details of exactly how cleaner fishes capture their prey are lacking. Here, we filmed lateral views (at 1000 frames/second) of individuals from four species of wrasses (cleaners and non-cleaners) feeding on attached prey. Our kinematic analyses revealed that cleaners exhibit smaller magnitudes of lower jaw rotation, cranial rotation and peak gape values. Additionally, when we examined the correlation of timing variables, we found a higher degree of coordination (indicated by higher correlations) in upper and lower jaw movements in the picking behaviors employed by cleaners when compared to the biting behaviors of non-cleaning taxa in our study. These results indicate that the kinematic basis for cleaning behavior lies in low-displacement, highly-coordinated movements of the jaws that enable cleaners to selectively acquire prey items that are attached to a substrate.

0306 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Charles Bangley, Roger Rulifson

East Carolina University, Greenville, NC, USA

Is Pamlico Sound, North Carolina a "New" Nursery Habitat for the Bull Shark (*Carcharhinus leucas*)?

The bull shark (*Carcharhinus leucas*) is a seasonal visitor to North Carolina nearshore and estuarine waters, but juveniles have historically been rare in the state's waters. Catch and environmental data from North Carolina Division of Marine Fisheries gillnet and longline surveys were used to determine the suitability of Pamlico Sound as bull shark nursery habitat. All sharks were classified as adult, age 1+, or neonate based on recorded total length (mm). Generalized linear models were used to identify environmental and spatial factors related to the presence of each bull shark demographic. From 2007-2014, a total of 48 bull sharks were captured within the sound, of which 36 fell within age 1+ or neonate ranges. Bull sharks within juvenile length ranges were not captured prior to 2011, but were documented every year since. Environmental preferences did not differ significantly between age 1+ and neonate sharks, but adults were found at significantly greater depths and in closer proximity to inlets. Juvenile bull shark abundance was significantly related to temperature and salinity. Significant increases in mean water

temperature and decreases in mean salinity occurred in Pamlico Sound from 2007-2014, particularly in May and June when parturition occurs in other bull shark nurseries. These environmental changes may have created favorable conditions for a bull shark nursery in Pamlico Sound.

0460 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Max Bangs

University of Arkansas, Fayetteville, AR, USA

Phylogenomics and Introgression in the Evolutionary History of *Catostomus*

Species boundaries have long been thought to be semipermeable (i.e., the ability of some genomic regions to introgress more readily than others), but have only recently been examined thanks to methodologies that can now discern historic introgression from its consort, incomplete lineage sorting. Yet despite this, confusion is still rampant, especially in non-model organisms. For one, historic introgression in *Catostomus* is poorly documented despite the fact that contemporary hybridization is widely acknowledged. This has become the subject of recent debate due to incongruence between morphological and mitochondrial phylogenies, with some authors attributing historic introgression without formal testing. To resolve this debate we applied double digest restriction-site associated DNA sequencing (ddRAD) to develop a molecular phylogeny for a species-subset, to include several in the subgenus *Pantosteus*. A series of D-statistics were applied to examine proposed introgression events. Results highlight the porous nature of species boundaries in catostomid fishes, in that several introgression events were identified. A well-supported molecular phylogeny was also generated, even in the presence of introgression, using >100,000 parsimoniously informative SNPs. Results help interpret several proposed taxonomic revisions, to include the elevation of Bonneville Bluehead Sucker (*C. (P.) virescens*), Little Colorado River Sucker (*C. cf. crassicauda*), and Zuni Bluehead Sucker (*C. (P.) discobolus yarrowi*).

0128 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Amanda Barker, John Gold, David Portnoy

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

Identification, Stock Assessment, and Habitat Usage of Cryptic Hammerhead Sharks

The scalloped hammerhead (*Sphyrna lewini*) and the recently discovered Carolina hammerhead (*Sphyrna gilberti*) are cryptic species that are sympatrically distributed in

the southeastern United States. Differing only in the number of precaudal vertebrae, scalloped and Carolina hammerheads are morphologically conserved; a way to distinguish them *in situ* has yet to be determined. Due to its recent discovery and lack of morphological differentiation Carolina hammerheads have likely been included in previous stock assessment for scalloped hammerheads, leading to an overestimation of scalloped hammerhead abundance. We will use double digest restriction-site associated DNA (ddRAD) sequencing to genotype individuals at thousands of single nucleotide polymorphisms (SNPs), and a panel of SNPs will be identified that can be used to reliably identify each species. Genetic and ecological data will be used to estimate relative abundance and habitat utilization of each species within known nurseries off the east coast of the United States. Because nursery utilization may not be equivalent between the species, one or more nurseries may be critical to one or both individual species persistence. For both species we will also generate estimates of baseline genetic diversity and conduct a preliminary assessment of stock structure to provide information useful for future species-specific management.

0353 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Henry Bart¹, Ray Schmidt¹, Dorothy Nyingi², Nathan Gichuki³

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Phylogeographies of Six Co-distributed Clades of Cyprinine Fishes in Kenya (Actinopterygii: Cyprinidae)

Collections taken at nearly 100 sites on streams and lakes of central and southern Kenya from 2010-2012, with funding from NSF's International Research Experiences for Students (IRES) program and the US Agency for International Development's Partnership for Enhancing Expertise in Research (PEER) program, yielded specimens and tissues of several little known fish species. Here we report the results of molecular phylogeographic studies, involving nuclear and mitochondrial genetic markers, for six clades or species complexes of cyprinine fishes (*'Barbus' apleurogramma*, *'B.' kerstenii*, *'B.' paludinosus*, *Garra* spp., *Labeo* spp., *Labeobarbus* spp.) collected from the Lake Victoria, Lake Naivasha, Ewaso Nyiro, Lake Natron, Athi, Tana and Pangani basins. Phylogenies produced for all of the groups contain more divergent lineages than the numbers of species currently recognized as valid. However, divergence histories differ across the groups, both in terms of numbers of distinct lineages and geographic patterns of divergence. Diversity and divergence histories for each of the groups will be discussed, and an attempt will be made to collate the histories into a general ichthyogeographic hypothesis for the region with divergence time estimates.

0438 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Ryan Barton¹, Matthew Davis³, W. Leo Smith², Joseph Munoz¹, Michael Ghedotti¹

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

Morphology and Evolution of Bioluminescent Organs in the Glow Bellies and Sweepers (Acropomatidae and Pempheridae).

Recent molecular phylogenetic analyses have consistently recovered a clade containing the Acropomatidae (glow bellies) and Pempheridae (sweepers). These families include a range of bioluminescent and non-bioluminescent taxa. The bioluminescent organ within this group has been reported to be an extension of the intestine harboring bioluminescent bacteria in the genus *Photobacterium*. The histology and gross anatomy of the bioluminescent organ and the homologous visceral structures in non-bioluminescent taxa are discussed within a phylogenetic context derived from multi-gene DNA-sequence data. These preliminary results suggest a complex history of origin and loss of visceral bioluminescence in this group.

0015 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Maria Delia Basanta¹, Andrés García²

¹Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, México, Distrito Federal, Mexico, ²Estación de Biología Chamela, Instituto de Biología, Universidad Nacional Autónoma de México, San Patricio, Jalisco, Mexico

Identification of Hotspots and Biological Corridors for Herpetofauna within two Priority Terrestrial Regions for Conservation in Western Mexico

The biodiversity crisis includes an important declination of many amphibian and reptile populations and species. The identification of species richness and endemism hotspots within a diverse region is important to prioritize conservation efforts. Western Mexico concentrates a third of Mexican biodiversity, species richness, endemism and endangerment, especially in reptiles and amphibians. This has been recognized by the establishment of several protected areas and the recognition of two terrestrial priority regions, the Chamela-Cabo Corrientes and the Manantlan-Colima Volcano. In this work, we modeled actual potential distribution of 129 amphibian and reptile species found in these regions and determined the correspondence of hotspots of species richness, endemism and endangerment with protected areas and vegetation cover and conservation status. We found 10 areas with high priority for conservation due to their coincidence in high values of richness, endemism and endangerment. Based on the analysis of such patterns along with the spatial distribution of vegetation types, roads and topography, we were able to identify potential biological corridors among those areas. The significant correspondence among areas of high richness, endemism and

endangerment, suggest these should be considered for official protection to complement the existing ones that failed to include most of these areas. Landscape heterogeneity across the study area with potential biological corridors and multiple ecosystems provides an excellent scenario for the implementation of conservation measures in such areas and their connection based not just on biodiversity but social, economic and political factors.

0108 Herp Physiology & Reproduction, Carson 4, Friday 17 July 2015

Steve Beaupre

University of Arkansas, Fayetteville, AR, USA

Reanalysis of Long-Term Field Metabolic Rate Data from Timber Rattlesnakes: Critical Factors and Implications

Mechanistic studies of energy flux facilitate development of a more predictive understanding of organismal responses to environmental change. Field metabolic rate (FMR) measures energy allocation to biochemical (anabolism/catabolism) and to physical activity. Energy expenditure can be affected by many factors (thermal environment, resource availability, social interactions) thus, FMR provides insight regarding ecological factors that influence the mass-energy condition, and rates of energy flux within individuals. I used the doubly-labeled water method to measure FMR in a large sample of radio-tagged Timber Rattlesnakes (*Crotalus horridus*) at a long-term study site in Northwest Arkansas. One hundred and ninety-five measurements of FMR were made among 59 individuals during the active season (May-September) for nine years (1996 to 2004 inclusive). FMR scaled allometrically with body mass following $0.477W^{1.13}$. Water efflux and influx was nearly isometrically related to body mass. Significant variation in the magnitude of FMR was apparent among years and among seasons (spring-summer transition, summer, and summer-fall transition). Supplemental feeding increased FMR by a factor of two over control snakes that foraged naturally. No effects of sex or ecdysis cycles on FMR were apparent. However, water efflux was significantly affected by ecdysis. Variability in FMR of Timber Rattlesnakes, especially with respect to annual variation, elicits caution when interpreting scaling relationships based on small samples from geographically focused and temporally limited studies. Mass scaling exponents that exceed 1.0 have been previously reported among snakes. These observations have potentially important implications for estimating energy budgets and interpreting of factors that influence FMR.

0427 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

Christine Bedore¹, Nicholas Wegner²

¹Georgia Southern University, Statesboro, GA, USA, ²Southwest Fisheries Science Center, National Marine Fisheries Service, La Jolla, CA, USA

Sensory Ecology of Elasmobranch Fishes

The sensory systems of chondrichthyan fishes are thought to represent the basal vertebrate condition from which more advanced modalities arose. Additionally, elasmobranch fishes inhabit nearly every marine environment and correspondingly represent a wide range of ecological adaptations. Therefore, elasmobranchs demonstrate an impressive array of sensory adaptations that correspond to their individual niches and provide ideal subjects for studying sensory adaptation to biological and physical environments. For example, most batoids possess duplex retinæ comprised of rod and cone photoreceptors, although the potential for a species to have color vision varies with the spectral composition of the habitat. Cownose rays, *Rhinoptera bonasus*, have two cone pigments with color sensitivity that corresponds to their turbid, green-dominated, estuarine habitat. Similarly, yellow stingrays, *Urolophus hannah*, have three cone pigments that correlate to their inhabitation in clear, spectrally rich reef-associated waters. Additionally, differences in visual temporal resolution, the ability to track moving objects, differs between these two species with the active, schooling cownose rays suffering a lower reduction in temporal resolution with decreases in ambient light levels and temperature. The reduced thermal sensitivity, combined with possession of a cranial rete, suggests that cownose rays may use cranial endothermy, or “brain warming”, to minimize reductions in nervous and sensory function when challenged with environmental temperature changes. Due to their small size relative to most cranial endotherms, as well as their ease of collection and maintenance in the laboratory, cownose rays make ideal models for testing unresolved hypotheses regarding sensory-driven evolution of cranial endothermy in fishes.

0415 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Katherine Bemis, Benjamin Marcy-Quay, Patrick Sullivan, Irby Lovette, William Bemis

Cornell University, Ithaca, NY, USA

Deep-water Dragonets (Teleostei: Callionymidae: *Foetorepus*) from the Mid Atlantic Bight: A Little-known Genus from the Edge of the Continental Shelf

The ranges of two relatively rare species of deep-water dragonets – the Spotfin Dragonet (*Foetorepus agassizii*) and the Palefin Dragonet (*F. goodenbeani*) – overlap on the outer continental shelf of North America in the Mid Atlantic Bight. We studied more than 400 specimens collected between 2009-2014 by the Northeast Fisheries Science Center and

their associated data. These samples allowed us to better characterize the geographic and depth distributions of the two species, describe aspects of their reproductive biology, and consider general questions about deep shelf and continental slope habitats. The two species occurred in a subset of locations within the sampled area (71 of 3887 stations), and their densities were related to latitude, longitude and depth. Density hotspots were associated with areas near submarine canyons. Although *F. agassizii* and *F. goodenbeani* occur at similar latitudes and longitudes in the western North Atlantic, *F. agassizii* occurs at greater depths, 50 m deeper than *F. goodenbeani*. Macroscopic and histological analysis of reproductive condition indicated active spawning by both species in September and October. Females collected in these months had oocytes in many stages, indicative of asynchronous oocyte development and batch spawning. Collection locations and depths in spring and fall were similar, suggesting *F. agassizii* and *F. goodenbeani* do not migrate seasonally, perhaps because they occur in habitats with stable year-round temperatures. Many species of outer continental shelf and slope fishes remain poorly known, and these two species of *Foetorepus* offer a window into the biology of shelf fishes.

0181 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kasey Benesh, Milton Tan, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Shape Variation and Evolution in the Genus *Phenacobius*

The genus *Phenacobius* contains five species of suckermouth minnows native to the United States. We investigated the correlation between shape variation of species in *Phenacobius* and their evolutionary relationships. We used geometric morphometrics to examine the shape difference between these species. We performed a principle component analysis to see what explained the most variation of shape between the species, and a canonical variate analysis to identify what shape variation contributed to the separation of these groups. We found that body depth explained a majority of the variation between the five species. We then constructed a phylogenetic tree based on genetic sequences obtained from GenBank. We then mapped the phylogeny into shape space to evaluate if the morphological data was an indicator of the evolutionary relationships of these species. We found that, in this case, phylogeny was not a good indicator of shape similarity, and the resultant tree had no phylogenetic signal. Ecological variation between species could explain these shape differences better than phylogeny, however there is little known about the ecological variation between species of *Phenacobius*.

0274 Herp Physiology & Reproduction, Carson 4, Friday 17 July 2015

Amanda Bennett, Jessica Longhi, Leslie Kerr, Dennis Murray

Trent University, Peterborough, Ontario, Canada

Terror at the Old Pond: The Acute and Chronic Physiological Response of Anuran Larvae to Predation Risk

Anuran larvae can decrease activity and modify tail shape upon detection of chemical cues released when conspecifics are consumed by odonate predators; these changes increase survivorship in high predation risk environments. The physiological mechanism underlying the morphological response to predation risk is corticosterone, a stress hormone released through the activation of the hypothalamic-pituitary interrenal axis. However, the mechanism behind behavioural plasticity remains enigmatic, possibly because the time scale of previous work has examined physiological changes between several hours to multiple weeks of exposure. Since tadpoles can alter behavioural responses to predation risk in less than one hour post-exposure, behavioural plasticity may be a reflection of corticosterone changes at an acute (< 1 hr post-exposure) time scale. Therefore, we characterized the acute response to odonate predator cues (and controls) by sampling whole-body corticosterone in wood frog (*Lithobates sylvaticus*) tadpoles every 10 minutes for 90 minutes of exposure. Tadpoles increased whole-body corticosterone levels to a peak at 20-30 minutes when exposed to predator cues. We then characterized the acute response to both a known and novel predator after three weeks of chronic exposure to predation risk, and noted an overall decline in reactivity. Last, we examined how chronic exposure to predators alters baseline corticosterone levels after three and six weeks of exposure in Northern leopard frog (*L. pipiens*) tadpoles, noting a four-fold increase in baseline corticosterone after three weeks and a drop back to controls after six. Thus, the perception of risk, as evidenced by a physiological response, changes during tadpole development.

0116 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4, Thursday 16 July 2015

Stephanie Benseman, Larry Allen

California State University, Northridge, Northridge, CA, USA

Distribution, Growth Estimates, and Ecology of Young-of-the-Year of Giant Sea Bass, *Stereolepis gigas*, off Southern California

Completed life history information on an ecologically, and once economically, important species such as the giant sea bass (*Stereolepis gigas*) is critical for the continued management of its fishery. Little is known about the life history of *S. gigas* due to the overexploitation of their stock in the early 1900's. Their depressed population has prevented detailed research for most of the 20th century. This species is therefore an excellent model for the recovery of long-lived, slow-growing, late-maturing organisms

aiding in future designs for other similarly threatened species. The goal of this study is to finally fill in gaps in the early life history of the young-of-the-year of giant sea bass by 1) determining distribution and general ecology for *S. gigas* in the wild, and 2) estimating growth rates based on site aggregations and otoliths analysis. SCUBA transects and laser measurements have been used to estimate cohort abundances and sizes in the field. Daily growth rings in otoliths from individuals collected will be analyzed to determine planktonic larval duration and daily growth rates. This study is the first of its kind to study these juvenile giants in their natural environment. An understanding of the growth rates will better inform future fisheries management decisions, while distribution information can be used to distinguish and protect important nursery areas. The early developmental information found in this study is a crucial missing piece of early life history of this critically endangered species, and will form a much needed baseline for the study of other polyprionids.

0409 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Andrea Bernard¹, Cassandra Ruck¹, Vincent Richards², Jim Gelsleichter³, Kevin Feldheim⁴, Mahmood Shivji¹

¹Save Our Seas Shark Research Center, Nova Southeastern University, Dania Beach, FL, USA, ²Clemson University, Clemson, SC, USA, ³University of North Florida, Jacksonville, FL, USA, ⁴Field Museum, Pritzker Laboratory for Molecular Systematics and Evolution, Chicago, IL, USA

The Genetic Connectivity of a Euryhaline Elasmobranch, the Atlantic Stingray (*Dasyatis sabina*)

Identifying the genetic connectivity of elasmobranchs inhabiting coastal waters remains an important global priority, as these species are particularly susceptible to human mediated impacts and declines given their close proximity to highly populated areas. The Atlantic stingray (*Dasyatis sabina*), a small, coastal species whose range spans the western North Atlantic (Florida to Chesapeake Bay) and Gulf of Mexico, is one of the few elasmobranchs capable of occupying both estuarine and freshwater habitats. Within Florida waters, a putative 'resident' population inhabits the freshwater St. Johns River System (SJRS); however, the extent of this population's connectivity to the remainder of its distribution remains unknown. To examine the genetic connectivity of the Atlantic stingray across its southern US distribution, including the SJRS, a total of 312 individuals from 11 sampling locations were genotyped at nine species-specific microsatellite loci. Population- and individual-level analyses identified high levels of genetic population structure among collections, with coastal populations within the Gulf of Mexico showing high genetic structure ($F_{ST} = 0.011 - 0.034$; $P < 0.05$) and a signal of isolation by distance ($R^2 = 0.957$; $P = 0.041$). Interestingly, individual-based analyses showed that freshwater SJRS animals were differentiated from other locations, suggesting that these individuals may truly represent a 'resident' freshwater population. The presence of high genetic population structure, coupled with what may be locally adapted populations, suggests that care must be taken to conserve this species, as the extinction of even a

single population may result in the irreversible loss of genetic diversity and adaptive potential.

0552 Herp Physiology & Reproduction, Carson 4, Friday 17 July 2015

Catherine Bevier

Colby College, Waterville, ME, USA

The Effects of Modulating the Skin Microbiome on Skin Secretion Proteins in Four Frogs from Maine

Amphibians produce many important compounds in their skin glands, including antimicrobial peptides (AMPs) important for protection against pathogens. Interesting evidence that AMP activity is modulated by the presence of epibiotic microbes, both beneficial and pathogenic, suggests that there are vital relationships among AMP production, epibiotic communities, and healthy amphibian populations. Here I tested the hypothesis that the production of skin secretions is stimulated by the presence of a microbial skin pathogen. I included male frogs of four species native to Maine that use different microhabitats during the breeding season. Woodfrogs and mink frogs, *Lithobates sylvaticus* and *L. septentrionalis*, spend significantly more time in the water than the terrestrial spring peeper and gray treefrog, *Pseudacris crucifer* and *Hyla versicolor*. Individuals from each species were placed in different groups, and we compared protein concentrations of skin secretions collected from frogs at different time points of the experiment. Higher protein concentrations likely reflect greater up-regulation of secretion production, presumably in response to a pathogen or other disturbance. Three control groups were used to account for effects of captivity and manipulations. Treatment frogs were sterilized with topical antibiotics for 72 h, then inoculated with the microbial pathogen, *Aeromonas hydrophila*. In general, protein concentrations of skin secretions varied greatly among individuals, even at the start of the experiment, and there were few consistent differences among species and among treatment and control groups within a species. Further analysis of these skin secretions is needed, especially given that some species in this study produce effective AMPs.

0028 Fish Ecology II, Carson 3, Sunday 19 July 2015

Jennifer Bigman¹, Brian Bergamaschi², Marina Brand³, Garrett Liles³

¹*Simon Fraser University, Burnaby, BC, Canada*, ²*U.S. Geological Survey, Sacramento, CA, USA*, ³*Delta Science Program, Sacramento, CA, USA*

Fishy Food Web Dynamics of the Sacramento-San Joaquin Delta

Severe declines of both native and non-native fishes in the Sacramento-San Joaquin Delta (Delta) have occurred over the past several decades (Moyle 2002, Kimmerer 2004),

and are thought to be caused by multiple factors but can be linked to a changing food web (Bigman et al. *in prep*). The food web in the Delta involves many complex relationships and dynamics across its constituents, and despite being highly studied, lacks synthesis which has confounded its effects on fishes in the system (Bennett et al. 1995, Kimmerer 2004, Lehman 2004, Glibert 2010). We synthesized how fishes in the Delta have been affected by a changing food web with respect to its constituents, habitat modification, nutrient dynamics, and hydrodynamics. We found that the current food web bears little resemblance to that of the past in terms of phytoplankton, zooplankton, and the factors that regulate these communities. Large shifts of phytoplankton and zooplankton abundance and species composition have occurred (Lehman 1996, Winder and Jassby 2011). These relationships are strongly influenced by various regulating factors that facilitate changes such as hydrodynamics, nutrient concentration, and invasive species, all of which have changed (Glibert 2010, Lucas et al. 2011, Thompson et al. 2013). Habitat modification has also influenced the food web (Nichols 1986), and has contributed to the decline of fishes. Understanding food web dynamics is crucial to providing insights regarding the overall functioning of the entire system. This effort resulted in a greater understanding of the intricacies of this complex system and has countless policy implications.

0606 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Joseph Bizzarro¹, Simon Brown², Heather Robinson², David Ebert², Adam Summers¹

¹*University of Washington, Seattle, WA, USA*, ²*Pacific Shark Research Center, Moss Landing, CA, USA*

How Can There Be So Many Skate Species?

Skates (Rajiformes: Rajidae) are an extremely diverse group of cartilaginous, marine fishes; yet, they have historically been considered to occupy unconsolidated habitats and serve similar trophic roles. The hypothesis of ecological redundancy in skates was evaluated using diet composition data from two eastern North Pacific skate assemblages (central California, western Gulf of Alaska). Species-specific diet compositions differed significantly in both regions, supporting the alternative hypothesis of trophic separation in skates. The timing and location of hauls was the most important consideration in explaining the substantial dietary variability in each assemblage and reinforces the perception that skates are generalist predators. Dispersion analyses were highly significant, however, indicating additional extreme within-group variability in skate diet among these variables. Canonical correspondence analysis was used to associate specific variable factors with prey taxa and supported the general concept of greater piscivory and less reliance on small crustaceans with increasing total length. Diet composition and trophic level of *Beringraja binoculata* and *Raja rhina* differed considerably between regions and indicated a greater reliance on crustaceans in Alaska and fishes in California. These results, coupled with those of a complementary study of spatial relationships, demonstrate that skates are more ecologically diverse than previously

reported. Pronounced differences in core resource use across broad, overlapping spectrums of trophic and spatial tolerances: 1) probably facilitate the coexistence of speciose skate assemblages, and 2) may explain the remarkable taxonomic diversity in this group. Ecological studies and fishery management plans that incorporate ecosystem considerations should incorporate species-specific data for skates.

0134 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Rebecca Blanton, C.M. Gienger, Floyd Scott

Austin Peay State University, Clarksville, TN, USA

Increasing Accessibility and Long-term Viability of the APSU David Snyder Museum of Zoology Natural History Collections

Austin Peay State University's David Snyder Museum of Zoology (APSU; established in 1963) is a significant collection of vertebrates from the Mid-South region of the United States. With over 50,000 cataloged specimens representing 759 species from 195 families, it includes the largest collection of amphibians and reptiles and fastest growing fish collection in Tennessee. Recent expansion from acquisition of orphaned collections, increased repository services, and research activities necessitated storage of specimens in areas not affording protection from fire and earthquake damage and restricted potential for future growth and continued service as a regional repository. Although collections are used in research, education, and outreach locally, use by the broader scientific community has been restricted by limited online accessibility. The goals of this project were to: (1) secure existing collections, and (2) increase their overall utility and accessibility. To accomplish these goals, high-density storage units were installed to eliminate space constraints and associated specimen damage from overcrowding and improper storage, while concomitantly providing adequate room for future growth and continued repository services. Efforts to increase accessibility are ongoing but will be expanded to include georeferencing all collections and integrating existing databases into a single Specify database made accessible through a newly developed APSU website and data-sharing portals, including iDigBio. These activities will ensure long-term viability of the APSU vertebrate collections and will transform a currently underutilized, yet regionally significant, collection into a broadly used resource that will enhance research and education of the faunally diverse Mid-south region.

0418 Fish Biogeography, Carson 3, Saturday 18 July 2015

Devin Bloom¹, Haley Ohms²

¹Willamette University, Salem, OR, USA, ²Oregon State University, Corvallis, OR, USA

On the Origins of Diadromy: A Conceptual and Empirical Evaluation of Alternative Hypotheses

Diadromous fishes undergo extraordinary migrations between oceans and freshwater habitats for feeding and reproduction. Despite a long-held fascination with diadromy and the iconic species such as salmon, eels, shad, lamprey and sturgeon that undergo these migratory loops, explanations for the evolutionary origins of diadromy remain elusive. There are two major modes of diadromy: catadromy and anadromy, which have mirror opposite migratory loops. Catadromous species feed in freshwater and reproduce in oceans, while anadromous fishes feed in oceans and reproduce in freshwater. The contrasting directionality of these migration patterns remains unexplained. The most widely accepted explanation for the evolution of diadromy is the productivity hypothesis, which suggests that individuals capitalize on productivity gains by feeding in oceans in temperate regions and freshwaters in tropical regions. An alternative explanation, the safe-site hypothesis, suggests diadromy evolves in response to differences in predation pressure across marine and freshwater environments. Here we consider the conceptual justification for these hypotheses and evaluate empirical evidence for these hypotheses in several groups of fishes, including shad, herring, anchovies, salmonids, tetraponids, and lamprey. We find little evidence supporting the productivity hypothesis and suggest alternative explanations for biogeographic patterns of diadromy, including the importance of paleographic events and competition. Finally, we propose integrating phylogenetic history and mathematical modeling to comprehensively evaluate alternative hypotheses for the evolution of diadromy.

0206 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Sarah K. Bolton, Matthew W. Russell, Ralph A. Saporito

John Carroll University, University Heights, OH, USA

Are Variable Alkaloid Defenses in the Dendrobatid Poison Frog *Oophaga pumilio* Perceived as a 'Palatability Spectrum' to Arthropods?

Conspicuously colored dendrobatid frogs sequester alkaloid-based chemical defenses exclusively from an arthropod diet, and differences in the availability of arthropods lead to variable alkaloid defenses. Although fundamental to understanding predator-prey interactions, little research has examined how predators perceive and respond to variable defenses in dendrobatids. Studies have demonstrated that variation in *Oophaga pumilio* alkaloids are related to differences in toxicity, using minimum lethal dose, LD₅₀, and irritability assays with laboratory mice; however, mice are not natural predators of

this species, and it is unclear how alkaloid toxicity translates to predator avoidance. Although toxicity is one measure of alkaloid defense, it is more likely that predator avoidance is based upon differences in the relative palatability of alkaloids. Arthropods that utilize chemoreception are among the natural predators of *O. pumilio*, and it is possible that alkaloid variation is perceived as a 'palatability spectrum'. Herein, we will report the results of a study aimed at determining if variation in alkaloid defenses among populations of *O. pumilio* are perceived as differences in palatability using the fruit fly *Drosophila melanogaster* as a general arthropod model. Fruit flies will be used in a series of 'palatability assays' to determine the link between variable alkaloid defenses and palatability. Due to the extensive variation in alkaloid defenses among and within populations of *O. pumilio*, we predict that *D. melanogaster* will perceive differences in alkaloids as a 'palatability spectrum'. Our results will represent an important first step in understanding how arthropod predators may perceive dendrobatids with variable alkaloid-based defenses.

0465 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Karine Bonatto, Priscilla Silva, Luiz Malabarba

Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil

Parasitic Catfish Feeding on Mulletts: An Unexpected Discovery

Fish diets are traditionally studied through the direct identification of food items found in their stomachs. Fish preys of the parasitic catfishes of the subfamilies Vandelliinae and Stegophilinae (Trichomycteridae), however, cannot be identified by usual methods due to their lepidophagic, hematophagic and mucophagic habits, being known from few records of direct observations. Herein we test the use of sequences of cytochrome oxidase subunit 1 (COI) to identify preys of the mucophagic and lepidophagic catfish *Homodiaetus anisitsi* through the mucous and scales found in their stomach contents, and test the results from different methods of preservation of the whole fish for analysis. We test GenBank as a source for the identification of fish preys versus local barcode inventories. Best results for the extraction and molecular identification of stomach contents were obtained from specimens fixed in ethanol 70%, than from those frozen or preserved in absolute ethanol. Prey species were successfully identified through comparison to local barcode inventory, with a single COI allele found in each stomach. The use of Blast tool of GenBank was unsuccessful, resulting in wrong identifications due to the lack of local species in that database. New and unexpected prey species (*Bryconamericus iheringii*, *Cyphocharax voga*, *Mugil liza*) were found in the stomach contents of *Homodiaetus anisitsi*, being all substrate feeders. We concluded that DNA sequencing analysis is an essential tool for the comprehension of dietary habits of parasitic catfishes feeding on mucous, scales or blood of other fish, but it needs local barcode inventories for accurate results.

0518 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Damien Bontemps¹, Rafael Joglar¹, Elvira Cuevas¹, Eileen Ortiz²

¹University of Puerto, Rio Piedras, San Juan, Puerto Rico, ²Department of Environmental and Natural Resources, San Juan, Puerto Rico

Use of Combined Stomach Content and Stable Isotope Analysis in Predicting Direct Foraging Impacts of the Introduced Spectacled Caiman (*Caiman crocodilus*) in Puerto Rico

The spectacled caiman (*Caiman crocodilus*) was introduced to Puerto Rico over 50 years ago in the Tortuguero Lagoon Natural Reserve (TLNR). It is now considered an established species counting among the exotic apex predators of the island. Concerns are raised in regards with potential foraging impacts at multiple trophic levels. Previous attempts to control its dispersion have failed in part due to the nearly non-existent information available. For this study, measurement data were obtained from 130 caimans across all life stages from October 2014 to March 2015 within the TLNR. Stomach contents were retrieved and analyzed based on prey category frequency of occurrence. Caiman muscle samples were collected for stable isotope analysis (SIA). Representative prey species were selected and collected based on principal prey groups observed in stomach contents. Isotopic signatures of predators and prey were analyzed using the SIAR statistical package to obtain nitrogen and carbon source proportion respective to different life stages. Aquatic insects were the most abundant prey items retrieved with 92.9% and 64.6% in hatchling and juvenile stomach respectively. In adult caimans, fish remains were the most significant prey items with 37.8% frequency of occurrence. Results obtained from SIA generally concurred with those obtained from stomach content analysis. This study provides novel information on dietary habits of spectacled caimans in Puerto Rico aiming to carefully design future management strategies. It further promotes the use of stable isotope analysis as a rapid and efficient tool to determine the diet of apex predator in introduced ecosystem.

0513 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4, Thursday 16 July 2015

Nassima Bouzid, Adam Leaché, Lauren Buckley

University of Washington, Seattle, WA, USA

Consequences of Geographic Variation in Lizard Body Size for Climate-Driven Range Shifts

Changes in species ranges in response to climate change are limited by the availability of suitable habitat. Western fence lizards (*Sceloporus occidentalis*) occupy a diverse range of environments, and populations in different habitat types are known to vary in body size, which may result in differences in performance, thermal ecology and ultimately different responses to climate warming. Using museum specimens, we quantify snout-

vent length for genetically distinct populations. We predict the operative temperatures of lizards using biophysical models tailored to the average body size of each population. Finally, we incorporate the energy and performance implications of operative temperatures in a demographic model to approximate geographic distributions under current conditions and a realistic climate change scenario. We plot projected distributions using both (a) body sizes estimated from empirical data and (b) simulated optimum body sizes. Our results suggest that increasing the biological specificity in theoretical models and scaling these models down to the population level, especially for wide-ranging species that inhabit diverse habitat types, will more reliably predict range shifts in response to climate change.

0186 Fish Ecology II, Carson 3, Sunday 19 July 2015

Katie Bowen, Tracey Sutton

Nova Southeastern University, Dania Beach, FL, USA

Pelagic Habitat Use by Juvenile Reef Fishes in the Northern Gulf of Mexico

The assemblage composition, abundance, biomass, and vertical distribution of juvenile reef fishes in the offshore pelagic habitat of the northern Gulf of Mexico are described. This study, a component of the NOAA-supported Offshore Nekton Sampling and Analysis Program, is the first to examine juvenile reef fish distributions across the oceanic northern Gulf of Mexico after the *Deepwater Horizon* oil spill. Results presented here are derived from a 3-month, spring/summer research cruise in 2011 on the M/V *Meg Skansi*. A 44-station sampling grid covering an area of 420 X 120 nautical miles was sampled with a 10-m² MOCNESS midwater trawl from the surface to a depth of 1500m, both day and night at each station. A total of 85,475 fish specimens were collected from 373 samples, including 767 reef fish specimens representing 52 species from 29 families. Initial analysis has revealed the presence of juveniles of some species in locations where adults are not known to occur. Juveniles were found almost exclusively in the uppermost 200m of the water column. A greater number of individuals were collected in nighttime trawls. Surprisingly, some individuals were sampled between 1000-1500m. During the MS7 sampling program, hydrographic profiles of the water column were recorded. This information provides the hydrographic background setting against which the coastal reef fish distributions in the offshore pelagic habitat of the Gulf of Mexico can be characterized. Results of fish distributions as a function of location (relative to the shelf break) and major mesoscale oceanographic features will be presented.

0293 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Beth Bowers, Stephen Kajiura

Florida Atlantic University, Boca Raton, FL, USA

Migratory Behavior of the Blacktip Shark (*Carcharhinus limbatus*)

The migratory behavior of the blacktip shark (*Carcharhinus limbatus*) in the Western Atlantic has been anecdotally described but not empirically studied. The sharks are thought to migrate from nursery areas along the southeastern coast of the United States in the summer, to South Florida, where they remain in large aggregations (up to 800 sharks km⁻²) from January to April before returning northward. The first recorded description of the blacktip shark migration states that they occur north of Cape Hatteras, NC “only as a rare stray.” Given that this description was published over 70 years ago, their range might have shifted poleward in response to warming ocean temperatures, as has been demonstrated in many other marine species. To investigate the current migratory pattern of this population, ten blacktip sharks were instrumented with acoustic transmitters, while they overwintered in South Florida, and passively tracked along the eastern coast in cooperation with the Florida Atlantic Coast Telemetry (FACT) and the Atlantic Cooperative Telemetry (ACT) networks. Seven of the ten individuals were detected after instrumentation. Three of those seven individuals were detected far north of the previously reported NC limit, off Delaware Bay, NJ (1) and Long Island, NY (2). Five individuals were detected at the original capture location in South Florida the following winter, including two of the sharks that were detected in Delaware Bay and Long Island. This study provides the first empirical evidence of blacktip sharks completing a full migration cycle and suggests that their northern limit may have expanded poleward.

0202 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

David Boyd, Lawrence Page

Florida Museum of Natural History, Gainesville, FL, USA

Review of the Horseface Loaches (Cobitidae, *Acantopsis*), with Descriptions of New Species from Thailand

Species of *Acantopsis* (Cobitidae), fishes with the English name of horseface loaches, are a morphologically unusual group that has received surprisingly little attention by systematists. The genus ranges from India to Laos and south to Borneo and Java. Populations show considerable morphological variation, most notably in general body shape, mouth morphology and color pattern. In spite of this variation, only six names are available throughout this very large area: *A. dialuzona* van Hasselt 1823, described from Java; *A. choirorhynchos* (Bleeker 1854), described from Sumatra; *A. spectabilis* (Blyth 1860) described from Myanmar; *A. octoactinotos* Siebert 1991, described from Borneo; *A. thiemmedhi* Sontirat 1999, described from Thailand; and *A. multistigmata* Vishwanath & Laisram 2005, described from Manipur, India. Of these, only *A. dialuzona*, *A. spectabilis*,

A. octoactinotos, and *A. thiemmedhi* are considered valid by recent researchers. However, data from throughout the range of *Acantopsis* suggest that all six names are valid and that several species have yet to be recognized and named.

0207 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Sean P. Boyle¹, Jacqueline D. Litzgus¹, Chad Chordes², Corina Brdar³, David Lesbarrères¹

¹Laurentian University, Sudbury, Ontario, Canada, ²Ministry of Natural Resources and Forestry, Peterborough, Ontario, Canada, ³Ontario Parks, Kingston, Ontario, Canada

You Want Me to Put That Where?!? Evaluating Methods of Identifying Road Mortality Hotspots

Road mortality is recognized as one of the most significant drivers of local and broad landscape scale extinctions in herpetofauna globally. Systems of mitigating road mortality for herpetofauna have varied greatly with regards to approach, scale, and design. This lack of consistency has hindered conservation of many at risk species, as well as the progress of road ecology in general. Here we discuss three critical elements for consideration when planning herpetofauna road mortality mitigation: a) rigorous sampling protocols and analytical methods for long term evaluation of effectiveness, b) appropriate temporal variation of surveys both within and between years to control for environmental stochasticity and c) comparative analyses of methods which can be used to identify road mortality hotspots. Using regular surveys over two years, road mortality hotspots were identified by statistically pinpointing spatial aggregations of herpetofauna, alive or dead, on the road. These hotspots were compared to those predicted by Circuitscape, a program which identifies movement through a landscape by treating animal movement like current moving through a circuit board. The results of our study demonstrate that road mortality hotspots vary from year to year, and as such multiple years are required for a comprehensive mitigation strategy. Furthermore, our comparative approach to hotspot identification provides managers with the tools they need to efficiently and effectively coordinate the usage of limited funds available for conservation.

0208 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Sean P. Boyle¹, Jacqueline D. Litzgus¹, Corina Brdar², David Lesbarrères¹

¹Laurentian University, Sudbury, Ontario, Canada, ²Ontario Parks, Kingston, Ontario, Canada

Road Work Ahead: Halfway Through a 5-year Road Mortality BACI

Reptiles and amphibians are facing major population declines, both locally and globally. One of the most significant sources of these declines is negative interactions with roads. Roads represent massive linear features leading to major habitat fragmentation and consequently altering meta-population dynamics, restricting access to critical resources, mating opportunities, and consequently gene flow. Still greater than this threat is danger of direct mortality via wildlife-vehicle collisions. Road mortality has been shown to be a major detriment to population persistence, especially in slowly maturing species such as turtles. In order to properly evaluate the effectiveness of road mortality mitigation being installed in a protected area, Presqu'ile Provincial Park in Ontario, we initiated a Before-After-Control-Impact study. Surveys for animals on the road are conducted simultaneously on both Control and Impact sites, four times per day during the summer. Our 'Before' period includes two seasons of summer monitoring (2013/14), and our 'After' period will consist two additional seasons of monitoring (2016/17). During our 'Before' seasons, mortality rates for those animals found on road surveys were approximately 28% for turtles, 63% for snakes and 90% for amphibians. Road mortality mitigation is scheduled to be installed by fall 2015; however, the Impact site was resurfaced fall 2014. This affords us the opportunity to detect if resurfacing of the road itself will result in a change in reptile and amphibian mortality. Preliminary data demonstrate high levels of mortality, especially among anurans.

0523 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kristina Bozanich, Chris Feldman

University of Nevada-Reno, Reno, NV, USA

The Impacts of Cheatgrass (*Bromus tectorum*) on Western Fence Lizards (*Sceloporus occidentalis*) in Nevada

Cheatgrass (*Bromus tectorum*) is a highly invasive plant that has encroached on much of the Great Basin Desert. Cheatgrass negatively impacts native ecosystems in a variety of ways, from altering fire regimes, to usurping water and nutrients used by native plants, to providing low quality food source for native herbivores. While much is known about the impact of cheatgrass on native plants, comparatively little is known on the impact of cheatgrass on small vertebrates, particularly reptiles. Using the western fence lizard (*Sceloporus occidentalis*) as a natural model, we set out to determine whether and how cheatgrass impacts the abundance of these ecologically important desert animals. We

show that sites dominated by cheatgrass have almost no lizards, while adjacent (control) sites with native vegetation contain healthy lizard populations. We then tested two mechanisms that might lead to the decline (or emigration) of fence lizards in cheatgrass invaded sites. First, we assessed whether cheatgrass supports a diverse or depauperate prey base for lizards. Second, we determined whether cheatgrass, which grows in dense patches, has the potential to impede the natural movements of lizards. Indeed, cheatgrass contains a lower diversity and abundance of insect prey. Cheatgrass also reduces the crawl speed of smaller lizards, potentially hindering foraging and escape behaviors, and increasing the energetic demands of movement. These mechanisms, and perhaps others, appear to render landscapes dominated by cheatgrass unsuitable for native fence lizards. Further investigation in other reptiles (and small vertebrates) is warranted so that the threat of cheatgrass is fully understood.

**0551 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Thursday 16 July 2015**

Kenzie Bozeman

Southeastern Louisiana University, Hammond, LA, USA

Dermal Gland Histology of *Amphiuma tridactylum* & Bioactivity of Skin Secretions against the Amphibian Chytrid Fungus, *Batrachochytrium dendrobatidis*

Amphiuma tridactylum, the three toed amphiuma, is a large-bodied fully aquatic salamander that inhabits freshwater habitats of the southeastern United States. The skin of *A. tridactylum* is heavily supplied with dermal glands (i.e., mucous and granular glands). Mucous and granular glands exhibit distributional, morphological, biochemical, and functional variation across taxa. These glands are associated with distinct secretion types. While mucous glands secrete a clear slimy mucus, granular gland secretions are often white and proteinaceous. The bioactivity of granular gland secretions has been hypothesized to offer protection against the amphibian chytrid fungus, *Batrachochytrium dendrobatidis* (Bd). Although dermal glands and skin secretions have been thoroughly studied for many frog and salamander species, data is lacking for fully aquatic salamanders such as *A. tridactylum*. This study provides the first histological description of the dermal glands of *A. tridactylum* and uses Bd growth inhibition assays to investigate the role of granular gland secretions in offering host protection against Bd. Skin samples were collected from preserved *A. tridactylum* and were analyzed using light microscopy. Crude peptides were eluted from the skin secretions of live *A. tridactylum* and subsequently combined with Bd zoospores to investigate peptide bioactivity. It was found that mucous and granular glands exhibit significantly different distributions and morphologies along the body of *A. tridactylum*. The findings also include evidence for sexual dimorphism. The complete histological and biochemical results will be presented.

0090 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Darcy Bradley¹, Eric Conklin², Yannis P. Papastamatiou³, Douglas J. McCauley⁴, Kydd Pollock², Amanda Pollock⁵, Bruce E. Kendall¹, Steve D. Gaines¹, Jennifer E. Caselle⁶

¹*Bren School of Environmental Science and Management, University of California Santa Barbara, Santa Barbara, CA, USA*, ²*The Nature Conservancy, Hawai'i, Honolulu, HI, USA*, ³*School of Biology, Scottish Oceans Institute, University of St Andrews, St Andrews, Scotland, UK*, ⁴*Department of Ecology, Evolution, and Marine Biology, University of California Santa Barbara, Santa Barbara, CA, USA*, ⁵*U.S. Fish and Wildlife Service, Honolulu, HI, USA*, ⁶*Marine Science Institute, University of California Santa Barbara, Santa Barbara, CA, USA*

Managing a Moving Target: A Spatially Explicit Capture-recapture Reef Shark Population Density Estimate at an Unfished Coral Reef

Baseline population estimates are lacking for most species of reef shark. The grey reef shark (*Carcharhinus amblyrhynchos*), which is listed as Near Threatened on the IUCN Red List of Threatened Species, is highly mobile and therefore particularly difficult to monitor. At the same time, its mobility is precisely what has stymied its protection in much of the world – without understanding the spatial behavior of reef sharks, it is impossible to design spatial management strategies to protect them. Shark abundance through both space and time can be better estimated by directly accounting for reef shark movement in population estimates without the biases inherent in diver-based visual surveys. A spatio-temporal understanding of animal movement and abundance also allows managers to identify critical habitats, movement between habitats, and track changes to population size and structure. To directly address and incorporate animal movement in estimates of reef shark population size and density, we used a spatially explicit capture-recapture model from an eight year capture-recapture program augmented with telemetry data to produce the first baseline population density estimate of grey reef sharks and to further describe their spatial and temporal distribution at Palmyra atoll, a remote U.S. National Wildlife Refuge in the central Pacific Ocean. We found that diver based visual surveys had significantly over estimated shark density at an island wide scale. While our analysis revealed density ‘hot spots’, sharks also underwent regular excursions around the atoll, indicating that large scale spatial protection is necessary to recover reef shark populations globally.

0093 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Darcy Bradley¹, Yannis P. Papastamatiou², Steven D. Gaines¹, Jennifer E. Caselle³

¹*Bren School of Environmental Science & Management, University of California Santa Barbara, Santa Barbara, CA, USA*, ²*School of Biology, Scottish Oceans Institute, University of St Andrews, St Andrews, Scotland, UK*, ³*Marine Science Institute, University of California Santa Barbara, Santa Barbara, CA, USA*

Do Non-extractive Human Impacts have Quantifiable Behavioral Effects on Palmyra's Reef Sharks?

Shark behavior can bias abundance estimates from diver-based visual surveys, thereby leading to a flawed understanding of population trends through time. The presence of this bias in diver-based visual surveys is ubiquitous in reef shark abundance estimates generated for Palmyra and the greater central Pacific. Failing to account for behavioral effects may be problematic as in most places it is impossible to differentiate changes in estimated population abundance due to behavioral modifications and those resulting from fishing. In Palmyra, we can isolate and quantify the behavioral response of reef sharks to human activities as human use of the waters surrounding Palmyra has not been constant: from 2001 to the present scientific diving, boating, and provisioning activities have significantly increased on Palmyra's reefs. We quantified each activity to create a spatially and temporally explicit human use map of Palmyra. We then used paired baited remote underwater visual surveys (BRUVS) in research (heavy-use) and non-research (no-use) sites to assess the impact of human presence on the behavior of three species of reef shark. We found significant differences in time of first arrival in frame ($p < 0.05$) but not maximum number of individuals in frame ($maxN$) for all reef shark species between heavy-use and no-use sites. In sites with minimal human impact, sharks arrived sooner, indicating greater attraction to human activity in no-use sites. By quantifying reef sharks' responses to human activities, we can correct biased population estimates produced from existing visual survey data throughout the central Pacific.

0241 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Jessica Bredvik¹, Christiana Boerger¹, Suzanne Graham², Anjali Kumar², Gwen Lattin³, Ann Zellers³

¹*United States Navy, Naval Facilities Engineering Command Southwest, San Diego, CA, USA*, ²*United States Navy, SPAWAR Systems Center Command, San Diego, CA, USA*, ³*Algalita Marine Research Institute, Long Beach, CA, USA*

Spatial and Temporal Distribution and Abundance of Ichthyoplankton from 2012-2013 in San Diego Bay

Bays and estuaries are vital nursery areas for nearshore marine fishes. San Diego Bay is the largest naturally occurring marine embayment between San Francisco and central

Baja California and is heavily industrialized. Despite anthropogenic influences, the bay serves as a nursery for several nearshore marine fish species. However, information regarding the distribution of planktonic fishes across the bay is limited. The purpose of this study was to describe the temporal, seasonal, and spatial variation of larval fishes in each of the four hydrographic regions in San Diego Bay. Monthly diurnal and nocturnal samples were collected from May 2012 - April 2013 along four transects via a surface manta net. Samples were processed and fishes were identified to the lowest taxonomical level. A total of 88 samples were collected, of which only three samples did not contain larval fish. Over the year, 4,562 fishes were collected including larvae of 16 species across 14 families. Overall, larval fish species were dominated by the family Atherinidae, mostly consisting of topsmelt (*Atherinops affinis*) and California grunion (*Leuresthes tenuis*). Several significant differences were identified including, higher abundances of fishes in the cool period (November-April) compared to the warmer months of May-October. Greater abundances and biomass of fish larvae were collected during the night sampling efforts and a higher number of plankton were found in the southern half of the bay. This study represents the first evaluation of ichthyoplankton within all ecoregions of San Diego Bay with continued exploration of potential drivers and larval fish community.

0469 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Heather Brekke², Nicholas Dulvy¹

¹Simon Fraser University, Vancouver, British Columbia, Canada, ²Royal Roads University, Victoria, British Columbia, Canada

Does it Matter How Many Sharks are Killed Each Year?

The number of elasmobranchs killed each year has become a key communication message used to raise public awareness of the plight of sharks, skates, and rays. The total number killed alone may divert attention from conservation success and the true problems, priorities, and actions. We illustrate this with an analysis of extent and pattern of catches of elasmobranchs within Canadian Pacific commercial fisheries over the past 30 years (1980–2013). In Canada, few elasmobranchs are subject to directed commercial fisheries, but some are incidentally caught in fisheries targeting teleosts. A total of 208,642 tonnes of elasmobranchs was recorded in Canadian Pacific waters over the thirty-year period, with most (93%) of weight comprised of the commercially valued elasmobranchs: Spotted Spiny Dogfish (*Squalus suckleyi*), Big Skate (*Raja binoculata*), and Longnose Skate (*Raja rhina*). Most (three-quarters) of the catch was retained and catch retention has changed little over the last 30 years. Overall, on average, nearly two million sharks, skates, and rays have been killed each year and there has been an 80% decline in catch over the last decade. While such statistics could be used to support what Hilborn has called the “litany of decline”, it seems instead that almost all of the recent catch has been sustainable and taken within scientifically set catch limits. Furthermore, the steep decline in catch is more likely to reflect a combination of declining market

demand and improved management resulting in the emergence of sustainable elasmobranch fisheries.

0041 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Casey Brewster

University of Arkansas, Fayetteville, AR, USA

Conservation of the Eastern Collared Lizard (*Crotaphytus collaris*) in Arkansas

The Eastern Collared Lizard (*Crotaphytus collaris*) is a saxicolous lizard adapted to open, xeric habitats. In Arkansas, suitable habitat for this species consists almost exclusively of “glade” habitats (xeric limestone prairies and calcareous cedar glades). Primarily as a result of fire suppression, healthy glade ecosystems have become rare in the state. In turn, many obligatory glade species, including *C. collaris*, have suffered population declines. Continued population declines have prompted the Arkansas Natural Heritage Commission to list *C. collaris* as “imperiled”. Recently, several government agencies have devoted efforts to restoring glade ecosystems, primarily through prescribed fire and tree removal. These actions are necessary to allow the opportunity for: 1) recovery of declining populations, 2) successful reintroductions to historic localities, and 3) remnant populations to exploit adjacent habitat. Here I discuss recent results of glade habitat restoration and conservation efforts. I provide data characterizing 4 healthy and 4 unhealthy populations (age-specific body size, body condition, reproductive frequency, % of historic habitat currently occupied, and population size) and discuss recent habitat restoration at those sites. I present protocols for recent reintroductions at restored habitat localities (number of individuals by age, sex and source population), initial monitoring data at reintroduction sites (survival and individual growth rates), and data on source populations used for reintroductions (haplotypes, population size and age specific body size). Lastly, I discuss future conservation efforts and anticipated impacts of these efforts.

0350 Fish Ecology II, Carson 3, Sunday 19 July 2015

Rachel Brewton, Matthew Ajemian, Gregory Stunz

Harte Research Institute for Gulf of Mexico Studies, Texas A&M University- Corpus Christi, Corpus Christi, TX, USA

Highly Opportunistic Foraging of Common Dolphinfish, *Coryphaena hippurus*, in the Western Gulf of Mexico

Understanding the feeding ecology of pelagic sportfish is essential to the management of these economically important fisheries species. The stomach contents of 357 Common Dolphinfish, *Coryphaena hippurus* (mean size = 72.22 ±24.29 cm TL) were examined to

investigate this species' food resources in the western Gulf of Mexico. Consistent with other studies, the observed diet was highly piscivorous, with fish comprising approximately 50% of the prey by occurrence. Fish from the order Tetraodontiformes comprised 30% of stomach contents that could be identified to family, with multiple prey items from families Balistidae, Monacanthidae, and Tetraodontidae. Also common were fish from the family Carangidae (23%). Additionally, crustaceans were important, mostly in the form of pelagic megalopae (5% of total observed diet). Other prey categories of note included squid and critically endangered Kemp's Ridley sea turtles. *Sargassum* sp. was found in 30% of the stomachs indicating these fish are feeding regularly from this drifting macroalgae. *Sargassum* was present more frequently in smaller Dolphinfish indicating less dependence on this resource as fish mature. Trematode parasites from the genus *Dinurus* were very common and were found in 30% of examined stomachs. Nematode parasites of the family Raphidascarididae were less common and observed in 8% of stomachs. Overall, Dolphinfish in the western Gulf of Mexico appear to be highly opportunistic carnivores and regularly bear gastrointestinal parasites consistent with other ocean basins. These conserved ecological characteristics are consistent with the circumtropical distribution of Dolphinfish and its association with dynamic pelagic communities.

0354 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Rachel Brewton, Megan Robillard, Judson Curtis, Matthew Ajemian, Gregory Stunz

Harte Research Institute for Gulf of Mexico Studies, Texas A&M University- Corpus Christi, Corpus Christi, TX, USA

Trophic Ecology of Red Snapper, *Lutjanus campechanus*, Among Various Habitat Types in the Western Gulf of Mexico

The ability of artificial reefs to serve as effective habitat for fishes remains a contested issue. Understanding the functionality of artificial reefs necessitates comparative ecological studies with natural habitats. We examined the impact of habitat type (natural vs. artificial) on the trophic ecology of Red Snapper (*Lutjanus campechanus*), a broadly distributed fisheries species with high economic value. Red Snapper (350-630 mm TL) were collected from three habitat types in the western Gulf of Mexico that included natural hard-bottom, standing oil production platforms, and toppled oil production platforms converted into artificial reefs. Epaxial muscle tissue was extracted from fish for stable isotope analysis. Tissue samples ($n=96$) were analyzed for carbon ($d^{13}C$) and nitrogen ($d^{15}N$) isotopes and isotopic ratios were compared between size classes of Red Snapper (350-400 and 550-600 mm TL), and among the three habitat types (artificial, natural, and standing). There was no overall effect of habitat type on C or N ratios. There was a significant difference in isotopic ratios between size classes of both C (ANOVA, $p = 0.002$) and N (ANOVA, $p = 0.004$); however, this effect was dependent on habitat type. Subsequent post-hoc comparisons indicated that smaller fish from both natural habitats and artificial reefs exhibited significantly higher C and N ratios than

larger fish from these habitats. At standing platforms, both size classes had similar isotopic signatures. These preliminary results suggest that Red Snapper are using artificial reefs similarly to natural habitats, but that standing platforms may modify the distribution or composition of their food resources.

0075 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Allison Bronson, Melanie Stiassny

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

Olfactory Anatomy of *Parauchenoglanis punctatus*, a Claroteid Catfish from the Congo Basin

Recent studies have revealed a series of anatomical specializations of the olfactory chamber that are unique to auchenoglanin catfishes (Claroteidae: Auchenoglaninae). Many features of the auchenoglanin olfactory chamber appear to mirror those predicted to function in augmenting flow to maximize the entrainment of odorants over the olfactory epithelium, including a novel membranous system for the intake of water. However, the nature of water flow in the olfactory chamber and how that flow is harnessed to ventilate the olfactory region in these fishes is poorly understood. By combining traditional histological methods and modern 3D reconstruction software, I describe the olfactory anatomy of the auchenoglanin catfish *Parauchenoglanis punctatus* and propose a functional model of water flow in this unusual system.

0534 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Richard Broughton

University of Oklahoma, Norman, OK, USA

Characterization of Transcriptomes of Hybridizing Cyprinid Species *Cyprinella lutrensis* and *Cyprinella venusta*

Hybridization appears to be more common among freshwater fishes than in other vertebrate groups and individuals of mixed ancestry are common in nature. Because various outcomes of hybridization may increase or decrease species diversity, anthropogenic habitat alteration and water flow modification that enhance conditions leading to hybridization may thereby directly influence biodiversity. To better understand genetic leading to hybridization or reproductive isolation, we characterized transcriptomes of the closely related cyprinid fishes *Cyprinella lutrensis* and *C. venusta*. These species hybridize in many localities throughout their overlapping ranges but there appears to be geographic variation in the propensity to hybridize. RNA was extracted

from brain tissue from individuals collected in areas of apparent allopatry. De novo assembly of sequence data using several algorithms and multiple k-mer values yielded >10,000 contigs from each species. Contigs were annotated by sequential Blast comparisons to the zebrafish proteome, Swiss-Prot, UniProt, and Pfam databases. Over half of the contigs aligned to annotated genes, while many others matched unidentified ORFs. All homologous contigs were compared between *C. lutrensis* and *C. venusta* identifying highly diverged loci that provide a set of candidate genes that encode differences between these species.

0569 Herp Ecology, Carson 4, Saturday 18 July 2015

Corey Brumbaugh¹, Alex Dornburg², Robert Weaver¹

¹Central Washington University, Ellensburg, WA, USA, ²Yale University, New Haven, CT, USA

Physiographic Factors Affecting the Distribution of Amphibians and Reptiles in Southeastern Washington State

Southeastern Washington State is a region of many different macrohabitat types, from shrub-steppe and Ponderosa pine forests, to dense high elevation spruce-fir stands. There are deep canyons with fast flowing rivers that cut through the basalt, as well as grasslands, and pristine expansive mountain meadows. The remoteness of this region has led to it being largely unexplored in terms of the distribution and abundance of amphibians and reptiles. Because of this we gathered data on 16 species of reptile and amphibian from five counties in southeastern Washington State. These data were gathered from the Washington Department of Fish and Wildlife State Database, the Connor Museum at Washington State University, as well as data gathered during field surveys from 2006-2009. Over 1200 individual data points were transformed and plotted using ArcGIS. Buffer zones of 500 and 1000 meters were created around each individual and maps from the United States Department of Agriculture allowed for analyses of soil type, vegetation type and density, as well as the nearest body of water. Using these parameters allowed us to model possible factors influencing the distribution of these species in this region. For this presentation we will discuss the abiotic and biotic factors that drive the distribution of these species across this landscape. It is our hope that these data will give us a better understanding of the ecological similarities and differences of the herpetofauna found within the varied ecosystems of southeastern Washington State.

0475 Herp Ecology, Carson 4, Saturday 18 July 2015

Gary Bucciarelli¹, H. Bradley Shaffer¹, David Green², Lee Kats²

¹UCLA, Los Angeles, CA, USA, ²Pepperdine University, Malibu, CA, USA

Temporal Variation of Toxin Levels in a Chemically Defended Amphibian

The potent neurotoxin, tetrodotoxin (TTX), sits at the interface of the ecological interaction between tetrodotoxic newts that are preyed upon by garter snakes. This relationship is a widely known, generally undisputed example of a coevolutionary “parallel arms race.” However, there is relatively little understanding of how newts control TTX, either at the proximate or ultimate level, whether newts can biosynthesize TTX or if it is the result of endosymbionts, and if TTX is genetically controlled and able to evolve in response to predation pressure. In light of these complexities, it seems pivotal to describe and more fully understand newts and the TTX phenotype. We have longitudinally quantified TTX concentrations of newts within and between breeding localities, tested whether TTX levels vary spatially and temporally, and whether the TTX phenotype responds to environmental changes. Five years of regular sampling of wild individuals and populations of newts across more than 30 sites spanning California indicate that individual and group mean TTX concentrations fluctuate tremendously within a breeding season and between years. Additionally, the results of field and laboratory research show that adults can be induced to produce greater concentrations of TTX and that environmental conditions affect TTX levels at multiple life history stages. Overall, these results imply that TTX is not a fixed phenotypic trait and provide a novel dimension to our understanding of TTX in nature, potentially requiring a reevaluation of the lockstep predator resistance model generally employed to explain the evolution of this potent toxin.

0258 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Scott Buchanan, Nancy Karraker, Bill Buffum

University of Rhode Island, Kingston, RI, USA

Understanding the Influence of Altered Habitat: Preliminary Results on Abundance and Demography of Aquatic Turtles in Rhode Island Along a Gradient of Forest Cover

Habitat loss and degradation, unsustainable human use, and climate change, have made freshwater aquatic turtles a taxa of particular conservation concern. The five aquatic turtle species native to Rhode Island use an array of upland habitats adjacent to wetlands, making a landscape-level understanding of what is driving distribution and abundance an important component of effective management. In Rhode Island, deforestation associated with development is the leading cause of habitat loss and fragmentation, but we know little about how aquatic turtle populations respond to this landscape-level alteration. An ongoing investigation was initiated in 2013 to study the effects of landscape composition and configuration on the distribution, abundance,

demography, and genetic diversity of aquatic turtles in Rhode Island. This study is focusing on a subset of wetlands throughout the state, namely isolated, non-riparian wetlands less than two hectares in size and of semi-permanent to permanent hydroperiod. As this will mostly preclude encounters with certain species, the study will focus on results from three species; *Chelydra serpentina*, *Chrysemys picta*, and *Clemmys guttata*. A mark-recapture approach has been used to sample 58 wetlands across a gradient of forest cover throughout Rhode Island. Preliminary results on abundance and sex ratio are presented herein.

0395 Herp Physiology & Reproduction, Carson 4, Friday 17 July 2015

Kiristin Budd¹, James Spotila², Laurie Mauger¹

¹*Southern Utah University, Cedar City, UT, USA*, ²*Drexel University, Philadelphia, PA, USA*

Preliminary Mating Analysis of American Crocodiles, *Crocodylus acutus*, in Las Baulas, Santa Rosa, and Palo Verde National Parks, Guanacaste, Costa Rica

Studying the mating system of wild populations of American crocodiles, *Crocodylus acutus*, has important conservation implications. We conducted a preliminary analysis of the mating system of *C. acutus* in Las Baulas (2007 and 2008), Santa Rosa (2007) and Palo Verde (2008 and 2009) National Parks in Guanacaste, Costa Rica. We captured hatchlings during crocodile surveys and analyzed them with 9 polymorphic microsatellite loci to determine relatedness values. High relatedness values indicated that full and half siblings were sampled in a single locality and season. We found full siblings between the years that hatchlings were collected in Las Baulas and Palo Verde National Parks, which suggested mate fidelity. The mate fidelity and high relatedness values could be a consequence of the smaller number of adult crocodiles found within these areas or indicative of a small number of dominant males in the populations. Our results support the need to conduct future studies describing the mating system and nesting success within populations of *C. acutus*. Understanding of these population factors is crucial to the continued success and maintenance of viable populations of *C. acutus*.

0358 Neotropical Ichthyological Association, Carson 3, Friday 17 July 2015

Michael D. Burns

Oregon State University, Corvallis, OR, USA

Modularity and Body Shape Evolution in Characiformes

The order Characiformes is a hyperdiverse group of South American and African fishes that exhibits an unparalleled amount of variation in body shape, trophic ecology, and habitat. I sought to analyze body shape evolution of the order to characterize and quantify morphological variation and test different hypotheses about the origin of the variation. I quantified body shape through geometric morphometric analysis of radiographed specimens. I digitized 24 landmarks from the head and body of 10 adult individuals per species for 134 genera with at least two genera from each family and summarized variation through a principal components analysis. The major axis of body shape variation was elongation, with three major morpho-types being described. The process of elongation differed between families, with species elongating in their caudal, precaudal, or cranium regions. A test of modularity confirmed that each of these three regions are diversifying as discrete units across examined species. Most of the variation was between families and indicates that body shape evolution occurred early in cladogenesis. Phylogenetic comparative analysis supported a relationship between body shape and trophic ecology, indicating that phylogenetic relatedness is not completely responsible for the shared morphologies. I hypothesize that trophic ecology was one key factor promoting morphological differentiation early in cladogenesis, and postulate that diversification in the three modules would differ across trophic groups.

0262 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Edward Burress, Milton Tan, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Craniofacial Diversification Across the Cichlid Fish Adaptive Radiation

Cichlids represent a major vertebrate radiation that exhibits impressive functional, morphological, and ecological diversity. Particularly, craniofacial adaptations associated with resource utilization are hypothesized to have facilitated their proliferation into many regions of the adaptive landscape. The benthic-to-pelagic axis has been a ubiquitous source of divergence, often associated with predictable craniofacial modifications such as skull elongation, jaw orientation and protrusibility, and biting force. Here, we quantified the relative shape of the skull and jaws using landmark-based geometric morphometrics on x-rays of more than 100 cichlid species representing all major lineages. We evaluated major axes of shape variation using principal component analysis and estimated phenotypic diversification rates across the cichlid phylogeny. Then, we tested for shifts in rates of craniofacial diversification and correlations between rates of speciation and craniofacial diversification to evaluate the role of craniofacial

evolution in the proliferation of cichlid fishes. We are particularly interested in contrasts between Neotropical and Afrotropical and between lentic and lotic lineages.

0091 General Ichthyology II, Crystal 3 & 4, Friday 17 July 2015

Thaddaeus Buser¹, Michael Burns¹, J. Andres Lopez²

¹*Oregon State University, Corvallis, OR, USA*, ²*University of Alaska Fairbanks, Fairbanks, AK, USA*

Morphological and Reproductive Divergence Associated with Habitat Shifts in Oligocottine Sculpins (Cottoidea)

Successful invasion of novel habitats can lead to rapid evolution and speciation of the colonizer from its ancestral stock. When colonization leads to high rates of speciation and adaptive morphological evolution, the event is recognized as an adaptive radiation. Members of the cottoid subfamily Oligocottinae inhabit both subtidal and intertidal habitats and have been suggested to represent an adaptive radiation into the latter. Intertidal and subtidal environments are markedly different across a broad range of physical and biological characteristics, which can be expected to differentially select the traits of fishes in these contrasting settings. Although there are many ways in which differentiation could manifest, we selected a set of three fundamental biological aspects that we felt would be able to capture the different suite of putative selective pressures acting on each group and thus exhibit signatures of adaptive evolution across habitat types: 1) general morphology, 2) prey acquisition, and 3) reproduction. We used a likelihood-based ancestral state reconstruction of relevant morphological, ecological, and behavioral characters on a phylogeny of Oligocottinae to test our hypothesis that there would be differences between subtidal and intertidal species. Additionally, we performed a principal components analysis of 10 digitized landmarks for each species to test for differences in body shape. Our results show a clear separation in body shape between tidepool residents and subtidal residents. They also show that in general, tidepool residents copulate, but do not care for their eggs, while subtidal residents do not copulate, but do exhibit parental care.

0348 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Joshua Cahal, Brian Crother

Southeastern Louisiana, Hammond, LA, USA

Biogeography of the Dinosauria

The Mesozoic had a rich diversity of animals that included some of the largest megafauna in Earth's history. Virtually all megafauna and much of the diversity of

smaller terrestrial vertebrates from this era come from a single clade, the Dinosauria. The Mesozoic dinosaurs are one of the most heavily studied extinct organisms and persisted through a geologically dynamic part of Earth's history, the breakup of Pangea. These three factors (rich diversity, substantial amount of research, geologically dynamic history) make dinosaurs a model organism for biogeographical studies of fossil organisms. Despite this, no study has attempted to discover areas of endemism for dinosaurs, the operational taxonomic unit for biogeographical studies. I propose to do the first study to assess the discovery of areas of endemism for dinosaurs using Parsimony Analysis of Endemicity (PAE) and Geographical Interpolation of Endemism (GIE). The history of these areas will also be assessed with cladistic biogeography and event based methods, analytical methods that are also rarely seen in dinosaur literature.

0165 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Alexander Cameron, Cari-Ann M. Hickerson, Carl D. Anthony

John Carroll University, University Heights OH, USA

Responses of Eastern Red-backed Salamanders, *Plethodon cinereus*, to Elevated Soil pH

Much of the research regarding the effects of environmental acidification on amphibian populations is focused on ecological and physiological responses to increases in acidity. However, few studies address how the restoration of acidic soils through the application of calcite materials, affects amphibians. We used previously established field sites undergoing long-term application of Hi-Ca lime to investigate the effects of increases in soil pH on body condition and population demography of Eastern Red-backed Salamanders, *Plethodon cinereus*. These variables were estimated for *P. cinereus* and compared between unmanipulated (control plots) and limed plots. We found no effect of soil liming on body condition of *P. cinereus* and both population demographics and density were similar between the treatment and control plots. Results are consistent with previous studies regarding the response of *P. cinereus* to soil liming, but unique in that they arise from the first long-term field investigation to examine effects of soil liming on density and demography in a wild population of *P. cinereus*.

**0289 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Griffin Capehart, Emily Taylor

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

No Drought About it: How Does Hydration Affect Rattlesnake Physiology and Behavior?

We conducted a study to determine how hydration affects an arid-adapted reptile species, the Northern Pacific Rattlesnake. We experimentally manipulated hydration levels in rattlesnakes and observed the effects on various aspects of their behavior and physiology, in order to provide information about how these snakes react to varying levels of hydration in the field. Total-distance moved was significantly higher for males than for females, and males tended to have larger home ranges than females. There was no difference in the rate of movement, or distance moved per day, between the sexes. Body size (snout-vent length) significantly co-varied with all of these movement parameters, with larger snakes moving longer distances and having larger home ranges. We found that experimental hydration did not affect movement patterns. All female snakes that were experimentally hydrated became pregnant. While hydration did not affect thermoregulatory patterns, pregnant females exhibited elevated body temperatures compared to other snakes. Additionally, hydrated males tended to have higher body condition than control males and females. Baseline corticosterone levels and stress reactivity were not affected by hydration or sex. Overall, hydration had little effect on the physiology and behavior of rattlesnakes in this short-term study, but the long-term effects of continued drought on arid-adapted organisms in the western United States deserves further study.

0063 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Aaron Carlisle¹, Mark Denny², Nishad Jayasundara³, Adrian Gleiss⁴, Elliot Hazen¹, Heidi Dewar¹, Salvador Jorgensen⁵, Barbara Block², Steven Bograd¹

¹NOAA Southwest Fisheries Science Center, Monterey, CA, USA, ²Stanford University, Pacific Grove, CA, USA, ³Duke University, Durham, NC, USA, ⁴University of Western Australia, Perth, WA, Australia, ⁵Monterey Bay Aquarium, Monterey, CA, USA

Linking Thermal Physiology with Habitat Availability in Juvenile Lamnid Sharks

Sharks in the family Lamnidae are unique in that they are endothermic, and maintain an elevated body temperature relative to ambient water temperature. An inability to maintain an elevated body temperature in response to thermal challenges can have serious consequences on the survival and fitness of these sharks. This is particularly relevant for neonates and small juveniles which may be thermally limited due to their low thermal inertia, potentially restricting them to moderate or warm water

temperatures in which they are able to maintain elevated core temperatures. These potential thermal requirements provide us with a unique opportunity to explore the thermal niche of young juvenile lamnid sharks and model potential nursery habitats based on temperature. We created a biophysical heat-balance model for three species of lamnid shark (white, mako, and salmon sharks) to investigate the theoretical lower thermal limits of juvenile lamnid sharks and explore how this limit changes with size. Model results were compared to the observed thermal niche of juvenile lamnid sharks based on survey, bycatch and electronic tag data from their shared nursery area of the California Current. Understanding the mechanisms which may define thermal limits for these sharks allows us to investigate how physiology interacts with environmental conditions to influence habitat availability across spatial and temporal scales and through ontogeny.

0094 Fish Conservation & Management, Carson 3, Saturday 18 July 2015

Chris L. Chabot, Holly A. Hawk, Larry G. Allen

California State University, Northridge, Northridge, CA, USA

Low Contemporary Effective Population Size Detected in the Critically Endangered Giant Sea Bass, *Stereolepis gigas*, Due to Fisheries Overexploitation

The giant sea bass, *Stereolepis gigas* (Polyprionidae), is the largest teleost distributed in the northeastern Pacific from California to northern Mexico and has been overexploited by fisheries for more than a century. As a consequence of this historic exploitation, populations collapsed throughout the region in the last century resulting in the classification of the species as Critically Endangered by the IUCN. Recently, numbers of giant sea bass have been increasing within the region due primarily to the banning of the near shore gill net fishery in California waters in 1994. To assess population structure, the impact of historic exploitation on the genetic diversity and effective population size of the species, and to detect signs of recent population expansions, individuals from throughout the northeastern Pacific (n = 61; Northern Channel Islands, CA to San Quintín, Baja California) were sequenced at the mitochondrial control region and genotyped using 12 nuclear microsatellite loci generated from next-generation sequencing. Based on these markers, a single population was detected with low genetic diversity resulting in an estimated contemporary effective population size of less than 500 individuals with evidence of recent expansion within the region.

**0127 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday
18 July 2015**

Prosanta Chakrabarty

LSU Museum of Natural Science (Ichthyology), Baton Rouge, LA, USA

Epistemological Concerns for Estimating Extinction

Extinction rates are unknowable; however, estimates of extinction, like all models – “are always wrong, but sometimes useful.” Here I review and examine some current models of extinction, and propose a potentially useful alternative approach based on minimizing ad hoc assumption. This more parsimonious approach to examining extinction is an alternative to the many overparameterized models currently available. (And it is perhaps one that Donn Rosen, who we honor at this symposium, might have preferred.) The assumption set for this new approach is based on the Hennigian model of speciation: in this model an extinction event (of the ancestor) occurs with every speciation event (the branching of two sister lineages), and so there should be a bifurcating branch at every node in a phylogeny. Assuming this background rate of extinction (one extinction for every node) all nodes lacking a bifurcation is an additional extinction event. A “null” (expected) tree model is proposed to aid comparison of extinction events (and other traits), versus an observed (empirical) tree with the properties of, (1) having all nodes bifurcating, (2) being completely symmetrical, and (3) having origination events occur at regular intervals. Although this model, like all models, is wrong: it may prove useful in comparative phylogenetics.

0035 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Chia-Hao Chang³, Fan Li⁴, Kwang-Tsao Shao², Yeong-Shin Lin³, Takahiro Morosawa⁵, Sungmim Kim⁶, Hyeyoung Koo⁷, Won Kim⁶, Jae-Seong Lee⁸, Shunping He⁹, Carl Smith¹⁰, Martin Reichard¹⁰, Masaki Miya¹¹, Tetsuya Sado¹¹, Kazuhiko Uehara¹², Sébastien Lavoué¹³, Wei-Jen Chen¹³, Richard L. Mayden¹

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Phylogenetic Relationships of Acheilognathidae (Cypriniformes: Cyprinoidea) as Revealed from Evidence of Both Nuclear and Mitochondrial Gene Sequence Variation: Evidence for Necessary Taxonomic Revision in the Family and the Identification of Cryptic Species

Bitterlings are relatively small cypriniform species and extremely interesting evolutionarily due to their unusual reproductive behaviors and their coevolutionary relationships with freshwater mussels. As a group, they have attracted a great deal of attention in biological studies. Understanding the origin and evolution of their mating system demands a well-corroborated hypothesis of their evolutionary relationships. In this study, we provide the most comprehensive phylogenetic reconstruction of species relationships of the group based on partitioned maximum likelihood and Bayesian methods using the nuclear and mitochondrial genes on 41 species, several subspecies and three undescribed species. Our findings support the monophyly of the Acheilognathidae. Two of the three currently recognized genera are not monophyletic and the family can be subdivided into six clades. These clades are further regarded as genera based on both their phylogenetic relationships and a reappraisal of morphological characters. We present a revised classification for the Acheilognathidae with five genera/lineages: *Rhodeus*, *Acheilognathus* (new constitution), *Tanakia* (new constitution), *Paratanakia* gen. nov., and *Pseudorhodeus* gen. nov. and an unnamed clade containing five species currently referred to as "*Acheilognathus*". This result highlights a potentially dramatic underestimation of species diversity in this family. Using our new phylogenetic framework, we discuss the evolution of the Acheilognathidae relative to classification, taxonomy and biogeography.

**0482 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Kristin Charles, Daniel Portik, Rayna Bell

University of California, Berkeley, Berkeley, CA, USA

**Investigating the Role of Riverine Barriers on Phylogeographic Structure of
Afrivalus paradorsalis (Anura: Hyperoliidae)**

The Congo River Basin Biome and the Gulf of Guinea Forest Biome together comprise approximately 20% of the world's floral and faunal diversity, yet we know relatively little about the evolutionary processes responsible for this exceptional diversity. The hyperoliid frog *Afrivalus paradorsalis* has a broad distribution throughout these biomes, making it a strong candidate for investigating effects of multiple biogeographic barriers on generating diversity in this region. Two major rivers, the Sanaga in Cameroon and the Ogooué in Gabon, occur within the range of *A. paradorsalis*. These rivers have been implicated in shaping phylogeographic patterns of diversity in several mammalian species, but whether the Sanaga and Ogooué are significant barriers to amphibian dispersal is less clear. I collected 16S mtDNA sequences for 36 individuals across 19 localities, and phylogenetic analyses of these data indicate there are three genetically distinct groups occurring throughout the range of *A. paradorsalis*. The geographic ranges of these haplotype groups appear to be delimited by the Sanaga and Ogooué Rivers, suggesting these rivers function as barriers to dispersal in this taxon. *Afrivalus paradorsalis* also occurs on Equatorial Guinea's Bioko Island, and 16S mitochondrial analyses indicate that these island populations are indistinguishable from the mainland clade north of the Sanaga. This corroborates the hypothesis of a recent land bridge connection between Bioko Island and the mainland.

0369 Fish Conservation & Management, Carson 3, Saturday 18 July 2015

Barry Chernoff, Helen Poulos

Wesleyan University, Middletown, CT, USA

Regime Shifts and Resilience in Fish Populations Following Dam Removal

In 2007 a dam was removed on the East Branch of the Eight Mile River. The dam that supported mill and agricultural activities had been in place since the 1760's. We have studied fish and benthic macroinvertebrate communities above and below the dam site before, during and after dam removal. We have shown previously that interannual variation in community structure for both fishes and macroinvertebrates was significantly higher above and just below the dam site than in reference communities. In this study we use gradient forest analysis and multivariate autoregressive models (MAR1) to examine: (1) the relationship of fish population dynamics to changes in the benthic macroinvertebrates; and (2) the interactions among the fishes themselves as a function of population densities and growth rates. The MAR1 analyses are carried out

with dam removal as a covariate. The results illustrate that the sites have distinctive models of metapopulation dynamics following dam removal. Furthermore, MAR1 statistics indicate that the reference population is “resilient” – able to absorb perturbations due to dam removal. Populations above and below the dam site are “reactive” – the perturbation due to dam removal has exceeded the threshold of their stability domains and that they are in the process of regime shifts. The regime shifts, however, do not seem to be in the direction of the domain exhibited by the reference community.

0506 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

Jacqueline Chivers, Craig Guyer

Auburn University, Auburn, AL, USA

Combing Morphological and Acoustic Techniques to Better Understand the Relationship Between Hybridizing Toads: *Anaxyrus americanus* and *Anaxyrus fowleri*

Morphology and advertisement calls of American toads (*Anaxyrus americanus*) and Fowler's toads (*A. fowleri*) have been used to differentiate between these species. However, previous methods of morphology used to classify individuals are based on a presence/absence system of characteristics and to some degree rely on subjectivity. In the field, calls of males are simply interpreted as being consistent with a particular species. In cases of potential hybridization, individuals may contain a combination of characteristics from both species or characteristics that appear intermediate. This study takes a closer look at morphology and male advertisement calls using precise measurements of species-specific characteristics in order to better estimate potential hybridization. Morphological characteristics used to identify each species are the size of tibial warts, number of warts per dorsal dark spot, and contact of the postorbital crest with the parotoid gland. Advertisement call characteristics measured were call duration (pulses/call), pulse rate (pulses/second), dominant frequency (kHz), length of call (second), time between calls (second), and length of one pulse (second). We restricted our examination to specimens from the state of Alabama, where hybridization between species and intergradation between subspecies is acute (Mount 1975). We compared *A. fowleri* from two populations that are sympatric with *A. americanus* to *A. fowleri* from two allopatric populations. Using a discriminate function analysis we documented a 7.2% (n=83) hybridization rate based on morphological characters. Call results showed *A. fowleri* individuals living in allopatry had greater variance in call characteristics than individuals living in sympatry.

0444 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Diana A. Churchill¹, Michael R. Heithaus¹, R. Dean Grubbs²

¹Florida International University, Miami, FL, USA, ²Florida State University, Tallahassee, FL, USA

Estimating the Trophic Position of Deep-water Sharks and Associated Species Using Compound-specific Nitrogen Isotope Analysis of Amino Acids

The ability to estimate trophic position is an important step in understanding the ecological roles of deep-sea animals. Determining absolute trophic levels using whole tissue stable isotope analysis is often problematic because of the inter- and intra-specific variation associated with trophic discrimination factors. Some of this variability may be eliminated by using compound-specific nitrogen analysis of proteinaceous amino acids. Using this technique, we were able to estimate the trophic position of numerically abundant deep-sea organisms. Tissue samples were collected from demersal fish (sharks, hake, tilefish, and cutthroat eels) and benthic scavengers (giant isopods, hagfish, crabs and shrimp) captured at depths of 200-1500 m along the northern slope (NGS) and the west Florida slope (WFS) of the Gulf of Mexico during 2011 and 2012. Whole muscle tissue $\delta^{15}\text{N}$ analyses reveal that these consumers span approximately 2 trophic levels, with the armed nylon shrimp (*Heterocarpus ensifer*) at the lowest relative trophic position and the little gulper shark (*Centrophorus cf. uyato*) at the highest. Compound-specific analyses will determine absolute trophic positions for the sampled deep-sea animals using source and trophic amino acid $\delta^{15}\text{N}$ values as well as examine possible isotopic baseline differences between the NGS and WFS.

0133 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Patrick Ciccotto, Lawrence Page

Florida Museum of Natural History, Gainesville, FL, USA

A Systematic Overview of the Cyprinid Genera *Crossocheilus* and *Lobocheilos* (Tribe Labeonini) from Southeast Asia

The family Cyprinidae comprises the most diverse family of freshwater fishes, with many groups exhibiting morphological similarities leading to taxonomic confusion. This issue of taxonomic uncertainty in both specific- and generic-level classifications is particularly evident in historically under-sampled regions of the world such as southeast Asia. An overview of the taxonomic diversity of *Crossocheilus* and *Lobocheilos*, two superficially similar cyprinid genera native to Asia, is presented with comparisons to other morphologically similar genera in the region. Species of *Crossocheilus* and *Lobocheilos* are benthic, algivorous species typically found in lotic habitats. Recent molecular phylogenetic data indicate *Crossocheilus* is paraphyletic, with a south Asian clade currently comprised of six species distributed within and west of the Salween River basin in Myanmar and Thailand to India, and a southeast Asian clade currently

comprised of 11 species distributed east of the Salween River on mainland Asia and into Indonesia. Morphological data from a subset of species examined support the recognition of these two clades as separate genera. The genus *Lobocheilos* is distributed in Thailand, Malaysia, and Indonesia. Eleven *Lobocheilos* species are formally recognized in Indonesia, with a greater degree of uncertainty in the identifications of species from Thailand. The systematics of the species in these two genera are discussed in light of recently collected specimens from throughout the region by the All Cypriniformes Species Inventory.

0061 ASIH STOYE AWARD ECOLOGY & ETHOLOGY II, Carson 4, Friday 17 July 2015

Brian Clark, Larry Allen

California State University, Northridge, Northridge, CA, USA

The Reproductive Behavior of Giant Sea Bass, *Stereolepis gigas*

Courting behaviors are important to reproductive success because they increase the likelihood of synchronized gamete release and production of viable offspring. Giant sea bass, *Stereolepis gigas*, are part of the northeastern Pacific nearshore fish fauna and have been historically overharvested placing them into the threat category, *Critically Endangered* by the IUCN. Giant sea bass are members of the wreckfish family, *Polyprionidae*, whose species are long-lived, late to mature and their reproductive behaviors remain unknown. The objective of this study was to describe the courting and spawning behavior of giant sea bass along the southern California coast. This was done by: 1) identifying the time of day when abundance was highest and 2) observing behaviors exhibited during courtship (spawning was not observed). SCUBA surveys were done June - August 2014 at Goat Harbor, Santa Catalina Island. Densities were sampled along transects three times per day (morning, afternoon and evening) and an HD video camera was used to record courting behaviors. Based on the surveys and observations, giant sea bass were most abundant during the afternoon, presumed sexual dimorphism was observed, and presumed courting behaviors were commonly observed when fish were in pairs. Understanding giant sea bass reproductive behavior could improve management of this endangered species and may give insight into reproductive behaviors of other polyprionid species.

0530 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Christopher Clark¹, Yukun Lin¹, Jerry Hsiung¹, Connor White², Christopher Lowe²

¹Harvey Mudd College, Claremont, CA, USA, ²California State University Long Beach, Long Beach, CA, USA

Planning, Control, and State Estimation for Animal Tracking with Autonomous Robots

The field of robotics has generated viable solutions to the planning, control and state estimation problems encountered when enabling mobile robots with autonomous capabilities. In this talk, such solutions are presented in the context of a particular application: the use of underwater robot systems for autonomous tracking of individual fish tagged with acoustic transmitters. Over the past 4 years, a multi-AUV (Autonomous Underwater Vehicle) system has been developed that is equipped with hydrophones and receivers to detect, localize, and autonomously follow tagged individuals. Experiments conducted in Big Fisherman's Cove, CA demonstrate localization errors on the order of 6 meters when tracking tagged boats. When deployed to track tagged leopard sharks, the AUVs are able to track and follow the individuals for hours at a time, while simultaneously obtaining environment data, (e.g. bathymetry). AUV Path Planning is accomplished via graph search algorithms that ensure AUV paths do not intersect with obstacles or kelp beds. Decentralized AUV control laws enable the AUVs to circle a moving individual without affecting the animal's behavior. Particle Filter state estimation algorithms are leveraged to successfully track the individual in real-time. Most recently, individuals have been tagged with a "smartTag" that houses an acoustic transmitter, video camera, automatic release system, and Inertial Measurement Unit. The use of this smartTag has decreased fish position estimation error by a factor of 2, and orientation estimation error by a factor of 4. Notably, the hardware and software techniques utilized are generalizable to a large class of tracking applications.

0141 Herp Behavior, Carson 4, Friday 17 July 2015

Rulon Clark

San Diego State University, San Diego, CA, USA

Predator-Prey Interactions Between Desert Kangaroo Rats (*Dipodomys deserti*) and Sidewinder Rattlesnakes (*Crotalus cerastes*)

Most animals live with some risk from predation and consequently have evolved a variety of mechanisms to dissuade predators, including communicating information about awareness or quality through predator-directed signals. Rattlesnakes, particularly sidewinders (*Crotalus cerastes*), are one of the most abundant predators in Mojave, Chihuahuan, and Sonoran desert ecosystems, and are likely to represent a significant source of predation for kangaroo rats. Desert kangaroo rats (*Dipodomys deserti*) respond

to many snakes with a series of antipredator displays involving close approaches, jump backs, foot drumming, and sand kicking. We use a combination of manipulative field experiments as well as natural observations that take into account the perspective of both predator and prey while investigating interactions between sidewinders and desert kangaroo rats. Specifically, we will present data addressing the following questions: (1) What behaviors do kangaroo rats display when they encounter an ambushing sidewinder rattlesnake? (2) How do kangaroo rats avoid envenomation when approaching snakes closely? (3) How do kangaroo rat interactions alter the behavior of ambushing rattlesnakes?

0580 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Will Clark¹, Robert Weaver²

¹Department of Math and Science, Western Wyoming Community College, Rock Springs, WY, USA, ²Department of Biological Sciences, Central Washington University, Ellensburg, WA, USA

Natural History of the Ring-necked Snake (*Diadophis punctatus*) in Washington State

The Ring-necked Snake (*Diadophis punctatus*) is a transcontinental species of snake with a continuous range throughout the eastern and mid-west United States. In the intermountain region of the west its distribution is less so, with several disjunct populations in Arizona, Nevada and Utah. However, on the west coast the range is less spotty and it is found from southern California, north through western Oregon and reaches its northernmost extent in south-central Washington State. Here we present ecological data on this population, and compare it to other populations, especially those in Utah and Arizona. We gathered data on habitat use, activity patterns, diet and reproductive data from 145 individual snakes collected from 2000-2014. Mature snakes ranged in size from 202-635 mm total length (TL), hatchlings were observed in the fall and had mean TL = 165 mm. The diet of adult male and females consisted solely of squamate reptiles, such as *Thamnophis* spp., *Contia tenuis*, and *Hypsiglena chlorophaea*, as well as *Plestiodon skiltonianus* and *Elgaria multicarinata*, while hatchlings and juveniles consumed invertebrates. Females with enlarged ova were found in late April and early May. Snakes showed a monthly bi-modal activity patterns, with few snakes (< 15 %) observed mid-summer. Only 2 snakes (1.3%) were observed to be nocturnal, and all others were found active on the surface or under cover objects (primarily rocks) by day. All snakes showed a preference for cooler temperatures, with more than 75% of snakes active when temperatures were between 18-26 °C.

0401 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Callahan Clarke¹, Bryenna Workman¹, Melissa Gall², Paul Hampton¹

¹Colorado Mesa University, Grand Junction, CO, USA, ²Carroll University, Waukesha, WI, USA

Single Large or Several Small: Prey Size Selection and its Effect on Swimming by Ribbon Snakes

Snake locomotion studies have suggested that extra weight in the form of developing offspring or ingested meals can affect terrestrial locomotion. However, information regarding the effects of a meal on swimming performance is lacking. Snakes use lateral undulations to propel themselves through the water. Consequently, a rigid prey item may confound the adverse effects of a meal on swimming by limiting spinal flexion. We hypothesized that consumption of several small fish will have less restriction on movement of the spinal column compared to a single large fish. We chose western ribbon snakes (*Thamnophis proximus*) as our study species. Ribbon snakes were fed meals approximately 20% of the snake's mass. The large meal treatment was a single fish that was approximately 20% of the snake's mass. For the several small treatment, snakes were fed four fish that were each approximately 5% of the snakes size, thus totaling an equivalent meal size. After feeding, individuals were video-recorded while swimming through a small pool. We determined the maximum swimming velocity using Logger Pro, a motion-analysis program. We used Image J to determine the amplitude and angle of spinal flexion from photo stills from the fastest trial for each snake. Results will be discussed.

0009 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Pamela Clarkson, Christopher Beachy

Southeastern Louisiana University, Hammond, LA, USA

Induction of Metamorphosis Causes Differences in Sex-specific Allocation Patterns in Axolotls (*Ambystoma mexicanum*) that have Different Growth Histories

We tested the hypothesis that salamanders growing at different rates would have allocation patterns that differ among male and female metamorphic and larval salamanders. We raised individual axolotls, *Ambystoma mexicanum*, on four food regimes: constant high growth (*ad libitum* throughout the experiment), constant low growth (restricted throughout the experiment), high growth switched to low growth (*ad libitum* switched after 140 days to restricted), and low growth switched to high growth (restricted switched after 140 days to *ad libitum*). Because axolotls are obligate paedomorphs, we exposed half of the salamanders to thyroid hormone to induce metamorphosis. We assayed growth and dissected and weighed gonads and fat bodies. The salamanders that were switched from a restricted to an *ad libitum* food regime

delayed metamorphosis. In all treatment groups, females had larger gonads than males and males had larger fat bodies than females. The association between storage and reproduction differed between larvae and metamorphs and depended on sex.

0008 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Pamela Clarkson¹, Eric Pulis², Roldan Valverde¹

¹*Southeastern Louisiana University, Hammond, LA, USA*, ²*Institute for Marine Mammal Studies, Gulfport, MS, USA*

Hook, Line, and Stressor? Corticosterone Concentrations in Juvenile Kemp's Ridley Sea Turtles

Stress dynamics of free-ranging prepubescent juvenile Kemp's ridley sea turtles, *Lepidochelys kempii*, will be examined throughout the 2015 fishing season along the coast of Mississippi. Incidental catch by hook and line is probably an intense stressor, sometimes causes severe injury, and rarely causes death. The objective of this study is to determine how much the activity of the hypothalamic-pituitary-adrenal (HPA) axis is altered by hooking, injury, and subsequent handling during rehabilitation. Corticosterone, the main stress hormone of reptiles, will be measured throughout the rehabilitation process. Plasma biochemistry will be measured at admittance and immediately prior to release to evaluate health. Corticosterone concentrations are expected to be highest initially and to decrease significantly throughout the rehabilitation process. We expect juvenile Kemp's ridleys to have a sensitive HPA axis that is highly altered during incidental hooking for three reasons: (1) small turtles are highly stress responsive (2) Kemp's ridleys are more stress responsive than other species of sea turtles (3) injury increases stress responsiveness. Stress has far-reaching effects on morphology, physiology, and behavior. Research and conservation efforts regarding Kemp's ridleys are critical to the population recovery of this critically endangered species.

0561 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Paul J. Clerkin¹, Jenny M. Kemper², David A. Ebert¹

¹*Pacific Shark Research Center, Moss Landing Marine Laboratories, Moss Landing, CA, USA*, ²*Hollings Marine Lab, Medical University of South Carolina, Charleston, SC, USA*

Investigation and Taxonomy of Southwestern Indian Ocean Chimaeridae

Historically understudied, the Chimaeriformes (Chondrichthyes: Holocephali) has received increased attention over the past decade and half, with the expansion of deep-

sea fisheries, with 19 species having been described. Despite this recent focus, 59% of all known chimaeras are data deficient as accessed by the IUCN. This lack of information is due to taxonomic uncertainty and the intrinsic complexities associated with sampling at great depth in remote areas. The Southwestern Indian Ocean (SWIO) offshore ecosystem is a poorly explored, remote region characterized by extreme topology that includes the massive Madagascar Ridge. This region is punctuated by seamounts that function as isolated underwater islands, supporting high abundance of fish, and a number of chimaera species. Currently, very little is known about SWIO Chimaeras, since only two species have been verified from the area, *Hydrolagus africanus*, and *Chimaera notafricana*. During two surveys (2012 and 2014) onboard a commercial deep-sea trawler in the SWIO offshore, six distinct species of Chimaeridae (4 Chimaera, 2 Hydrolagus) were collected. A comprehensive set of morphometric and meristic measurements, and genetic samples were collected from each specimen encountered. Comparisons with geographic congeners using standard morphological methods along with comparative genetic samples were made between SWIO offshore chimaeras and those from South Africa, Australia, and New Zealand to investigate similarities and differences between these geographical regions. Taxonomic resolution of this enigmatic Chondrichthyan group will lead to improved species-specific identification.

**0140 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Friday 17 July 2015**

Jonathan Clinger, C.M. Gienger

Austin Peay State University, Clarksville, TN, USA

Metabolic Cost of Reproduction in Female Eastern Box Turtles (*Terrapene carolina*)

Life history strategies can be shaped by the energetic effort that is allocated toward reproduction, with the magnitude of this effort having a direct impact on reproductive success and future fecundity. Thus to fully understand the life history of a species, it is crucial to assess the magnitude of the parental reproductive effort. One part of this reproductive effort is the energetic cost associated with producing offspring. Our objective was to assess the cost of reproduction in female Eastern Box Turtles (*Terrapene carolina*) throughout the entire brooding period. For each gravid female, metabolic measurements were taken weekly until the time of oviposition to estimate the gravid metabolic rate and then again one week following oviposition to measure the non-gravid metabolic rate. We also measured the metabolic rate for each clutch in order to separate the contribution of the embryonic metabolism from the gravid maternal metabolic rate. In comparing reproductive state, the gravid female metabolic rate was significantly higher than the non-gravid metabolic rate. This resulted in a 3.27 ± 1.48 mL O₂•h⁻¹ mean whole animal metabolic cost of reproduction (0.009 ± 0.006 mL O₂•h⁻¹ mass specific metabolic rate) and a 36.4% whole animal increase in metabolic rate (42.9% mass specific increase) compared to a resting metabolic rate.

0101 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Daniel Coffey, Kim Holland

Hawaii Institute of Marine Biology, University of Hawaii at Manoa, Kaneohe, HI, USA

In Situ Measurements of Dissolved Oxygen from a Vertically Migrating Deepwater Shark, the Bluntnose Sixgill (*Hexanchus griseus*)

Advances in biologging technology have enhanced our understanding of the ecology of marine animals and have been central to identifying how contemporary oceanographic conditions establish patterns in their distribution and behavior. In particular, the impact of dissolved oxygen on the vertical distribution of marine animals is becoming increasingly recognized. Insights into the impact of oxygen on vertical movements would be advanced by in situ measurements of dissolved oxygen from animal-borne sensors instead of relying on model-derived, climatological data. Here we demonstrate the capabilities of a novel dissolved oxygen pop-up satellite archival tag (DO-PAT) by presenting the results from calibration experiments and trial deployments on bluntnose sixgill sharks (*Hexanchus griseus*). The DO-PATs provided fast, accurate, and stable measurements in calibration trials and conductivity-temperature-depth (CTD) vertical profiles. In addition, initial deployments on *H. griseus* effectively captured the oceanography of the region when compared with World Ocean Atlas 2013 values. This is the first study to demonstrate the use of an animal-borne device for measuring in situ dissolved oxygen saturation. The information returned from DO-PATs is relevant not only to the study of the ecology of marine animals but will also become a useful new tool for investigating the physical structure of the oceans.

0378 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Jared Cole, Casey Brewster, Brenna Levine, Bradley Martin, Whitney
Anthonysamy, Marlis Douglas, Michael Douglas

University of Arkansas, Fayetteville, AR, USA

Identifying Evolutionarily Significant Units in Eastern Collared Lizard (*Crotaphytus collaris*) from Arkansas

Eastern Collared Lizard (*Crotaphytus collaris*) populations in Arkansas have become highly fragmented because of anthropogenic habitat loss. Further, Arkansas is at the periphery of the species' range, and populations are characterized by small size and concomitant low genetic diversity both contributing to increased risk of local extirpation. To mitigate further population decline a genetic analysis is needed for development of conservation strategies. This study examined evolutionary history of *C. collaris* in Arkansas using sequence analysis of two mitochondrial DNA genes. Distinct haplotype data were identified and genetic diversity characterized within and among

populations. Estimates of gene flow were used as a proxy to determine dispersal among suitable habitat patches. Results of this study will help devise more salient management strategies to maintain *C. collaris* populations in the region.

0277 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kathleen Cole¹, David Noakes², Neil Thompson³, Michael Blouin³, Bruce Morrison⁴, Carl Schreck⁵, Joseph O'Neil⁶, Ryan Couture⁶

¹Department of Biology University of Hawaii at Manoa, Honolulu, HI 96822, USA, ²Department of Fisheries and Wildlife and Oregon Hatchery Research Center, Oregon State University, Corvallis, OR 97331, USA, ³Department of Zoology, Oregon State University, Corvallis, OR 97331, USA, ⁴Lake Ontario Management Unit, Ontario Ministry of Natural Resources, Glenora, Ontario, Canada, ⁵USGS Fisheries Coop Research Unit and Department of Fisheries and Wildlife, Oregon State University, Corvallis, OR 97331, USA, ⁶Oregon Hatchery Research Center, Oregon Department of Fish and, Alsea, OR, USA

Effects of Elevated Temperature, Stock Source and Parentage on Sexual Development and Growth in Steelhead, *Oncorhynchus mykiss*

Oncorhynchus mykiss, known as steelhead and rainbow trout in its anadromous and freshwater resident forms, respectively, is one of several salmonid species that normally express multiple phenotypes. Investigations have shown that conditions experienced during early development can have a significant impact on phenotypic variation and subsequent life history options in such species. Using several steelhead pairs as a parental source of embryos, we compared wild and hatchery-sourced *O. mykiss* to evaluate to what extent stock source, genotype (chromosomal sex) and differing rearing temperatures influenced growth and sexual development. Among fish of all treatments raised at 5 C° above ambient from fertilization to swim up, sex ratios based on histological examination of gonadal tissue were not significantly different from 1:1. Subsequent genotyping of a subsample demonstrated full concordance between genotypic and phenotypic sex. Therefore, **early exposure to elevated temperature did not affect sexual development**. In addition, genetic sex did not affect growth rates. However, temperature regime and stock source did. Fish exposed to elevated temperatures were larger on average, resulting in larger terminal size. At termination of the study, wild sourced fish tended to be larger on average than hatchery sourced fish regardless of temperature regime in which they were raised. These growth differences associated with rearing temperature and stock source suggest that phenotypic variation in *O. mykiss* is likely to increase with projected climate change, with unknown consequences to life history trajectories.

0311 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Bruce Collette¹, Katherine Bemis²

¹*Smithsonian Institution, Washington, D.C., USA*, ²*Cornell University, Ithaca, NY, USA*

Fifty Years in the Making: Beloniformes of the Western North Atlantic

Beloniformes is a diverse order of fishes found worldwide in marine and freshwaters that contains six families and at least 230 extant species. Four of these families, Belonidae (needlefishes), Scomberesocidae (sauries), Hemiramphidae (halfbeaks) and Exocoetidae (flyingfishes) occur in the western Atlantic Ocean with about 40 living species and subspecies. *Fishes of the Western North Atlantic* is a large-format monographic series started in the 1940s. Designed to summarize everything known about the fishes of our region, this series provides a thorough examination of specific groups. Our new volume on Beloniformes is a comprehensive review of the group, and is based on 50 years of research by Bruce Collette (National Systematics Laboratory), Nikolai Parin (Shirshov Institute of Oceanology, Russian Academy of Sciences) and Robert Gibbs (Smithsonian Institution). In *Beloniformes of the Western North Atlantic* we provide updated keys for species from our region as well as extended species accounts. Each species account includes taxonomic information and synonymies, diagnostic features, information on reproduction and development, diet, predators, parasites, and notes on importance to humans. Figures include drawings of adults and juveniles, including early developmental stage for many species, as well as distribution maps for each species and tables of morphometric and meristic data based on specimens examined for this project. This compilation reveals gaps in our knowledge, which may inspire future research efforts. The volume is nearing completion, but we are still gathering information from colleagues, and welcome your comments, citations, or suggestions for information to include.

0221 General Ichthyology I, Crystal 3 & 4, Friday 17 July 2015

Bruce Collette¹, John Graves², Valerie Kells³

¹*National Marine Fisheries Service Systematics Laboratory, Washington, DC, USA*,
²*College of William and Mary, Gloucester Point, VA, USA*, ³*Marine Science Illustration, Charlottesville, VA, USA*

Tunas and Billfishes of the World

Tunas and mackerels (family Scombridae) and billfishes (families Xiphiidae and Istiophoridae) comprise 61 species of epipelagic (surface-dwelling) fishes. Many of the species are important for commercial and/or recreational fisheries. They display marvelous adaptations to their epipelagic life which are of great interest to evolutionary biologists and ecologists. While there are many publications that focus on different aspects of their commercial and recreational value, their unique morphological

adaptations, or the threats they face, up to now there has been no single source that contains comprehensive, inclusive, and up-to-date information on all 61 species. This book, to be published by Johns Hopkins Press, will contain accurate color illustrations of all the species, keys to their identification, distinguishing characters, distribution maps, biology (food, reproduction, predators and parasites), fisheries interests, and threats to their survival. Bruce Collette's 55 year career has focused on the anatomy, taxonomy, and evolution of these fishes. John Graves has dealt with genetics and population biology of many species of tunas and billfishes. Val Kells is known for the accuracy and beauty of her illustrations. Much of the information on morphology comes from the FAO species catalogs on Scombridae and billfishes. Some of the information on biology, fisheries, and threat status comes from the IUCN Red List accounts of these species. Recently published material is being added and we are eager to receive new information on any of the tunas and billfishes.

0212 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Michael Colley¹, Stephen Lougheed², Kenton Otterbein³, Jacqueline Litzgus¹

¹Laurentian University, Sudbury, Ontario, Canada, ²Queens University, Kingston, Ontario, Canada, ³Killbear Provincial Park, Nobel, Ontario, Canada

An Evaluation of the Effectiveness of Mitigation for Reducing Road Mortality of Eastern Massasauga Rattlesnakes

Reducing road mortality is essential to reptile conservation. The Georgian Bay, Ontario population of the Eastern Massasauga rattlesnake (*Sistrurus catenatus*) is designated as Threatened by COSEWIC, in part because of high road mortality. Killbear Provincial Park has taken steps to reduce reptile road mortality through construction of four ecopassages and barrier fencing along three busy park roads. Although mitigation has been widely recommended, its effectiveness has rarely been evaluated. Park roads were monitored twice daily on bicycles, and again at night by car to document locations of both living and dead Massasaugas and other reptile species in 2013 and 2014. Road mortality rates were compared pre-mitigation, during mitigation construction, and post-mitigation. Automated PIT tag readers and trail cameras were installed at each ecopassage to monitor snake activity. A "willingness to utilize" (WTU) experiment was conducted to further explore the effectiveness of the ecopassages. We found a significant decrease in road mortality of Massasaugas on park roads over time as mitigation was constructed. Monitoring techniques showed that Massasaugas and other reptiles used the ecopassages, observations that were further supported in the WTU experiment. Our evaluation of the mitigation structures determined that they are successful at reducing road mortality and connecting bisected habitat, provided that intense annual maintenance of the fencing is conducted. This project provides a template for construction of similar mitigation in other key locations where road mortality is prevalent.

0210 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Michael Colley¹, Stephen Lougheed², Kenton Otterbein³, Jacqueline Litzgus¹

¹Laurentian University, Sudbury, Ontario, Canada, ²Queens University, Kingston, Ontario, Canada, ³Killbear Provincial Park, Nobel, Ontario, Canada

PVA Reveals Importance of Road Mortality Mitigation for Preventing Extirpation of a Massasauga Population in a Protected Area

Snake populations worldwide are declining, in part because of road mortality. Post-construction monitoring of road mortality mitigation measures has become more common, but few of these assessments look at the overall effect on population viability. Killbear Provincial Park, Ontario recognized the damaging effects of road mortality on local snakes and began monitoring populations of the threatened Eastern Massasauga rattlesnake (*Sistrurus catenatus*) in 1992. To address concerns about declining populations, Killbear installed barrier fencing and four ecopassages along three busy park roads between 2007 and 2013. A population viability analysis (Vortex) was done using local demographic data and road mortality rates to determine if mitigation installed in Killbear would allow Massasauga populations to persist into the future with low risk of extinction. We found that the post-mitigation road mortality levels corresponded with a low probability of extinction, suggesting that the mitigation is effective at promoting a sustainable population. That being said, the population is highly sensitive to female mortalities, and the death of more than 2 females/year could result in an extinction risk greater than 85%. Furthermore, we found that had mitigation not been constructed, the study population would have experienced an almost 100% probability of extinction over 100 years. Analyzing the effects of road mortality at the population level ensures stakeholders are adequately informed about the status of populations, ensuring proper management can be taken for their long-term viability.

0341 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Friday 17 July 2015

Paul Converse¹, Tim King², Shawn Kuchta¹, Willem Roosenburg¹

¹Ohio University, Athens, OH, USA, ²US Geological Survey, Kearneysville, WV, USA

Reduced Contemporary Gene Flow in Diamondback Terrapins, *Malaclemys terrapin*

The diamondback terrapin (*Malaclemys terrapin*) is a brackish water dwelling turtle that inhabits the Gulf and Atlantic seaboard of the United States. Historically overexploited, the terrapin still faces conservation concerns, namely habitat loss and accidental drowning in crab and eel pots. Conservation studies recover disparate results pertaining

to terrapin dispersal and population structure. Ecological and life history studies indicate the terrapin has low vagility and highly structured populations, while molecular studies detect weak or no population structure and infer high levels of gene flow. Here, we estimate gene flow in diamondback terrapins in Chesapeake Bay over evolutionary and contemporary timescales. Tests for population structure indicate Chesapeake Bay contains four terrapin populations that are highly admixed and harbor high levels of genetic diversity. Despite high levels of admixture, we find terrapin populations have low levels of gene flow connecting them. We also find that terrapin gene flow has decreased over time within Chesapeake Bay, although we detected a large influx of gene flow from outside the bay. Decreased terrapin population connectivity could be caused by habitat loss due to coastline development and the presence of a large network of crab pots throughout Chesapeake Bay. We hypothesize that female-biased sex ratios and male-biased dispersal maintain high levels of population admixture in the presence of low levels of gene flow.

**0605 Donn Rosen and the Assumptions Symposium II, Crystal 3 & 4, Sunday
19 July 2015**

Kevin W. Conway

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

**Dragonets, Blennioids, or None of the Above: A Morphological Perspective on
the Gobiesocid Sistergroup**

Clingfishes (Gobiesocidae) are highly derived acanthomorph teleosts characterized by a sophisticated ventral adhesive disc that is formed by elements of the paired fins and girdles. The relationships of clingfishes to other acanthomorphs have been a matter of considerable debate since the late 1800s. Based on morphological evidence, the Gobiesocidae has been considered either: (1) *incertae sedis* within Paracanthopterygii; (2) sistergroup to a clade comprising Batrachoidiformes plus Lophiiformes within Paracanthopterygii; (3) sistergroup to Callionymidae within Acanthopterygii; or (4) sistergroup to Blennioidei within Acanthopterygii. In his last published work, Rosen (in Rosen & Patterson, 1990) dismissed putative paracanthopterygian and callionymid affinities for gobiesocids and instead advocated a close relationship between blennioids and clingfishes based on characters of the upper gill arch skeleton. In this contribution I summarize previous hypotheses on the phylogenetic position of gobiesocids inferred from morphological characters, critically reassess these characters, and introduce a new character from the upper jaw that tentatively supports a sistergroup relationship between the gobiesocids and the blennioids.

0449 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

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Taxonomic Revision of the Seagrass Dwelling Clingfishes of the Genus *Acyrtops* (Teleostei: Gobiesocidae)

Members of the clingfish genus *Acyrtops* are small (>23mm SL) obligate inhabitants of seagrass beds throughout the western central Atlantic. The two valid species of *Acyrtops*, the Emerald clingfish *A. beryllinus* (Hildebrand & Ginsburg, 1927) and the flarenose clingfish *A. amplicirrus* Briggs 1955, are morphologically similar and difficult to distinguish based on external characteristics. This has led some authors to question the validity of *A. amplicirrus* and has hampered attempts to circumscribe the geographic range of both species, especially within the Caribbean Sea. Using a combination of museum specimens and COI sequence data, we plan to clarify: (1) how many species of *Acyrtops* are present in the western central Atlantic; (2) the geographic range of each species; and (3) which morphological characters are useful for distinguishing between species of *Acyrtops*. Our preliminary results suggest that *A. beryllinus* and *A. amplicirrus* are distinct and should be considered valid and that a third species of *Acyrtops* is present within the southern Caribbean Sea and could potentially bear the name *Acyrtops brevis* (Briggs, 1969).

0545 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Justin Cordova, David Ebert

Moss Landing Marine laboratories, Moss Landing, CA, USA

Species Grouping Within the Genus *Apristurus* Garman, 1913 Using Dermal Denticles

Apristurus is one of the largest shark genera, which encompasses 48 nominal species. Multiple morphological and molecular studies have shown the genus can be subdivided into three distinct subgroups: the *A. brunneus* subgroup, *A. spongiceps* subgroup, and *A. longicephalus* subgroup. This study examines the dermal denticles of three *Apristurus* species, one representative of each subgroup; specimens were collected off the coast of Monterey Bay CA, and Tai-chi, Taiwan. The three-species used for this study includes *A. kampae* for the *spongiceps* group; *A. brunneus* for the *brunneus* group; *A. herklotsi* for the *longicephalus* group. Dermal denticles were taken from four different locations on the specimens and observed under a dissecting microscope. Morphological features including cuspid counts, denticle size, and spacings are compared in order to find any noticeable differences. Observations reveal that the denticles of *A. kampae* are widely

spaced and have a unicuspid structure, where the other specimens exhibited a tricuspid structure with overlapping denticles. These differences will be further examined as a means of further organizing the genus taxonomically, and to investigate whether these differences may have ecomorphological significance relative to their preferred associated habitats.

0421 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Jeffrey Corneil¹, Chad Montgomery¹, Víctor Hugo Reynoso²

¹Truman State University, Kirksville, MO, USA, ²UNAM, Mexico City, Mexico

Conservation Assessment of the Critically Endangered Oaxacan Spiny-Tailed Iguana (*Ctenosaura oaxacana*)

The understudied and Critically Endangered Oaxacan Spiny-Tailed Iguana, *Ctenosaura oaxacana*, described in 2001, is restricted to the coast of Oaxaca, Mexico. In 2004 the species was estimated at fewer than 2,500 mature individuals with fewer than 1,800 expected to remain today. Therefore, information is urgently needed to inform present and future conservation decisions. The objective of the study is to develop an understanding of the species as a basis for conservation management practices and to update the current IUCN Red List status. Utilizing mark-recapture and radio-telemetry, we are gaining useful information regarding the natural history, demography, and range of the species. We are determining the species' current occurrence relative to habitat. In addition, we are examining home range and movement rates to understand habitat requirements. An *in situ* education and outreach component has been implemented to incorporate Oaxacan students and decision makers into the project. Since March 2014 we have captured 140 individuals (44 F: 51 M: 45 J) and tracked 13 individuals (7 F: 6 M) for up to eight weeks. No capture bias has been observed. Males (129mm SVL, 69g) are significantly larger than females (110mm SVL, 47g). *Ctenosaura oaxacana* prefers dry tropical forest with sparse understory and relatively open canopy and requires tree hollow refugia found in fewer than 10 tree species. We have expanded the known range of the species 100km to the west and the 20km to the east. We have also identified two natural predators.

0436 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Maria Correa, Thomas Near

Yale University, New Haven, CT, USA

Molecular Phylogeny of Sand Darters (*Ammocrypta*) Inferred from Nuclear and Mitochondrial Genes

Molecular phylogenetics provides useful insight into the relationships between closely related and morphologically similar species. The darter clade *Ammocrypta*, or sand darters, comprises six species: *A. beanii*, *A. bifascia*, *A. clara*, *A. meridiana*, *A. pellucida*, and *A. vivax*. A previous phylogenetic analysis of mtDNA gene sequences resolved *A. beanii* as paraphyletic where populations from the Mobile Basin were resolved as the sister lineage of *A. bifascia*. With regards to relationships among species of *Ammocrypta*, the mtDNA gene tree differed from a hypothesis based on external morphology. To further resolve phylogenetic relationships within *Ammocrypta* and assess the delimitation of species, we present new Bayesian and maximum likelihood phylogenies inferred from DNA sequences for the mtDNA cytochrome *b* and the two nuclear genes, *S7* ribosomal protein intron 1 and *RAG1*, for 165 individuals sampled from all six described species of *Ammocrypta*. Our phylogenies confirm the paraphyly of *A. beanii*, show that nuclear gene trees differ from those inferred from mtDNA, and reveal mtDNA introgression involving *A. vivax* and *A. beanii* in the Hatchie River system. These phylogenetic inferences are coupled with meristic data to assess species delimitation in the clade. The phylogenetic relationships and morphological data support the recognition of Mobile Basin populations of *A. beanii* as a new species.

0453 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday 16 July 2015

Joel Corush

University of Tennessee, Knoxville, TN, USA

The Evolutionary Significance of a Biphasic Lifestyle: A Case Study Assessing Diadromy in Ray-finned Fishes

Many fishes are limited to either marine or freshwater environments, however, roughly 250 of the nearly 32,000 teleost fishes are diadromous, or migratory between marine and freshwater during a particular stage of their life. Evolutionarily, diadromy is of interest due to its rare, yet widespread occurrence in nearly 30 families of fishes. To test rates of transition to and from diadromy and between wholly freshwater and marine lifestyles, I used a phylogeny of 7822 fishes and MUSSE analysis in R. Additionally, rate of diversification as a function of speciation and extinctions were examined in marine, freshwater and diadromus fishes. Results indicate that transitions to diadromy are rare from both marine and freshwater clades, yet once diadromy is acquired, diversification rates tend to be high when compared to marine and freshwater fishes. Additionally

transition out the diadromy occurred at a rate that was orders of magnitude higher than transitions out of marine or freshwater to any other state. This information does not support the hypothesis that diadromy is simply an intermediate state while transitioning between freshwater and marine systems. Instead this study suggests that diadromy is a source of diversification.

0295 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Joel Corush, Elizabeth Wolfe, Benjamin Keck

University of Tennessee, Knoxville, TN, USA

Patterns of Natural Hybridization in North American Minnows (Cyprinidae)

Hybridization occurs throughout the Tree of Life, yet patterns of rates and frequencies of hybridization within more inclusive taxonomic groups remains poorly documented. Identifying correlations between hybridization and the breeding behaviors and environmental preferences can shed light on factors facilitating hybridization. This study addresses these interactions in the largest clade of North American freshwater fishes, the minnows (Cyprinidae). To understand the dynamics of hybridization, we created a list of North American minnows and a list of observed hybrids from multiple ichthyological collections and the scientific literature. Frequencies of hybrids among the 418 species were recorded. Characteristics such as breeding methods and habitat preferences were assigned to each species to measure frequencies of hybridization for each characteristic. Preliminary results are based on 13,123 individual specimens contained in 1446 lots, representing 215 unique crosses involving 106 species. Among those, 62 crosses occurred within genera, while the remaining 153 crosses occurred between different genera. This large number of between genera crosses suggests that factors other than direct relatedness may be important in facilitating hybridization.

0117 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Taylor Cotten

Arizona Game and Fish Department, Phoenix, AZ, USA

SWPARC *Thamnophis eques* and *Thamnophis rufipunctatus* in Arizona, Current Research and Conservation

Recently listed as Threatened under the Endangered Species Act, the current US range of both *Thamnophis eques* and *Thamnophis rufipunctatus* largely occurs in Arizona. The Arizona Game and Fish Department and partners have initiated multiple monitoring, survey and restoration measures aimed at recovery and conservation of both species. We present the current distribution, status, and threats to both species within the state of

Arizona as well as current and future management and conservation efforts established for both species. By approaching gartersnake conservation from a multi-species perspective we can identify, create, and preserve intact native riparian systems.

**0375 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Dan Crear¹, Chris Lowe¹, Jeff Seminoff³, Dan Lawson², Tomo Eguchi³, Robin LeRoux³

¹California State University Long Beach, Long Beach, CA, USA, ²NOAA Southwest Regional Office, National Marine Fisheries Service, Long Beach, CA, USA, ³NOAA Southwest Science Center, National Marine Fisheries Service, La Jolla, CA, USA

Comparing Diel Differences in Habitat Use of East Pacific Green Sea Turtles, *Chelonia mydas*, Between an Urbanized River and Estuary Environment

Juvenile green sea turtles, *Chelonia mydas*, forage and rest within coastal habitats. However, identifying when and where these behaviors occur can be difficult. Further, these behaviors are often dictated by the quality of habitat. Six juvenile green sea turtles were fitted with acoustic transmitters and one was also fitted with an accelerometer. These turtles were tracked for two non-consecutive 24 hr periods within an urbanized coastal river and an estuary in southern California. A seventh turtle was tagged with an accelerometer and acoustic transmitter and tracked using a passive acoustic array in the river. Those fitted with accelerometer tags indicated that turtles were less active at night ($0.58 \pm 0.56 \text{ m/s}^2$ and $0.50 \pm 0.63 \text{ m/s}^2$) than during the day ($0.86 \pm 0.63 \text{ m/s}^2$ and $0.78 \pm 0.60 \text{ m/s}^2$) at both sites. Turtles spent more time near bridge pilings and runoff outflows in the river and near a culvert in the estuary while resting. Turtles indicated significantly larger core use areas in the river ($0.0118 \pm 0.0066 \text{ km}^2$) than in the estuary ($0.0051 \pm 0.0028 \text{ km}^2$). This may be due to the patchy resources in the river compared to the large dense eelgrass beds within the estuary. These aforementioned manmade structures in the river may be important habitat features used for resting by juvenile green sea turtles to shelter them from tidal flow. We show that combining high-resolution geospatial data with accelerometer data can provide accurate inferences of the behaviors of green sea turtles.

0230 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kristine Crippen, Eriek Hansen

Colorado Mesa University, Grand Junction, CO, USA

Quantifying Proximate Body Composition in Catostomids Using Bioelectrical Impedance Analysis

Methods for determining the condition of organisms are valuable tools for assessing the health of populations. Traditionally, length-weight relationships are used to quantify fish condition, but this method cannot differentiate among the components of proximate body composition (water, lipid, and lean masses). Current methods used to quantify proximate body composition are lethal. Many fish species in the Colorado River are classified as imperiled and nonlethal techniques are needed to quantify proximate body composition. Bioelectrical impedance analysis (BIA) is a nonlethal method which measures resistance and reactance, and has been used to quantify human proximate body composition. Our goal is to develop BIA techniques for studying sensitive and endangered species. Our objectives are 1) refine BIA techniques for Catostomids and Cyprinids, 2) compare effects of invasive needle electrodes versus noninvasive surface electrodes, 3) develop a multiple regression model for predicting proximate body composition, 4) evaluate if the model is species specific or can be used for multiple species or among families. We will report on the development of a BIA protocol, a comparison between needle and surface electrodes, and on models for quantifying the proximate compositions of white suckers (*Catostomus commersonii*; a representative for the native Catostomids).

0089 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Brian Crother

Southeastern Louisiana University, Hammond, LA, USA

Skepticism, Evolution, and Donn E. Rosen

In the spring of 1985 at the University of Miami in Coral Gables, FL., Donn Rosen taught a mini-course titled Evolving Evolutionary Thought. At the end of the course Rosen left the students with a list of assumptions that inhibit scientific progress in comparative biology, including for example, "Competition theory is important and well formulated." To me, it seems clear that Rosen was a skeptic, a Humean skeptic, and he used his skepticism to advance knowledge and to teach. I will review Rosen's list and attempt to reveal the origin of his skepticism through his writings. For instance, early in Rosen's writings he argued for the adaptive significance of structures, a stance he later changed to questioning the importance of adaptive scenarios, which in the skeptical list became "Adaptation scenarios have important general explanatory powers."

0439 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Karen Crow

San Francisco State University, San Francisco, CA, USA

Multiple Paternity, Female Bateman Gradients, and Cryptic Female Choice in the Live-bearing Surfperches

According to Bateman's principle, female fecundity is limited relative to males, setting the expectation that males should be promiscuous, while females should be choosy and select fewer mates. However, several surfperches (Embiotocidae) exhibit multiple paternity within broods suggesting that females benefit from polyandry. We found evidence for multiple paternity in a basal embiotocid taxon (*Hyperprosopon anale*), indicating that this tactic is a shared reproductive strategy among surfperches. Previous studies found no correlation between mating success and reproductive success (i.e., a Bateman gradient). However, by utilizing genomic scale variable markers, and including samples from a broader range of reproductive size classes, we found evidence consistent with a Bateman gradient in two surfperch species for the first time. Female Bateman gradients in the surfperches indicate that sexual selection is likely complex in this system, with the potential for conflicting optima between sexes. We argue that the complex reproductive natural history of surfperches is characterized by several traits that may be associated with cryptic female choice, including protracted oogenesis, uterine sac complexity, and sperm storage.

0260 Fish Conservation & Management, Carson 3, Saturday 18 July 2015

Clayton Crowder

Arizona Game and Fish Department, Phoenix, AZ, USA

The Attempted Establishment of Roundtail Chub *Gila robusta* in a Warm-water Riverine System in Eastern Arizona

Fulfilling objectives identified in the multi-partner Blue River Native Fish Restoration Project to protect and restore the native fish assemblage within the Blue River drainage in eastern Arizona, personnel from Arizona Game and Fish Department, US Bureau of Reclamation, and private contractors collected Roundtail Chub *Gila robusta* from an extant population in a neighboring creek in 2009 and 2010 and held the fish in captivity for reproduction and captive rearing. In June 2012, Roundtail Chub collected from the wild (n=27) as well as offspring from the captive bred Roundtail Chub (n=195) were stocked into the lower Blue River. Post-stocking monitoring conducted in the fall of 2012, 2013, and 2014 resulted in the capture of 42, 3, and 48 Roundtail Chub respectively within the project area. Additional sampling performed in 2014 detected Roundtail

Chub in two size classes (<50 mm and >150 TL) indicating that 2013 was the first year Roundtail Chub reproduced.

0485 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Paul Cupp

Eastern Kentucky University, Richmond, KY, USA

Substrate Avoidance Behavior in Green Salamanders, *Aneides aeneus*

Green salamanders, *Aneides aeneus*, sometimes assume postures that reduce body contact with the substrate such as the floor of a rock crevice or paper towel. Due to the body configuration of this salamander with the limbs splayed out to the side, the body is almost always in direct contact with the substrate. Various factors or properties of the substrate may affect the salamander, such as: temperature, ph, water content, etc. Physiological and behavioral responses of the animal may occur as a result to changes in the substrate in regard to these factors. While, typically, *A. aeneus* occur in humid but not wet crevices, they may be exposed to wet crevices temporarily, especially after heavy rains. Also, water may be standing in the bottom of some crevices for a few hours or days. Here, I report field and laboratory observations of green salamanders responding to prolonged direct contact with wet substrates. In six instances (equally divided in lab and field), individual adult *A. aeneus* were observed in a posture in which the limbs were raised high and the head and tail were raised off the substrate thereby significantly reducing exposure of the skin to direct contact with the substrate. One of these salamanders shifted to an alternate posture in which all four feet were in contact with the substrate with limbs extended, and the mid-body arched above the substrate. These postures may allow terrestrial salamanders, such as *A. aeneus*, to remain in home crevices thereby reducing exposure to predation without becoming overhydrated.

0582 Fish Morphology & Histology, Crystal 1 & 2, Saturday 18 July 2015

Wasila Dahdul

University of South Dakota, Vermillion, SD, USA

How to Accelerate the Transformation of Comparative Anatomy into Computable Anatomy?

The diversity of living form documented in the literature of comparative anatomy and phylogenetics is not readily available in a computable format, hindering its integration across studies and fields. By developing informatics tools, prototyped on teleost fishes, that apply ontology terms to free-text anatomical descriptions, the Phenoscope project has enabled the synthesis of character data and the linking of novel species anatomy to the genes that may underlie them. These data are desired by many biologists. However,

given the vastness of the legacy literature, how can this computational integration be applied efficiently at scale? Here I describe the workflow and effort required for phenotype curation and the prospects for streamlining the process. The currently manual workflow largely consists of data preparation, ontology development, and phenotype annotation, with the latter two tasks being the most time consuming. Improved community data practices can reduce time spent on data preparation, whereas ontology development remains a necessarily manual and specialized task. Phenotype annotation may be accelerated using natural language processing (NLP) tools to semi-automate the process of applying ontology terms to free-text descriptions. I describe an evaluation of an NLP system using the consistency of annotations created by humans as a baseline, and an assessment by the original authors of how well the semantics of their character descriptions are represented by the ontology-based logical expressions generated by humans or NLP. Finally, I discuss extending this workflow to enable links between phenotypes and habitat/environmental data to examine the repeated evolution of miniaturization in fishes.

0100 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Caio Isola do Amaral Dallevo-Gomes¹, George Mendes Taliaferro Mattox²

¹*Universidade de São Paulo, São Paulo, São Paulo, Brazil*, ²*Universidade Federal de São Carlos - campus Sorocaba, Sorocaba, São Paulo, Brazil*

An Annotated Checklist of the Syngnathidae of the New World, Current Diversity and Historical Perspective (Teleostei, Syngnathiformes)

The family Syngnathidae contains more than 300 extant species of seahorses and pipefishes, the majority of which occurs in the Indo-Pacific, but a significant number of species occur in the New World (i.e. the Americas). Information about the species diversity of New World syngnathids is scattered in different literature sources, hindering significant advances in the taxonomic knowledge of many members of the family. Moreover, studies dealing exclusively with New World syngnathids are largely lacking, with most works including the Eastern Pacific syngnathids together with the Indo-Pacific fauna. In addition, freshwater species have been usually treated separately from estuarine and marine ones. Taxonomic studies on the New World syngnathids are mainly focused on local checklists and species descriptions, often included in more general works. The present study was aimed at gathering the scattered information about New World syngnathids, and complement this information with regional records about the distribution of some species, along with museum records in order to review the distribution of the Syngnathidae in the New World. A total of 14 genera and 49 species were found to occur in the New World including freshwater, estuarine and saltwater species. Seven genera and 20 species occur in the Pacific Coast and 13 genera and 30 species in the Atlantic coast, with six genera and one species occurring on both oceans. Of all the species and genera, only *Pseudophallus* is strictly a freshwater genus. This work is funded by FAPESP Process 2013/19979-7.

**0113 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Caio Isola do Amaral Dallevo-Gomes¹, George Mendes Taliaferro Mattox²,
Mônica Toledo-Piza¹

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Osteology of the Freshwater Pipefish *Pseudophallus mindii* (Meek & Hildebrand): Setting the Path for Future Systematic Studies within Syngnathids (Teleostei: Syngnathiformes)

Syngnathidae contains over 300 species of seahorses and pipefishes, all characterized by having a small mouth, brooding pouch in males and bony rings covering the body. Although the majority of species occurs in the Indo-Pacific, 49 occur in the New World. The only truly freshwater pipefish genus in the Americas is *Pseudophallus*, which includes species with potential taxonomic problems. The osteology of *Pseudophallus mindii* was studied herein to provide data for future taxonomic and systematic studies within the genus. Some characteristics of syngnathids are related to osteological modifications. The tubular snout results from the elongation of the suspensorium and anterior bones of the neurocranium, reduction of jaw bones and displacement of infraorbitals and the opercular series. Bony rings begin at the level of the pectoral girdle and consist of seven bony plates decreasing in number posteriorly to four bony plates that encase the body from the nuchal plates to the caudal-fin base. Each plate interlocks with adjacent plates from the same ring through ligaments and bony grooves, and each plate has a forked flange anteriorly that connects with the plate of the anterior ring. Vertebrae possess strong lateral processes that anchor bony rings along the body. The caudal-fin skeleton is composed of only two hypural plates. The osteology of *P. mindii* will be compared to that of other species of the genus and family, not only to clarify the taxonomic problems of *P. mindii* but also to establish a base for future phylogenetic studies. Study funded by FAPESP process 2013/19979-7.

0406 AES Biogeography, Carson 2, Friday 17 July 2015

Toby Daly-Engel¹, Dean Grubbs², Rebecca Varney¹, Erin Pereira¹, Shawn Larson³

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Strange Things Happen When You Turn Back the Molecular Clock: Evolution and Speciation in Sixgill Sharks (Genus *Hexanchus*)

It is largely unknown what selective forces impact evolution and speciation in the deep ocean, though this ecosystem is thought to be largely unchallenged by climatic change

relative to shelf and coastal habitat. Fossil records and recent genetic analyses indicate that sixgill sharks (*Hexanchus*, Hexanchidae) are members of the first extant shark taxon to emerge following the shark batoid-split approximately 300 MYA. Unlike other Squalomorph lineages, many of which moved inshore to shallower shelf habitat and consequently diversified widely over evolutionary time, sixgills remain a primarily deep-water group, which may have contributed to their low speciation rates. Here we explore the factors that shape sixgill shark diversification in the deep ocean. DNA was collected from 130 *Hexanchus griseus* and 9 *H. nakamurai* from 13 collection sites across a global range. We sequenced four mitochondrial and nuclear genes plus 11 microsatellite loci, and found low molecular diversity across the genome relative to other shark species of a similar size. Coalescent analysis indicates a deep evolutionary split within *H. griseus* resulting in multiple well-defined global clades, one Indo-Atlantic and one restricted to the Pacific. We also show a deeper split within *H. nakamurai* that has resulted in at least one previously-unknown cryptic species, located in the West Indian Ocean. A molecular clock for the mtDNA control region and calibrated to the emergence of the Isthmus of Panama confirmed that rates of evolution in sixgills is dramatically lower than that of other shark taxa.

0491 Fish Ecology I, Carson 3, Sunday 19 July 2015

Solomon David¹, Matthew Herbert³, Ashley Moerke⁴, Mary Khoury³, Patrick Doran³, Eugene Yacobson³, Peter McIntyre²

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Connecting the Largest Surface Freshwater System on Earth: Life History and Distribution of Great Lakes Migratory Fishes

The Laurentian Great Lakes are comprised of a variety of aquatic habitats and diversity of fishes, nearly 200 species, many of which make seasonal spawning migrations connecting ecosystems. Aside from game species, many Great Lakes migratory fishes are understudied, nor are their distributions and life history traits comprehensively documented. To categorize the life history variation among native and exotic migratory fishes of the Great Lakes, we surveyed literature, field reports, and polled Great Lakes fishes experts to generate a comprehensive list of 55 species, focusing only on spawning migrants. We then created a “trait matrix” of 25 life history characteristics (e.g. iteroparous versus semelparous, facultative versus obligate migrants) classifying Great Lakes migratory species. To better understand the distribution of Great Lakes migratory species, we developed a presence-absence map of migratory species by coastal watershed for the entire Great Lakes region. Finally, we focused on several “migratory hotspots” in the Great Lakes region to compare and describe localized biodiversity, phenology, and habitats. Our study provides a comprehensive overview of the diversity, life history, and distribution of Great Lakes migratory fishes. Because these species traverse and connect a variety of aquatic habitats, they can serve as

environmental indicators of ecosystem health; therefore understanding their life history and distribution are important components of conserving biodiversity in the largest surface freshwater system on Earth.

0554 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Lindsay Davidson, Nicholas Dulvy

Simon Fraser University, Burnaby, Canada

Conservation Priorities and Political Responsibilities for Chondrichthyans

Global areas with concentrations of biodiversity (hotspots) are often prioritized for conservation and management action. The first hotspot analysis found that 1.5% of the earth's land surface area contained almost half of the world's threatened endemic plants and 30% of threatened vertebrates. The term hotspot has heretofore become a blanket term for finding concentrations of biodiversity using a variety of measurements. For example, the majority of marine analyses have described hotspots based on species richness patterns. Species richness patterns, however, are driven by common species. Therefore basing conservation and management actions on species richness patterns would not protect the most rare or vulnerable species. Here, we use a systematic conservation planning approach to determine the location of global marine hotspots as originally defined by Myers (2000). We define hotspots as global marine areas with concentrations of threatened, endemic chondrichthyans. We found the highest counts of threatened endemics in the national marine waters of, in descending order, Brazil, Taiwan, Uruguay, Argentina, and South Africa. Just over half of the 13 countries with the greatest number of threatened endemics in their national waters have a National Plan of Action (NPOA) for Sharks or finning regulation in place. Only one of the countries, Australia, has a NPOA that meets >65% of the objectives of sustainable fishing. This information can be used to inform the use of limited resources for the conservation of marine threatened species.

0056 AES Morphology & Physiology, Carson 2, Sunday 19 July 2015

Jonathan Davis

Texas Parks and Wildlife Dept, Pleasure Island, TX, USA

Plasma Solute Properties, Movements, and Structure of Bull Shark, *Carcharhinus leucas*, Populations in Sabine Lake and Lake Pontchartrain: A Comparative Study

The euryhaline bull shark, *Carcharhinus leucas*, is found in many coastal habitats throughout the Gulf of Mexico. The *C. leucas* populations were sampled in two estuarine systems to assess structure, movements, and osmoregulatory parameters: Lake

Pontchartrain, Louisiana and Sabine Lake, Texas. The population structures were similar in both locations with mean size and sex not being significantly different through analysis of University of New Orleans's Nekton Research Laboratory data from 2000-2013 and Texas Parks and Wildlife Coastal Fisheries data from 1986-2015. The *C. leucas* movements were seasonally influenced based on temperature in both areas according to an acoustic receiver monitoring array and seasonal collections. The plasma solute concentrations were determined from blood taken during the last year in each location. The Na⁺, K⁺, Cl⁻, Mg²⁺, Ca²⁺, urea and TMAO concentrations were significantly different between locations. Lake Pontchartrain is more stable in regards to salinity than Sabine Lake and as a result Sabine Lake bull sharks exhibited more fluctuation in these solute concentrations throughout the seasons. In summary, comparisons of two *C. leucas* populations from two distinct coastal habitats resulted in similar movements and structure while revealing a fluctuation in plasma solute concentrations due to variable salinity levels.

0429 Fish Systematics II, Carson 3, Sunday 19 July 2015

Matthew Davis

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

Evolutionary Relationships of the Deep-Sea Pearleyes (Aulopiformes: Scopelarchidae) and a New Genus of Pearleye from Antarctic Waters

This study investigates the evolutionary relationships among species in the family Scopelarchidae with molecular (eight genes) and morphological data. A new genus of pearleye is diagnosed, *Lagiacrusichthys*, new genus, from a previously described species (*Benthalbella macropinna*) distributed in Antarctic waters. The diagnosis of *Lagiacrusichthys* is based on molecular and anatomical information, including a highly reduced dorsal fin (5-6 rays) and a long anal fin (35-39 rays). The results represent the most taxonomically comprehensive molecular and total evidence hypotheses of the evolutionary relationships of the pearleyes to date (13 of 18 species), and these frameworks are used to comment on the historical biogeography of this widespread group. It is inferred that the pearleyes likely first evolved in central- tropical waters, with two independent invasions into Antarctic waters.

0400 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Matthew Davis, Toby Daly-Engel

University of West Florida, Pensacola, FL, USA

Atlantic Sharpnose Shark (*Rhizoprionodon terraenovae*) Rangewide Genetic Stock Structure

The Atlantic Sharpnose shark is a small coastal species in the family Carcharhinidae that is common throughout the Gulf of Mexico and the Western Atlantic from Maine to Honduras. This species is regularly fished, representing as much as 45.9% of the artisanal elasmobranch fishery in the Gulf of Mexico. However, little is known about its population size, range, and movement patterns. We seek to delineate the stock structure and dispersal of this species using mixed marker molecular analysis. To date we have accumulated *R. terraenovae* tissue samples from a variety of locations in the Atlantic and northern Gulf of Mexico, and collections are ongoing. Connectivity will be assessed through statistical comparison of DNA sequences from both the mitochondrial and nuclear genome, including the control region and microsatellites. With these data we will delineate detailed patterns of gene flow and dispersal in *R. terraenovae* throughout its range, information that will enable managers and conservationists to better protect this species in the future.

0328 AES Reproduction, Carson 2, Friday 17 July 2015

Melissa Gonzalez De Acevedo, Jim Gelsleichter

University of North Florida, Jacksonville, FL, USA

Hormone Regulation of Sperm Storage in Female Bonnethead Sharks (*Sphyrna tiburo*)

Female sperm storage is a phenomenon that has evolved in many different taxa, allowing viable sperm to be retained in the reproductive tract for an extended time period. Previous studies have determined that reproductive hormone may play an important role in regulating various aspects of sperm storage in certain vertebrates, including the long-term survival of sperm and its release near the end of the storage period. However, to date, no published studies have investigated the hormone regulation of sperm storage in the reproductive tract of female elasmobranchs despite evidence for this phenomenon in several shark species. Therefore, the purpose of this study was to investigate if gonadal steroid hormones such as 17 β -estradiol, androgens, and progesterone, which have been shown to increase in circulation during various periods of sperm storage, may play in regulating this poorly understood process. To accomplish this, circulating concentrations of gonadal sex hormones and the distribution of sex steroid receptors in the oviducal gland, the sperm storage organ of female sharks, were examined in the bonnethead (*Sphyrna tiburo*), an annually-reproducing species

known to store sperm for a 3-6 month period between copulation and ovulation/fertilization. As demonstrated in previous studies, female bonnetheads exhibited increases in circulating steroid concentrations both during (testosterone, 17 β -estradiol) as well as near the end (progesterone) of the sperm storage period. Immunocytochemical analysis of androgen, estrogen, and progesterone receptors in the oviducal gland demonstrated that epithelial cells of sperm-storage tubules and spermatozoa itself are direct targets for these hormones.

0549 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Christina De Jesús-Villanueva¹, Wilfredo Falcón², Ximena Vélez-Zuazo¹, Catherine Stephen³, Riccardo Papa¹

¹University of Puerto Rico Río Piedras, San Juan, Puerto Rico, ²Institute of Evolutionary Biology and Environmental Studies University of Zurich, Zurich, Switzerland, ³Utah Valley University, Orem, UT, USA

Genetic Population Structure and Origin of the Invasive Green Iguana (*Iguana iguana*) in Puerto Rico

Green Iguanas (*Iguana iguana*) have become an established and widespread invasive in Puerto Rico. Due to economic loss in agriculture and degradation of road infrastructure, they are categorized as an invasive nuisance by the local Department of Natural Resources and the Environment. Although their presence is conspicuous throughout the island, little is known about their genetic population structure or origins. In this study, we describe the distribution of genetic diversity of *I. iguana* across the island and determine their geographical origins using up to 200 samples (20 individuals from each of two populations within five regions across the island). We investigate how genetic diversity is partitioned among and between Puerto Rican populations of *I. iguana* using DNA sequence data from three loci and up to 10 microsatellite markers. Preliminary mtDNA sequence data show a high number of distinct haplotypes (10) dispersed throughout the island; suggesting multiple introduction events and highly diverse populations. By analyzing the recovered haplotypes on Puerto Rico along with previously published, native range haplotype data, we find the Puerto Rico populations have origins from both Central American and Colombian iguana populations. Within Puerto Rico, individuals from different sources are found in the same population. To date, 3 polymorphic msat loci (2-6 alleles) have been optimized for this study. Our results will ultimately be used to inform management practices.

0160 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Kevin de Queiroz

Smithsonian Institution, NMNH, Washington, DC, USA

Nomenclatural Assumptions that Inhibit Scientific Progress

Donn Rosen's 1985 list included several traditional taxonomic assumptions that he criticized from the perspective of phylogenetic systematics. At that time, methods for reconstructing phylogenies based on explicit tree-thinking had already been developed, and tree-based methods were starting to be extended into other areas of comparative biology. They had not, however, been developed for biological nomenclature – the area of taxonomy dealing with methods for naming taxa and applying existing names in the context of new phylogenetic hypotheses. The idea that supraspecific taxon names ought to be applied only to clades was gaining acceptance, but those names were still being applied using methods based on taxonomic ranks. In the early 1990s, tree-based methods were developed for biological nomenclature, and they highlighted that the traditional rank-based methods failed to maintain the associations between names and clades. Nevertheless, some 25 years later, tree-based nomenclatural methods still have not gained wide acceptance. Instead, rank-based methods continue to be assumed, and this assumption is inhibiting scientific progress by contributing to continual disruptions of the associations between names and clades. The magnitude of these disruptions has been amplified by recent progress in molecular sequencing and phylogenetic inference methods, which have led to many new phylogenetic hypotheses and a related large number of recent changes in the names of clades and species, many of which are both unnecessary and counterproductive. Examples will be provided using names applied to various amphibian and reptile clades.

0384 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Raelynn Deaton Haynes, Julian Rios

¹St. Edward's University, Austin, TX, USA

Fighting with Swords: Genital Combat as an Alternative Explanation for Same Sex Mating in a Coercive Livebearer?

Sexual selection does not explain the seemingly counter-adaptive nature of homosexual behavior, which is widespread in nature. Homosexual behaviors often result in males using genitalia to mate, but these behaviors may be mistaken for combat. Livebearing fishes provide an excellent system to test these alternative hypotheses because mosquitofish (*G. affinis*) and guppies (*P. reticulata*) display same sex mating behaviors when in male-biased populations and in the absence of female conspecifics. It is plausible that males use armaments (often in the form of genital structures) as weapons during competitive encounters. Here, we attempt to tease apart these two potential mechanisms of male genital contact (same sex mating vs. combat) in the coercive

western mosquitofish. If males are engaging in genital combat, we expect gonopodial scarring caused by genital contact, whereas if males are engaging in same sex mating, we expect to see elevated levels of sperm expenditure. To date, our data show that males engage in increased genital contact when females are not present, and that virgin males have signs of gonopodial scarring (using SEM) when placed into an all-male competitive situation (relative to isolated control virgins and males exposed to females). Our next step is to determine sperm expenditure under the differing social conditions (all male vs. mixed male and female). These data also will be presented. Our study will test the conventional assumption that livebearing males engage in same sex mating, and will explore the novel prediction of genital combat, which has rarely been shown in vertebrate systems.

0071 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Simon Dedman¹, Rick Officer¹, Deirdre Brophy¹, Maurice Clarke², David Reid²

¹*Galway-Mayo Institute of Technology, Galway, Co. Galway, Ireland,* ²*Marine Institute, Rinville, Co. Galway, Ireland*

Modelling Abundance Hotspots for Data-poor Irish Sea Rays

Skates and rays represent one of the most vulnerable components of the fish community in temperate demersal fisheries such as the Irish Sea. They also tend to be data poor in comparison to commercially exploited teleost fish. Spatial management has been suggested as an important tool in protecting these species, but requires an understanding of the abundance distribution, and its relationship with the environment at both adult and juvenile life history stages. In this analysis, delta log-normal boosted regression tree models were used with bottom trawl survey data to derive rays' spatial abundance, and environmental links. The modelling approach allowed the development of detailed predictive maps of abundance of four common and rare skate and ray species implicated in the fishery: thornback, spotted, cuckoo and blonde rays. The distributions were driven by a general preference for sand and courser substrates, higher salinities, temperatures and currents speeds. The abundance distribution maps were examined together with maps of skate and ray commercial landings, suggesting that the main hotspots for the species were away from the main commercial fishing areas. The maps were also compared to potential MPAs proposed for wider ecosystem protection, and the main hotspots were well covered by the proposed MPAs. This combination of the main abundance hotspots in areas of low fishing, and wider potential ecosystem protection, suggests good potential for spatial management measures to protect these species in the Irish Sea.

0080 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Simon Dedman¹, Rick Officer¹, Deirdre Brophy¹, Maurice Clarke², David Reid²

¹*Galway-Mayo Institute of Technology, Galway, Co. Galway, Ireland,* ²*Marine Institute, Rinville, Co. Galway, Ireland*

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0014 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Hayley DeHart, Gavin Naylor

College of Charleston, Charleston, SC, USA

Comparing Demographic and Genetic Estimates of Population Sizes in Three Coastal Shark Species

Sharks are widely held by the scientific community to be threatened with extinction, and yet they remain some of the most poorly understood marine vertebrate organisms. There is belief among marine conservation biologists that population genetics based approaches can be used to distinguish species, populations, and even population sizes for these threatened animals. Estimating population sizes using multiple estimates, as well as multiple species, is critical to understanding true population sizes and life history traits that affect these estimates. This study aims to estimate census population size (N_c) and compare this demographic value to the genetically determined effective number of breeders (N_b). Census size will be estimated from an on-going demographic mark and recapture study conducted by South Carolina Department of Natural

Resources and estimated using the program MARK. Effective number of breeders will be estimated using a cross-species gene capture method and variability will detected in these data to estimate effective number of breeders using the program NeEstimator. These methods will be deployed on three separate shark species: bonnetheads (*Sphyrna tiburo*), finetooth sharks (*Carcharhinus isodon*), and sandbar sharks (*Carcharhinus plumbeus*). These species all exhibit different population structure, life history, and recapture rates, which may in turn affect their N_b/N_c ratio, a value that may be used for future conservation regulation. It is believed that the comparisons between these estimates and species may be used for population assessment and management of coastal shark species.

0085 AES Genetics, Carson 2, Friday 17 July 2015

Hayley DeHart¹, Gavin Naylor¹, Bryan Frazier²

¹College of Charleston, Charleston, SC, USA, ²South Carolina Department of Natural Resources, Charleston, SC, USA

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0174 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Brian Deis, Kathleen S. Cole

University of Hawaii at Manoa, Honolulu, HI, USA

Reproductive Behavior and Social Behavior of a Cryptobenthic Reef, Eviota Fish in Hawai'i

Cryptobenthic reef fishes that reach <5cm as adults, account for a considerable amount of fish biodiversity on tropical reefs, but only recently have studies begun to elucidate the importance of the trophic role they may play in reef ecosystems (Depczynski and Bellwood 2003). *Eviota epiphanes*, a small (2cm TL), cryptobenthic species of goby (family Gobiidae) has been documented as the most abundant fish on near shore reefs in Hawai'i (Greenfield 2003). The high abundance of *E. epiphanes* in both larval and adult forms, suggests this species may make a significant contribution to the trophic structure of Hawaiian reefs. The goal of this study is to document the social and reproductive behavior of *E. epiphanes*, to better understand its biology. Individuals are being collected around Oahu and observed in aquaria in social groups ranging from two to five adults. Behavioral observations and, when appropriate, the associated presence of eggs, will be recorded daily. From these data we will characterize reproductive and other social behaviors, and evaluate the social structure of this species. This research is the first in-depth look into the social and reproductive behavior of *E. epiphanes* and, as such, will contribute to the growing literature on the biology of cryptobenthic reef fishes.

0592 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Robert del Carlo¹, Edmund Brodie, Jr², Normand Leblanc¹, Chris Feldman¹

¹*University of Nevada, Reno, Reno, NV, USA*, ²*Utah State University, Logan, UT, USA*

Muscle Performance of Garter Snakes Entangled in an Arms-race: Evidence of a Physiological Tradeoff?

The interaction between toxic newts (*Taricha*) and several resistant garter snakes (*Thamnophis*) provides a model system for the study of predator-prey coevolution. Pacific newts possess tetrodotoxin (TTX), a potent neurotoxin that binds selectively to the outer pore of voltage-gated sodium channels, blocking the movement of sodium ions across the cell membrane and thereby paralyzing muscles and nerves. Nevertheless, three species of garter snakes prey on sympatric newts and have independently evolved high tolerance to TTX, partly through structural changes in the outer pore (P-loop) of the skeletal muscle sodium channel (Na_v1.4) that reduce the affinity of TTX to this protein. However, these countermeasures may come at a cost; P-loop changes in sodium channels are expected to alter the biophysical properties of the protein, which may impact tissue functioning and organismal performance. We tested this hypothesis by examining various aspects of muscle physiology in TTX-resistant and non-resistant

grater snakes. We then correlated physiological performance of muscle tissue to whole animal TTX-resistance, and genotypic variation in the skeletal muscle sodium channel. Our data showed that muscles from TTX-resistant animals displayed reduced excitability and performance relative to wild-type snakes, suggesting a possible physiological tradeoff in TTX-resistance.

0243 Fish Systematics II, Carson 3, Sunday 19 July 2015

Maria Laura S. Delapieve¹, Roberto E. Reis¹, Pablo A. Lehmann²

¹*Pontifícia Universidade Católica do Rio Grande do Sul (PUCRS), Porto Alegre, Rio Grande do Sul, Brazil,* ²*Universidade do Vale do Rio dos Sinos (UNISINOS), São Leopoldo, Rio Grande do Sul, Brazil*

Phylogenetic Relationships of the Species of Hypoptopomatini (Siluriformes: Loricariidae)

The discovery of two possible genus-level new taxa of Hypoptopomatini prompted a reanalysis of the phylogenetic relationships of the tribe. Therefore, in order to elucidate the phylogenetic relationships of the hypoptopomatins and to test its monophyly, the present study aims to provide an encompassing hypothesis of relationships among the hypoptopomatins, comprising most species of *Hypoptopoma*, three new taxa and the other genera of the tribe. We analyzed a data matrix of 108 morphological characters with the inclusion of 63 terminals. The analyses were conducted using the heuristic searching algorithm of multiple Random Addition Sequence (RAS) followed by extensive branch swapping with the algorithm Tree Bisection and Reconnection (TBR). The analysis resulted in 120 maximally parsimonious trees of 446 steps, consistency index of 0.35 and retention index of 0.82. The 120 primary cladograms were then summarized in a strict consensus tree. The result confirms the monophyly of Hypoptopomatinae and Hypoptopomatini. The tribe comprises five known genera (*Acestridium*, *Hypoptopoma*, *Niobichthys*, *Otocinclus* and *Oxyropsis*) and two new genera. Additionally, *Hypoptopoma* (*sensu* Aquino & Schaefer, 2010) is not found to be monophyletic, *Otocinclus* is found to be the most basal member of the tribe; *Acestridium* and *Niobichthys* are sister to each other and closely related to a group formed by *Hypoptopoma* + New Taxa "A", and New Taxa "B" + *Oxyropsis* + *Hypoptopoma*. Based on this framework, changes to the classification and the taxonomy of the Hypoptopomatini are suggested.

0126 General Ichthyology II, Crystal 3 & 4, Friday 17 July 2015

John Denton¹, Dean Adams²

¹American Museum of Natural History, New York, NY, USA, ²Iowa State University, Ames, IA, USA

A New Phylogenetic Test for High-Dimensional Evolutionary Rate Differences among Body Regions Reveals Complex Interplay of Evolutionary Rates and Modularity in Lanternfish (Myctophiformes; Myctophidae) Photophore and Body Shape Evolution

Interplay between evolutionary rates and shape modularity influences the evolution of body plans by both promoting and constraining the magnitude and direction of trait response to ecological conditions. We develop a new phylogenetic comparative method for assessing differences in evolutionary rates among groups of geometric landmark coordinates that are subsets of a single configuration, and apply this method in combination with fits of alternate modularity hypotheses to body shape evolution in bioluminescent lanternfishes. We ask two fundamental questions – first, do maximal differences in evolutionary rates among body shape regions align with the optimal hypothesis of modularity, and second, do lanternfish lateral photophores exhibit an evolutionary signature independent of body shape? We show that: (1) the highest evolutionary rate differences within body shape do not necessarily correspond to best-fit modularity hypotheses; and (2) bioluminescent lateral photophores evolve along the same axis of covariation, and at a similar rate, as body shape in lanternfishes. These results suggest that photophore position in lanternfishes informs on body shape, but is likely a passive outcome of ecological pressures on life history.

0287 Herp Conservation II, Carson 1, Saturday 18 July 2015

Anne Devan-Song, Margarete Walden, Nancy Karraker

University of Rhode Island, RI, USA

"Viper Season" in South China: *Trimeresurus albolabris* Movements Explain Patterns of Snake-human Conflict

Trimeresurus albolabris is an arboreal pit viper that contributes significantly to human-wildlife conflict in tropical East Asia. In this region people refer to 'snake season' as the time of year when snakes are more frequently encountered. However, no previous research has attempted to determine what is responsible for this phenomenon. We hypothesized that conflict rates are related to vertical and horizontal viper movements, as increased horizontal movements may elevate encounter rates by humans, while vertical movements down from the canopy place vipers within human height. We tracked 16 female vipers and four male vipers for during the active season in 2012 and 2013 in Hong Kong. Female vipers exhibited synchronized descents from trees in October and November, coinciding with rains after dry periods. Males descended

between July and August, remained at low heights throughout most of the active season, and increased in average daily movements during the breeding season from September to November. The highest human-viper conflict rates occurred in October and November, which coincided both with female descent and increased male mate-searching movements. 'Nuisance' vipers were often found on garden shrubs or artificial substrates resembling branches near people's homes. Our results show that human-viper interactions may be reduced by seasonally clearing potential perch substrates around homes, and anticipating increased viper presence during the breeding season and during rains that occur after a dry period. Lowered encounter rates have beneficial implications for both snakes and humans, with reduced translocation or culling of nuisance snakes, and decreased bite morbidity in humans.

0027 General Herpetology, Carson 1, Friday 17 July 2015

Daniela Dick

Helmholtz Centre for Environmental Research - UFZ, Leipzig, Saxony, Germany

Patterns of Amphibian Community Organization in Central European Floodplains

River floodplains are important biodiversity hotspots. They function as primary habitats and dispersal corridors for many amphibian species. Nonetheless, especially in densely populated regions such as North America or Central Europe, most floodplains are heavily degenerated due to river regulations despite their importance for the maintenance of a rich biodiversity. Thus, the conservation need of river floodplains is high, but especially the successful implementation of amphibian conservation actions in floodplains is difficult due to our limited understanding of amphibian habitat requirements. In my study, I identified general patterns in amphibian community organization in floodplain habitats. I used literature data of 19 Central European amphibian species for 17 life history traits to investigate species ability to cope with floodplain hydrological dynamic and functional groups within communities to better understand habitat requirements. I found four functional groups of species representing floodplain habitats of different hydrological variability, ranging from species specialized to dynamic environments to species generally absent from floodplains. Overall, I found most Central European amphibian species being better adapted to hydrologically highly dynamic environments than to more permanent habitats. My results underline the importance of natural dynamics in floodplains as a major determinant of habitat preferences of amphibian species and therewith for the amphibian community at a given site.

**0517 ASIH STOYE AWARD PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY,
Carson 3, Friday 17 July 2015**

Matthew Dickson¹, Sigfrido Zimmermann¹, Tanja Wolmeyer¹, Gillian Larson¹,
Heather Liwanag², Robert Espinoza¹

¹California State University, Northridge, Northridge, CA, USA, ²Adelphi University,
Garden City, NY, USA

**Evolution in Your 'Hood: Rapid Continental Spread and Local Adaptation of a
Successful Invasive Gecko**

Invasive species can provide insights into adaptive evolution. Introduced species are likely to rapidly adapt to new local climates because of small founder populations and strong selective pressures. Ectotherms may be particularly sensitive to climatic challenges, requiring swift adaptive change. To test these ideas, we compared body sizes, thermal tolerances (CT_{\min} and T_{pant}), and temperature-dependent rates of evaporative water loss (EWL) and resting metabolism (RMR) of introduced populations of Mediterranean House Geckos (*Hemidactylus turcicus*) from climatically distinct regions across the USA. These geckos first appeared in Florida in 1910 and now occur in 24 states. Eleven populations were studied from across the USA representing four climates: desert ($n = 3$ populations), Mediterranean ($n = 2$), subtropical ($n = 5$), and continental ($n = 1$). We hypothesized that geckos would exhibit phenotypic differences consistent with adaptation to local climates. Geckos from drier climates were smaller, and those experiencing cooler daytime temperatures had lower CT_{\min} compared to those from hotter climates. We found no differences in T_{pant} among populations. At higher body temperatures, arid-climate geckos had rates of EWL that were two-thirds the EWL of geckos from humid climates, which was explained by correspondingly lower RMR in the arid populations. Interestingly, a recently founded (~3 yr) Mediterranean population did not show evidence of local adaptation. Current studies include sprint performance and testing for developmental plasticity. Ultimately our data will be used to predict the range expansion of this species in the USA.

0250 Fish Systematics II, Carson 3, Sunday 19 July 2015

Casey Dillman¹, Brian Sidlauskas², Richard Vari¹

¹National Museum of Natural History, Washington, D.C., USA, ²Oregon State
University, Corvallis, OR, USA

**A Morphological Supermatrix-based Phylogeny for the Neotropical Fish
Superfamily Anostomoidea (Ostariophysi: Characiformes): Phylogeny,
Missing Data, and Homoplasy**

Phylogenetic systematics of the four families and 281 species of the ecomorphologically diverse Anostomoidea have been addressed in 11 morphological studies, but a global hypothesis of species-level relationships remains absent. Synthesizing characters from

these studies yielded a supermatrix with 463 morphological characters with which to infer phylogenetic hypotheses for 174 ingroup species using parsimony and Bayesian optimizations. We evaluate the applicability of the supermatrix approach to morphological datasets, test its sensitivity to missing data, determine the impact of homoplasious characters on phylogenetic resolution, and determine the distribution of homologies and homoplasies on the topology. Despite 60% plus missing data, analyses supported the monophyly of all families in a pattern consistent with previous results. Phylogenetic structure degraded only when species with a high percentage of missing data were included, and in those analyses restricted to solely homoplasious characters. Results of the latter differed modestly from full optimization indicating phylogenetic signal even in highly mutable characters. Homology versus homoplasy distributions differ across the phylogeny, with a greater prevalence of homologies at deeper nodes and homoplasies nearer the tips than expected by chance. This suggests early diversification into distinct bauplans with subsequent diversification of mutable character systems. The morphological supermatrix approach is powerful and allows integration of classical data with modern methods to examine the evolution of multiple character systems.

0214 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Pavel Dimens, David Portnoy

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

Structural Ambiguity: Population Demography of the Blacknose Shark in the Florida Keys

For marine species existing along seemingly continuous habitats, identifying regional groups poses challenges because it limits the ability to define *a priori* hypotheses with respect to population structure. Further, in species that feature large migrations, individuals from independent populations may co-occur seasonally on feeding grounds. A recent study using microsatellite markers identified five distinct populations spread across an area from South Carolina to the Yucatan and the Bahamas but found ambiguity in the Florida Keys, an area that spans the divide between the U.S. Atlantic and eastern Gulf of Mexico populations, as well as their management units. This study aims to use double-digest restriction associated DNA sequencing (ddRAD-seq) to identify single nucleotide polymorphisms (SNPs) and provide high-resolution population genetic data for blacknose shark in the Florida Keys. The goal is to distinguish between three possible scenarios of population structure and gene flow in the region: 1) the Keys are a zone of admixture between Atlantic and east Gulf of Mexico populations, 2) individuals from both populations are seasonally present in the keys but there is no gene flow, 3) the Keys are a unique population, separate from Atlantic and Gulf of Mexico populations.

0052 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Drew Dittmer¹, Joseph Bidwell²

¹University of Newcastle, Callaghan, NSW, Australia, ²East Tennessee State University, Johnson City, TN, USA

Baffled by Buffel Grass (*Cenchrus ciliaris*): The Negligible Effect of an Invasive Grass on Reptile Community Structure and Diversity at an Australian World Heritage Site

In 1969 buffel grass (*Cenchrus ciliaris*) was established to control erosion at the base of the inselberg Uluru in Uluru Kata-Tjuta National Park. Since that time, the grass has spread and is now considered an invasive. This has raised concerns about potential impacts on native animal communities. The mix of native vegetation and buffel grass that occurs around Uluru offers the opportunity to compare the herpetofaunal community associated with the two vegetation types. In May 2014, we assessed vegetation coverage at 26 pitfall arrays surrounding the inselberg. We performed 100 metre vegetation transects at each pitfall array, and measured the percent ground cover for 36 genera of plants and percent dead vegetation. Sixteen of 26 sample sites had some measure of buffel grass, of these, buffel grass varied from less than 1% to as much as 50% of ground cover. We looked for patterns in the reptile and amphibian community that correlated with vegetation using Nonmetric Multidimensional Scaling (NMS). Despite being one of the most abundant vegetation species around Uluru, buffel grass had a weak association with herpetofaunal community structure compared to native species of vegetation. We also used Indicator Species Analysis (ISA) to determine an objective number of vegetation communities. From the communities determined from ISA, we compared the overall herpetofaunal diversity; communities dominated by buffel grass had some of the highest herpetofaunal species diversity of all sites sampled. We suggest buffel grass has a negligible impact on reptile biodiversity at Uluru.

0066 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Drew Dittmer¹, Brett Goodman², Joseph Bidwell³

¹University of Newcastle, Callaghan, NSW, Australia, ²University of Adelaide, Adelaide, SA, Australia, ³East Tennessee State University, Johnson City, TN, USA

Is This Inselberg Insulating? How a Large Inselberg Influences Microclimates and Thermoregulatory Opportunity for a Diverse Reptile Community

The namesake inselberg, Uluru, at Uluru Kata-Tjuta National Park, offers a unique opportunity to study a shadow effect on the temperatures available to a diverse reptile community. In general the base of Uluru is insulated from extreme temperature fluctuations of the open desert; the north base of Uluru being warmer at night, and the

south base being cooler during the day. We placed 6 optimal temperature models (OTMs) at each of eight pitfall sampling locations (N=48 OTMs) to analyse variation in temperatures available to reptiles for thermoregulation around the base of the inselberg. Each OTM contained a single iButton® that was programmed to record the temperature every 10 minutes. OTMs were deployed for a total of 30 days during the months of January and February 2015. We used Multivariate Analysis of Variance (MANOVA) to determine if OTM sampling locations differed in daily minimum, maximum, mean and standard deviation of temperature. In addition to the pitfall and OTM sampling, we also determined the preferred body temperatures (T_{pref}) for 15 reptile species using thermal gradients and a hand-held infrared thermometer. For the OTM data, we present preliminary analyses which show the north face of Uluru is warmer than all other locations and that the high reptile diversity on the north face of Uluru can be partly attributed to the availability of more thermoregulatory opportunities. Additionally, we show that cooler temperatures on the south face of Uluru and the presence of a daily shadow likely exclude heliothermic reptiles with high T_{pref} .

0560 AES Morphology & Physiology, Carson 2, Sunday 19 July 2015

Michael Doane, Elizabeth Dinsdale

San Diego State University, San Diego, CA, USA

Revealing a Physiological Role of Shark Skin Through Microbial Community Analysis

Sharks are apex predators that support an unnoticed yet diverse consortia of microbial organisms. Microbial life is inherently involved in the health of sharks but little is known of baseline composition of the shark microbiota. Shark skin is the first line of defense against pathogenic environmental microbiota. We hypothesized the boundary layer would yield structured microbial communities that were distinct from the water column microbiota. Microbes were collected from the base of the first dorsal fin of 6 Common thresher sharks (*Alopias vulpinus*) in the California Bight using a “supersucker” method. DNA was processed for shot-gun metagenomics and sequenced using Ion Torrent technology. The MG-RAST platform was used to annotate the resulting genomic data, which yielded an average of 936,614 high quality sequences having an average sequence length of 180 base-pairs. Each metagenome yielded an average of 577,797 sequences with protein coding motifs but of those only 2.9 to 8.2% matched known protein sequences in the SEED database. Microbial communities were more similar within shark samples than the water column microbial communities (PERMANOVA, $p=0.003$). Potential functional composition of microbial communities was also more similar to other shark samples than to the water column (PERMANOVA, $p<0.001$). Highly structured, distinct microbial communities on the skin surface suggest sharks possess physiological processes that are selective on microbial associates. Sharks produce a thin integument mucus layer that likely acts to regulate microbial activity, similar to that of teleost fishes. Our findings build on the understanding of shark interactions with their surrounding environment.

0054 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Terry Donaldson

University of Guam Marine Laboratory, Mangilao, Guam, USA

Lek-like Reproductive Behavior and Mating Success of *Cheilinus trilobatus* (Labridae) on a Resident Aggregation Site

A number of species of wrasses (Family Labridae) utilize resident spawning aggregation sites to reproduce, often on a daily basis. Many of these species utilize a lek-like mating system in which males arrive at the aggregation site first in order to establish mating territories and then attract females to mate. I examined the behavior of *Cheilinus trilobatus* at a spawning aggregation site to describe patterns of territorial and reproductive behavior, and to measure differential mating success of males distributed within this site. Terminal-phase (TP) males established temporary territories and defended them against rival males and sneaker initial-phase (IP) males, while attempting to attract females that visited the spawning aggregation site. Visitation by females typically began in the morning with up to several females assembling at the landmark over the course of 2-5 hours depending upon the species and the male territory holder. Males would often court females well into the afternoon. Males holding temporary territories directly adjacent to the outer reef slope of this site, where current exposure appeared to be greatest, had significantly higher rates of mating success compared to those males holding temporary territories away from the outer slope or in the interior of the site. The results of this study suggest that dominant males that defend these outer reef slope sites successfully against rival males within this resident spawning aggregation achieve greater mating success through increased access to females, and that females may be selecting these males on the basis of the location of their territories.

**0016 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Friday 17 July 2015**

Caroline Dong¹, Tag Engstrom², Robert Thomson¹

¹*University of Hawaii at Manoa, Honolulu, HI, USA*, ²*California State University, Chico, CA, USA*

Origins of Softshell Turtles in Hawaii with Considerations for Conservation

Non-native species have the potential to induce large-scale ecological changes that threaten native ecosystem biodiversity, particularly on islands. However, aside from strongly invasive species, the majority of non-natives receive relatively little scientific attention making it difficult to predict the severity of their impact. In addition to ecological and natural history data, genetic approaches help address the status of non-natives, particularly for introductions that involve multiple sympatric and

morphologically cryptic species to clarify their taxonomic identities and geographic origins. We used these approaches to investigate softshell turtles (family: Trionychidae) introduced to the Hawaii in the late 1800s: *Palea steindachneri* and *Pelodiscus sinensis*. In light of the extended importation and inter-island dispersal, revised understanding of diversity and taxonomy in the previously monotypic *P. sinensis*, and native range conservation concerns, we comprehensively characterized the populations of Hawaii. Extensive surveying efforts reveal a present distribution markedly different from the historical one with the current ranges of *P. steindachneri* limited to Kauai and *Pelodiscus* limited to Oahu. Analysis of the 12S rRNA, ND4, and Cyt b gene regions revealed two species of the *Pelodiscus* complex (*P. sinensis* sensu stricto and *P. maackii*) and low genetic diversity in *P. steindachneri*. This work suggests continued research efforts to assess their impacts on Hawaiian species with the aim of developing management policies to either protect them as 'assurance colonies' for the declining native populations or alternatively support the eradication of this introduced aquatic predator that may threaten native fauna.

0257 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kate C. Donlon¹, John B. Jensen², Thomas C. McElroy¹

¹*Ecology, Evolution and Organismal Biology, Kennesaw State University, GA, USA,*

²*Wildlife Resources Division, Department of Natural Resources, GA, USA*

Conservation Genetics and Mark-Recapture Monitoring of a Rare Salamander, *Plethodon petraeus*, with a Highly Restricted Range

Globally, amphibian species are experiencing declines at an alarming rate largely due to habitat loss, disease and climate change. Species with limited ranges are at an elevated risk of a significant decline in population numbers and extinction due to an inability to avoid and recover from these impacts. One such species is the Pigeon Mountain salamander. The Pigeon Mountain salamander, *Plethodon petraeus*, is restricted to a roughly 15 km area on the eastern flank of Pigeon Mountain in northwest Georgia. Consequently, *P. petraeus* is highly vulnerable to the impacts associated with amphibian declines, a fact that placed the salamander on the list of rare and protected species in Georgia. The entirety of *P. petraeus*' distribution is highly correlated with patchily distributed rocky outcrops, providing an efficient management target. However, the development of an effective, long-term management plan requires an understanding of genetic diversity, gene flow and levels of population connectivity. We will present data on the population genetic structure of *P. petraeus* estimated from mitochondrial haplotypes and nuclear DNA profiles from eight polymorphic microsatellite loci identified from cross-species amplification. All loci were found to be in Hardy-Weinberg equilibrium and not in linkage disequilibrium. We will also include preliminary results from a mark-recapture study using visible implant elastomer marking.

0294 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Maureen Donnelly

Florida International University, Miami, FL, USA

What Does Use of a Limited Resource Have to do with Biodiversity?

"Survival of the fittest" during the "struggle for existence" suggests that competition is the driving force behind evolutionary change as a result of natural selection. Competition occurs when a resource is limited, but the limiting resource is rarely identified in most studies. Donn E. Rosen was the first scientist who challenged me to think critically about the role competition played in evolution when he asked me what "natural selection had to do with why there are lions, tigers, and bears." To measure the importance of competition for the generation of diversity, I used Google Scholar to search for publications on speciation. Because over 600,000 papers are included in the results of this search, I sampled papers every five years starting in 1965 (e.g., 1965, 1970, 1975, . . . 2015) and determined what mechanism was implicated in the generation of diversity. The number of papers that implicate competition is small, and the importance of competition theory will be compared with a facilitation model recently presented by McIntire and Fajardo.

0547 Cypriniformes Biology, Crystal 1 & 2, Sunday 19 July 2015

Thomas Dowling¹, Paul Marsh², Robert Clarkson³

¹Wayne State University, Detroit, MI, USA, ²Marsh & Associates, Tempe, AZ, USA,

³US Bureau of Reclamation, Phoenix, AZ, USA

Molecular Markers Identify Segregation of Two Species of Chubs (Genus *Gila*) in an Arizona Stream

Two species of cyprinid fish, *Gila robusta* and *G. nigra*, were once common to rivers and headwater streams of the Gila River drainage of the southwestern US, but are now being considered for listing. These taxa have been difficult to discriminate with morphology and also show high levels of genetic divergence among local populations but not species. Here we report on a study of these species from Fossil Creek, a spring-fed tributary of the Verde River that was managed extensively for hydropower generation beginning in the early 20th century. Projects were implemented in 2004-2005 to decommission the power facility and return full flows following construction of an artificial fish barrier near the terminus, chemical renovation upstream to remove non-native fishes, and subsequent repatriation of the native fish community. We examined genetic consequences of these management activities on the two chubs by comparing patterns of microsatellite and mtDNA variation from a temporal longitudinal series of post-project samples collected from above and below an enhanced barrier falls. Our data demonstrate that *G. robusta* has become more common downstream of the falls over

time, with *G. nigra* becoming rare; however, *G. nigra* is able to persist upstream of the barrier in the absence of *G. robusta*. Results are consistent with specific status for *Gila robusta* and *G. nigra*, and have specific implications for the conservation and management of these forms.

0388 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Charles Downey, Rachel Brewton, Jennifer Wetz, Matthew Ajemian, Gregory Stunz

Harte Research Institute for Gulf of Mexico Studies, Texas A&M-Corpus Christi, Corpus Christi, TX, USA

Reproductive Biology of Red Snapper, *Lutjanus campechanus*, on Natural and Artificial Reefs in the Western Gulf of Mexico

Energy exploration in the Gulf of Mexico (Gulf) has resulted in the addition of numerous oil and gas production platforms that have added structurally complex habitat to an area otherwise comprised of primarily bare bottom. The impact of these artificial structures on fish populations is largely unknown and there is ongoing debate about their functionality. Red Snapper (*Lutjanus campechanus*) is an ecologically and economically important sportfish that uses natural reefs as well as the artificial reefs created by standing and reefed (toppled or cutoff) oil and gas platforms. Little is known about the reproductive characteristics of Red Snapper in the western Gulf, and how they may differ between natural and artificial habitats. Red Snapper (155-855 mm TL) were collected from standing rigs, reefed rigs, and natural hard-bottom in the western Gulf. Physical parameters (sex, total weight, gonad weight, TL) were recorded and ovaries were preserved for histological analysis. Sex ratios, gonadosomatic indices (GSI), reproductive stages, and weights were compared among habitat types. Sex ratios were nearly 1:1 at natural habitats and standing rigs, with reefed rigs having a higher percentage of males (59.8%) than females. Preliminary GSI data suggest a similar spawning season among structure types. While histological analyses of ovaries are ongoing, these initial results suggest that the functionality of artificial reefs and natural reefs could be similar for Red Snapper reproduction in the western Gulf.

0480 General Ichthyology I, Crystal 3 & 4, Friday 17 July 2015

Alan Downey-Wall, Derek Hogan, Jason Selwyn

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

Examination of Habitat Utilization Patterns and Source-Sink Dynamics in the Indo-Pacific Lionfish, *Pterois volitans*, for Insights into Habitat-Specific Targeted Removal

The Indo-Pacific lionfish, *Pterois volitans*, is one of the most prominent marine invasive species of the past decade, successfully spreading into most regions of the subtropical and tropical Western Atlantic. Management of the species is primarily done through local removal efforts, which can be successful but very labor intensive. Here we examine several demographic metrics; size, sex, and female spawning across five major coastal tropical marine habitats including; lagoon, mangrove channel, mangrove, back-reef (collectively "nursery" habitats) and fore-reef) in order to assess habitat utilization patterns and source-sink dynamics of lionfish in their invaded range. We incorporated the demographic data into a stage-based population growth model to determine the viability of each of the five habitats. We found a significant difference in size, sex ratio, and proportion of spawning females at the fore-reef compared to the protected, nursery habitats. Macroscopic inspection of the gonads of each lionfish revealed that nursery habitats had a higher proportion of juveniles (16-49%), while the fore-reef had comparatively fewer (2%). The proportion of spawning females was <15% in all protected habitats and ~68% in the fore-reef; there were no spawning females found in the mangrove sites. The population growth model found only the fore-reef was self-sustaining ($\lambda = 1.18$), suggesting that nursery habitats likely require larval recruits from the fore-reef in order to persist. We propose two competing habitat-specific removal strategies that take into consideration the identified source and sinks, under two alternative juvenile movement scenarios; (i) migration between habitats, and (ii) no migration between habitats.

0278 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Danielle Drabeck¹, Antony Dean², Sharon Jansa¹

¹*University of Minnesota, Saint Paul, MN, USA*, ²*Laboratory of Microbial Evolution Sun Yat-sen University, Guangzhou, China*

Molecular and Functional Characterization of an Evolutionary Arms Race: Opossums and Pit Vipers

Opossums are among the few mammals resistant to pit-viper venoms, but the molecular basis of resistance is incompletely characterized. Recently, a protein involved in blood clotting (von Willebrand Factor) has been found to have undergone rapid adaptive evolution in venom-resistant opossums. This protein is a known target for snake venom

C-type lectins (CTLs) such as Botrocetin (from *Bothrops jararaca*) in susceptible species. Several amino acid changes in vWF unique to these opossums could explain their resistance. However, experimental evidence that these changes disrupt binding to snake venom CTLs was lacking. Using *E.coli* expressed opossum vWF and purified Botrocetin I quantified binding affinity for venom-resistant and venom-susceptible taxa. I also used platelet agglutination assays to further elucidate how tertiary binding of vWF-Botrocetin to the platelet binding protein GPIIb/IIIa contributes to resistance. Together, these data describe how this adaptive modified binding site on opossum vWF helps to mitigate venom-induced coagulopathy from venom C-type lectins.

0527 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Kristina Drake¹, Todd Esque², Ken Nussear⁴, Lizabeth Bowen², Shannon Waters², Keith Miles², Rebecca Lewison³

¹University of California, Davis, CA, USA, ²US Geological Survey, Henderson, NV, USA, ³San Diego State Univ., San Diego, CA, USA, ⁴University of Nevada, Reno, NV, USA

Using Genetics to Identify Subtle or Hidden Health Conditions in the Mojave Desert Tortoise

The desert tortoise (*Gopherus agassizii*) is a threatened species that inhabits the Mojave Desert of California, Nevada, Arizona, and Utah. Despite dedicated management effort, protection, and study over the last 25 years, tortoise populations continue to decline. Tortoises are often slow to respond to environmental stressors and seldom display clinical signs of physiological distress. This slow and subtle physiological response to stressors often hinders our ability to accurately assess their condition and identify specific environmental settings linked to declining animal health. We assessed juvenile and adult tortoises in the western and northeastern Mojave Desert to evaluate the effects of disease, disturbance, and habitat alteration on the physiology and health of tortoises. We conducted physical health assessments, collected blood samples, and monitored behavior and activity from 2011-2014. Blood samples were evaluated using a gene transcription quantitative polymerase chain reaction (qPCR) assay, incorporating multiple genes that are indicative of physiological responses to stressors (i.e. disease pathogens, trauma, or temperature and environmental disturbances). This transcription panel targets conserved genes known in other species to change in response to bacteria, viral, inflammatory thermal stress, nutritional stress, environmental toxicants, and overall cellular function and metabolic conditions. As hypothesized, gene transcript profiles did not correlate with standard desert tortoise health assessments, or with known animal condition and disease status, highlighting the need for the development of alternate assessment techniques, such as molecular diagnostics.

0203 AES Genetics, Carson 2, Friday 17 July 2015

Drew Duckett, Gavin Naylor

College of Charleston, Charleston, SC, USA

Maximizing Statistical Power in Shark Population Structure Analyses

Next Generation Sequencing technologies developed in recent years allow for the collection of substantially more DNA sequence data than has previously been possible. However, the comparative utility of the various kinds of molecular markers now available for exploring population genetic questions has not yet been thoroughly evaluated. Few population genetics studies test the statistical power of the marker types used or the sampling schemes employed for answering the question posed. Using too few loci, the incorrect marker type, or inadequate sampling can severely compromise the statistical significance of research findings obtained. The present study explores the differences in statistical power associated with different molecular marker types, different numbers of marker loci, and different sampling schemes for analyzing population structure. These issues are addressed through both computer simulation and empirical data sets of three shark species with different life history characteristics. The results of the present study will serve to guide researchers as to which markers are most appropriate for different kinds of questions and increase knowledge of the population structures of the shark species evaluated.

0152 Herp Conservation II, Carson 1, Saturday 18 July 2015

Andrew M. Durso, Ryan P. O'Donnell

Utah State University, Logan, UT, USA

The Future of Herpetological Citizen Science

Citizen scientists have vast potential to contribute to our knowledge of amphibian and reptile distribution, abundance, and ecology. In addition to recording where particular species are observed, an ideal citizen science database would 1) imply non-detections using a checklist-based format, 2) allow reporting of effort and other ancillary information, 3) encourage reporting of abundance, and 4) encourage frequent reporting by building and encouraging a community of contributors. Many existing databases collect only presence data, which are useful for certain purposes but have more limited analytical potential than presence-absence data. Reporting all species using checklists generated from global reptile and amphibian range maps would allow data analysts to engage in occupancy modeling, the most robust, versatile, unbiased, and universally accepted tool for examining species occupancy at landscape scales. Quantifying effort is critical for assessing two unavoidable sources of bias: imperfect detection and unequal sampling effort. Counting individuals conveys important information about relative abundance, which in turn allows analysis of population trends at a variety of spatial scales. Finally, the greatest advantage that a citizen science database can provide that is

not provided by the work of professional herpetologists is the great statistical power that is achieved from the accumulated efforts of thousands of volunteers around the world. An ideal database would serve as the focal point of a global social network of recreational herpers and professional herpetologists working together to achieve common goals in amphibian and reptile conservation.

0382 Donn Rosen and the Assumptions Symposium II, Crystal 3 & 4, Sunday 19 July 2015

Mallory Eckstut

University of Nevada Las Vegas, Las Vegas, NV, USA

Does Vicariance or Dispersal Drive Biogeographic Patterns and Diversity?

Rosen was skeptical of several statements regarding biogeography, including those stating that all biogeographic patterns are formed by either vicariance or dispersal. Reconstructive methods are often used to identify either vicariant- or dispersal-based patterns of diversity. A modification was made to Phylogenetic Analysis to Compare Trees (PACT) to distinguish unique and general diversification events among areas; degree of uniqueness may be useful for discerning unique dispersal events from general geodispersal or vicariant events. This method was tested on a variety of reptiles and an amphibian from the North American warm deserts. The results of this analysis revealed that both unique and general events led to the formation of the current North American warm desert biota. Additionally, pseudo-congruent diversification patterns were observed, which means that similar diversification patterns were produced by historically dissimilar events. This result underscores Rosen's skepticism of the statements "All distribution patterns result from [vicariance/dispersal]" and emphasizes the importance of including a temporal framework when conducting community-level biogeographic analyses to distinguish unique from general events, such as dispersal from vicariance and geodispersal.

0163 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Cameron Eddy, Carl Anthony, Cari-Ann Hickerson

John Carroll University, University Heights, OH, USA

Great Lakes Island Biogeography of *Plethodon cinereus*: Effect of Island Elevation on Color Polymorphism

Many current questions in ecology and evolutionary biology have been addressed in island systems. For example, factors involved in the genetic divergence of populations are easier to discern in island populations because confounding effects of gene flow from adjacent populations are limited. This study focused on isolated island populations

of the polymorphic Eastern Red-backed Salamander (*Plethodon cinereus*) in the Great Lakes. Color morph frequencies of *P. cinereus* populations on these islands are largely unknown, but reports of monomorphic unstriped populations suggest that this form may be favored on islands and peninsulas. The goal of this project was to census island populations throughout the Great Lakes to determine morph frequencies on the islands, and to explore whether phenotypic differences between island and mainland populations are related to island attributes (e.g. size, distance to mainland, and elevation). We compiled morph frequency records from 26 islands and 14 paired mainland sites occurring in each of the five Great Lakes using literature records, museum specimens, and field surveys. In the census, we found nine islands to be polymorphic and 17 to be monomorphic (2 unstriped and 15 striped). Island elevation above lake level was positively correlated with an increased difference in morph frequencies between island and adjacent mainland sites. However, contrary to our expectation, island populations were not more likely to be monomorphic unstriped, suggesting that selection for the unstriped morph varies from island to island or that genetic drift plays a stronger role than selection in determining morph frequencies.

0077 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Michael Edgehouse, Michael Skinner, Christopher Brown, Brigette Schwimmer
Lewis-Clark State College, Lewiston, ID, USA

**Seasonal Diet of a Population of Western Terrestrial Garter Snake,
Thamnophis elegans, Along the Grande Ronde River, Southeastern
Washington**

Garter snakes (*Thamnophis spp.*) are historically considered generalist predators. However, recent studies have demonstrated several populations of the western terrestrial garter snake (*Thamnophis elegans*) to be dietary specialists during different life stages or different seasons. We investigated the spring and summer time diet of a population of *Thamnophis elegans* along the Grande Ronde River in southeastern Washington. Our data, coupled with previous studies, demonstrate that this population of *Thamnophis elegans* are dietary specialists. Snakes from this population show a 100% preference for sculpin fish (*Cottus spp.*) as their food source during spring and summer and a 92% preference for *Cottus spp.* throughout the year.

0296 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Robert Edman¹, Gorka Sancho¹, Bryan Frazier², John Kucklick³, Walter Buble²

¹College of Charleston, Charleston, SC, USA, ²South Carolina Department of Natural Resources, Charleston, SC, USA, ³National Institute of Standards and Technology, Charleston, SC, USA

Movement Patterns and Trophic Ecology of Tiger Sharks (*Galeocerdo cuvier*) Caught off the Southeast Coast of the United States

Exploitation of sharks has markedly increased in the past three decades, and this exploitation, coupled with degradation of essential habitats, can contribute to declining species abundance. Understanding the movement patterns and diet composition of sharks is central to creating and enacting appropriate management actions to preserve these animals and their habitats. Despite the large number of Tiger Sharks (*Galeocerdo cuvier*) in the western North Atlantic Ocean, the majority of research on Tiger Shark movement and diet has been concentrated in the Pacific and Indian Oceans. The present study seeks to fill these gaps of knowledge through analyses of the movement and diet of Tiger Sharks caught in coastal waters of the southeast United States. A multi-tag approach, utilizing passive acoustic telemetry and satellite telemetry, will provide insight into the movement patterns of Tiger Sharks both inshore along the coast and offshore throughout the Atlantic Ocean. Stable isotope analysis will be used to determine the trophic position of Tiger Sharks and estimate diet composition. Captured Tiger Sharks were sampled for skin, blood, and muscle to use in stable isotope analysis. Select sharks were surgically implanted with acoustic tags, and a number of these sharks were dual tagged with Smart Position or Temperature Transmitting (SPOT) tags as well. Preliminary data indicate that these Tiger Sharks repeatedly visit inshore areas but do not venture offshore of the continental shelf. Stable isotope analyses are ongoing and monitoring of tagged sharks will continue with additional sharks tagged and sampled this summer.

0021 General Herpetology, Carson 1, Friday 17 July 2015

Omoyemwen Edo-Taiwo, Martins Aisien

University of Benin, Benin City, Edo State, Nigeria

Amphibians in Cocoa Plantations, Southwestern Nigeria

Agricultural activities could lead to deforestation with resultant consequences on biodiversity. Biodiversity is supported by forests which invariably provide habitat for wildlife. Habitat loss and degradation usually increase the threat faced by amphibians. In the tropics, the largest percentage of human land-use is agriculture because it is the economic mainstay of many African countries. The increasing use of pesticides and other agricultural chemicals especially in cocoa farming are likely to affect the existence

and health of amphibians. An area can be made unsuitable for amphibian reproduction and survival by land-use changes in some cases nevertheless a number of original amphibian community could be supported by disturbed/converted areas. Data on amphibian diversity in cocoa plantations are lacking. This study aimed at determining species richness, relative abundance and community composition of amphibians in cocoa plantations. This study was conducted in cocoa plantations located in southwestern Nigeria. Amphibians were collected from their breeding sites and vegetation within the plantations. A combination of visual (VES) and acoustic (AES) encounter survey was used. Amphibians were collected at night. Collected specimens were identified following laid down protocols. Each identified species was photographed and the snout-vent length (SVL) taken. 912 amphibians belonging to 7 families, 10 genera and 36 species were encountered. 23 species were identified while 13 species were unidentified. The number of amphibians recorded in this study is rather high which probably suggests that there could be several species that can tolerate altered environment and among the unidentified species could be potential new species.

0247 General Ichthyology II, Crystal 3 & 4, Friday 17 July 2015

Josh Egan, Andrew Simons

University of Minnesota, St. Paul, MN, USA

Evolution of Microphagy in Anchovies

Microphagy is the consumption of prey too small to be sensed and engulfed individually. This feeding mode has evolved many times in fishes and is typically associated with modifications of the jaws, gill arches, and gill rakers. Paired sac-like epibranchial organs are also present in the oral cavities in many microphagous fishes. Preliminary functional morphology studies indicate these organs help fishes consume extremely small food particles, but this hypothesis has not been tested in a comparative phylogenetic framework. Several anchovy species (Family: Engraulidae) are microphagous, but it is not known how many times microphagy evolved within anchovies and if it is accomplished using morphological structures similar to those in other microphagous fishes. To investigate these questions: (1) I characterized aspects of cranial morphology for anchovy species from all major engraulid lineages, (2) surveyed the literature and examined specimens to determine which anchovy species have epibranchial organs, (3) reconstructed ancestral diets, and (4) used phylogenetic comparative methods to identify suites of morphological characters associated with the evolution of microphagy in anchovies. In this talk I will discuss the origins and convergent and alternative morphologies associated with microphagous diets in anchovies.

0423 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Samantha Ehnert, Jim Gelsleichter

University of North Florida, Jacksonville, FL, USA

Mercury Accumulation and Effects in the Brain of Atlantic Sharpnose Sharks (*Rhizoprionodon terraenovae*)

Studies have shown that sharks often bio-accumulate mercury concentrations that threaten the health of human consumers. However, few studies have examined mercury in the central nervous system of sharks or how mercury affects shark neurophysiology. This study's goal is to determine if elevated levels of mercury often found in shark muscle also occur in the brain, and if mercury accumulation is associated with damage to the shark's nervous system. Muscle and brain mercury concentrations in the Atlantic sharpnose shark (*Rhizoprionodon terraenovae*) are being measured and compared. Brain mercury concentrations with S100b concentrations, bioindicator of mercury-induced neurodegeneration, in shark cerebrospinal fluid (CSF) are being compared. Sharks were collected along the U.S. Southeastern coast. Total mercury concentrations in dried muscle and brain samples were measured using a Direct Mercury Analyzer. Levels of S100b were measured in shark CSF using an ELISA. Preliminary results show strong correlations between mercury in the muscle and brain. Brain mercury levels were significantly lower than the muscle and most known thresholds for biological effects; suggesting limited potential for neurological impacts. Data on S100b concentrations in CSF support this premise, as increased brain mercury levels were not correlated with increased S100b, suggesting mercury levels are below the threshold needed for release of S100b as a function of neurotoxicity. Measurements of oxidative stress, another marker of mercury-induced neurotoxicity, are being analyzed. This study will be one of the first to examine the direct impacts of mercury uptake in sharks, and therefore contribute significantly to the field of shark ecotoxicology.

0433 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Diego Elias, Kyle Piller

Southeastern Louisiana University, Hammond, LA, USA

Diversification of Percidae: Is clade Age Enough?

Percidae is a family of freshwater fishes composed of more than 238 species distributed throughout North America and Eurasia. Prior studies hypothesized that Percidae arose during the Cenozoic era in Eurasia, and later dispersed into North America. One of the most striking patterns in this diverse family is the disparity in species richness between these two regions. Approximately 94% of the described species within Percidae inhabit North America and are distributed among 7 genera. In contrast, the remaining 6% of species inhabit Eurasia and are distributed among 6 genera. The North American darter

genera *Etheostoma* and *Percina* account for approximately 66% and 20% of the total species richness of the family, respectively. The objective of this study was to evaluate if the disparity in species richness within the family could be explained by the age of the clades. A fossil calibrated phylogeny of the family was constructed with the software BEAST using two mitochondrial (Cyt b; ND2) and two nuclear (RAG1; S7 intron 1) markers. A MEDUSA analysis was used to estimate diversification rates within the family. Significant changes in the rates of diversification were not detected within Percidae, but the extant species richness of the genus *Etheostoma* is higher than expected giving the age of the clade. This result suggests that historical and geological events, rather than clade age alone, are likely the major drivers in the diversification of *Etheostoma*, the most speciose genus in the family Percidae.

**0457 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Diego Elias¹, David Camak¹, Caleb McMahan², Kyle Piller¹

¹*Southeastern Louisiana University, Hammond, LA, USA*, ²*The Field Museum of Natural History, Chicago, IL, USA*

Comparative Phylogeography Within the Grijalva-Usumacinta Area of Endemism

The Grijalva-Usumacinta area of endemism, in northern Middle America, comprises a complex geologic region, located in the southeast portion of México (Campeche, Quintana Roo, and Yucatán), northern Guatemala (El Petén), and northern Belize. In this complex geographic area, many different types of aquatic environments are present, including lakes, ponds, sinkholes, and rivers. Many of these water bodies are recognized as closed basins and most of the lakes in this area were formed by dissolution of the limestone. Some of these water bodies have gone through periods of wet and dry cycles, which has resulted in changes in the size and depth of water bodies, as well as modified connections among water bodies in the recent past (Holocene-Pleistocene). The objective of this work was to evaluate if co-distributed species of freshwater fishes in this region (*Gambusia sexradiata*, *Petenia splendida*, *Thorichthys meeki*, and *Paraneotroplus melanurus*), with substantial differences in life history traits, display congruent phylogeographic patterns. Phylograms were constructed using two mitochondrial markers, and haplotype networks were constructed using TCS. The results indicate that there are substantial differences in phylogeographic patterns for these co-distributed species.

**0346 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Lilly Eluvathingal, Maureen Donnelly

Florida International University, Miami, FL, USA

A Global Analysis of Factors Driving Amphibian Diversity in Plantations

Anthropogenic conversions of natural areas to agriculture and monoculture plantations are a large threat to flora and fauna, especially in biodiversity hotspots which harbor large numbers of endemic species. Plantations in the tropics are established in areas which are characterized by high species richness and they tend to support subsets of species with narrow distribution ranges found in the surrounding “natural areas”. We review studies on amphibians in plantations and examine factors affecting number of species with a focus on tropical plantation systems. We summarize preliminary data on anurans in an active tea plantation from Kerala, India. We compare our field data from a large tea plantation in Munnar, Kerala, India to those obtained from the literature. Tea is a globally popular beverage whose flavor is dependent on the elevation at which it is grown. This plantation is nestled in the Western Ghats and Sri Lanka biodiversity hotspot, a center of radiation for amphibians, spiders, orchids, balsams, and several other phyla. We report on known species of amphibians from a 350 square km area of heterogeneous, actively managed tea plantations with a large number of cryptic species expected to be described in the coming years. Of the reported 22 species, all but one are endemic to the Western Ghats, reinforcing the need to educate plantation managers about conservation practices that can be implemented without affecting production, including selective protection of breeding micro-habitats and reduced pruning, in turn increasing the attractiveness of the product to an increasingly socially conscious, international market.

0579 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Erica Ely, Chris Feldman

University of Nevada, Reno, Reno, NV, USA

Geographic and Ontogenetic Variation in the Food Habits of the Sierra Garter Snake (*Thamnophis couchii*)

Thamnophis is a wide-ranging, abundant and ecologically important group of North American snakes. Previous studies have indicated that most garter snake species are generalist predators, consuming the most abundant prey available, which can vary spatially and temporally. Here, we take the first overview of dietary habits across the entire range of the Sierra garter snake (*T. couchii*), a western endemic restricted to the Sierra Nevada and lower Cascade Range of California. We assessed diet habits by examining stomach contents of preserved museum specimens collected from across the species' range over the past 120 years. Feeding frequency was overall low, and most of

the specimens with stomach contents contained a single prey item. The identifiable stomach contents contained mainly fish, frequently frogs and occasionally tadpoles, salamanders and even invertebrates, contributing to the growing evidence of ecological plasticity of *Thamnophis* species across North America. We discuss how the dietary habits of *T. couchii* vary across latitude and ontogeny and in the context of the arms-race with toxic Pacific newts (*Taricha*).

0290 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Alison Enchelmaier, Nicholas Perni, Laurel Zaima, Neil Hammerschlag
University of Miami, Miami, FL, USA

Changes in Fish Diversity in a Restored Mangrove Habitat

Habitat restoration and monitoring are important tools for ongoing marine conservation efforts focused on areas that have been historically subjected to human-impacts and selection. Bill Baggs Cape Florida State Park, located on Key Biscayne, has been subjected to synergistic impacts resulting from urban development and hurricanes, which lead to the destruction of over 80 hectares of the park's wetlands, including a mangrove forest. Significant restoration efforts were implemented that continue to grow the health and diversity of the coastal mangrove ecosystem of the park. While many marine fish species use this critical habitat across their ontogeny, current data on fish abundance and diversity in this area is lacking. We evaluated the long-term efficacy of the restoration efforts in the man-made mangrove pools at Bill Baggs' Park using BRUVS (baited underwater camera systems). We then compared our data with previous studies from 1998 and 2004. We discuss results as they relate to the efficacy of small-scale restoration efforts in human-dominated ecosystems in subtropical regions.

0373 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Thursday 16 July 2015

Julia Ersan¹, Brian Halstead¹, Erica Wildy², Michael Casazza¹, Glenn Wylie¹
¹*U.S. Geological Survey, Dixon, CA, USA*, ²*California State University, East Bay, Hayward, CA, USA*

Diet and Prey Preference of Neonate Giant Gartersnakes (*Thamnophis gigas*) from the Sacramento Valley of California

The introduction of exotic species can change the trophic dynamics of native species. The giant gartersnake, an endemic predator in the Central Valley of California, is listed as threatened due to the conversion of its once vast wetland habitat to agriculture. Further contributing to this snake's changing ecology is the introduction of non-native

prey species resulting in a diet that is almost completely comprised of exotics. I examined prey preferences of neonate giant gartersnakes using behavioral trials of naïve neonates of wild-caught females from three field sites. The first set of trials entailed an examination of prey preference in neonate snakes when they are presented with olfactory cues. The second set of trials evaluated prey selection in neonates when presented with different live prey items. Results from olfactory trials suggest that neonates do indeed prefer native prey species and results from consumption trials suggest that other factors contribute to prey selection. These results contribute to understanding the mechanisms underlying giant gartersnake diets in the contemporary landscape, and can inform improved management of prey communities for giant gartersnakes.

**0271 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Evan Eskew, Michael Miller, Janet Foley, Brian Todd

University of California, Davis, CA, USA

**Both Sides of the Coin: Host and Pathogen Influence Chytridiomycosis
Disease Outcome**

The emerging disease chytridiomycosis, caused by the fungal pathogen *Batrachochytrium dendrobatidis* (*Bd*), has devastated amphibian populations worldwide. Despite causing significant declines, *Bd* can have extremely variable impacts on different amphibian hosts. Some species are thought to act as asymptomatic *Bd* carriers, yet relatively little is known about mechanisms that allow these species to combat disease. To further understand amphibian host responses to fungal infection, we conducted an experimental exposure trial with a disease-susceptible species, the wood frog (*Lithobates sylvaticus*), and a disease-resistant species, the American bullfrog (*L. catesbeianus*). These two species were each exposed to two isolates of *Bd* known to differ in virulence, Section Line Lake (SL) *Bd*, which has a high virulence phenotype, and Carter Meadow (CM) *Bd*, which has demonstrated only mild virulence in other amphibian species. Over the course of a seven-week experiment, wood frogs exposed to SL *Bd* suffered significantly greater mortality than frogs exposed to CM *Bd* or sham controls. In contrast, there were no differences in American bullfrog survival attributable to *Bd* exposure treatment despite the fact that American bullfrogs were exposed to *Bd* doses three times greater than wood frogs. Finally, there was evidence of negative, sublethal effects of *Bd* exposure on body mass in wood frogs. Our results suggest that both amphibian host and *Bd* isolate strongly influence disease outcome of amphibian-*Bd* interactions. Ongoing gene expression work on tissues collected during the course of this experiment will investigate potential genetic mechanisms underlying the mortality patterns reported here.

0607 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

Robert Fisher¹, Jone Niukula², Heidi Davis³, Peter Harlow⁴

¹US Geological Survey, San Diego, CA, USA, ²The National Trust of Fiji, Suva, Fiji, ³San Diego Zoo Institute for Conservation Research, San Diego, CA, USA, ⁴Taronga Conservation Society Australia, Sydney, NSW, Australia

Biogeography and Conservation Systematics of Pacific Iguanas (*Brachylophus* sp.)

Pacific Basin iguanas (genus *Brachylophus*) are an enigmatic element of Fijian and Tongan Island biodiversity and have a long history (> 35 MY) in the region. At least two species have become extinct since humans have arrived in the region, and now iguanas are rare or absent from many islands. There are three living species in the genus as currently described. Over the last decade we have surveyed iguana populations on many of the islands in Fiji and collected genetic and morphological samples from these relict populations. Analysis of these data indicates that there is a much greater diversity of iguanas still extant in Fiji than is currently described. Many of these are apparently now single island endemics, probably due to extirpations of nearby populations, and most or all would be considered critically endangered. Overall these data support that there was a much greater distribution and species diversity in the genus in the recent past and continued investigation of unsampled islands is a critical priority. This information is vitally important to setting conservation goals and strategies, as the conservation focus for this genus from 1980 - 2005 was primarily on Yadua Taba Island crested iguanas, whereas assumptions about "banded" iguanas were that their extinction risks were relatively low. Description of this new diversity is currently underway, although continued risk of extinction is a real threat for most of these species.

0604 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Samuel Fisher¹, Sophia Alcaraz¹, Ramón Gallo-Barneto², Clara Patiño-Martínez³, Carlton Rochester⁴, Miguel Ángel Cabrera-Pérez⁵, Robert Fisher⁴

¹Steele Canyon High School, Jamul, CA, USA, ²Área de Medio Ambiente. Gestión y Planeamiento Territorial y Ambiental, Las Palmas, Spain, ³Asociación para el Desarrollo Sostenible y Conservación de la Biodiversidad, Las Palmas, Spain, ⁴US Geological Survey, San Diego, CA, USA, ⁵Servicio de Biodiversidad. Dirección General de Protección de la Naturaleza. Gobierno de Canarias, Las Palmas, Spain

SWPARC - Rapid Ecological Adaptation of a Snake Following Invasion of a Novel Island Ecosystem

Many species adaptations to novel ecosystems can be predicted, but measures of their morphological and reproductive changes are often lacking. Frequently, the tempo and mode of these changes are not often identified because many invasive species are not studied until they are already well established. In the Canary Islands, the California

kingsnake (*Lampropeltis californiae*), including albino variations, is a novel invasive species that was first detected in 1998. The source of the introduction was the international pet trade with captive bred animals originating from California. Studies of the invasive populations on Gran Canaria have shown that they are divergent from the qualitative literature regarding the natural history within their native range. We studied 1538 museum specimens and 780 field captured kingsnakes from the native range in California and Mexico. Based on the measurements of 277 individuals from Gran Canaria, the snakes have increased in snout vent length an average of 33%, and in reproductive output, as measured by follicle and egg counts, by 240%. Within the invasive population 53.6% of females were gravid versus 10.4% in the native range. Another ecological difference is in the frequency of tail breaks, with the invasive population having 14.5% versus 6.6%, respectively. This can indicate greater incomplete predation and/or increased wounds inflicted by prey (e.g. *Gallotia stehlini*) in the novel habitat. This rapid adaptation to the novel environment (where they are now the apex predator and are not yet food limited), shows how ecological conditions in their natural range constrain their adaptive potential.

0120 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

James P. Flaherty, C.M. Gienger

Austin Peay State University, Clarksville, TN, USA

Habitat Selection and Movement Patterns of Copperheads (*Agkistrodon contortrix*) in Fire-altered Landscapes

Fire can functionally alter habitat available to wildlife through alteration of structural and micro-climatic characteristics. Reptiles, due to their reliance on behavioral thermoregulation and crypsis, can be especially susceptible to these post-fire changes in habitat characteristics. The copperhead (*Agkistrodon contortrix*) is a widely distributed snake throughout the southeastern US, and is found in a variety of habitats. Previous studies suggest that copperheads decrease in abundance immediately after fire events, but to our knowledge there has been no work investigating this species' habitat selection and movements in a fire-altered landscape. We tracked 11 adult male copperheads captured in burned and unburned sites at Land Between the Lakes National Recreation Area, KY using radio-telemetry. Copperheads were tracked during the active season (May-October) of 2014. Home ranges were calculated by minimum convex polygons (MCP) and fixed kernel density estimation (KDE). Movement patterns were assessed by measurement of straight-line distances between successive copperhead relocations. At each copperhead location, a suite of structural and environmental habitat variables were recorded. In order to measure habitat availability, each snake relocation point was paired with a randomly selected point. There was no significant difference between MCP home ranges and movement patterns of copperheads captured in burned and unburned sites. KDE home ranges were significantly larger in copperheads captured in unburned sites than those captured in burned sites. Available habitats in burned sites exhibited significantly greater heterogeneity than unburned sites, but overall,

copperheads selected habitats more similar to those available in burned sites than in unburned sites.

0178 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

Brooke Flammang

New Jersey Institute of Technology, Newark, NJ, USA

Biomechanics of Shark Swimming

The mechanics of the heterocercal tail in sharks is a classic problem in functional vertebrate biology. Because sharks lack a buoyant swim bladder, their ability to produce lift and balance torques while swimming has long been a subject of research and debate in the field of vertebrate locomotion. Just as understanding the kinematic motions of the shark tail required three-dimensional analysis, new three-dimensional fluid dynamics tools allow us to view complex swimming instantaneously without trying to assimilate data from multiple two-dimensional data sets. Recently, I have discovered not only how sharks are able to produce lift, but also how they are able to modulate their tail stiffness to generate nearly continuous thrust.

0493 Herp Conservation II, Carson 1, Saturday 18 July 2015

Noelle Fletcher, Erika Nowak, Erik Nielsen

Northern Arizona University, Flagstaff, AZ, USA

Citizens and Serpents: The Effectiveness of Citizen Science in Improving Knowledge and Conservation of Two Threatened Gartersnake Species

Research is underway to develop recovery plans for two federally threatened species, the northern Mexican (*Thamnophis eques megalops*) and narrow-headed (*T. rufipunctatus*) gartersnakes. Though declines in both snakes have been documented, aspects of their natural histories make them difficult to detect using traditional field survey methods. Missing information includes current distributions of each species and habitat requirements. Given its worldwide utility in garnering wildlife information, citizen science may help address knowledge gaps for these species. In Arizona's Verde River Watershed, known populations of these snakes occur in high-use areas that include riparian restoration projects, recreation, development, and agricultural water diversion. Our study evaluated the usefulness of citizen science in obtaining data on each species' distribution and habitat use in Northern Arizona. We created a citizen science website and Smartphone application which allowed volunteers to report sightings of snakes. Volunteers were surveyed at the beginning and end of the 2014 field season to gauge whether project participation and snake education increased knowledge and

appreciation for the target species. Results were based on trained and untrained survey participants. Trained volunteers reported higher knowledge growth than those who had not, however untrained participants reported more positive snake attitudes. Citizen scientists recorded sightings on the app, including two new locations. I will detail successes and struggles of this project, including which tactics worked best with public outreach and education.

0564 Fish Biogeography, Carson 3, Saturday 18 July 2015

Brook Fluker¹, Bernard Kuhajda²

¹*Arkansas State University, Jonesboro, AR, USA*, ²*Tennessee Aquarium Conservation Institute, Chattanooga, TN, USA*

Testing Predictions of Peripatric Speciation in the Mobile Basin of the Southeastern United States

Peripatric speciation, in the form of peripheral isolation, has been invoked as a possible mode of speciation for several North American freshwater fishes, yet few examples have been confirmed and others are indiscernible from allopatric speciation. With its lower reaches in the Gulf Coastal Plain and upper reaches restricted to a small portion of the southern Appalachian Highlands, the Mobile Basin represents an intriguing system to study peripheral isolation in freshwater fishes. This study used phylogeographic, population genetic, and morphological data from three species of upland, spring-adapted darters and their lowland, widespread stream-inhabiting relatives to test four main predictions of peripatric speciation. Phylogeographic reconstructions of each spring-stream sister pair supported expected patterns of peripatric speciation; each isolate rendered its widespread stream progenitor paraphyletic and was most closely related to geographically proximate populations of stream relatives near the lowland-upland boundary. While initial upland colonizations by each isolate differed temporally, adaptation to spring habitats by each (as evidenced by population differentiation) closely overlapped with the onset of extended glacial cycles during the Pleistocene (approx. one million years ago). Additional predictions of peripatric speciation were supported for the three spring species, i.e. high levels of population structure, reduced dispersal ability, low levels of genetic variation, and prolonged bottlenecks compared to stream sisters. Further, spring species showed parallel reductions in development of the lateral-line system. Collectively, these results suggest Pleistocene divergence of marginal spring inhabitants and peripatric speciation has been a relatively rapid process facilitated by adaptation to novel habitats.

0487 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Sonja Fordham

Shark Advocates International, Washington, DC, USA

Spotlight on the Small and Flat: Conservation Status Updates for Select U.S. Atlantic Dogfish, Skates, and Rays

While large sharks continue to be a popular focus for conservation attention, smaller, flatter species actually hold the national titles for elasmobranch depletion, recovery, and landings, as well as most and least protected species. As the most commercially important U.S. shark, the spiny dogfish (*Squalus acanthias*) has been driven to depletion and back, regulated through quotas that once severely restricted fishing yet now grossly exceed demand. Lagging more than a decade behind in basic assessment and management is the similarly sized Atlantic smoothhound or "smooth dogfish" (*Mustelus canis*), which feeds poorly understood markets and is the nation's sole subject of the world's weakest ban on shark "finning." A complex of Northwest Atlantic skates (Family Rajidae), used for food and bait, supports the country's largest elasmobranch fishery, yet the American public's concern for the overfished species is outweighed by growing appreciation for eating skate wing, thereby allowing for less than rigorous recovery actions. Despite the now notorious "Save the Bay, Eat a Ray" industry campaign, Americans appear more interested in appreciating cownose rays (*Rhinoptera bonasus*) in touch tanks than on their plates. Still, this exceptionally vulnerable, un-assessed species continues to be taken without limit as bycatch and in tournaments. The focus for ensuring the recovery of Florida's Endangered Smalltooth Sawfish (*Pristis pectinata*) has shifted from securing legal safeguards to restoring adequate funding for implementing the recovery plan, particularly programs to prevent mishandling. Following the latest conservation status updates, recommendations for improvement will be offered.

0459 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kimberly Foster, Kyle R. Piller

Southeastern Louisiana University, LA, USA

Variation in Trophotaenial Structures of Five Goodeids

The freshwater subfamily Goodeinae (Goodeidae) contains approximately 42 viviparous species. Species in the subfamily possess a pseudoplacental structure that facilitates nutrient transfer to the embryos from the maternal lumen. These structures are known as trophotaeniae (from the Greek for feeding ribbons). Historically, the taxonomy of the subfamily was based, in part, on the external morphology of the trophotaeniae, with the most common trophotaenial form being "irregular ribbon-shaped." The purpose of this project was to use high-resolution scanning electron microscopy (SEM) to visualize shape and surface characteristics for five species of goodeids. All species included in the

study (*Ilyodon furcoidens*, *I. whitei*, *Chapalichthys peraticus*, *C. encaustus*, and *Allodoniichthys tamazulae*) were originally described as having "irregular ribbon-shaped" trophotaeniae. The trophotaeniae were run through a series of graded ethanol washes, critically point dried, mounted to aluminum studs, and sputter coated with gold palladium. Initial inspections of the external anatomy and shape of the trophotaeniae support the original "irregular ribbon-shape" designations. However, scanning electron microscopic images show substantial differences in surface morphology between the five species and indicate that additional taxonomic characters, not previously imaged, may be present.

**0468 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Kimberly Foster, Kyle R. Piller

Southeastern Louisiana University, Hammond, LA, USA

Body Shape Diversification Within the Goodeidae (Teleostomi)

The Goodeidae (Teleostomi: Cyprinodontiformes) is a diverse and conservationally imperiled family of freshwater fishes. The family is comprised of two main evolutionary lineages differentiated at the subfamily level. The subfamily Empetrichthyinae possesses 10 taxa (species and subspecies), exhibit oviparity, lack pelvic fins, and are limited to the Great Basin of the United States. The other subfamily, Goodeinae, is more diverse containing 42 viviparous species, and only occur in the Mesa Central of Mexico. Others have suggested that the Goodeinae represent an adaptive radiation as a result of the group's high diversity, limited geographic distribution, occurrence in a broad range of habitats, and the existence of a wide range of morphologies and body shapes. The disproportionate features and species richness within the two subfamilies make them an excellent group for evolutionary study. The purpose of this study was to assess the rates of morphological diversification within the Goodeidae using body shape data. In particular, we hypothesized that the Goodeinae will show elevated rates of morphological diversification associated with its radiation in the Mesa Central. Geometric morphometric data was gathered from all species in the family, and we analyzed the data using a time-calibrated phylogenetic tree and various R statistical packages. Within subfamily evolutionary rates were obtained and support the hypothesis of elevated rates of phenotypic evolution in the Goodeinae, which is consistent with the radiation hypothesis for the subfamily.

0539 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Dewayne Fox¹, Bradley Wetherbee², Symone Johnson¹, James Kilfoil¹

¹Delaware State University, Dover, DE, USA, ²University of Rhode Island, Kingston, RI, USA

Development of a Multifaceted Conservation Plan for Sand Tigers (*Carcharias taurus*) in the Delaware Bay and Nearshore Coastal Waters

Due to their large size, feeding habits, abundance, and prolonged periods of occurrence, Sand Tigers (*Carcharias taurus*) serve as apex predators for the Delaware Bay and much of the surrounding nearshore coastal waters. Likely a result of their restricted summer movements and overlap with humans, they unfortunately suffer the consequences of intentional and accidental takes in fisheries. Most problematic is the recently developed and apparently increasing recreational sector targeting this prohibited species. Adding to our concerns is the fact that the fishery has increased in size and popularity after Sand Tigers were listed as a Species of Concern by NOAA-NMFS. Facing a growing problem, the State of Delaware implemented regulatory changes in 2011 in an effort to increase survival of recreationally landed Sand Tigers. While these changes have likely led to reductions in angling pressure, a more unified approach is required to conserve and recover this species. Our plan includes enhanced protection of core Sand Tiger habitats, working with anglers to change practices and/or implement use of conservation engineering approaches, as well changes in cooperative tagging programs and scientific/aquaria collections. While the State of Delaware has taken large steps to educate the public on the need for improved angling practices, the lack of higher level support cannot help but undermine the state's efforts. Ultimately, to be successful and applicable to the US northwest Atlantic Sand Tiger population as a whole, a number of state and federal agencies, as well as local stakeholders must cooperate.

0510 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday 16 July 2015

Benjamin Frable, Brian Sidlauskas

Oregon State University, Corvallis, OR, USA

Differential Gill Arch Evolution and Ancient Divergences in the Neotropical Superfamily Anostomoidea (Ostariophysi:Characiformes)

The hyper-abundant Neotropical freshwater fish superfamily, Anostomoidea contains two clades with seemingly disparate evolutionary strategies. The first group, the anostomids, represent ~150 species with a wide variety of body coloration, mouth position, tooth shape and trophic strategies ranging from generalist to herbivory to insectivory. The other major group, the families: curimatids, chilodontids and prochilodontids, contains around the same number of species but members are silvery with some pigmentation, have little variation in mouth position, possess reduced or no

teeth and all feed mostly on detritus. Although the detritivores may be superficially similar, there is substantial variation in the arrangement of the gill arches, which are used in processing food, within each family and even within genera. We investigate 1) how a group of species that presumably all feed on the same resource can exhibit similar species diversity to the Anostomidae, 2) if detritivore gill arches are more diverse than those of anostomids, 3) if detritivore gill arch morphology evolves faster or differently than anostomid gill arches and 4) whether morphologies converge. Additionally, we estimate divergence times of major lineages within the superfamily and detritivorous clades. This system provides crucial information on the role of ecomorphology in diversification and demonstrates that detritivory probably encompasses a spectrum of morphological and ecological specialization.

0455 Fish Systematics I, Carson 3, Saturday 18 July 2015

Ethan France, Thomas Near

Yale University, New Haven, CT, USA

Molecular and Morphological Data Reveal a Cryptic Species Masquerading as *Percina palmaris* (Percidae: Etheostomatinae).

The Bronze Darter, *Percina palmaris*, is distributed throughout the Coosa and Tallapoosa River systems in the eastern Mobile Basin. Previous analyses of meristic traits uncovered differences between specimens sampled from the Coosa and Tallapoosa systems. We investigated the phylogeography of *P. palmaris* using DNA sequences from a single mtDNA gene and two nuclear loci. Our analyses resolve both the Coosa and Tallapoosa populations as reciprocally monophyletic in the mtDNA gene tree, and nearly monophyletic in each of the two nuclear gene trees. Divergence time estimates between these two lineages range between approximately 2 and 5 million years. We present a new meristic dataset sampled from 134 specimens and show little morphological divergence between the two resolved clades. We identify the Tallapoosa populations of *P. palmaris* as a new and undescribed species, which marks the first identification of a true cryptic species among darters. Our analyses demonstrate the utility of combining classic morphological data and molecular phylogenetics for future biodiversity discovery in the well-studied North American freshwater fish fauna.

0526 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Bryan Frazier¹, Dana Bethea², William Driggers³, Robert Hueter⁴, John Tyminski⁴

¹South Carolina Department of Natural Resources, Charleston, SC, USA, ²NOAA Southeast Fisheries Science Center, Panama City, FL, USA, ³NOAA Southeast Fisheries Science Center, Pascagoula, MS, USA, ⁴Mote Marine Laboratory, Pensacola, FL, USA

Growth Rates of Bonnetheads (*Sphyrna tiburo*) from the Western North Atlantic Ocean Estimated from Tag-Recapture Data

Regional variation in growth has been observed for multiple species of elasmobranches. Recently, published age and growth models for bonnetheads (*Sphyrna tiburo*) reported larger than expected life history differences between sharks from the eastern Gulf of Mexico and off the coast of South Carolina. Growth can be estimated independent of age by using length based growth models. A maximum likelihood approach (GROTAG) was used to analyze direct growth estimates from tag-recapture derived data. Region and sex-specific models were generated allowing investigation of regional growth, and likelihood ratio tests were used to determine optimal parameterization of the models. Parameters explored included individual growth variability, seasonal growth, measurement error and outliers for each data set. A comparison of region-specific length based models to published age-based models for bonnetheads will be discussed.

0095 Herp Conservation I, Carson 1, Saturday 18 July 2015

Kealoha Freidenburg¹, Alex Shepack², David Skelly¹

¹Yale University, New Haven, CT, USA, ²Southern Illinois University, Carbondale, IL, USA

Species Loss in Developed Landscapes: An Experimental Evaluation

Anthropogenic changes to the landscape are widely associated with biodiversity loss, and declines in amphibian populations have been linked to habitat fragmentation and conversion. We were interested in assessing how well amphibians perform in a range of habitats, from developed landscapes (e.g., urban settings) to less developed, forested landscapes. In particular, we focused on the contribution of wetland degradation in developed landscapes to local population extinctions. We conducted a translocation experiment with wood frog larvae (*Rana sylvatica* = *Lithobates sylvaticus*) across 12 ponds. Seven ponds had existing wood frog populations (=present ponds), while five ponds had no wood frogs (=absent ponds). Each pond received two enclosures, and wood frog larvae were reared within enclosures until some individuals in each treatment began to reach metamorphosis. Survival, growth rate, and development rate were equivalent between 'present' and 'absent' ponds. We found no evidence that the heavily developed landscape surrounding the absent ponds negatively affected the wood frog larvae. Instead, it may be that influences outside the pond basins contribute to the absence of amphibians within the ponds. Because urban wetlands are often

presumed to be degraded, our results offer unexpected evidence of their functional value and provide reasons to examine whether wetland restoration practices will improve outcomes for some wetland dependent wildlife.

0074 General Ichthyology I, Crystal 3 & 4, Friday 17 July 2015

Bryan Frenette

University of Oklahoma, Norman, OK, USA

Aspects of Growth and Morphology of the Spotted Gar *Lepisosteus oculatus*

The spotted gar is one of seven members of the family Lepisosteidae. The gars are a poorly studied group of fishes, largely due to their reputation as ‘trash’ fish. The spotted gar is a freshwater predator that ranges from southern Canada south throughout the eastern and central United States. At the northern periphery of its range, it is a species of conservation concern and may be impacted by habitat degradation as a result of anthropogenic change. I provide demographic data on length, weight, sex, and body morphology of adult spotted gar from a population in the Lake Thunderbird reservoir near Norman, Oklahoma. This data expands the limited demographic information that exists for this species. In a laboratory experiment I examined the effect of turbidity on the growth of juvenile spotted gar, and detected no effect of turbidity on growth. Mortality was high for juvenile spotted gar, particularly among smaller same-aged juveniles. High mortality resulted in low statistical power for this study, which may have led to type II error. Finally, I described the spawning of spotted gar being held in captivity without the use of hormone injection. Fish spawned naturally in the spring of 2014 while being held in a one tenth hectare pond at the University of Oklahoma’s Aquatic Research Facility.

0327 Fish Morphology & Histology, Crystal 1 & 2, Saturday 18 July 2015

Sarah Friedman, Peter Wainwright, Samantha Price

University of California Davis, Davis, CA, USA

Ecomorphological Convergence in Zooplanktivorous Surgeonfishes

Morphological convergence plays a central role in the study of evolution. Often induced by shared ecological specialization, homoplasy hints at underlying selective pressures and adaptive constraints that deterministically shape the diversification of life. Though midwater zooplanktivory has arisen in surgeonfishes (family Acanthuridae) at least four independent times, it represents a highly specialized state, requiring the capacity to swim, locate, and suck small prey items out of the water column. While this diet has commonly been associated with specific functional adaptations in fishes, acanthurids present an interesting case study as all other species feed by grazing on benthic algae and detritus, requiring vastly different ecomorphology. We examined the feeding

morphology in 30 acanthurid species and, combined with a pre-existing phylogenetic tree, compared evolutionary models fit across two diet regimes: zooplanktivores and non-zooplanktivorous grazers. Accounting for phylogenetic relationships, the best-fitting model indicates that zooplanktivorous species are converging on a separate adaptive peak from their grazing relatives. Driving this bimodal landscape, zooplanktivorous acanthurids tend to develop reduced facial features, smaller teeth, weakened jaw adductor muscles, and shorter pectoral fins. However, despite these phenotypic changes, model fitting suggests that lineages have not yet reached the adaptive peak associated with plankton feeding even though some transitions appear to be over 10 million years old. These findings demonstrate that the selective demands of pelagic feeding promote repeated-albeit very gradual-ecomorphological convergence within surgeonfishes, while encouraging local divergences between closely related species, contributing to the overall diversity of the clade.

0591 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Jared Fuller¹, Richard Kazmaier², Rocky Ward²

¹University of Nevada, Reno, Reno, NV, USA, ²West Texas A&M University, Canyon, TX, USA

Genetic Response of a Texas Horned Lizard (*Phrynosoma cornutum*) Population to a Catastrophic Wildfire in South Texas

The Texas horned lizard (*Phrynosoma cornutum*) is listed as a threatened species in Texas reflecting the great public concern for its survival. In March of 2008, the Chaparral WMA experienced a catastrophic wildfire that burned approximately 95% of the managed land and abundance of horned lizards was dramatically reduced because of the fire. This event provides a unique opportunity to look at the effects of an extreme fire event on genetic diversity of a heavily studied population of Texas horned lizards. Pre- and post-fire samples were examined to determine changes in genetic structure. We tested the hypotheses that 1) genetic structure remained constant over the period prior to the fire, and 2) measures of genetic diversity declined after the fire, reflecting a population bottleneck. Eight pairs of microsatellite primers were used to construct composite genotypes, which were analyzed to assess within-sample year genetic diversity, among sample genetic diversity, and to compare between pre-fire and post-fire populations. There were no significant changes in observed heterozygosity when pre- and post-fire samples were compared. An AMOVA found the vast majority of variation (99.7%) within populations. A suite of exploratory statistics using different methods of ordination plotted and demonstrated no distinct clustering patterns, which, suggests the wildfire had no significant effects on the genetic structuring in the population.

0218 Herp Ecology, Carson 4, Saturday 18 July 2015

Meaghan Gade, Ralph Saporito

John Carroll University, University Heights, OH, USA

Color Assortative Mating in a Mainland Population of the Strawberry Poison frog, *Oophaga pumilio*

Assortative mating is a common reproductive strategy in which individuals tend to mate with partners that share similar traits (genotypic or phenotypic) with themselves. This reproductive strategy has been proposed as one of the main mechanisms in the evolution and maintenance of color polymorphism among polytypic populations of the strawberry poison frog, *Oophaga pumilio*, in Bocas del Toro, Panama. Evidence of assortative mating in *O. pumilio* is largely based upon mate choice experiments conducted in the lab, but very few studies have investigated this mating strategy in natural mating pairs in the field. Herein, we report the results of a field-based behavioral study at La Selva Biological Station in Costa Rica, in which the color phenotype of naturally paired male and female *O. pumilio* were examined for evidence of assortative mating. The hue, brightness, chroma, and pattern was recorded for 69 natural reproductive pairs, and female *O. pumilio* were most often paired with males who shared similarities in coloration. Our results indicate that color assortative mating is operating within this population of *O. pumilio*, and provide support for the experimental studies in Bocas del Toro that have found similar results. The color phenotype of *O. pumilio* is likely under both sexual and natural selective pressures, optimizing mating success and reducing predatory pressures. Therefore, assortative mating may be beneficial for *O. pumilio* because it results in offspring that are most suited to their environment, leading to increased mating success and decreased predation pressures.

0611 Chemical Ecology Symposium, Crystal 3 & 4, Sunday 19 July 2015

Brian Gall¹, Edmund Brodie III³, Edmund Brodie, Jr.²

¹*Hanover College, Hanover, IN, USA*, ²*Utah State University, Logan, UT, USA*, ³*The University of Virginia, Charlottesville, VA, USA*

Complex Ecological Interactions between Newts and Aquatic Invertebrates Modulated by the Powerful Neurotoxin Tetrodotoxin

Tetrodotoxin (TTX) is a powerful neurotoxin found in a wide variety of aquatic and terrestrial organisms, including newts of the genus *Taricha*. In newts, TTX has played a pivotal role in their evolution serving as the central molecule in an arms race with toxin-resistant garter snakes (*Thamnophis*). Despite these advancements, there has been little investigation into other potential predators. Here we report the results of various experiments exploring the ecological interactions between toxic newts and caddisfly larvae, which consume the toxic eggs. Caddisfly larvae are voracious predators of the newt eggs and have caused modifications in oviposition behavior in female newts to

increase the success of their offspring. In addition, caddisfly larvae appear to be resistant to the negative effects of TTX intoxication, indicating an additional player may be involved in the evolution of extreme toxicity in *Taricha*.

0365 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Tony Gamble¹, Aaron Bauer², Eli Greenbaum³, Todd Jackman²

¹University of Minnesota, Minneapolis, MN, USA, ²Villanova University, Villanova, PA, USA, ³University of Texas at El Paso, El Paso, TX, USA

Diurnality Evolved Multiple Times in Geckos.

Geckos are the only major lizard group comprising mostly nocturnal species. Nocturnality is presumed to have evolved early in gecko evolution and geckos possess numerous adaptations to functioning in low light and at low temperatures. However, not all gecko species are nocturnal and most diurnal geckos have their own distinct adaptations to living in warmer, sunlit environments. We reconstructed the evolution of gecko activity patterns using a newly generated time-calibrated phylogeny. Our results provide the first phylogenetic analysis of temporal activity patterns in geckos and confirm an ancient origin of nocturnality at the root of the gecko tree. We identify multiple transitions to diurnality at a variety of evolutionary time scales. In addition, transitions back to nocturnality occur in several predominantly diurnal clades. The patterns revealed will be useful in reinterpreting existing hypotheses of how geckos have adapted to varying thermal and light environments. These results can also inform future research on gecko ecology, physiology, morphology, and vision as it relates to changes in temporal activity patterns.

0403 ASIH STOYE AWARD ECOLOGY & ETHOLOGY II, Carson 4, Friday 17 July 2015

Donnell Gasbarrini¹, Edward Morris², Anna Sheppard²

¹Laurentian University, Sudbury, Ontario, Canada, ²Ontario Parks, Northeast Zone, Sudbury, Ontario, Canada

An Investigation into the Cause of a Mass Mortality Event of Blanding's Turtles (*Emydoidea blandingii*) in Misery Bay Provincial Park, Ontario, Canada

Mass mortality events (MMEs) can devastate populations by removing up to 90% of individuals, which is especially damaging in long-lived species. While MMEs are being documented with increased frequency, a limited understanding of the causes and consequences of MMEs remains. This study aims to determine the causes of a MME of Blanding's turtles (*Emydoidea blandingii*), a species at risk, in a relatively pristine habitat in Misery Bay Provincial Park (MBPP), Ontario, Canada. The typical anthropogenic

threats to turtles are minor or virtually absent in the MBPP setting, and yet 59 turtles (49 Blanding's turtles and 10 painted turtles) were found dead without obvious cause in 2013. The potential causes of death under consideration include predation in the active season and failed overwintering through either metabolic/respiratory acidosis, freezing, and winter predation. Telemetry and mark-recapture studies are being used to determine areas of importance within MBPP and to generate a population size estimate, respectively. Motion-sensor activated trail cameras have been paired with a Blanding's turtle decoy, as a novel strategy to identify predators within the park. Overwintering sites have been located through telemetry, and characteristics such as temperature and dissolved oxygen content of water are being measured to determine differences between overwintering sites and sites which yielded carcasses. The results of this study will be informative for the conservation of this population, and for the management of future MMEs.

0550 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Ava Ghezelayagh¹, Raymond Simpson¹, Carol Baldwin², Thomas Near¹

¹*Yale University, New Haven, CT, USA*, ²*Smithsonian Institution, Washington, DC, USA*

Molecular Phylogeny of Seabasses and Groupers (Perciformes: Serranidae)

The family Serranidae, consisting of ~545 species, is classified in the recently delimited Perciformes. Molecular phylogenetic analyses consistently result in serranid paraphyly, with the Serraninae and Epinephelinae resolved as a clade, the Anthiinae with uncertain resolution within Perciformes, and Niphon resolved as the sister lineage of Percidae. In this study we include 97 additional species of Serranidae, with representative species from all of the recognized subfamilies and tribes. Bayesian and maximum likelihood phylogenies will be inferred using DNA sequences of ten nuclear genes that provided the basis for recent studies examining relationships within Percomorpha. The newly generated phylogenetic trees provide a basis to incorporate morphological characters in a phylogenetic based classification of perciform teleosts.

0376 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Missy Gibbs, Patrick Watson, Kelsey Johnson-Sapp

Stetson University, DeLand, FL, USA

**Rapid Change in Reproductive Patterns of the Invasive Catfish
Pterygoplichthys disjunctivus in a Florida Spring System**

Ten years ago, we began to collect data for a description of reproductive patterns in a relatively new population of *Pterygoplichthys disjunctivus* (Loricariidae) in Volusia Blue Spring, Florida. Three years and 340 catfish later, we were able to describe seasonal reproductive patterns, but our data suggested that aspects of catfish reproductive patterns (length of spawning season, gonadosomatic index, age at first maturity, proportion of the population in reproductive ready mode, and batch fecundity) were beginning to change. We have continued to collect data (n=1100), and are now able to demonstrate clear changes in reproductive strategy over the years. Although catfish nesting season is still limited by the temperature of the adjoining St. Johns River, instead of recrudescing in winter, most catfish are now maintaining reproductive readiness in the warmer spring run throughout the winter. We also found that gonadosomatic index, overall fecundity and batch fecundity have all gone up during all seasons, while average oocyte size has decreased.

**0053 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Sarah Gibson

University of Kansas, Lawrence, KS, USA

**Multidentaculate Teeth in the Lower Actinopterygian Fish †*Hemicalypterus*:
Evidence for a Specialized Feeding Niche in the Late Triassic**

Fishes occupy multiple ecological niches, and many have evolved specialized multicuspid dentition that is often associated with benthic scraping, feeding primarily on algae. Extant fishes with such dentition occur in both marine (e.g., rabbitfishes, surgeonfishes) and freshwater systems (e.g., haplochromine cichlids, characiforms). The fossil record for fishes displaying dentition often associated with herbivory extends only into the Eocene. I report evidence of the oldest example of specialized multidentaculate dentition in a ray-finned fish, †*Hemicalypterus weiri*, from the Upper Triassic Chinle Formation of southeastern Utah (□210–205 Ma). †*Hemicalypterus* is a unique lower actinopterygian with a deep, disc-shaped body and ganoid scales covering only the anterior portion of the flank, the posterior flank being scaleless. †*Hemicalypterus* has been hypothesized to belong within either Semionotiformes or Dapediiformes, but are phylogenetically remote from modern fishes. Recent excavations recovered new specimens of †*Hemicalypterus*, and these new specimens clearly indicate that †*Hemicalypterus* had evolved specialized teeth that converge with those of several living

teleost fishes (e.g., characiforms, cichlids, acanthurids, siganids), with a likely function of these teeth being to scrape algae off a rock substrate. This finding contradicts previously held notions that fishes with multicuspid, scoop-like dentition were restricted to teleosts, and indicates that ray-finned fishes were diversifying into different trophic niches and exploring different modes of feeding earlier in their history than previously thought, fundamentally altering our perceptions of the ecological roles of fishes during the Mesozoic.

0266 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Matthew Girard, Wm. Leo Smith

University of Kansas, Lawrence, KS, USA

The Inter- and Intrarelationships of Pacific Ocean Sculpins in the Genus *Icelinus*

The sculpin genus *Icelinus*, described by Jordan in 1885, contains eleven species of phylogenetic and biogeographic interest. In previous publications, the phylogenetic placement of *Icelinus* has been inconsistent. The majority of previous morphological analyses have placed the genus sister to Eastern Pacific psychrolutids. Alternatively, molecular analyses and a subset of morphological studies have placed the genus sister to Western Pacific psychrolutids. However, all previous phylogenetic analyses of *Icelinus* have lacked inclusion of the two Western Pacific species. In this study, we combined several mitochondrial and nuclear genes with a novel morphological dataset for all eleven *Icelinus* species and numerous psychrolutids to establish the placement of the genus *Icelinus* and its intrarelationships. Our preliminary results suggest that *Icelinus* is nested within a Western Pacific clade of psychrolutid species indicating that the genus originated in the Western Pacific and underwent trans-Pacific dispersal across the Bering Sea.

0574 ASIH STOYE AWARD PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY, Carson 3, Friday 17 July 2015

Scott Goetz¹, Mary Mendonça¹, Elizabeth Hiltbold¹, Christina Romagosa², Craig Guyer¹

¹*Auburn University, Auburn, AL, USA*, ²*University of Florida, Gainesville, FL, USA*

Assessing Immunocompetence in Anurans: An in Vitro Assay Measuring Innate, Cell-Mediated, and Humoral Responses

Global amphibian declines and other conservation concerns relating to animal health have fueled an increase in the application of ecoimmunologically based investigations.

As the field of ecoimmunology matures there is a growing need for assays providing more detailed immunological assessments of non-model organisms. Specifically, there are few available tools for measurement of acquired immune responses. Here we introduce an in vitro flow cytometric analysis of frog splenocyte proliferation, providing a detailed evaluation of innate, cell-mediated, and humoral immune responses. Innate immune response can be assessed by measurement of nitric oxide production in culture supernatants using Griess reagents. Lymphocytes involved in acquired immunity are tagged with the vital dye CFSE (carboxyfluorescein diacetate, succinimidyl ester) and stimulated with either phytohemagglutinin (PHA; cell-mediated) or Lipopolysaccharide (LPS; humoral). Proliferation is measured by serial halving of the fluorescence intensity of CFSE as the lymphocytes undergo mitosis. Inclusion of CD3+ FITC antibodies, which exhibit a high affinity and specificity to T cells, in culture medium allows for distinction of T cell and B cell lymphocytes. This technique allows for concise evaluation of cell subsets. This is an improvement over current and commonly used in vivo assays that provide only limited information regarding which cell populations are responsible for observed effects. Further, this method enables the recognition of discrete cycles of cell division rather than measuring lymphocyte transfer to an infection site. An added advantage of this technique is the ability to simultaneously evaluate all three major components of the immune system in a single individual.

0103 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Tamera Goetz¹, Peterson Cullimore¹, H.J. Walker², Kevin Tang¹

¹University of Michigan-Flint, Flint, MI, USA, ²Scripps Institution of Oceanography, La Jolla, CA, USA

Molecular Phylogeny of the Surfperches (Teleostei: Embiotocidae)

Surfperches (family Embiotocidae) are unique fishes distributed on both sides of the Pacific Ocean. The family currently includes 13 genera and 23 recognized species, with the bulk of the diversity found off the west coast of the United States. Embiotocids are biologically interesting because all species are viviparous, a trait not observed in any of their presumed close relatives and found in very few marine bony fishes overall. We are collecting sequence data from mitochondrial (12S, 16S, ATPase 8/6, cytochrome *b*, cytochrome *c* oxidase I) and nuclear genes (ectodermal-neural cortex 1, histone 3, recombination activating gene 1, tmo-4c4, and Zic family member 1) from all 13 genera (*Amphistichus*, *Brachyistius*, *Cymatogaster*, *Ditrema*, *Embiotoca*, *Hyperprosopon*, *Hypsurus*, *Hysterocarpus*, *Micrometrus*, *Neoditrema*, *Phanerodon*, *Rhacochilus*, and *Zalembeius*) and all 23 species. Species from several other percomorph families are also examined to investigate the higher level relationships of Embiotocidae. A phylogeny of surfperch relationships will be presented and the monophyly of the family and its genera will be discussed.

0151 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Shawn Goodchild, Craig Stockwell

North Dakota State University, Fargo, ND, USA

An Experimental Test of Novel Multi-species Refuges for Conserving Protected Fishes

Establishing refuge populations as a hedge against extinction has been a very useful tool for conserving western fishes, but this important tool is often constrained by the scarcity of suitable refuge sites. One novel solution might be to establish multi-species refuges which may even include resident populations of invasive species. To determine suitability of such refuges, we established experimental communities that included allopatric and sympatric communities of three fish species; endangered Pahrump poolfish (*Empetrichthys latos*), Amargosa pupfish (*Cyprinodon nevadensis*), and invasive mosquitofish (*Gambusia affinis*). Mosquitofish larval survival was not significantly affected by the presence of other species. By contrast, pupfish persisted in sympatry with both poolfish and mosquitofish, having higher survival in allopatry (557.0 ± 248.2 (mean \pm SE)) and in the presence of poolfish (425.3 ± 35.7) compared to poolfish and mosquitofish (242.3 ± 31.9). Mean poolfish larval survival was high in allopatry (123.2 ± 16.6), but significantly reduced in the presence of pupfish (6.6 ± 1.2), in the presence of mosquitofish (1.0 ± 0.5), and a community of all three species (0.5 ± 0.4). This suggests that pupfish may be able to persist in multi-species refuges. However, our findings also suggest that poolfish are not compatible with the other species and the current management of poolfish in single species refuges is appropriate.

0502 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Thursday 16 July 2015

Michelle Gordon, CR Tracy

University of Nevada, Reno, NV, USA

Morphological Insights into the Relationships Among Isolated Populations of *Anaxyrus boreas* in Northern and Central Nevada

The Hydrological Great Basin covers most of Nevada and parts of Oregon, Utah, and California, and is one of the driest regions in the United States. Much of the Great Basin's extensive biodiversity relies on isolated aquatic systems, which are home to specialized endemics with limited ranges. Studies focused on the biogeography of the region have long suggested that much of the biological diversity within the Great Basin has resulted from species' expansions and contractions during wet and dry periods during and since the Pleistocene. The region is projected to continue to become more arid, and with increasing anthropogenic groundwater demand, the unique species, which are dependent upon these isolated refuges, face challenges to their continued persistence. Of concern are the western toad (*Anaxyrus boreas*), and its congeners that comprise the

western-toad species complex. Research to uncover the fine scale relationships among isolated populations of these bufonids has been difficult because of similar morphology among individuals in these populations. Genetic analyses have suggested that western toad diversity is likely underrepresented by current taxonomy, leaving unique populations open to mismanaged conservation. Preliminary genetic analysis has evaluated the relatedness of toads in this species complex. Using morphometric analyses, our research characterizes three new species, linking these toads to relatives within the western toad complex. Our study provides an important step informing conservation policy to protect these unique bufonids, and the critical habitat upon which they depend.

**0119 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Andrew Gottscho

San Diego State University, San Diego, CA, USA

**Species Delimitation of Fringe-toed Lizards (Squamata: Phrynosomatidae:
Uma notata complex) in the Colorado Desert**

Here, I used nuclear DNA sequence and genome-wide SNP data to thoroughly investigate the systematics of fringe-toed lizards (*Uma notata* complex), including the federally threatened/state endangered Coachella Valley fringe-toed lizard (*U. inornata*), in the deserts of southwestern North America. I analyzed both ten nuclear loci collected using Sanger sequencing and genome-wide sequence and single-nucleotide polymorphism (SNP) data collected using restriction-associated DNA (RAD) sequencing. I used concatenated phylogenetic methods, parametric and non-parametric clustering algorithms and coalescent species tree models to test hypotheses regarding genetic diversity, phylogeny, species delimitation, and historical biogeography. I detected five species-level lineages within this complex, three of which were previously described as full species, one which was described as a subspecies but later synonymized, and one undescribed species from Mohawk Dunes, Arizona, USA. All but one of these lineages were recovered as monophyletic with strong support in the concatenated analyses and by clustering algorithms, while all were decisively supported as distinct species by ranking hierarchical nested models with Bayes factors in a coalescent species tree model. My time-calibrated and geospatial analyses support the hypothesis that Pleistocene glacial cycles promoted allopatric speciation via dispersal across a landscape matrix shaped by older tectonic events, but I also recovered evidence for a vicariant role of the Colorado River during the Pleistocene. I recommend that the six lineages each be recognized as distinct species, and I outline possible conservation implications and recommendations of this study.

0445 AES Ichthyology, Carson 2, Thursday 16 July 2015

Mark Grace¹, Michael Doosey², Henry Bart², Gavin Naylor³

¹NOAA/NMFS, Pascagoula, MS, USA, ²Tulane University Biodiversity Research Institute, Belle Chasse, LA, USA, ³Hollings Marine Institute, Charleston, SC, USA

First Record of a Pocket Shark (*Mollisquama* sp.) from the Gulf of Mexico

Kitefin sharks of the family Dalatiidae (Squaliformes) comprise 7 genera of which five are monotypic; the highest percentage of monotypic genera for any family in the order Squaliformes. One of the rarest monotypic dalatiids, *Mollisquama parini* Dolganov, 1984 was described from a single female specimen collected from the Nazca Submarine Ridge in the southeast Pacific Ocean. A second *Mollisquama* specimen was captured during a 2010 midwater trawl survey of the northern Gulf of Mexico conducted by NOAA/NMFS Southeast Fisheries Science Center, Mississippi Laboratories. Both the holotype of *M. parini* and the Gulf of Mexico specimen possess the remarkable pocket gland with its large slit-like external opening located just above the pectoral fin. Features found on the Gulf of Mexico specimen that were not noted in the description of *M. parini* include a series of ventral photophore agglomerations and a modified dermal denticle surrounded by a radiating arrangement of denticles just posterior to the mouth. Phylogenetic analysis of NADH2 gene sequences places *Mollisquama* sister to *Dalatis* plus *Isistius* within the family Dalatiidae.

0450 Herp Behavior, Carson 4, Friday 17 July 2015

Michael Grace¹, Adam Safer²

¹Florida Institute of Technology, Melbourne, FL, USA, ²Georgia State University, Atlanta, GA, USA

Neural Correlates of Complex Behavior: Brainstem Neuroanatomy Correlates with Pit Organ Arrangement Habitat Use in Infrared-Imaging Snakes.

Boid and pythonid snakes exhibit a wide variety of pit organ sizes, shapes and orientations, and amazing diversity in the organization of pit organ arrays. Pit vipers all possess a single loreal pit organ on each side of the face, but the anatomy of their pit organs varies among species. Given this diversity, the processing of neural information from pit organs may vary considerably among species, and may provide different species with varying thermal imaging capabilities (including fields of view, stereoscopic imaging and depth perception, spatial resolution, etc.). As one component of an effort to better understand infrared information processing, we analyzed the brainstems of pitviper *Crotalus horridus*, the viper *Bitis gabonica*, the boid snakes *Calabaria reinhardtii*, *Boa constrictor* and *Corallus hortulanus*, the pythons *Python molurus* and *Aspidites ramsayi*, and the ratsnake *Elaphe guttata*. Results show that all boid and pythonid snakes examined possess a nucleus of the lateral descending trigeminal tract (nLTTD), the projection site of thermosensitive trigeminal ganglion neurons (although in *Calabaria* and

Aspidites, the presumptive nLTTD was small and indistinct). Furthermore, nLTTD relative cross-sectional area varied among species, being greatest in arboreal species, and those with more extensive arrays of deeply-invaginated pit organs. Neither *B. arietans* nor *E. guttata* displayed nLTTD morphology. These results indicate, as hypothesized, that a greater amount of brainstem space is dedicated to processing pit organ information in snakes targeting in three-dimensional space and with larger arrays of pit organs, and further support the lack on infrared imaging capability in the genus *Bitis*.

0017 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Molly Grace

University of Central Florida, Orlando, FL, USA

How Does Traffic Noise Influence Wildlife Abundance? An Investigation Using Anurans as a Model

Roads are associated with reduced abundances of many animal species, from arthropods to mammals, and it is hypothesized that traffic noise is a contributing factor. However, very few studies have experimentally tested the effects of noise, and observational studies are confounded by other stimuli provided by roads, e.g. direct mortality via roadkill or chemical and light pollution. In this project, I played back traffic noise in previously noiseless areas and studied the reactions of anurans (frogs and toads) as a model group. I hypothesized that noise could impact anuran abundance in at least one of three ways: (1) deterrent effect, such that traffic noise deters individuals from accessing roadside areas; (2) masking effect, such that traffic noise interferes with communication by spectral overlap and masking of breeding signals reduces reproductive success and therefore abundance over time; or (3) physiological effect, wherein loud traffic noise is a physiological stressor, reducing survival and therefore abundance over time. Measurement of relative anuran abundance, reproductive success (in this case, eggs/individual) and stress hormone levels (corticosterone) provides an indication as to which of these three effects may be operating in natural systems and which is the most detrimental. The results of this research can guide management actions in how to ameliorate the harmful effects of traffic noise on wildlife.

**0182 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

River Grace, Michael Grace

Florida Institute of Technology, Melbourne, FL, USA

**Evolution of Nervous System Function and Behavior in a Micro-Vertebrate,
the Brahminy Blindsnake (*Ramphotyphlops brahminus*)**

The subterranean brahminy blindsnake (*Ramphotyphlops brahminus*) is among the smallest vertebrate animals on Earth, and it is thought to be the most widespread vertebrate species (except perhaps man). This study is the first part of a comprehensive analysis of what may be the simplest nervous system in any terrestrial vertebrate on the planet. This series of studies investigated whether *R. brahminus* can light with its rudimentary eyes, and whether these snakes can use light sensitivity to modify behavior. It was hypothesized that (1) *R. brahminus* possess eyes that contain functional retinas, even if very small and simple, (2) they can detect light, and (3) *R. brahminus* uses light for simple, non-visual tasks including navigation and predator avoidance. Scanning electron microscopy and visible light microscopy revealed an eye-like structure underneath the skin and scales of the head. Electroretinography showed that the snakes respond to light using their apparently rudimentary eyes, but the ERG waveform is very small its unusual shape suggests that the functional architecture of the *R. brahminus* retina is distinct from that of other vertebrates. Finally, a series of behavioral experiments revealed these snakes do not respond to shadows (as a means of predator avoidance), but are able to navigate with the aid of light. This research provides new knowledge of the anatomy, physiology, and behavior of one of the world's smallest vertebrate animals, and it provides new insight into the evolutionary adaptations of micro-vertebrate life.

0352 Herp Physiology & Reproduction, Carson 4, Friday 17 July 2015

Katherine Graham¹, Cecilia Langhorne¹, Carrie Vance¹, Andrew Kouba², Scott Willard¹

¹*Biochemistry and Molecular Biology Department, Mississippi State University, Mississippi State, MS 39762, USA,* ²*Conservation Research Department, Memphis Zoo, Memphis, TN 38112, USA*

Use of Exogenous Hormone Treatments to Induce Ovulation in the Critically Endangered Mississippi Gopher Frog (*Lithobates sevosa*)

The Mississippi gopher frog (*Lithobates sevosa*) is a critically endangered species with an estimated 150 adults in the wild. Because this species has failed to reproduce naturally in captive breeding programs, our research focuses on the development of assisted reproductive technologies (ART). One challenge in developing ART for Mississippi gopher frogs has been difficulty obtaining eggs from females. Thus, we developed a study examining four exogenous hormone treatments to induce ovulation in gopher

frogs. Hormone treatments (n=5 animals/treatment) include: A) gonadotropin-releasing hormone agonist (GnRH_a); B) GnRH_a and the dopamine antagonist metoclopramide hydrochloride; C) GnRH_a and human chorionic gonadotropin (hCG); and D) GnRH_a and hCG following two low priming doses of hCG. Ultrasound data were collected concurrently to monitor follicular development. The number of animals ovulating, relative fecundity (number of eggs/body weight of female), and the fertilization rate of eggs were compared between the four hormone treatments. Preliminary results suggest no significant difference ($P>0.05$) between treatments for the number of females ovulating and relative fecundity. However, there was a significant difference ($P<0.05$) in fertilization rate between treatments, with Treatment C resulting in a significantly lower fertilization rate compared to the other treatments. Ultrasound analysis revealed that ovulating frogs had an increase in follicular development following hormone treatment, and ultrasound was useful in predicting which frogs may ovulate. By determining the optimal hormone treatment protocol for ovulation in this species, we have a greater opportunity to conduct *in vitro* fertilization trials and produce more offspring for captive assurance colonies and reintroduction programs.

0326 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Dan A. Greenberg, Wendy J. Palen, Arne Ø. Mooers

Simon Fraser University, Burnaby, BC, Canada

Predicting Disease-Induced Extinctions in Amphibians Based on Host Traits and Evolutionary History

Conservation practitioners require methods to predict species' responses to threat processes even when data are scarce. The global decline of amphibians represents an urgent case in point. In many regions the fungal pathogen *Batrachochytrium dendrobatidis* (Bd), which causes the disease chytridiomycosis, is a major driver of local extinctions. While epidemics of chytridiomycosis result in a great loss of local species diversity, there are many species that manage to survive these events. Why do some species decline while others persist during a disease epidemic? Host traits are likely to influence several facets of a species' disease susceptibility, and therefore may represent a way to predict extinction outcomes during disease epidemics a priori. To examine this possibility we gathered a global dataset on Bd infection prevalence for 320 species of amphibians and 100 sites. We examined how different life history and ecological traits predicted susceptibility to infection using phylogenetic comparative methods. Subsequently, we tested whether these traits similarly correlate to patterns of local extinction during disease epidemics. We found that patterns of Bd infection prevalence in amphibians are phylogenetically non-random, with certain clades bearing typically high levels of infection while others display very low infection prevalence. Similarly, several life history and behavioural traits were associated with heightened infection prevalence in the wild. Using commonly available data on host traits and phylogeny may represent an

effective method to prioritize species for conservation management in the event of future disease epidemics.

0040 Herp Ecology, Carson 4, Saturday 18 July 2015

Patrick Gregory

University of Victoria, Victoria, BC, Canada

A Large Communal Den of Garter Snakes (*Thamnophis elegans*) in Southwestern British Columbia

In February 2015, during planning for repair work on a dike in Delta, British Columbia, it was learned that the site was used by garter snakes (*Thamnophis*) as a hibernaculum. To mitigate negative effects of the work on the snakes, the den was carefully taken apart and the snakes removed and maintained in artificial hibernation until the den could be restored and the snakes released there in time for the mating season. A total of 534 *T. elegans* were found in the den. Although much larger communally denning populations of garter snakes are known, especially in cold climates, this is a large aggregation by any standard, especially for the mild winter climate of southwestern British Columbia. Most reports of hibernating snakes in this region consist of isolated individuals or relatively small aggregations. This large sample of hibernating snakes also presented an excellent opportunity to collect data on the structure (sex, size, etc.) and other characteristics of this denning population and to mark the snakes for later recapture. Future work will involve monitoring the site to ascertain whether snakes continue to use the hibernaculum and to determine patterns of dispersal from the hibernaculum as well as basic features of the ecology of these snakes.

0142 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Ashley Grimsley¹, Daniel Leavitt¹, Robert Lovich², Nicholas Heatwole³

¹Arizona Game and Fish Department, Phoenix, AZ, USA, ²Naval Facilities Engineering Command, San Diego, CA, USA, ³Bureau of Reclamation, Yuma, AZ, USA

SWPARC Flat-tailed Horned Lizard (*Phrynosoma mcallii*) Demographic Monitoring within the Yuma Desert Management Area, Arizona

The Yuma Desert Management Area represents the majority of the Flat-tailed Horned Lizard's (*Phrynosoma mcallii*) range in the state of Arizona. Demographic monitoring has been carried out since 2008 on two separate plots in the Yuma Desert Management Area, including one plot on the Barry M. Goldwater Range (YD 1) and another on the Bureau of Reclamation (YD 2). Monitoring was continued (for the 7th year) in 2014 with intense 10-day surveys at each plot during the active season of *P. mcallii*. Mark-recapture techniques were carried out using PIT tags (toe clips for juveniles). Population models,

using data on adult *P. mcallii* from 2008 to 2014, were then created using program MARK. Population parameter estimates suggest there is steady population size, growth, and movement for both plots, the YD 1 ($N = 20.92 \pm 2$) and YD 2 ($N = 25.57 \pm 2$). Emigration and immigration were estimated higher in the YD 1 than the YD 2. Population stability may be determined by a variety of independent or combined factors including changes in seasonal environmental conditions, habitat conditions, predation levels, and unknown factors. Continued monitoring will result in a greater understanding of *P. mcallii* populations within these locations.

0235 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Luke Groff¹, Aram Calhoun¹, Cynthia Loftin²

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Habitat Features Mediate Wood Frog Hibernaculum Microclimate

Winter in northern latitudes is a period of scarcity (e.g., food) and extremes (e.g., temperature) and, thus, is critical for non-migratory species. Freeze-tolerant wood frogs (*Lithobates sylvaticus*) endure harsh winters using complex physiological processes; however, hibernal habitat selection may also affect individual fitness. For example, deep snowpack insulates frogs from cold, variable temperatures, thereby facilitating winter survival, and hibernacula nearer to breeding sites may yield reproductive advantages. Laboratory research has focused on the species' physiology, but few studies have investigated ecological strategies used to cope with harsh winters. Our research was conducted in northern Maine during 2011- 2013. Our objectives were to (1) describe the hibernaculum and measure temperature and relative humidity, (2) evaluate hibernal habitat selection at micro (1 m plots) and macro (5 m plots) spatial scales, and (3) describe the spatial arrangement of breeding, post-breeding, and hibernal habitats.

**0233 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Thursday 16 July 2015**

Luke Groff¹, Cynthia Loftin², Aram Calhoun¹

¹University of Maine, Department of Wildlife, Fisheries, and Conservation Biology, Orono, ME, USA, ²U.S. Geological Survey, Maine Cooperative Fish and Wildlife Research Unit, Orono, ME, USA

Local- and Landscape-scale Predictors of Breeding Site Occupancy by Pool-breeding Amphibians in Wetland-limited, Montane Landscapes

The importance of local- and landscape-scale features to amphibian breeding habitat selection varies across a species' range. Maine is ecologically diverse with 19 US-EPA Level IV ecoregions, abundant wetlands with a range of hydroperiods, and a steep climate gradient. Because Maine's high elevation landscapes are topographically rugged and wetland-limited, the relative importance of individual wetlands to pool-breeding amphibians may be greater than in wetland-rich landscapes. We evaluated breeding habitat use by wood frogs (*Lithobates sylvaticus*) and spotted salamanders (*Ambystoma maculatum*) in six Upper Montane/Alpine Zone Ecoregion landscapes in 2013 and 2014 by repeatedly surveying 135 potential breeding sites. We modeled each species' detectability and breeding site occupancy at three spatial scales (site, migration, dispersal) and quantified landscape features with buffers generated from a terrain ruggedness index, a cost surface, and the species' known movement distances. Top-ranked wood frog and spotted salamander detection models included Julian day and survey length, respectively. Occupancy probability models incorporating site-scale covariates had greatest support, whereas migration- and dispersal-scale covariates had essentially no empirical support. Wood frog occupancy was correlated (+) with basin area and percent shallow water (≤ 1 m deep), and spotted salamander occupancy was correlated (+) with basin area and beaver presence. Pool-breeding amphibians in our high elevation study area use atypical breeding habitats (e.g., large, long-hydroperiod wetlands), as classic vernal pools are uncommon in montane landscapes. Information about montane breeding habitats in northern New England will enhance the efficacy of conservation efforts targeting pool-breeding amphibians.

0104 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Elizabeth Grolle, Michelle Lopez, Marina Gerson

California State University, Stanislaus, Turlock, CA, USA

City Lizard, Country Lizard: Flight Initiation Distance Differs Between Urban and Rural Populations of Western Fence Lizards (*Sceloporus occidentalis*)

Flight initiation distance (FID) is the distance to which a predator is permitted to approach before the prey initiates flight behavior. This can be influenced by factors including predator density and distance to cover. We measured flight initiation

distances in two populations of Western fence lizards (*Sceloporus occidentalis*), one in a rural and one in an urban environment. Lizards at the rural site initiated flight at significantly longer distances than those at the urban site. These results support the prediction that lizard behavior can be influenced by differences in human exposure and predator recognition in their environments. Lizards develop tolerance to humans in urban areas in order to maximize fitness by reserving energy and utilizing resources for longer periods of time. The findings from this study demonstrate that researchers should be aware of differences in human exposure between populations of study animals and should choose study sites appropriately when designing FID studies.

0105 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Chaiwut Grudpan, Jarungjit Grudpan

Department of Fisheries, Faculty of Agriculture, Ubon Ratchathani University, Ubon Ratchathani, Thailand

Cypriniformes: The Symbolic Fishes for the Lower Mekong Basin (LMB)

The Mekong River basin (MB) is the largest in mainland Southeast Asia (795,000 km²) and the seventh largest globally in terms of discharge (16,000 m³/s). The Mekong River is the 10th longest river (4,909 km) in the world. It flows from the Tibetan Plateau in China through Myanmar, Lao PDR, Thailand, Cambodia, and Vietnam. This watershed has a diverse landscape with massifs, plateaus, karsts, volcanic swamp, floodplains, forests and grasslands, and is considered a globally significant biodiversity hotspot. The Lower Mekong Basin (LMB), through Lao PDR, Thailand, Cambodia and Vietnam, covers 609,000 km² (77% of MB) with 55.3 million people, intensive agriculture, urbanization, and industrialization. Fisheries is a significant source of income for local communities, especially in the Tonle Sap Lake (the largest flooded area in Southeast Asia). The estimated economic value in Cambodia alone is US\$233 million, 10-20% of the Cambodian GDP, based on an annual average harvest of 400,000 tons. Based on the catch of the most effective gear (DAI stationary giant bag net), eight species of Cyprinidae and one species of Cobitidae are among the 10 most commonly caught species. Since 2006, the Nagao Environmental Foundation (NEF) has supported intensive field surveys in four countries in the LMB region, and 235,000 specimens of 540 species have been catalogued at partnering facilities. Cypriniformes formed the largest group, with 216 species in four families: Balitoridae, Cobitidae, Cyprinidae, and Gyrinocheilidae. These are the most regionally symbolic fishes for long-term monitoring of environmental impacts related to global change.

0332 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Hongyi Guo, Ya Zhang, Xuguang Zhang, Jiakun Song, Wenqiao Tang

Shanghai Ocean University, Shanghai, China

Analysis of Otolith Microchemistry in Seawater and Freshwater Life Phase of Japanese Glass Eel, *Anguilla japonica*, Collected in the Lower Reaches of the Yangtze River

Japanese eel larvae were collected in the lower reaches of the Yangtze River from January to April, 2012. Otolith elemental concentrations in seawater and freshwater growth zones were examined by synchrotron radiation X-ray fluorescence (SRXRF). It was found that Sr, Ba, Fe, Mn, Zn, Cr, Ni, Se, Co, Cu and Au whose concentrations revealed significant differences between seawater and freshwater growth zone of otoliths. The concentration coefficients of trace elements in the seawater and freshwater growth zone of otoliths follow the increasing order of Hg>Cr>Mn>Se>Co>Ba>Sr>Fe>Zn>Cu>Ni>V and Hg>Sr>Co>Se>Cr>Zn>Cu>Ba>Mn>Ni>Fe>V, respectively. For the elemental contents within otoliths, dynamic responses to aquatic environment hydrochemistry are different due to different otolith types. The first kind of element, such as Sr, Ba, Fe, Mn, Cr, Ni, Co, V, which concentrations in the sagitta were under the positive influence of their concentrations in the water, and the differences of elemental concentrations between sea and freshwater were more than its in the seawater and freshwater growth zone of otoliths. However, the second kind of element, such as Zn, Hg, Cu, Se, which concentrations in the sagitta were under the negative influence of their concentrations in the water, and the differences of elemental concentrations between sea and freshwater was less than its in the seawater and freshwater growth zone of otoliths. The results indicated that the first type can make the corresponding elements in water respond and these elements can be used as the target elements to monitor environmental hydrochemistry.

**0536 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Thursday 16 July 2015**

Jacquelyn C. Guzy¹, Kelly M. Halloran¹, Jessica A. Homyack², John D. Willson¹

¹*University of Arkansas, Fayetteville, AR, USA*, ²*Weyerhaeuser Company, Vanceboro, NC, USA*

Contributions of Streamside Management Zones to Conservation of Herpetofauna in Intensively Managed Forests in the Ouachita Mountains, USA

A majority of forest in the United States is actively managed for the production of commercial wood products. Thus, it is imperative to determine how to maximize the value of managed forests as wildlife habitat. A primary tool for maintaining ecological integrity in managed forest landscapes are streamside management zones (SMZs),

buffers of mature forest retained along streams. Although research confirms that implementation of SMZs protects water quality, very little is known regarding SMZ contributions as wildlife habitat. Our study examined the importance of SMZs surrounding headwater streams for maintenance of amphibian and reptile biodiversity in the Ouachita Mountains of west-central Arkansas, USA. We focused particularly on stream-associated salamanders, an understudied group, known to be sensitive to anthropogenic disturbance. During 2014-2015 we conducted four surveys at each of 84 headwater streams across a gradient of SMZ widths and adjacent stand ages. We used a hierarchical Bayesian species-richness model to estimate herpetofaunal species richness and species-specific occupancy responses to SMZ and stand characteristics, while accounting for variation attributable to other site and sampling covariates. Additionally, we used binomial mixture models with Bayesian inference to examine the influence of SMZs on abundance of two stream-associated salamanders, the Ouachita dusky salamander (*Desmognathus brimleyorum*) and many-ribbed salamander (*Eurycea multiplicata*), that displayed high occupancy, but variable abundance. Our results revealed interspecific variation in responses of amphibians and reptiles to intensive forestry and add to our understanding of the contributions of SMZs to conservation of herpetofaunal biodiversity.

0585 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Nicholas Haertle², Brad Moon¹

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Effect of Feeding Frequency on Digestion in Cottonmouth Snakes (*Agkistrodon piscivorus*)

Optimal foraging theory states that a predatory animal should generally optimize prey preference based on the energy acquired during consumption per unit time. Further, the degree of prey type specialization should be based on the relative abundance of different prey types in the environment. I have previously demonstrated that in cottonmouth snakes (*Agkistrodon piscivorus*), a model generalist predator, a continuum may exist between the benefit of consuming endothermic prey versus ectothermic prey. However, I have also shown the consumption of endothermic prey, specifically rodents, may present a cost in consumption time. The current study suggests that, in cottonmouth snakes, consuming abundant prey more frequently may decrease the costs associated with digestion, allowing a greater proportion of energy to be allocated to maintenance, growth, reproduction, and storage. Specifically, there appears to be a lower digestive scope and lower cost towards specific dynamic action (SDA) associated with consuming prey on a more frequent basis. Decreasing these associated costs may allow for a decreased time to adult size, maturity, and overall fitness.

0297 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Bridgette Hagerty, Brandon Perrone, Carrie Reall, Stephani Lane, Tina Vesnic

York College of Pennsylvania, York, PA, USA

Trends in Ranavirus Prevalence in Amphibian Larvae and Adults at a Breeding Pool in South-Central Pennsylvania

Widespread declines in amphibian populations are a well-documented and complex conservation problem. Emerging infectious diseases such as chytrid fungus and several types of virus within the genus *Ranavirus* have been implicated as causes of major mortality events among amphibians and other ectotherms. In natural populations, prevalence is influenced by a complex web of interacting factors, including species composition, density, and environmental stressors. This study was designed to evaluate temporal trends in the prevalence of ranavirus in one amphibian community near York, PA and assess external factors that affect prevalence by initiating long-term monitoring. Additionally we tested the adult host reservoir hypothesis, which suggests that adults act as reservoirs, thus reinfesting the pool each breeding season and contributing to interspecific transmission. Tissue samples from 10% of the sampled larvae in the vernal pool and all sampled adults in the surrounding forest buffer were used to detect the presence of the FV3 strain by quantifying a portion of the major capsid protein gene using dye-based real-time PCR. Our initial two years of sampling suggest that ranavirus was present in all four amphibian species and prevalence increased over the larval developmental season. We documented a mortality event in 2013, however, prevalence increased between 2013 and 2014 in *Anaxyrus americanus* and *Abystoma maculatum*. Additionally, adults from every sampled species, including *Plethodon cinereus*, had viral DNA present, which supported the adult reservoir hypothesis. These trends contribute to the growing initiative to assess and explain annual variability in ranavirus prevalence within natural amphibian communities.

0505 Fish Systematics I, Carson 3, Saturday 18 July 2015

Dominik Halas

University of Minnesota, Minneapolis, MN, USA

Reconstructing Species Trees when Introgression is Common: A Case Study in the *Etheostoma zonale* (Teleostei: Percidae) Group

Introgression at both mitochondrial and nuclear loci is increasingly being recognized as a common phenomenon in many freshwater fish species. To date, all species tree methods assume that any incongruence between gene trees is due to incomplete lineage sorting, and cannot account for the effects of introgression. As a result, reconstructing species trees of taxa which have undergone introgression poses considerable problems. In this study, I have examined the effects of introgression at several mitochondrial and nuclear loci on the resolution of the species tree of the banded darter and its near

relatives, the *Etheostoma zonale* group. These freshwater fish species are widespread throughout the eastern United States, predominantly in the Mississippi River basin. In the Upper Tennessee River drainage, one member of the group has been introgressed by another, more widespread member, to the extent that its distinctiveness has only recently been recognized. Standard species tree analysis does not reveal the distinctiveness of this lineage unless the introgression it has undergone is taken explicitly into account. I examine several potential ways in which introgression at both mitochondrial and nuclear loci can be recognized and dealt with in species tree analyses, and suggest some future directions for the discovery and analysis of introgression patterns in a species tree context.

0490 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kelly M. Halloran¹, Jacquelyn C. Guzy¹, Jessica A. Homyack², John D. Willson¹

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Effect of Timber Harvest on Survival and Movement of the Ouachita Dusky Salamander (*Desmognathus brimleyorum*)

Clearcut timber harvesting drastically alters forest ecosystems. In addition to conspicuous structural changes, timber harvesting can negatively affect some plethodontid salamanders. Using a Before-After-Control-Impact design, we are examining the effects of clearcut timber harvesting on a stream-dwelling salamander endemic to the Ouachita Mountains, *Desmognathus brimleyorum*. Due to their sensitivity to anthropogenic habitat alteration, amphibians like *D. brimleyorum* are considered bioindicators of ecosystem health, but few studies of forestry effects have focused on stream-dwelling salamanders or evaluated mechanisms driving observed shifts in abundance (e.g., mortality vs. movement). Under a robust design sampling framework, we conducted a capture-mark-recapture study at two streams within intensively-managed pine forests in west-central Arkansas from May 2014-June 2015. The pineland surrounding one of the study streams was harvested in January 2015. For each capture/recapture, we recorded the location of each individual salamander to assess movement in the stream before and after harvest. Using program MARK, we estimated salamander abundance and survival over the course of the year and compared rates of change between the harvested and control stream. The results of this study will help inform management decisions aimed at conserving biodiversity and ecosystem integrity in landscapes managed for timber production.

0242 Herp Conservation II, Carson 1, Saturday 18 July 2015

Brian Halstead, Shannon Skalos, Glenn Wylie, Michael Casazza

U.S. Geological Survey, Western Ecological Research Center, Dixon, CA, USA

Terrestrial Ecology of Semi-aquatic Giant Gartersnakes (*Thamnophis gigas*)

Wetlands are a vital component of habitat for semiaquatic herpetofauna, but for most species adjacent terrestrial habitats are also an essential resource. We examined the use of terrestrial environments by state and federally threatened Giant Gartersnakes (*Thamnophis gigas*) to provide behavioral information relevant to conservation of this rare species. We used radio telemetry data of adults from several sites throughout the Sacramento Valley, California, collected between 1995 and 2011, to examine Giant Gartersnake use of the terrestrial environment. Giant Gartersnakes were found in terrestrial environments more than half the time during the summer, with the use of terrestrial habitats increasing to nearly 100% during brumation. While in terrestrial habitats, Giant Gartersnakes were found underground more than half the time in the early afternoon during summer, and the probability of being underground increased to nearly 100% of the time at all hours during brumation. Extreme temperatures also increased the probability that Giant Gartersnakes would be found underground. Under most conditions, Giant Gartersnakes were found to be within 10 m of water at 95% of observations. For females during brumation and individuals that were found underground, however, the "average" individual had a 10% probability of being located > 20 m from water. Individual variation in each of the response variables was extensive; therefore, predicting the behavior of an individual was fraught with uncertainty. Nonetheless, our estimates provide resource managers with valuable information about the use of terrestrial habitats by a rare semiaquatic snake.

0584 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Erik Halverson, Richard Mahoney, Todd Huspeni, Justin Sipiowski

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

Black Spot Parasitism of *Luxilus cornutus* (Cyprinidae: Actinopterygii) in Wisconsin: A Statewide, 65-year Perspective

We are currently constructing a dataset comprising all specimens of the Becker Memorial Ichthyology Collection (University of Wisconsin- Stevens Point Museum of Natural History) for the Common Shiner (*Luxilus cornutus*). Specimens have been collected from throughout the state of Wisconsin over the past 60 years. Our accessioning and cataloging is ongoing, and to date we have currently gathered data from over 10,000 specimens. This represents approximately 30% of the total individuals in this collection. For each specimen cataloged, we recorded total length (mm), preserved mass (g), gonad mass (g) and estimated age. We also recorded the number of individual Black Spot parasites (metacercariae of *Uvilifer ambloplites*) on the left side of each specimen. Considering size classes of fish over 30 mm and sample sizes of at least

30 fish, prevalence (% individuals with at least one parasite) varied across populations from 100% to 25%. Considering similar size classes and sample sizes, average intensities (average number of parasites on the left side of infested individuals) varied from 0 to 213. Separate analyses were conducted for each sex for individuals ranging from 30 – 80 mm (ages I & II; Becker 1983). Multiple regression analyses were calculated to evaluate the relationships among parasite intensity, sex, location, season, latitude, and total length. The results of these are reported here.

0593 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Bryan Hamilton¹, Beverly Roeder¹, Margaret Horner²

¹Brigham Young University, Provo, UT, USA, ²Great Basin National Park, Baker, NV, USA

SW PARC - Survival and Detectability in Great Basin Rattlesnakes - A 15 Year Study

The Great Basin is one of the most remote and most threatened regions of North America. One of its few endemic reptiles is the Great Basin rattlesnake (*Crotalus lutosus*). Little is known about their ecology and life history. Great Basin rattlesnakes hibernate communally in large numbers, utilize high elevation habitats and an array of vegetation types. They are also prone to local extirpation and are sensitive to changing land use and vegetation cover. As the only rattlesnake species occurring in a cold desert, climate likely places constraints on reproduction. We conducted capture-mark-recapture surveys for Great Basin rattlesnakes from 1999 to 2014 at four sites, using a combination of ventral scale clipping and PIT tags to mark individuals. Sites varied in elevation, proximity to humans, land use status, climate, and vegetation. We captured 445 individuals, 160 females and 264 males, during 780 capture events. Sex was biased toward males (1.65), suggesting lower survival in females or sex specific differences in recapture probability. Females have high costs associated with reproduction and can lose up to 50% of their mass per reproductive event. Recapture rates averaged 75% and varied by location and sex. Females were recaptured at lower rates than males (56% versus 92%). Site specific recapture probability varied from 39% to 103%. We will analyze these data in RMark using Cormack-Jolly-Seber models and present survival and detection probabilities, factors that influence survival and detection, particularly sex and capture aversion, information that will be useful in rattlesnake conservation.

0508 Herp Ecology, Carson 4, Saturday 18 July 2015

Paul Hampton

Colorado Mesa University, Grand Junction, CO, USA

Ontogeny of Prey Size: A Functional Explanation for Prey Size Selection Patterns in Snakes

As body size increases some snake species eliminate relatively small prey from their diet exhibiting an ontogenetic shift toward larger prey. In contrast, other species exhibit a telescoping pattern in which the consumption frequency of large prey increases with body size but relatively small prey are retained in the diet. I compared feeding performance among two snake species (*Nerodia fasciata* and *N. rhombifer*) which exhibit ontogenetic shifts in prey size and *Thamnophis proximus* which exhibits telescoping prey size selection. Polynomial regression was a significantly greater fit for the data comparing snake body size and handling performance for the two *Nerodia* species. Specifically, both species exhibited a point at which relatively small prey became increasingly difficult to handle. However, for *T. proximus*, time and effort were negatively correlated with snake morphology. I also used character mapping on a composite phylogeny to compare morphology among the two diet strategies with various aspects of foraging ecology across a broad diversity of snake taxa, but no conspicuous pattern was observed. Finally, preliminary data analysis with phylogenetic independent contrast indicates positive correlation between the magnitude of change in SVL and the slope of mandible length to SVL, with telescoping species appearing separate from the ontogenetic shifters in morphospace. It appears that prey size shifts in snakes are related to the allometry of trophic morphology and limitations to handling efficiency.

0188 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Sang-Yun Han¹, Jin-Koo Kim¹, Yoshiaki Kai², Hiroshi Senou³

¹Department of Marine Biology, Pukyong National University, Busan, Republic of Korea, ²Maizuru Fisheries, Research Station, Field Science Education and Research Center, Kyoto University, Maizuru, Kyoto, Japan, ³Kanagawa Prefectural Museum of Natural History, Kanagawa, Japan

Cryptic Diversity of the *Hippocampus coronatus* Complex (Pisces, Syngnathidae) from Korea and Japan

The taxonomy within the *Hippocampus coronatus* complex is controversial among ichthyologists. Some consider the *H. coronatus* complex to belong to a single species because it is presumed that the various skin filaments and coloration arise from the characteristics of their habitats. However, others insist that the *H. coronatus* complex comprises two distinct species, *H. coronatus* and *H. sindonis*, based on the size of the coronet. To clarify the taxonomic status of the *H. coronatus* complex, we conducted

morphological and molecular analyses of 156 individuals of *Hippocampus* spp. collected from Korea, Japan, and Vietnam in 1933-2015. Based on the shape of the coronet, 120 individuals were identified as undescribed species, 21 were *H. coronatus*, nine were *H. sindonis*, and the remaining belonged to other *Hippocampus* species (four *H. mohnikei*, one *H. kuda*, and one *H. trimaculatus*). Neighbor-joining trees constructed from mitochondrial DNA cytochrome *b* (670 base pairs, bp), 16S rRNA (405 bp), and 12S rRNA (343 bp) gene sequences showed that 120 individuals did not correspond to either *H. coronatus* or *H. sindonis*. Therefore, further research is required to clarify the taxonomic status of *Hippocampus* sp. by comparing the type specimens of *H. coronatus* and *H. sindonis*.

**0170 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday
18 July 2015**

James Hanken

Harvard University, Cambridge, MA, USA

Ontogeny and Homology – A Cautionary Tale

Embryological and other developmental data have been used for well over a century to infer the homology of morphological structures and substantiate claims of evolutionary relatedness. Indeed, Darwin relied heavily on embryological development as evidence for his claims of common ancestry among disparate adult forms. However, a growing body of empirical data demonstrates divergent patterns of development of otherwise homologous structures in independent lineages. There are now several instances of interspecific divergence in developmental processes that underlie homologous characters occurring with little or no concomitant change in adult phenotype, a phenomenon termed “developmental system drift.” These results caution against the use of ontogenetic data as an exclusive or infallible criterion for evaluating homology. Instead, they reinforce recent claims that routine application of a so-called ontogenetic criterion of homology may be unjustified, if not downright misleading in specific instances, and thereby obscure, rather than reveal, important trends in comparative and evolutionary biology. Examples of these relationships and data will be provided from recent comparative studies of the development of the vertebrate skull, which employ sophisticated cell-labeling and genomics techniques to resolve the embryonic derivation of individual bones.

0164 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Alexander Hansell¹, Steve Kessel³, Lauran Brewster⁴, Steve Cadrin¹, Greg Skomal⁵, Samuel Gruber⁶, Tristan Guttridge²

¹University of Massachusetts - Dartmouth, Fairhaven, MA, USA, ²Bimini, Biological Field Station, Bimini, Bahamas, ³University of Windsor, Windsor, Canada, ⁴University of Hull, Hull, UK, ⁵Massachusetts Division of Marine Fisheries, New Bedford, MA, USA, ⁶Rosenstiel School of Marine and Atmospheric Science, Miami, FL, USA

Coastal Shark Assemblage, 11 – Year Fishery-Independent Shallow Water Longline Survey in Bimini, Bahamas

Understanding population dynamics is essential for implementing effective conservation and management of coastal sharks. Fishery-independent surveys can offer valuable information for data-limited situations. An 11-year (2004-2014) standardized, shallow water longline assessment was conducted monthly in the eastern coastal waters of Bimini, Bahamas. Each survey was comprised of five longline sets of 15 hooks with a soak time of 24 hours. A total of 684 sharks from nine species were caught over the course of the study with tiger (*Galeocerdo cuvier*), nurse (*Ginglymostoma cirratum*), blacktip (*Carcharhinus limbatus*) and lemon (*Negaprion brevirostris*) sharks comprising 94.9% of the catch. Based on total length, the majority of tiger (91.3%), nurse (54.4%), and lemon (81%) sharks were immature, while most blacktip sharks (84.6%) were mature. A sexual bias was noted in the data. The tiger (77.3%) and blacktip (58.3%) sharks were more often female, while the majority of lemon (73%) and nurse (56.8%) sharks were male. Seasonal trends indicate an abundance of nurse, blacktip, and lemon sharks during the warmer months. Over the course of the study, there was an increase in the tiger shark population. Nurse, blacktip, and lemon shark numbers were relatively stable. Preliminary general additive models indicate that catch rates are influenced by month, year, temperature, tide, soak time, and lunar cycle.

0357 AES Morphology & Physiology, Carson 2, Sunday 19 July 2015

Hannah Hart¹, Andrew Evans², Jim Gelsleichter¹, Greg Ahearn¹

¹University of North Florida, Jacksonville, FL, USA, ²University of Southern Mississippi Gulf Coast Research Lab, Ocean Springs, MS, USA

Molecular Identification and Functional Characteristics of Peptide Transporter 1 (PEPT1) in the Bonnethead Shark (*Sphyrna tiburo*)

Elasmobranchs are considered top predators with worldwide distribution, and in general these fish play an important role in the transfer of energy from the lower to the upper trophic levels within marine ecosystem. Despite this, little research regarding the rates of prey ingestion, digestion, and processes of energy and nutrient absorption have been explored. Specifically understudied is enzymatic digestion within the intestinal brush border that functions to break down macromolecules into smaller subunits for

luminal absorption across the gastrointestinal epithelium. Given their carnivorous diet, the present study sought to expand knowledge on nutrient intake in elasmobranchs by focusing on the uptake of products of protein metabolism. To accomplish this, Peptide Transporter 1 (PEPT1), a protein found within the brush border membrane (BBM) of higher vertebrates that is responsible for the translocation and absorption of small peptides released during digestion by luminal and membrane-bound proteases, was molecularly identified in the bonnethead shark (*Sphyrna tiburo*) using degenerate primers based on conserved portions of known PEPT1 sequence in Atlantic stingray. The transporter was also localized by immunocytochemistry with rabbit polyclonal anti-rat PEPT1 and the Vector ImmPRESS anti-rabbit kit in all the same organs. Vesicle studies were used to identify the affinity of the transporter, and to quantify the rate of uptake using 3H-glycylsarcosine. Such results provide insight into the rate and properties of food passage within *S. tiburo*, and can lead to topics such as physiological regulation of protein metabolism, and how it may vary in elasmobranchs that exhibit different feeding strategies.

0255 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Pamela Hart, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Systematics of the Southern Cavefish Species Complex in the Southeastern U.S.

The Southern Cavefish (*Typhlichthys subterraneus*) is one of the most fascinating stygobites of the Amblyopsidae because it has been hypothesized to represent a species complex (i.e. encompassing multiple species). Multiple divergent lineages have been recovered based on multilocus genetic analyses. As many as 15 lineages (representing potential new species) may exist throughout the range of *T. subterraneus*, however results based on different analyses have been inconclusive about the number of populations present that may represent evolutionary lineages. Thus, the taxonomic status of the complex remains unresolved. Using aforementioned molecular assessments and preliminary morphological data, we hypothesize the number of morphologically diagnosable evolutionary lineage is vastly underestimated. We investigate the number of species of *T. subterraneus* within the Southeastern U.S. with both morphological and molecular data. We also examine populations not previously included in molecular assessments.

0048 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Malorie Hayes, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Morphological Investigation of the African Minnow Genus *Enteromius*

Morphological characteristics are commonly used to diagnose species and to classify members of a genus; however, these methods can sometimes be misleading due to homoplasious characters and convergence toward similar body types or coloration. These factors have been a major problem for the group of small, African minnows named *Enteromius*. Only recently has genetic information been generated to better understand the evolutionary history of members of the genus *Enteromius*. Using a recently published phylogeny based on genetics as a backbone for this investigation, we use the concept of reciprocal illumination to find morphological synapomorphies for the clades recovered in the genetic analysis, and identify additional areas on the phylogeny where more data is needed. This study examines the shared counts, measures, and other physical structures of members of *Enteromius*. The findings of this study suggest that previously suggested synapomorphies for the group need to be examined in further detail to create a robust understanding of the relationships within *Enteromius*.

0509 Fish Conservation & Management, Carson 3, Saturday 18 July 2015

Edward Heist¹, Jennifer Eichelberger¹, Paul Hartfield², George Jordan³, Bernie Kuhajda⁴

¹*Southern Illinois University Carbondale, Carbondale, IL, USA*, ²*U.S. Fish and Wildlife Service, Jackson, MS, USA*, ³*U.S. Fish and Wildlife Service, Billings, MT, USA*,

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Morphological and Genetic Variation in Lower Mississippi River *Scaphirhynchus* Part 2: Congruence Between Morphological and Genetic Assignments with Perspectives on Hybridization

Previous genetic studies suggested high levels of hybridization between federally endangered Pallid Sturgeon (*Scaphirhynchus albus*) and Shovelnose Sturgeon (*S. platorhynchus*) in the lower Mississippi River. Morphological species identification in those studies were based either on field identification and/or an inconsistent suite of morphological characters. For this study more than 200 specimens of *Scaphirhynchus*, including fish that were identified in the field as Pallid Sturgeon, Shovelnose Sturgeon, and "Intermediate Sturgeon" were analyzed using both morphological and genetics characters. Thirty-seven morphological and twelve meristic characters were used to assess species identification on formalin-fixed specimens. Nineteen DNA microsatellites and two Single Nucleotide Polymorphisms were scored on the same specimens using ethanol-preserved fin clips collected prior to fixation. Bayesian analysis of the genotypes using STRUCTURE detected the presence of two weakly differentiated

groups with few genotypes strongly assigning to either group. While field-identified Pallid and Shovelnose sturgeon tended to assign more strongly to different STRUCTURE groups, the assignments were far weaker than they are in the Missouri River where hybridization is presumably less common. Assignment to species based on species-specific allele frequency baselines from the Missouri River identified few pure Pallid Sturgeon in the lower Mississippi River. The small number of specimens identified as pure morphological Pallid Sturgeon were not the same specimens identified as pure Pallid Sturgeon using genetics. Figures comparing genetic and morphological assignments will be presented. The implications for Pallid Sturgeon recovery in the lower Mississippi River will be discussed.

0304 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Clint Henke

University of Colorado, Denver, CO, USA

SWPARC - Tribute to Hobart Smith and David Chiszar - and A Journey Across the Southwest

Hobart Smith is one of the grandfathers of herpetology. With over 1,600 publications he still remains one of the most published scientists of all times. Not only did he father the study of herpetology in Mexico, but he furthered knowledge of the subject here in the United States as well. David Chiszar was a well-known animal behaviorist who made enormous strides in the subjects of predatory behavior of rattlesnakes, brown tree snake biocontrol in Guam, and making sure Hobart's need for field adventures were carried out during his later years. The two of them were sort of an Abbot and Costello who kept each other entertained and intellectually engaged. They shared their adventures and knowledge with countless other professionals and friends that were lucky enough to know them (including many individuals involved in SWPARC). I will share the story of one of my adventures with them and try to pay tribute to who they were.

0168 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Diana L. Herrera-Rodelo, Fredys F. Segura-Guevara, Charles W. Olaya-Nieto

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

Multiannual Length-Weight Relationship of *Liseta Leporinus muyscorum* in the Sinu River, Colombia

The length-weight relationship of *Liseta Leporinus muyscorum* in the Sinu River between January 2000 and December 2002 was estimated. The size ranged between 12.7 and 44.0 cm TL, the total weight between 36.8 and 1025.0 g and the mean length in the catch was

25.8 cm TL. The length–weight relationship was $TW = 0.014 (\pm 0.05) LT^{2.92 (\pm 0.03)}$, $r = 0.96$, $n = 4300$, with isometric growth coefficient, ranging between 2.83 (2000) and 3.09 (2002) with statistically significant differences with 2002 year. The condition factor ranged from 0.019 (2000) to 0.008 (2002); this factor decreased 5.3% from 2000 to 2001 year and 55.6% from 2001 to 2002 year, showing statistically significant differences between 2001 and 2002. A correlation between the condition factor, hydrological cycle of the Sinu River and the spawning season of the Liseta, March to September, was observed. We conclude that the population dynamics of the Liseta has changed during the study period. These changes may be due to overfishing and/or the new hydrological conditions that crosses the Sinu River since 2000 year, when the Urra hydroelectric became operational and began generating electricity.

0414 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Toby Hibbitts¹, Timothy Garrett¹, Connor Adams², Johanna Harvey¹, Gary Voelker¹

¹Biodiversity Research and Teaching Collection, Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, TX, USA, ²Institute of Renewable Natural Resources, Texas A&M University, College Station, TX, USA

Skinks of the South Texas Sand Sheet: Do We Have a New Species?

Two skink species from the genus *Plestiodon* are known to occur throughout southern Texas. We have discovered populations of skinks in the South Texas sand sheet that are morphologically distinguishable from both known *Plestiodon* species (*obsoletus* and *tetragrammus*). They most closely resemble *P. obsoletus*; however, they mature at a smaller size, are more elongate, and have shorter legs. Also, if they were *P. obsoletus* most specimens encountered would be small enough to either be black or transitioning from black. Here we use mtDNA (ND1) to compare these skink populations to other sympatric skink species as well as other *Plestiodon* species from the USA and Mexico.

0342 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Eric Hilton¹, Andrew Williston², Peter Konstantinidis¹

¹Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, VA, USA, ²Harvard University Museum of Comparative Zoology, Cambridge, MA, USA

Osteology of *Parabrotula plagiophthalma* (Parabrotulidae) Based on Cleared and Stained Specimens and X-ray Computed Tomography

Parabrotulidae comprises two species of the genus *Parabrotula* and the monotypic *Leucobrotula*, and has been allied to aplyonids, zoarcids, and other groups; in *Fishes of the*

World Nelson calls them a "family without a home." These are small (<50 mm TL), eel-like fishes of the bathypelagic. As a first step in better understanding the relationships of the parabrotulids, we studied the skeletal anatomy of *P. plagiophthalma* based on cleared and stained specimens and x-ray computed tomography of alcohol-stored specimens. The skeleton is highly reduced and the bones that are present are weakly ossified. The posttemporal and supracleithrum are thin rods of bone (although the cleithrum is relatively massive and well ossified) and the chondral portion of the pectoral girdle is unossified. The dentary is the only tooth-bearing bone of the oral jaws and the vomer only variably has teeth. The ectopterygoid is extremely thin, and the *pars autopalatina* is entirely separate from the more posterior regions of the chondral suspensorium. The interopercle is broad anteriorly but tapers to a threadlike posterior region that broadly overlaps an equally thin subopercle. Most remarkably, the fifth ceratobranchials are represented only by a pair of small, weakly formed cartilages; it has not been determined if this is due to delayed development or secondary ontogenetic reduction. Among teleosts, the loss of ceratobranchial five is otherwise seen in only in some anguilliforms, in which it is an ontogenetic loss. These and other aspects of the morphology of *Parabrotula* will be discussed in a comparative framework.

0578 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Brian Hinds¹, Bryan Hamilton²

¹North American Field Herping Association, Los Angeles, CA, USA, ²Great Basin National Park, Baker, NV, USA

SWPARC - NAHERP Citizen Science Program

The North American Herpetological Education and Research Project (HERP) database is a repository of sightings and information on North American herpetofauna contributed by citizen scientists and professional herpetologists, which is fully incorporated. The goal of HERP is to provide datasets for the conservation of North American herpetofauna. Sightings are collected and moderated with the goal of disseminating data to scientific, academic, governmental, regulatory, research agencies and other approved projects. The North American Field Herping Association (N.A.F.H.A.) is a nonprofit volunteer organization. Our mission is to unite amateur, private and professional herpetologists from North America toward the common goal of better understanding, conserving and managing native North American reptiles and amphibians. Founded in 2006, with input from professional, private and amateur herpetologists from all regions of North America, NAFHA is rapidly becoming a primary source of herpetological information and field assistance for researchers, conservationists, legislators and wildlife management organizations working with North American herp species. The Herpetological Educational and Research Project (HERP) database is a continually expanding collection of current herpetological data, gathered daily from the field by NAFHA members working in Canada, Mexico and the U.S.A. As of 3/31/2015, 2,676 users had entered 206,539 records. We welcome you to explore the database (www.naherp.com), read about the regional projects our members are involved in, and

visit our various forums. We also extend an invitation to you to become a member of NAFHA and help us achieve our goals of creating better conservation and management of our native North American reptiles and amphibians.

0010 Fish Biogeography, Carson 3, Saturday 18 July 2015

Christopher Hoagstrom¹, Kathie Taylor²

¹Weber State University, Ogden, UT, USA, ²Argenta Ecological Consultants, Salt Lake City, UT, USA

Deep Endemism of Fishes in the Ozarks and Pre-Pleistocene Highland Vicariance

Fish endemism in the Ozark Plateaus has received considerable study. Mayden's inspirational hypothesis of highland vicariance, circa 1987, used phylogenetic evidence to cast some Ozark endemics as vestiges of a contiguous, pre-Pleistocene highland fauna that was fragmented by geomorphic evolution in the Pleistocene. However, the Ozark Plateaus encircle a dome that was independently uplifted in the Paleozoic and then leveled by erosion in the Mesozoic. Mesozoic erosion exposed strata susceptible to dissolution. Subsequent dissolution created an insular, karst province with myriad caverns and springs. That is, strata subject to dissolution remain largely buried in surrounding provinces. Several revised fish phylogenies include Ozark endemics with late Tertiary origins, meaning these taxa arose when the Ozarks were an eroded, presumably karstified, plain. The Ozarks likely provided spring-fed refugia in a geomorphically stable setting, especially in the Oligocene and again in the Late Miocene when climatic cooling and sediment flux impacted surrounding provinces. All but one pre-Pleistocene endemic occupies the Salem Plateau where karst is prevalent (the Springfield Plateau endemic is troglobitic). In the Plio-Pleistocene, regional erosion lowered the surrounding base level and drainage divides of Miocene age were uplifted. Eventually, in-facing escarpments and annular rivers with entrenched valleys encircled the dome. Pre-Pleistocene endemics appear to be ancient peripheral isolates. Their ancestors likely invaded from adjacent plains. Tributaries to the Mississippi Embayment with more equitable climates harbor most isolates. Variation in estimated times of origin and disparities among distributions of sister taxa are consistent with expectations from the centrifugal-speciation and taxon-pulse hypotheses.

0011 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Christopher Hoagstrom¹, Thomas Archdeacon², Stephen Davenport², David Propst³, James Brooks²

¹Weber State University, Ogden, UT, USA, ²USFWS New Mexico Fish & Wildlife Conservation Office, Albuquerque, NM, USA, ³New Mexico Department of Game & Fish Conservation Services Division, Santa Fe, NM, USA

Last-stand Population Ecology in Fragmented Rivers and Conservation in De-facto Refugia

Habitat destruction and subdivision associated with dams increasingly restrict sensitive riverine taxa to isolated reaches with residual habitat (i.e., de-facto refugia). Population dynamics in these reaches must be well understood to determine critical habitat features. We used 20 years of population-monitoring data to assess population trends and habitat associations for three imperiled, pelagic-broadcast spawning minnows (*Notropis girardi*, *Notropis jemezanus*, and *Notropis simus pecosensis*). The study reach had a regulated flow regime and three distinct sub-reaches with, from upstream to downstream, "discontinuous" (i.e., degraded) habitat, relict-ecosystem (i.e., high quality) habitat, and channelized (i.e., degraded) habitat. We assessed population and flow-regime influences on recruitment and summarized distributional patterns of cohorts. Each population was persistent and dominated by a single year class. In two species, high-flow events regulated recruitment, which is typical for riverine, pelagic-broadcast spawning minnows. Populations of all three species centered in unchannelized habitat. Intra-reach habitat connectivity was important to facilitate movement to unchannelized habitat from climatic refugia and, in the case of *N. s. pecosensis*, to allow upstream return of juveniles displaced into channelized habitat as propagules or small age-0 individuals. Over-winter recruitment and climatic refugia appeared to help species withstand streamflow intermittence. Recognition that fragmentation has destroyed all but isolated refugia should motivate proactive place-based conservation where species make a "last stand". Monitoring provides the basis for comprehensive assessment, but only threat alleviation ensures conservation.

0562 General Ichthyology II, Crystal 3 & 4, Friday 17 July 2015

Jennifer Hodge, Francesco Santini, Peter Wainwright

University of California, Davis, CA, USA

Causes and Consequences of Sexual Dichromatism in Labrid Fishes

Fishes display an array of color patterns from drab and uniform to strikingly brilliant and complex. The question as to why some fishes are so spectacularly colored has intrigued biologists for over a century. Color pattern in general is used by organisms to avoid detection and to communicate. Communication is an important component of sexual selection. Phenotypic differences in color between males and females, or sexual

dichromatism, are often used as a measure of the strength of sexual selection. The magnitude of sexual dichromatism has been hypothesized to account for the increased diversification rate of parrotfishes within the family Labridae. Here, we ask whether the degree of sexual dichromatism affects rates of lineage diversification and whether sexual dichromatism has evolved adaptively, with shifts to coral reef habitats. Using quantitatively scored sexual dichromatism and habitat traits with a new time calibrated phylogeny for 404 labrid species we found no evidence for increased rates of diversification in highly dichromatic lineages. However, we did find positive evidence for a correlation between dichromatism and associations with coral reef habitat such that more dichromatic species tend to be found on coral reefs. While our results do not support previous expectations of a positive effect of the intensity of sexual selection on the rate of speciation, we suggest that the bright colors found in many male labrids on reefs evolved both because of competition with other males and to communicate species identity, reducing the chances of hybridization in species-rich coral reef communities.

0150 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Hillary Hoffman¹, Daniel Leavitt¹, Daniel Steward²

¹AZ Game & Fish Department, Phoenix, AZ, USA, ²U.S. Army Garrison Yuma, Yuma, AZ, USA

Occupancy and Habitat Use of Sonoran Desert Tortoises on Yuma Proving Ground, La Paz County, AZ

In 2014, we returned to the United States Army Yuma Proving Ground to conduct occupancy surveys for Sonoran Desert Tortoises (*Gopherus morafkai*). Rising concern regarding the status of the Sonoran Desert Tortoise in Arizona resulted in further effort to understand a population on the western edge of its distribution. We conducted a focused survey in the Trigo and Dome Rock Mountains of Yuma Proving Ground to determine Sonoran Desert Tortoise occupancy and habitat use. Previous surveys of the military base suggested that this was a low density population. Here we provide evidence contrary to previous assessments. Between March and October we detected 20 tortoises on 32 occasions during occupancy surveys. We placed VHF transmitters and GPS tracking units on 9 tortoises in order to better understand Sonoran Desert Tortoise habitat use on the installation. Here we report on the status of this population, what we have learned about their habitat use patterns, how this survey compares to previous surveys, and what we expect continued surveys will tell us.

0249 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Sarah Hoffmann, Steven Warren, Andrea Hernandez, Marianne Porter

Florida Atlantic University, Boca Raton, FL, USA

Swimming Kinematics of Juvenile *Sphyrna lewini*

Hammerhead sharks (Sphyrnidae) have a unique, dorso-ventrally compressed head that may act as a hydrofoil, generating lift and increasing maneuverability in the horizontal plane during swimming. Previously, researchers hypothesized that the cephalofoil acts as a stabilizer during swimming to maintain the shark's position parallel to the substrate. This is different than more streamlined sharks, which use whole body rolling during swimming. Furthermore, hammerheads have greater hypaxial musculature allowing for a larger range of motion of the head. As a result, a slight change in the angle of attack of the cephalofoil could produce a significant change in pitch angle of the shark with limited energy expenditure. Our goal is to examine the whole-body swimming kinematics of juvenile scalloped hammerhead sharks, *Sphyrna lewini*, to better understand how head morphology has shaped swimming performance. From previous kinematics data on lift generation in elasmobranchs, we predict that the cephalofoil is generating lift. Kinematic data was assessed using synched dorsal and lateral video of *S. lewini*. We measured volitional straight swimming performance variables by tracking the movements of anatomical landmarks through time. These landmarks included points on the body midline, cephalofoil, pectoral fins, and caudal fin. The movements of these points were correlated with performance variables such as whole body velocity, body curvature, tailbeat frequency, tailbeat amplitude, head yaw, and cephalofoil and pectoral fin angles of attack. From these data, we are able to quantify swimming performance and better understand how the cephalofoil of hammerhead sharks may be increasing maneuverability and generating lift.

0528 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Eric Hoffmayer¹, Jennifer McKinney², Jill Hendon³, James Franks³, Brett Falterman², William Driggers¹

¹National Marine Fisheries Service, Pascagoula, MS, USA, ²Louisiana Department of Wildlife and Fisheries, Baton Rouge, LA, USA, ³Gulf Coast Research Laboratory, Ocean Springs, MS, USA

Northern Gulf of Mexico Whale Shark Research Program: What We Have Learned about Whale Shark Aggregations in the Northern Gulf of Mexico

The *Northern Gulf of Mexico Whale Shark Research Program* was initiated in 2003 to increase our knowledge of whale shark occurrence and distribution within the region. A primary component of this program is a whale shark sighting website, which accommodates reports of regional sightings by "citizen scientists." Whale sharks aggregate in areas of high prey abundance and our hope was to examine factors driving

this behavior in the northern Gulf of Mexico. To date, over 600 whale shark sighting reports have been received. Reports were provided by a number of groups, including recreational anglers, divers, helicopter pilots and petroleum industry personnel and were categorized as sightings of solitary individuals, small aggregations (2-9 individuals) or large aggregations (10 or more individuals). Whale shark aggregations represented 190 (31%) of reported sightings, 47 (25%) of which were large aggregations between 10-150 individuals. All of the reported large aggregations occurred during summer, almost exclusively along the continental shelf edge, with 19 (41%) occurring at Ewing Bank off Louisiana. Directed research efforts were made to encounter aggregations to determine the size and sex of the sharks within the aggregation and to identify the primary prey source(s) by collecting plankton samples. Five aggregations were encountered and appeared to consist of largely juvenile males that were feeding on little tunny (*Euthynnus alletteratus*) eggs. The use of sightings data provided by "citizen scientists" has proven to be an inexpensive and effective technique for characterizing whale shark distribution, seasonality and aggregation locations in the northern Gulf of Mexico.

0286 Fish Ecology II, Carson 3, Sunday 19 July 2015

J. Derek Hogan¹, Peter J. Lisi², Peter B. McIntyre², Michael J. Blum³, James F. Gilliam⁴, Nate Bickford⁵

¹Texas A&M University - Corpus Christi, Corpus Christi, TX, USA, ²University of Wisconsin - Madison, Madison, WI, USA, ³Tulane University, New Orleans, LA, USA, ⁴North Carolina State University, Raleigh, NC, USA, ⁵University of Great Falls, Great Falls, MT, USA

Variability in Migration of an Amphidromous Goby (Gobiidae): Causes and Consequences

Variation in migratory behaviors has been documented for a wide variety of fish species. The causes and consequences of this variability are still poorly understood for most species. Here we investigate variability in migratory histories of a Hawaiian amphidromous goby, *Awaous stamineus*, across the species' entire geographic range. Amphidromous species undergo a brief marine larval phase followed by a return to freshwaters as juveniles. Using otolith microchemistry, we determined that 62% of individuals did not migrate to the ocean, completing their life cycle entirely within freshwater, demonstrating that amphidromy is not obligate for this species. We show that variation in migratory histories among populations is driven by environmental factors. Specifically hydrologic variability appears to drive migratory patterns, whereby watersheds with more variable water flow show higher rates of oceanic-migrations. Comparing early life history outcomes based on daily otolith growth rings, we find that marine migrating larvae have shorter larval durations and exhibit faster larval and adult growth, compared to purely-freshwater counterparts. These benefits of maintaining marine migrations presumably balance against the challenge of finding and re-entering an island stream from the ocean. The facultative nature of amphidromy in this species

highlights the selective balance between costs and benefits of migration in life history evolution.

0347 Chemical Ecology Symposium, Crystal 3 & 4, Sunday 19 July 2015

Matthew Holding¹, H. Lisle Gibbs¹, James Biardi²

¹The Ohio State University, Columbus, OH, USA, ²Fairfield University, Fairfield, CT, USA

Adaptive Variation in a Complex Chemical Phenotype: Northern Pacific Rattlesnake Venom Shows Environmentally-structured Local Adaptation to Venom Resistance in Ground Squirrels.

Interactions between species are widely regarded as important drivers of diversification, especially when geographic variation in the nature of these interactions favors local adaptation of key traits. Recently, the importance of trait complexity in the evolution of species' interactions has gained attention, where it seems that complex traits are more likely to be locally adapted. Snake venoms are highly variable chemical phenotypes with a well-characterized molecular basis, and venoms serve as the direct chemical link between a snake and its prey. The discovery of prey species with evolved resistance to snake venoms suggests that venoms may have coevolved with prey resistance, and that venoms are shaped by selection acting through diet at fine spatial scales. We demonstrate a high degree of population-level differentiation in the venom phenotypes of Northern Pacific Rattlesnakes (*Crotalus oreganus oreganus*) from across their range in California. We then unveil a functional signal of local adaptation of these snakes to dealing with high levels of venom resistance in one of their primary food sources, the California Ground Squirrel (*Otospermophilus beecheyi*) by quantifying venom resistance in 1690 unique snake-squirrel combinations. Local adaptation of a predator with a longer generation time than its prey is an unexpected result, and may represent an empirical example of phenotypic complexity and evolutionarily labile venoms at work as diversity generators in these interactions.

**0292 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Parker House, Larry Allen

*Nearshore Marine Fish Research Program, California State University, Northridge,
Northridge, CA, USA*

**The Return of the King: Giant Sea Bass (*Stereolepis gigas*) Reproductive
Population Assessment off Santa Catalina Island, CA**

Giant sea bass (*Stereolepis gigas*) are the resident apex predator and largest teleost of the rocky reefs and kelp forests within the Southern California Bight. After their population crash due to overfishing in 1935, giant sea bass were largely absent in southern California waters for much of the 20th century. However, recent surveys suggest the southern California population may be returning. This study provides the first assessment of the reproductive population of giant sea bass off Santa Catalina Island, CA. Eight sites were surveyed on both the windward and leeward side of Santa Catalina Island every two weeks from 6/9 - 8/13/2014. Of the eight sites, three spawning aggregations were identified at Twin/Goat, The V's, and Little Harbor, CA. Over the course of the summer the giant sea bass population was primarily made up of individuals 1.2 - 1.3 m TL with several small and newly mature fish observed in aggregations. However, the majority of the biomass within the population was held among larger and older individuals. Overall, mean biomass densities of the spawning stock of giant sea bass were much higher than expected. Comparing mean biomass of all kelp forest fish trophic levels during the summer season revealed a nearly top-heavy biomass pyramid for the fish community off the island. The large trophic presence of giant sea bass provides support for their promising return to the rocky reefs and kelp forests off Santa Catalina Island, and possibly the Southern California Bight.

0082 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kyle J. Hovey¹, Megan A. Boyk¹, Erin E. Johnson¹, Taran Grant², Ralph A. Saporito¹

¹*John Carroll University, University Heights, OH, USA*, ²*Universidade de São Paulo, São Paulo, SP, Brazil*

Do Variable Alkaloid Defenses in the Red-belly Toad *Melanophryniscus simplex* Provide Equal Protection from Microbial Pathogens?

Amphibians produce the majority of their defensive chemicals, but alkaloid defenses in poison frogs are sequestered entirely from dietary arthropods. Alkaloids function as a defense against predators, and certain alkaloids appear to inhibit microbial growth. However, alkaloid defenses vary considerably among populations of poison frogs, reflecting geographic differences in availability of dietary arthropods. Consequently, environmentally driven differences in alkaloid defenses of poison frogs may have

significant implications in their protection against pathogens. While natural alkaloid mixtures in poison frogs have recently been shown to inhibit growth of non-pathogenic bacteria and fungi, no studies have examined the effectiveness of alkaloids against microbes that infect frogs. Herein, we examined how alkaloid defenses in the red-belly toad, *Melanophryniscus simplex*, affect growth of the known anuran pathogens *Batrachochytrium dendrobatidis*, *Aeromonas hydrophila*, and *Mycobacterium* sp. Frogs were collected from six locations throughout Brazil that are known to vary in their alkaloid profiles. Alkaloids were isolated from individual skin samples, and extracts were assayed against each pathogen. Microbe subcultures were inoculated with extracted alkaloids to create dose-response curves, and spectrophotometry was used to compare growth between treatments. GC-MS was used to characterize and quantify alkaloids in frog extracts, and our results suggest that variation in alkaloid defenses lead to differences in inhibition of pathogenic microbes. This study provides the first evidence that alkaloid variation in a bufonid poison frog is associated with differences in inhibition of frog pathogens. Furthermore, our study provides support that alkaloid defenses in poison frogs confer protection against both pathogens and predators.

0256 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Hua Hsun Hsu¹, David A. Ebert², Shouu Jeng Joung¹, Kwang Ming Liu¹, Chia Yen Lin¹

¹National Taiwan Ocean University, Keelung City, Taiwan, ²Moss Landing Marine Laboratories, Moss Landing, CA, USA

Catch and Preliminary Fishery Biological Information of Megamouth Sharks *Megachasma pelagios* in Eastern Waters off Taiwan

Megamouth shark *Megachasma pelagios* is rare and one of three filter-feeding shark species. Prior to this study, only 65 megamouth sharks have been recorded during 1976-2015; 6 from the Atlantic Ocean, 6 from the Indian Ocean, and 53 individuals from the Pacific Ocean. In fact, an additional 32 megamouth sharks were caught by gill nets off Hualien, eastern Taiwan between 2013 and 2014. All sharks were caught at night before dawn from April to August, with most of them caught with ocean sunfish (Molidae), the primary target species of drift net fishery. Of the 32 specimens, body weights (BW) ranged from 210-1147 kg, and lengths measured from 220-560 cm in precaudal length, 250-710 cm in total length (TL); sexes were 20 females (250-710 cm TL), 11 males (363-484 cm TL), and sex was unknown for one individual (500 cm TL). Reproductive condition was determined for 17 sharks, two females were determined to be mature, 11 (5 females 6 males) were maturing, and 4 other females were immature. Stomach contents of 12 individuals examined, indicated that 5 were vacuous, 6 were with partial prey, and 1 was full of prey. Parasites were collected from pectoral fins, mouth, gill slits, stomach, and intestine of 14 individuals. The BW-TL relationships were estimated to be $BW=2.316 TL - 524.06$ ($r^2=0.72$, $n=11$) for male, and $BW=0.198 TL^{1.286}$ ($r^2=0.42$, $n=20$) for female, respectively. Eastern waters of Taiwan may be a very important feeding ground for juvenile and subadult megamouth sharks.

0303 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Daniel Huber¹, Bethany Loya¹, Summer Decker², Jonathan Ford²

¹The University of Tampa, Tampa, FL, USA, ²University of South Florida, Tampa, FL, USA

Structural Mechanics of Sixgill and Mako Shark Jaws: Evolutionary Considerations

Jaw morphology has changed dramatically over the course of shark evolutionary history, and this diversity of morphology has been postulated to reflect variability in feeding mechanism, behavior, and ecology. The purposes of this study were to 1) compare the structural mechanics of the jaws of the bluntnose sixgill shark *Hexanchus griseus* and longfin mako shark *Isurus paucus*, which approximate relatively ancestral and derived jaw morphologies respectively, and 2) investigate the mechanical consequences of the transition from bone to cartilaginous jaws, which occurred early in the evolutionary history of chondrichthyan fishes. Jaws were CT scanned, segmented, and modeled to represent various character states of skeletal composition (unmineralized cartilage, composite mineralized/unmineralized cartilage, bone). Stress, strain, and strain energy density were determined using finite element analysis. *Isurus paucus* exhibited comparable stress, but less strain and strain energy density than *H. griseus*, indicating that the material and morphology of jaws have become more efficient at handling stress and strain. The heterogeneous model (composite mineralized, unmineralized cartilage) resulted in low stress, intermediate strain, and intermediate strain energy density for all jaws. These results suggest that shark jaws may have been structurally modified over time to better resist stress and strain by virtue of changes in their geometry and that emergent mechanical properties derive from the combination of mineralized and unmineralized cartilage.

0542 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Jeanette Huber, Gavin Naylor, Lei Yang

College of Charleston, Charleston, SC, USA

Extraction of DNA from Historical and Contemporary Samples of Sawfish (Pristidae) for Population Genomics

Population genetic research on large marine vertebrates can be limited by time, money, and small sample sizes. This is particularly true for rare species or those that are only represented by archival specimens in museum collections. Improved DNA extraction techniques along with next-generation sequencing technologies and target gene capture methods that require only small amounts of input DNA hold promise for studying

demographic processes in rare populations. Sawfish (family Pristidae) are among the most critically endangered marine vertebrate species, and they have already been locally extirpated from some of their historical ranges. It is thus difficult to obtain adequate sample sizes from populations in remote areas or in areas where they have been severely overharvested. However, due to their iconic and unique appearance, sawfish rostra are often well represented in museums around the world. Archival sawfish tissues can supplement contemporary samples in genetic studies, as well as provide a baseline for examining historical population structure and genetic diversity prior to exploitation. This requires however, that sufficient DNA be extracted from archival specimens, but it is often low quantity and degraded. The current study aims to evaluate the efficacy of several extraction methods applied to different sawfish tissue types including fresh tissue as well as dried skin, teeth, and bone from historical samples of rostra ranging from ten to two hundred years old. Results from this study will be utilized in future work to assess population structure, size and history of critically endangered sawfish species.

0345 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Sarah Huber, Peter Konstantinidis, Eric Hilton, Deborah Steinberg

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

Organization, Expansion, and Digitization of the Larval Fish Collection at the Virginia Institute of Marine Science

The Virginia Institute of Marine Science Nunnally Ichthyology Collection contains a large collection of uncatalogued larval fishes (ca. 50,000+ lots). This collection is unique among all ichthyoplankton collections on the East Coast in its scope and size, and consists of collections made in the Caribbean, the Mid- and South Atlantic Bights, and the Chesapeake Bay, as well as ichthyoplankton in samples from long-term time-series and other plankton studies from the Atlantic, Pacific, and Southern Oceans. Many of the plankton samples deriving from these large, interdisciplinary research projects are complemented by extensive environmental data, including depth, temperature, salinity, and dissolved oxygen, and by phyto- and zooplankton assemblage information. Here we will report on the current progress of sorting, identification, and digitization of this collection, which was recently funded by the National Science Foundation. As part of our current NSF CSBR grant, we will host two-week long workshops at VIMS that will include a three-day primer on larval fish identification led by four invited guest larval fish taxonomists, followed by identification of selected samples from VIMS collections will focus on specimen identification and other topics in larval fish taxonomy. Participants will sort and identify ichthyoplankton samples to the family level under expert guidance. In this poster we will provide additional details on the workshop scheduled for the fall of 2015.

0106 Herp Ecology, Carson 4, Saturday 18 July 2015

Geoffrey N. Hughes, Jacqueline D. Litzgus

Laurentian University, Sudbury, ON, Canada

Thermal Landscape Ecology of Wood Turtles (*Glyptemys insculpta*) in the North

The features of a physical landscape (topography, canopy cover, water, and soil) generate a dynamic thermal landscape over daily and seasonal cycles. For ectotherms like turtles, this thermal landscape may be of greater relative importance for fitness than the physical landscape. Previous thermal ecology studies have focused on thermal selection at the organism and site levels, but not the landscape level, and the thermal landscape concept has primarily been applied in an urban planning context, not an ecological context. Our project explores the thermal landscape as an ecological concept, and its implications for conservation of the wood turtle (*Glyptemys insculpta*), a species that uses a wide variety of terrestrial and aquatic habitats during the course of its active season. Using temperature dataloggers attached to radio-tagged turtles and to operative thermal models placed throughout the study area, we examined the relative importance of the thermal landscape compared to the habitat landscape on wood turtle habitat use and movements. Using thermal imaging cameras, we compared the importance of physical and thermal properties of soil in nest-site selection by female wood turtles. We also placed operative thermal models within nearby forestry sites and aggregate pits; comparisons to the thermal model data from the turtle study site will allow us to examine the thermal impact of resource development on wood turtle habitat. This study will further our understanding of the thermal ecology of ectotherms, in addition to informing habitat restoration for an Endangered species. Preliminary data will be presented.

0107 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Geoffrey N. Hughes, Jacqueline D. Litzgus

Laurentian University, Sudbury, ON, Canada

The Thermal Landscape as a Predictor of Wood Turtle (*Glyptemys insculpta*) Nest-site Selection

For oviparous species with no parental care, like wood turtles (*Glyptemys insculpta*), nest-site selection represents the only point at which a mother may behaviourally invest in her offspring. Previous studies in the Sudbury District determined that wood turtle females select nest sites for high-but-variable nest temperatures; lab studies have shown that variable incubation temperatures speed development of wood turtle embryos. By studying both the thermal and physical properties of known nesting beaches at the study site, and comparing them to the specific thermal and physical selections made by nesting wood turtle females, we will determine whether wood turtles navigate a thermal

landscape on the microhabitat scale, and if this thermal landscape is more important in determining their behaviour than the physical landscape. Thermal imaging cameras will be placed on three known nesting beaches to measure their thermal characteristics. These beaches will be divided into 1x1 metre grids; soil samples will be collected from each grid prior to the commencement of nesting activity to measure soil organic content and grain size distribution, to measure the physical characteristics of the beaches; we will also take daily soil moisture measurements during the nesting period. When we observe a female nesting on a beach, we will compare the thermal and physical characteristics to assess relative importance in the female's nest-site selection. This study will improve our knowledge of the surface cues used by female wood turtles in nest-site selection, and can lead to new techniques for surveying nesting habitat. Preliminary data will be presented.

0245 General Ichthyology II, Crystal 3 & 4, Friday 17 July 2015

Peter Hundt, Andrew Simons

University of Minnesota, St. Paul, MN, USA

Evolution of Trophic Morphologies and Diet in Combtooth Blennies (Blenniidae)

Combtooth blennies (387 species) are small (most < 100 mm), common fishes found in most tropical and subtropical shallow marine communities. The oral teeth of blennies are in a single row on the jaws and the teeth may number from as few as 20 to as many as 400. In addition, there is substantial variation in shape from short and incisiform to thin and long teeth. Furthermore, the teeth have a range of modes of attachment from firm attachment to the jaw to a weak attachment via loose connective tissue with no direct tooth contact to bone. Beyond their remarkable teeth, some blennies have an extra point of articulation, the intramandibular joint, in the lower jaw between the dentary and articular bones. Trophic morphologies such as these are often strongly correlated with specific diets. The diet of blennies varies widely between species and includes species that specialize on coral polyps, detritus, polychaetes, or fish scales. However, the most species rich clade, containing species with unique trophic morphologies, appears to feed almost exclusively on detritus. Herein, I use stomach content analysis, morphological evaluation and phylogenetic analyses of 5 nuclear loci, from 130 blenny species, to explore the evolution of trophic morphologies and diets.

0540 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Kelly Hunt, Jason L. Jones, Amanda Northrup

Nevada Department of Wildlife, Las Vegas, NV, USA

Monsters in Our Midst, Or Are They? A Humble Exercise in Estimating Detection Probability (Southwest PARC)

The Gila monster (*Heloderma suspectum*) is a notoriously hard to detect reptile species, in part due to its rarity and secretive behavior. Few attempts have been made to quantify detection probabilities for this species, presumably because Gila monsters spend upwards of 95% of their time in shelters. An estimation of detection probability is necessary for making reliable inference about species occurrence and may provide insight into the factors influencing these parameters. Past studies on Gila monsters have largely relied on trackway surveys and radio telemetry to confirm occupancy. Although trackway surveys increase detection probability, they require sandy substrate and are temporally short-lived, thus they have limited applicability in sites lacking sandy substrate and for studies with infrequently surveys. Radio telemetry is labor intensive, costly, and invasive, but results in a more targeted effort that can directly evaluate detection (i.e., activity above ground). In an attempt to estimate detection probability, eight radio telemetered Gila monsters were tracked for upwards of two years. The variables that were hypothesized to influence detection included environmental covariates (e.g., temperature, humidity), season, time of day, and gender of the individual Gila monsters. Although our estimates of Gila monster detection probabilities are site specific, they may provide managers and researchers with a better understanding of the amount of effort required to confirm occupancy and the environmental variables that influence detection rates in biogeoclimatically similar areas where Gila monsters are predicted to occur.

0494 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2, Thursday 16 July 2015

Sarah M. Hykin¹, Ke Bi², Jimmy A. McGuire¹

¹*Museum of Vertebrate Zoology, Berkeley, CA, USA*, ²*Computational Genomics Resource Laboratory (CGRL), California Institute for Quantitative Biosciences (QB3), Berkeley, CA, USA*

Fixing-formalin: A Method to Recover DNA Sequence Data from Formalin-fixed Museum Specimens Using High-Throughput Sequencing

For a century or more, specimens were routinely collected and deposited in natural history collections without preserving fresh tissue samples for genetic analysis. In the case of most herpetological specimens, attempts to extract and sequence DNA from formalin-fixed, ethanol-preserved specimens – particularly for use in phylogenetic analyses – has been laborious and largely ineffective due to the highly fragmented

nature of the DNA. As a result, tens of thousands of specimens in herpetological collections have not been available for sequence-based phylogenetic studies. Massively parallel High-Throughput Sequencing methods and the associated bioinformatics, however, are particularly suited to extracting meaningful genetic markers from severely degraded/fragmented DNA sequences such as DNA damaged by formalin-fixation. In this study, we compared previously published DNA extraction methods on three tissue types subsampled from formalin-fixed specimens of *Anolis carolinensis*, followed by sequencing. Sufficient quality DNA was recovered from liver tissue, making this technique minimally destructive to museum specimens. Sequencing was only successful for the more recently collected specimen (collected ~30 ybp) which could be due to variables regarding the conditions of preservation. For the successfully sequenced sample, we found a high rate of base misincorporation. After rigorous trimming, we successfully mapped 27.93% of the cleaned reads to the reference genome, were able to reconstruct the complete mitochondrial genome, and recovered an accurate phylogenetic placement for our specimen. The technique we present will greatly improve the value of museum collections by making many formalin-fixed specimens available for phylogenetic analysis.

0220 AES Morphology & Physiology, Carson 2, Sunday 19 July 2015

Johanna Imhoff¹, R. Dean Grubbs²

¹Florida State University, Tallahassee, FL, USA, ²FSU Coastal and Marine Laboratory, St. Teresa, FL, USA

Methylmercury Contamination in Six Species of Deepwater Sharks in the Northeastern Gulf of Mexico

As mid to upper trophic level predators, elasmobranchs are at risk of carrying high loads of bioaccumulating toxicants. Methylmercury (MeHg) is of particular concern in fishes because high levels of contamination can put humans at risk for reproductive and neurological problems via fish consumption. Research on MeHg contamination in deepwater sharks has shown that MeHg concentration increases with the size of the shark, often exceeds recommended values for safe human consumption, and generally increases with increasing trophic level and dependence on benthic versus pelagic food webs. MeHg is one of several pollutants that are of particular concern after an oil spill. It has been hypothesized that oil spills create ideal conditions for blooms in the bacteria that methylate mercury. As mid to upper trophic level predators, deepwater sharks have the potential to bioaccumulate high concentrations of MeHg and their high longevity may facilitate the persistence of high levels of MeHg in the system for long periods of time. Therefore mercury analysis of coexisting deepwater sharks in a habitat near a source of anthropogenic pollution (i.e. the Deepwater Horizon oil spill) could provide useful information on the roles of taxonomy and depth habitat in toxicological response of mesopredators after an oil spill. Methylmercury speciation and levels will be analyzed in six shark species that range from the continental shelf edge to the mid-slope

and include both Carcharhiniformes (*Mustelus canis*, *M. sinusmexicanus*) and Squaliformes (*Squalus cubensis*, *S. cf. mitsukurii*, *Centrophorus uyato*, *C. granulatus*).

0244 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Siobhan Ingersoll¹, Rebecca Farr², Kevin Tang¹

¹University of Michigan-Flint, Flint, MI, USA, ²Wayne State University, Detroit, MI, USA

Cusk-eel Phylogeny Based on Molecular Data

Cusk-eels of the family Ophidiidae are an enigmatic group of marine bony fishes. They are mainly found in temperate or tropical waters around the world. The purpose of this project is to expand upon a previously presented phylogenetic tree to understand and determine their relationships to other fishes in the order Ophidiiformes. Nine genes were amplified and sequenced using standard molecular biology techniques. To generate the tree of relationships, the data will be combined and analyzed using modern phylogeny reconstruction methods. The results of this study will provide an evolutionary framework that will be used to revise the classification.

0558 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Laura Jackson, Paula Mabee

University of South Dakota, Vermillion, SD, USA

Automated Integration of Morphological Data Sheds Light on Paired Fin Loss in Actinopterygian Fishes

Surveying the taxonomic distribution of characters across multiple studies is a laborious and time-consuming task. We show that tagging anatomy with computer-readable terms automates this process, enabling rapid views of integrated data, and extending author observations to include inferred data. We used this approach to explore the frequency of pectoral and pelvic fin loss across actinopterygian fishes. Data for paired fins were extracted from the Phenoscape Knowledgebase (KB, kb.phenoscape.org), which contains 19,024 morphological characters for 4,399 vertebrates from 139 studies. 491 observed and inferred morphological characters were automatically compiled into a synthetic supermatrix for 4052 taxa, and a corresponding tree was simultaneously generated. This supermatrix identified 111 of 545 extant families of actinopterygian fishes having one or more species that as adults lack pectoral fins, pelvic fins, or both.

As compared to previous studies investigating fin loss, this study provides additional data for 14 families. This is the first study showing the frequency of pectoral fin loss, which was documented in 21 families. Ancestral state reconstruction determined 72

independent evolutionary events for paired fin loss, with this number representing the maximum number of possible diverse genetic pathways leading to fin loss. However, additional pathway analysis is necessary to conclude whether the number of independent fin loss events is significant. Because fin data are linked to genes for zebrafish in the KB, this enabled us to extract a list of 25 candidate genes known to cause paired fin loss. This data provides great research potential for understanding fin and limb development.

0238 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Jessica Jang, Catarina Pien, David Ebert

Moss Landing Marine Laboratories, Moss Landing, CA, USA

Unlocking the Mystery of Western Indian Ocean Electric Rays (Torpedinidae: *Torpedo*, Duméril 1806)

The Torpedinidae consists of two genera, *Torpedo* Duméril 1806, consisting of 15 species, and *Tetronarce* Gill 1862 that consists of 12 species. *Torpedo* species although morphologically similar, typically exhibits an ornate coloration, with distinct dorsal surface markings, and by the presence of spiracular papillae. *Tetronarce* species on the other hand are drably colored, and lack these distinctive papillae. As part of a broader investigation into the ecology, life history and taxonomy of southwestern Indian Ocean (SWIO) Chondrichthyans we are currently investigating the electric ray genus *Torpedo*. Three species are represented in the SWIO: *Torpedo fuscomaculata*, Peters 1855, *Torpedo panthera*, von Olfers 1831, and *Torpedo sinuspersici*, von Olfers 1831, but these may each involve species complexes given the striking color variation of specimens collected from different island groups within the region. Regional species each have distinctly different markings and patterning, orbital papillae/protrusions, and life history characteristics suggesting some of these island groups be home to regionally endemic electric rays. Here we present our findings to date on the mysterious electric rays of the SWIO.

0147 Herp Behavior, Carson 4, Friday 17 July 2015

Bruce Jayne, Steven Newman, Michele Zentkovich, Henry Berns

University of Cincinnati, Cincinnati, OH, USA

Incline, Peg Height, Peg Shape and Body Shape Have Interactive Effects on the Arboreal Locomotion of Snakes

The height and shape of ridges in tree bark vary substantially, and the convergently evolved ventrolateral keels in some specialized arboreal snakes seem well suited for catching such structures. However, the combined effects of body shape, ridge height

and incline on locomotor performance are poorly understood. Hence, we used cylindrical surfaces with different inclines (N=5) and heights (N=5), and shapes (N=2) of pegs to simulate and test how bark texture and incline affect the maximal speed and locomotor behavior of snakes. Of our three study species, both corn snakes and brown tree snakes formed a conspicuous ventrolateral keel, but boa constrictors did not. Unlike the other two species, brown tree snakes performed lateral undulation on pegs that were only 1 mm high on all inclines ranging from horizontal to vertical. Brown tree snakes were faster and used lateral undulation on more surfaces than the other two species.

Corn snakes often performed lateral undulation when pegs were 2 mm but not 1mm high, and steep surfaces with short pegs were often impassable for this species. Boa constrictors used more concertina locomotion than the other species, and they usually did not perform lateral undulation until peg height exceeded 2 mm. Some trade-offs between proficient concertina and undulatory locomotion occurred between corn snakes and the stouter boa constrictors. By contrast, every aspect of the arboreal locomotor performance known for brown tree snakes appears to equal or exceed those of the other two more muscular study species, which also regularly climb trees.

0201 Chemical Ecology Symposium, Crystal 3 & 4, Sunday 19 July 2015

Adriana Jeckel¹, Taran Grant¹, Ralph Saporito²

¹Universidade de São Paulo, São Paulo, Brazil, ²John Carroll University, University Heights, OH, USA

Sequestered and Synthesized Chemical Defenses in the Poison Frog *Melanophryniscus moreirae* (Bufonidae)

Bufonid poison frogs of the genus *Melanophryniscus* contain a diversity of alkaloid-based chemical defenses that are derived from a diet of alkaloid-containing arthropods. In addition to these dietary alkaloids, bufadienolide-like compounds and indolealkylamines have also been identified in certain members of *Melanophryniscus*. Our study reports, for the first time, the co-occurrence of large quantities of alkaloids sequestered from diet and a synthesized indolealkylamine in skin secretions from individual specimens of *Melanophryniscus moreirae* from Brazil. GC-MS and GC-MS-FTIR analysis of 55 individuals of *M. moreirae* revealed 38 dietary alkaloids and the biosynthesized indolealkylamine bufotenine. On average, pumiliotoxin **267C**, bufotenine, and allopumilitoxin **323B** collectively represented 90% of the defensive chemicals present in individual toads. Skeletochronology was used to examine the relationship between defensive chemicals and toad age, and our findings demonstrate that older toads possess larger amounts of defenses. In addition, the average quantity of defenses differed between sexes, with males possessing significantly less dietary alkaloids and bufotenine than females. Most dietary alkaloids in *M. moreirae* have structures with branched-chains, indicating they are derived from oribatid mites. Interestingly, the ratio of bufotenine:alkaloid quantity decreased with increasing quantities of alkaloids, suggesting that *M. moreirae* might regulate bufotenine synthesis in relation to sequestration of dietary alkaloids. Finally, the occurrence of both

sequestered and synthesized defenses appears to be present among other members of *Melanophryniscus*, and therefore our current understanding of the taxonomic distribution of this dual defensive strategy will be discussed as it relates to different species groups.

0060 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Dale Jefferson¹, Maud Ferrari², Alicia Mathis³, Keith Hobson⁴, Eric Britzke³, Adam Crane¹, Douglas Chivers¹

¹Department of Biology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada, ²Department of Biomedical Sciences, WCVN, University of Saskatchewan, Saskatoon, Saskatchewan, Canada, ³Department of Biology, Missouri State University, Springfield, MO, USA, ⁴Environment Canada, Saskatoon, Saskatchewan, Canada

Shifty Salamanders: Transient Trophic Polymorphism and Cannibalism within Natural Populations of Larval Salamanders

Many species of ambystomatid salamanders utilize temporary wetlands for breeding and subsequent larval development. Such habitats are inherently variable and require larvae to exhibit plasticity in foraging, growth and development. In instances where larval densities are relatively high some species may rapidly adapt a distinct head morphology that could facilitate cannibalism. In this study we examined larval long-toed (*Ambystoma macrodactylum*) and ringed salamanders (*A. annulatum*), collected from distinct populations where the cannibalistic morphology had previously been observed. Head morphometrics and stable isotopic values of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) were used to identify the presence or absence of structural cannibalism. Weather conditions for collection sites and years were also analyzed as a potential factor associated with the expression of cannibalistic morphology. Populations of salamander larvae did not consistently exhibit cannibalistic morphologies throughout collection periods. Trophic polymorphisms were observed among larval long-toed salamanders during collection years when precipitation for the collection area was relatively low. Larval ringed salamanders did not exhibit polymorphisms in this study and were cannibalistic. Our results suggest that structural cannibalism could be transient within populations for both species. This morphology appears necessary to facilitate cannibalistic behaviour in long-toed salamanders. Size hierarchy within populations of larval ringed salamanders facilitates cannibalism without morphological adaptations, however, the expression of the cannibalistic morphology may prolong the viable time period in which individuals may consume conspecific prey. Additionally, expression of structural cannibalism may be related to weather conditions that result in increased population densities through reductions in wetland hydroperiod.

**0058 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Dale Jefferson¹, Keith Hobson², Brandon Demuth¹, Maud Ferrari³, Douglas Chivers¹

¹*Department of Biology, University of Saskatchewan, Saskatoon, Saskatchewan, Canada,*
²*Environment Canada, Saskatoon, Saskatchewan, Canada,* ³*Department of Biomedical Sciences, WCVN, University of Saskatchewan, Saskatoon, Saskatchewan, Canada*

Competitive Eaters: Cannibalism as a Response to Perceived Competition Among Larval Wood Frog (*Lithobates sylvaticus*) and the Conditional Benefits of Conspecifics as a Diet

Wood frog tadpoles exhibit considerable adaptive plasticity. When population densities become high tadpoles may become cannibalistic. Conspecific tissues potentially represent an ideal diet by composition and should be beneficial to the growth and development of cannibalistic individuals. To test the relative efficacy of cannibalism to growth and development we conducted multiple feeding experiments. Results indicate that while cannibalism represents a better alternative to starvation and provides some benefit to development and survival of tadpoles over low quality diets. However, cannibalism appears less effective at promoting tadpole growth and/or development relative to diets of similar protein content. This may be the result of differences in risk aversion among individuals. Tadpoles raised individually appear to avoid consuming the cannibalistic diet until they face the risk of starvation. Conversely, when tadpoles perceived the presence of competitors their feeding response to all diets, including a diet of conspecific tissues was hastened. Our results suggest that competition, rather than dietary quality is likely the driving force behind cannibalistic behaviour unless tadpoles otherwise face the risk of starvation.

0492 Chemical Ecology Symposium, Crystal 3 & 4, Sunday 19 July 2015

Christopher Jeffrey, Lora Richards, Lee Dyer

University of Nevada, Reno, Reno, NV, USA

Powerful Chemical Tools for Understanding Organismal Interactions

Recent advances in chemistry have revealed tremendous opportunities for addressing unanswered questions in biology. We apply modern methods of organic spectroscopy, synthesis, and analytical chemistry to address ecological questions at unprecedented taxonomic and geographic scales, and with a high level of molecular resolution. This presentation will highlight new applications of chemical methods toward addressing a variety of important questions in modern chemical ecology research, specifically focusing on the discovery of the sea lamprey migratory pheromone and our work related to untangling the chemical origin of complex plant-insect interactions.

0291 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Matthew Jew, David A. Ebert

Moss Landing Marine Laboratories, Moss Landing, CA, USA

Redescription of the Bigeye Chimaera, *Hydrolagus macrophthalmus*, de Buen, 1959, (Chimaeriformes: Chimaeridae), with Comments on the Family Chimaeridae from the Southeastern Pacific Ocean

Hydrolagus macrophthalmus de Buen, 1959 is a little known chimaeroid species from the Southeastern Pacific Ocean. It was described based on two specimens by Fernando de Buen, and at the time it was the only chimaeroid species, other than *Callorhynchus callorynchus* (Linnaeus, 1758) known from the region. At least four other species are now known to occur in the area therefore making improved identification between species all the more important. *Hydrolagus macrophthalmus* can be distinguished from the other regional species by a combination of uniform height of the elongated second dorsal fin, a long curved first dorsal fin spine that extends past the origin of the second dorsal fin when laid flat and uniform dark brown coloration with no light markings or spots laterally on the body. The species is compared to four other species reported to occur in the Southeastern Pacific Ocean: *H. alphus*, *H. melanophasma*, *H. mccoskeri* and *H. trolli*. Improved identification of Southeastern Pacific Ocean chimaeras will help in developing better management practices and conservation of these little known Chondrichthyans.

0183 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

Tereza Jezkova¹, Jef Jaeger², Viktoria Olah-Hemmings², Bruce Jones³, Rafael Lara-Resendiz⁴, Daniel Mulcahy⁵, Brett Riddle²

¹University of Arizona, Tucson, AZ, USA, ²University of Nevada, Las Vegas, Las Vegas, NV, USA, ³Desert Research Institute, Las Vegas, NV, USA, ⁴University of California, Santa Cruz, Santa Cruz, CA, USA, ⁵Smithsonian Institution, Washington, DC, USA

Range and Niche Shifts in Response to Past Climate Change in the Desert Horned Lizard (*Phrynosoma platyrhinos*)

During climate change, species are often assumed to shift their geographic distributions in order to track climatic niches to which they are adapted. Recent work, however, suggests that niches of species do not always remain conserved during climate change but shift instead, allowing populations to persist in place or expand into new areas. We assessed the extent of range and niche shifts in response to the warming climate after the Last Glacial Maximum (LGM) in the desert horned lizard (*Phrynosoma platyrhinos*). We used mitochondrial DNA sequences to approximate the species range during the LGM by identifying populations that exhibit a genetic signal of population stability versus those that exhibit a signal of a post-LGM geographic expansion. We then compared the

climatic niche that the species occupies today with the niche it occupied during the LGM using two models of simulated LGM climate. The genetic analyses indicated that *P. platyrhinos* persisted within the southern Mojave and Sonoran deserts throughout the latest glacial period and expanded northwards, into the western and eastern Great Basin, after the LGM. The climatic niche comparisons revealed that *P. platyrhinos* expanded its niche after the LGM towards novel, warmer and drier climates that allowed it to persist within the southern deserts. We concluded that climatic changes at the end of the LGM promoted both range and niche shifts in this lizard. The mechanism that allowed the species to shift its niche remains unknown, but phenotypic plasticity likely contributes to the species ability to adjust to climate change.

0340 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Rebecca John, Robert Gitzen

Auburn University, Auburn, AL, USA

Movement Patterns of the Green Salamander (*Aneides aeneus*) in Alabama

The green salamander (*Aneides aeneus*) has suffered localized population and abundance declines over the past several decades resulting in increased conservation concern. The species is associated with rock outcrops buffered by mixed hardwood forest cover at an elevation range of 140-1350 meters throughout the Appalachians. The morphology of the species and the ecology of the genus suggest that the species is highly mobile, however, limited studies have looked at the movement patterns, which are critical for developing effective management plans for habitat and surrounding areas. We used fluorescent tracking powder as a temporary method of tracking salamander movement. This method uses an ultra-violet light to illuminate the path of individual salamanders over a twenty four hour period. Fluorescent powder is safe for amphibians and not known to inhibit movement, alter behavior, or disrupt respiration rates. Daily movement patterns were examined at Redstone Arsenal in Madison County and at Bankhead National Forest in Lawrence, Winston, and Franklin Counties in northern Alabama. Specific objectives were to 1) quantify daily movement patterns of male and female green salamanders, and 2) determine rock crevice refugia fidelity.

**0612 Donn Rosen and the Assumptions Symposium II, Crystal 3 & 4, Sunday
19 July 2015**

David Johnson¹, Peter Konstantinidis²

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

Homology of the Upper Jaw and Suspensorial Elements of the Deep-Sea Telescope Fish, *Gigantura* (Aulopiformes:Giganturidae): Rosen (1973) Revisited

The monogeneric family Giganturidae comprises two extraordinarily specialized bathypelagic species occurring circumtropically between 500 to 2000 m. During a brief transformational period in early ontogeny, giganturids undergo one of the most drastic developmental transformations among fishes. Accordingly, the adults are characterized by numerous, extreme skeletal reductions that obfuscate the identification of some of the remaining elements. The most problematic of these are the paired, tooth bearing elements of the upper jaw. In 1925, C. Tate Regan proposed that they represent the premaxillae or an amalgamation of premaxillae and maxillae. Thirty-six years later Vlad Walters presented a compelling argument that the large, toothed "upper jaw" bone represents the autopalatine rather than the premaxilla/maxilla. Among his four reasons for rejection of Regan's homology assessment was his observation that the maxilla is represented by a small, weakly ossified lamina lying above the posterior end of the gape. In his 1973 seminal paper on higher euteleost interrelationships, Donn Rosen resolutely rejected Walter's seemingly well-reasoned argumentation and agreed with Regan that the large tooth-bearing element represents a fusion of the premaxilla and maxilla. As part of his evidence, Rosen argued that Walters' maxilla is, in fact, an infraorbital element. Remarkably, in our opinion, Rosen's hypothesis has been accepted uncritically by most subsequent authors, including Bob Johnson and Eric Bertelsen, whose monograph thoroughly documented the transformation from the larval "Rosaura" to the adult. We reexamine the evidence presented for previous homology assessments and draw on a previously unconsidered line of evidence - the associated musculature.

0187 Fish Genetics, Carson 3, Saturday 18 July 2015

John Johnson¹, Michelle Johnston², Derek Hogan¹, Alex Fogg³

¹Texas A&M University - Corpus Christi, Corpus Christi, TX, USA, ²Flower Garden Banks National Marine Sanctuary, Galveston, TX, USA, ³University of Southern Mississippi, Ocean Springs, MS, USA

Genetic Composition of Invasive Lionfish Throughout the Atlantic

Lionfish have recently invaded Atlantic waters and rapidly spread through the Caribbean and into the Gulf of Mexico (GOM). Genetic analyses have determined that

there are two species involved (*Pterois volitans*/*P. miles*) and suggest that there are two differentiated populations of *P. volitans*, one in the Atlantic and one in the Caribbean. Observational data suggest that populations in the Florida GOM may have come from the Florida Atlantic population, but little is known of the composition of the GOM invasion. Here we determine the genetic composition of lionfish throughout the Gulf, Caribbean and Atlantic to ascertain; (1) which species have invaded the northern Gulf of Mexico (NGOM) and, (2) to determine the likely route (i.e. Florida/ Atlantic or Caribbean) that lionfish invaded the NGOM. Understanding the genetic composition and patterns of connectivity of lionfish can aid in multi-agency management efforts to control lionfish populations.

0270 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Cristina Jones¹, Audrey Owens¹, Bradley Poynter², Stuart Wells²

¹*Nongame Wildlife Branch, Arizona Game and Fish Department, Phoenix, AZ, USA,*

²*Conservation Center, Phoenix Zoo and Arizona Center for Nature Conservation, Phoenix, AZ, USA*

SWPARC - Ask Me about Turtle Trapping

Freshwater turtles are among the most traded pets, and an increasing number of species are easily available and released by owners into urban ponds. To prevent the spread of nonnative turtles into adjacent natural waterways, we initiated a nonnative turtle trapping in the 1.2 ha pond at the entrance of the Phoenix Zoo in 1999, and have conducted this effort annually since 2007. This event has allowed us to determine turtle population demographics at the pond, and provide outreach on the impact of releasing pet turtles. Turtles were trapped using 35 baited hoop nets (1.5 and 2.5 ft diameter) over 7 trapping periods. We recorded species, gender, mass, and length of all turtles captured. Male turtles were marked with unique identification number. Males are released back into the pond as they are an attraction for Zoo visitors; nonnative females and restricted species go to the Phoenix Herpetological Society where they are adopted into homes or placed with institutions. Through 2014 we have captured 851 individual turtles, and removed 546 nonnative female turtles and restricted turtle species. These represent 17 species, of which 1, the Sonora mud turtle (*Kinosternon sonoriense*), was native. Over 90% of the 851 turtles were pond sliders (*Trachemys scripta*), 235 were recaptures. Through partners and up to 125 volunteers, we provided outreach to up to 6,000 members of the public annually. Data suggests that this project has been successful in reducing the size of the breeding population and in providing outreach to the public.

0524 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Jason L. Jones

Nevada Department of Wildlife, Las Vegas, NV, USA

SWPARC - The Citizen and the Snake

The management of hard to detect species can be inherently complex, due to the paucity of information regarding the life history and ecology of these species. Unfortunately, sampling strategies can be intensive, expensive, and ineffective at estimating species' distribution and habitat use patterns, particularly for hard to detect, non-game, wildlife species (i.e., reptiles, amphibians, small mammals). Snakes, as a taxonomic group, are relatively difficult to sample/detect and are generally underrepresented in species occurrence databases, resulting in a limited understanding of their distribution.

Although snakes are difficult to systematically sample, many species are encountered on roads, making snakes an ideal group for which to collect incidental observation data. Road cruising is a common method for opportunistically finding rare or hard to detect snake species, particularly by citizen scientists. With an increasing number of interested citizens on the road, an increased opportunity exists for vouchering (photo, tissue, whole body) specimens and collecting high resolution occurrence/locality data. Citizen scientists are integral for collecting information on hard to detect species and are increasing our collective understanding of the distribution, habitat use, phylogeography, and status of many snake species. By providing basic training, equipment (i.e., Geneti-kits), and a venue for accessioning specimens into museum collections, citizens can greatly improve our understanding of the life history and general ecology of hard to detect species.

0586 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Jason L. Jones¹, Sarra L. Jones²

¹Nevada Department of Wildlife, Las Vegas, NV, USA, ²Amphibian Reptile Conservancy, Las Vega, NV, USA

A Year in a Desert Hole

In 2011 a camera trap (game camera) was placed in southern Nevada. We hoped to document the occurrence of a specific Gila monster (*Heloderma suspectum*); we ended up capturing a menagerie of species in this seemingly hot and remote desert. This short documentary film highlights a year in a Mojave Desert hole from winter to winter. The story begins in 2011 and ends in 2012, with highlights from two subsequent years at the end of the film.

0590 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kenny Jones¹, Brook Fluker¹, Bernard Kuhajda²

¹Arkansas State University, Jonesboro, AR, USA, ²Tennessee Aquarium Conservation Institute, Chattanooga, TN, USA

Conservation Genetics of the Blueface Darter (*Etheostoma* sp. cf. *zonistium*), a Rare Undescribed Fish in Northwest Alabama

Previous morphological work revealed that select populations of the Bandfin Darter (*Etheostoma zonistium*) in northwest Alabama represent a rare, undescribed fish species; the Blueface Darter (*E. sp. cf. zonistium*). With the description of the Blueface Darter forthcoming, its rarity, extremely small distribution, and fragmented landscape will make it a potential candidate for listing under the Endangered Species Act shortly following its formal description. The Blueface Darter has a peculiar distribution in small tributaries of two distinct drainage basins; the upper reaches of Bear Creek (Tennessee River drainage) and the Sipsey Fork (Black Warrior River drainage). Further, population connectivity of Blueface Darters in tributaries of the upper Bear Creek system is potentially restricted by the Upper Bear Creek Reservoir. This study uses mitochondrial (mt) cytochrome *b* DNA sequence data and microsatellite loci to test multiple hypotheses involving patterns of genetic variation and population fragmentation within the Blueface Darter. Phylogenetic analysis of DNA sequence data recovered a well-supported relationship between Blueface Darters and *E. zonistium* plus other members of the species group. Three mtDNA haplotypes were identified within the Blueface Darter, differing by only one base pair each, suggesting low levels of intraspecific genetic variation. However, patterns of mtDNA variation suggest that individuals in the Sipsey Fork were the result of recent or ongoing inter-drainage transfers from Bear Creek. Microsatellite DNA analyses will be used to further evaluate inter-drainage transfers and reservoir-induced fragmentation, in addition to providing measures of genetic variation that will help to prioritize conservation needs on a population-by-population basis.

0532 ASIH STOYE AWARD GENERAL HERPETOLOGY II, Crystal 1 & 2, Friday 17 July 2015

Leonard Jones, Adam Leaché

University of Washington, Seattle, WA, USA

The Patterns and Processes Underlying the Global Diversification of Viperids

Identifying the ecological, geographic, and morphological traits that are related to species diversification is a central focus in macroevolutionary research. New methods are available for detecting shifts in diversification rates along a phylogeny and for identifying the traits associated with rate shifts. The evolutionary success of the Viperidae (~320 species) has been subject to multiple studies concerning the clade's

taxonomic relationships, biogeographic history, ecology, and morphological diversity. However, statistical inferences aimed at investigating the global diversification pattern of viperids are lacking. Using a phylogeny estimated from publically available genetic data from all viperid genera (179 species), I investigate the global patterns of viperid species richness. I contrast the results from two Bayesian macroevolutionary rate analysis methods that use either character state-dependent or Brownian motion evolutionary models. I also comment on the effects of the phylogeny, data type, sampling scheme, and model selection on diversification rate inference. The results highlight the importance of assessing the legitimacy of detected diversification rate shifts along phylogenies.

0166 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Ryan Jorgensen, Bruce Jayne

University of Cincinnati, Cincinnati, OH, USA

Three-dimensional Trajectories Affect the Axial Muscle Activity of Arboreal Snakes Bridging Gaps

In arboreal habitats many animals must traverse gaps between branches with different three-dimensional trajectories that alter the mechanical demands, especially for elongate animals such as snakes. However, no previous study has determined how snakes use their muscles when crossing gaps. From dorsal to ventral, the three largest epaxial muscles of snakes involved in vertebral flexion are: the semispinalis-spinalis (SP), longissimus dorsi (LD), and iliocostalis (IL). We used electromyography and motion analysis to test the effects of different three-dimensional trajectories on the activity of these three muscles in brown tree snakes (*Boiga irregularis*) crossing gaps that were straight up, straight down, horizontal and straight, and horizontal with a right angle turn. Extensive bilateral activity occurred in the SP segments as they crossed the edge of the starting perch, but SP activity ceased after the head of the snake touched the edge of the destination perch. For the trajectories without a sideways turn, the activity of the SP muscle was greatest for the horizontal, intermediate for the upward, and least for the downward trajectories. While turning sideways, muscles on the convex side had little or no activity compared to the concave side. Unlike any known mode of terrestrial locomotion, extensive bilateral activity of the IL occurred, and the IL was active when the SP and LD were inactive. Hence, not only did the orientation relative to gravity while crossing gaps affect muscle activity, these complex three-dimensional movements involved several previously undescribed variations in motor pattern.

0385 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kathlene Joyce, Jacqueline Chivers

Auburn University, Auburn, AL, USA

Phylogeography of Slimy Salamanders in Alabama

The genus *Plethodon* is one of the largest clades of salamanders in North America and includes the slimy salamander complex, a widespread lineage of large, black, woodland salamanders. In Alabama, three members of the glutinosus complex converge, with *Plethodon mississippi* occupying the western quarter of the state, *Plethodon grobmani* occupying the lower third, and *Plethodon glutinosus* occupying the rest of the state. However, no morphological or color feature distinguishes the three putative species from each other and geographic limits of each lineage toward the center of the state are unknown. In this study we examined the phylogeography of the glutinosus complex in the state of Alabama. We sequenced a nuclear gene (RPL12) found in a paper written by Fisher-Reid and Weins (2011) for 20 specimens collected throughout the state. To these data we added 5 specimens available on genbank assigned to the three lineages found in Alabama. We used Sanger sequencing and then aligned these data using MEGA v6 software. A maximum likelihood tree was then generated from these data. This tree failed to recover three distinct lineages within Alabama. Instead, our analysis suggests gene flow within a single, widespread species. This interpretation is supported by additional analysis of the mitochondrial genome.

0019 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Ingrid Kaatz¹, Donald Stewart¹, Phillip Lobel²

¹*SUNY-ESF College of Environmental Science and Forestry, Syracuse, NY, USA,*

²*Boston University, Boston, MA, USA*

Stridulation Morphology of Callichthyid Catfishes: Vocal Ridge Variation Across Species Within the Corydoradinae

Callichthyid catfishes produce sounds by pectoral spine stridulation in agonism and reproduction. Vocal ridge shape can be acute and rounded within individuals for the subfamily Corydoradinae and is similar across species. Dorsal process ridge width and inter-ridge distance is similar across species. To determine whether species' mechanisms are convergent or have diverged we counted dorsal process ridge number for adult specimens (17 species, four genera) using scanning electron and dissecting microscopes. *Scleromystax* ridges ranged 34 to 45 (39 + 4 SD, n = 6 individuals). *Aspidoras* ridges ranged 19 to 44 (36 + 9, n = 6). *Brochis* ridges ranged 59 to 81 (68 + 8, n = 6). *Corydoras* pooled species ridges ranged 38 to 76 (55 + 9, n = 70). Ridge number correlated with body size (SL) for *Corydoras* species pooled ($r^2 = 0.2293$, $p < 0.00002$). Total ridges per species for 14 *Corydoras* species (n = 4 to 9 individuals/species) positively correlated with body size (SL) for three species ($r^2 = 0.6834$ to 0.9772 , $p < 0.04$ to 0.001). Specimen

standard length was similar (4.0 cm + 0.8 SD, 2.3 - 7.5 cm, n = 89). The presence of vocal ridges in all specimens suggests that both sexes could vocalize. Correlation of ridge number with body size for some species and the similarity in adult size for many species in the Corydoradinae suggests that if species differ in vocal communication signals this would have to be accomplished by variation in vocal muscles, their origins or insertions and neural control.

0149 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Dovi Kacev¹, Shannon Corrigan³, Rebecca Lewison¹, John Hyde²

¹San Diego State University, San Diego, CA, USA, ²Southwest Fisheries Science Center, La Jolla, CA, USA, ³College of Charleston, Hollings Marine Lab, Charleston, SC, USA

Identifying Multiple Paternity in Two Species of Pelagic Shark

Polyandry is common throughout kingdom *Animalia*. There are several evolutionary explanations for the rise of this reproductive strategy including increasing genetic diversity, allowing for sperm competition as a proxy for male fitness, or high cost to females of mating avoidance. Several recent studies have found that multiple paternity is common among coastal and benthic shark species but to date, pelagic shark litters remain unstudied. Due to lower expected rates of conspecific interaction and higher opportunity costs, pelagic sharks may be less likely to have multiple matings than their coastal counterparts. In this study we opportunistically sampled single litters from shortfin mako (*Isurus oxyrinchus*) and common thresher (*Alopius vulpinus*) sharks (eight and four pups respectively). We used microsatellite markers to test for the possibility of multiple paternity in these species and discuss the possible implications. In the litters for both species, multiple paternity was detected. The mako litter was found to have at least two but more likely three sires, while the thresher litter has most likely two sires.

0167 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Stephen Kajiura, Shari Tellman

Florida Atlantic University, Boca Raton, FL, USA

Seasonal Shark Abundance in South Florida

Southeast Florida experiences an enormous seasonal influx of upper trophic level marine predators each year as blacktip sharks (*Carcharhinus limbatus*) form massive aggregations in nearshore waters. The narrow shelf and close proximity of the Gulf Stream Current to the Palm Beach County (PBC) shoreline constrain tens of thousands of sharks to the shallow, coastal environment. This natural bottleneck provides a unique opportunity to estimate abundance. Over a four year period, a biweekly aerial survey

was flown along the length of PBC and the number of sharks within 200m of shore was directly counted. Shark abundance peaked in the winter (January-March) at over 12,000 individuals, and declined to nearly zero in the summer months. This corresponds to a maximum density of over 800 sharks km⁻². Because these numbers represent only the sharks immediately adjacent to the shoreline, they are a gross underestimate of the total number of sharks present. Shark abundance was inversely correlated with water temperature with sharks found in large numbers only when water temperatures were less than 25°C. These baseline abundance data can be compared to future studies to determine if shark population size is changing and if sharks are restricting their southward migration as global water temperatures increase.

0368 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Larry Kamees, Steven Beaupre, Jason Ortega, Craig Lind, Jill Guillette

University of Arkansas, Fayetteville, AR, USA

Validation of the Use of Leukocyte Profiles for Determining Stress in the Prairie Rattlesnake (*Crotalus viridis*)

Stress undermines routine physiological and behavioral mechanisms in all organisms and is commonly assayed by measuring corticosterone levels in plasma. Stress-related research would benefit from additional techniques, less costly in time and money. An alternative approach to assessing stress involves evaluating leukocyte profiles in blood smears. Although the use of leukocyte profiles is well established in mammals and birds, studies involving reptiles are not well represented in the literature. In general, a stressor induces a redistribution of leukocytes, particularly heterophils and lymphocytes (H/L). In comparison to measuring increases in plasma corticosterone due to stress, leukocyte redistribution occurs over hours instead of minutes, potentially diminishing the confounding effects of handling stress and providing a more accurate indication of stress. Thus, the H/L ratio may be a useful indicator of acute and long-term environmental stress. We hypothesized an increase in the H/L ratio would occur in response to increased corticosterone. We used laboratory animals (*C. viridis*) to validate the use of leukocyte profiles in assessing stress. Snakes (N=20) were randomly assigned to one of two groups, treatment or control. Snakes in the treatment group had their corticosterone levels manipulated via dermal exposure of corticosterone dissolved in sesame oil and the control group was treated with sesame oil. Plasma corticosterone concentrations and leukocyte counts were compared prior to and 24 hours after being dosed to determine if they are correlated. Detecting a stress response using a rapid and inexpensive technique could provide useful information to resource managers when planning and implementing management strategies.

0396 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Nicole Karres, Nicholas Geist

Sonoma State University, Rohnert Park, CA, USA

The Carnivorous Feeding Behavior of Western Pond Turtles (*Emys marmorata*) in Urban Waterways

I learned that Western Pond Turtles (*Emys marmorata*) living in 2 urban creeks are carnivores. I did this by using radio telemetry and visual sightings to track turtles while they foraged to observe them eating. After observing the turtles eat, I captured them, and collected their stomach contents for examination. I tracked and captured turtles over a 3-year period collecting observation information and 54 stomach content samples. My results show that *E. marmorata* are unable to separate prey from the nearby habitat. Therefore, they often incidentally ingest abiotic and biotic material nearby their prey. For example, I observed *E. marmorata* eat crayfish on the stream bank and in filamentous algae. Afterwards, I found the prey along with the stream substrate material or algae in the contents of the turtle's stomach. Further, I found that if I waited a few days and then collected stomach content samples, the soft-tissue was absent. However, the less easily digested body parts along with abiotic material, vegetation, or filamentous algae were still present in the samples.

0316 ASIH STOYE AWARD GENERAL HERPETOLOGY II, Crystal 1 & 2, Friday 17 July 2015

Nicole Karres¹, Andrea Goodnight², Nicholas Geist¹

¹*Sonoma State University, Rohnert Park, CA, USA*, ²*Oakland Zoo, Oakland, CA, USA*

The Gastric Lavage Method, a Safe and Effective Way to Collect Stomach Contents from Freshwater Turtles in the Field

The Gastric Lavage Method (GLM) I developed to collect stomach content samples in the field has a number of features. First, GLM uses "veterinary best practices" and chemical restraint. This makes collecting stomach contents a comfortable experience for the researcher and the turtles. Furthermore, GLM meets the current Institutional Animal Care and Use Committee standards for the treatment of research animals. Specifically, GLM uses drugs that induce full anesthesia, thereby making it easy to completely evacuate all of the contents from the turtle's stomach. Afterwards, the effects of the drugs are easy to reverse. As a result, turtles that undergo GLM are back in the water feeding 6-hours later. I used GLM 87 times on 2 species of turtles over a 4-year period without injuring any of them.

0246 General Herpetology, Carson 1, Friday 17 July 2015

Kristopher Karsten

California Lutheran University, Thousand Oaks, CA, USA

Sexual Dimorphism in Morphology, Signaling, and Performance in Two Species of *Sceloporus* Lizards

Sceloporus lizards are often dimorphic in size and signals (blue ventral and throat patches). Most commonly, males are larger in body and signal size. In southeast Arizona, two sympatric species deviate from this typical pattern in contrasting ways. Both sexes in *S. jarrovi* have large body size and extensive signals whereas both sexes of *S. virgatus* have smaller body size, no ventral signals, and minimal throat patches. My aims were to explore dimorphism in body and signal size in both species and determine if these signals correlated with a potentially sexually-selected trait, bite force. *S. jarrovi* were not dimorphic in body size or ventral patch size but were in throat patch size and bite force (males > females in both). I found no relationship between the sizes of either signal and bite force in males. In contrast *S. virgatus* were dimorphic in body size (females > males) but not in signal size. There was no dimorphism in size-corrected bite force. However, there was a surprising negative correlation between signal and bite force in males. My findings indicate that the relationship between signals and performance in these 'atypical' *Sceloporus* species is complex.

**0543 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Thursday 16 July 2015**

Jade Keehn, Chris Feldman

University of Nevada, Reno, Reno, NV, USA

Demography and Predation Ecology of Lizards at Wind Energy Farms

Wind energy is a vital part of our nation's goal to increase the sustainability of our society. However, wind farms may affect local ecology as organisms respond to novel and potentially unsuitable habitat conditions. This research addressed whether turbines affect demography and predation ecology in a lizard system (*Uta stansburiana*). To test whether survival declines in populations near turbines relative to control populations, we estimated survival rates of marked lizards using robust-design models. To test the hypothesis that energy-disturbed sites have increased predator activity, we estimated predator abundances, compared attack rates on clay lizard models, and measured wariness behavior (approach distance, or, observer distance at time of lizard retreat). Survival models did not support a difference in mortality rates between turbine and control sites. On average, control sites had greater densities of *U. stansburiana*, mammalian carnivores, large invertebrates, avian lizard specialists, hawks, and songbirds. Turbine sites had more snakes, lizards (competitors and predators of *U. stansburiana*), and scavengers. Clay models were most-frequently attacked by birds, and

bird, mammal, and lizard attack rates were higher at control sites. Approach distance did not differ between control and turbine sites; however, lizards were more wary with reduced plant cover and increased lizard density. In all, these results suggest that natural variation in site quality influences organisms more than disturbance from human activities. While wind energy has been shown to negatively affect reptiles with slow life-history strategies, it does not appear to reduce survival or increase abundance of predators of these r-selected lizards.

**0437 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Matthew G. Keevil¹, Brittainy Hewitt¹, Ronald J. Brooks², Jacqueline D. Litzgus¹

¹Laurentian University, Sudbury, Ontario, Canada, ²University of Guelph, Guelph, Ontario, Canada

You Should See the Other Guy: Sex and Body Size Effects on Injuries from Intraspecific Aggression in Snapping Turtles

Turtles exhibit a large range of sexual size dimorphism (SSD) and the roles of body size and aggression in chelonian mating systems has long been a subject of interest focusing on the role of coercion, female choice, and male-male competition. Patterns of SSD in turtles are correlated with ecological mode (terrestrial, semi-terrestrial, aquatic, bottom-walking) and it has been hypothesized that mating systems are also shaped by ecological mode. Male combat and coercive mating are competing explanations for male-biased SSD but are difficult to assess empirically in aquatic, bottom-walking species with cryptic behaviour. We compiled observations of presence/absence of putative combat wounds collected from over 500 captures and recaptures of Snapping Turtles (*Chelydra serpentina*) in Algonquin Provincial Park, Ontario, to test hypotheses of mate competition and coercion. We found that both sex and body size were important predictors of risk of wounding, consistent with the hypothesis that male-male sexual competition is the primary driver of intraspecific aggression. Low wounding rates among females suggests that resource competition and coercive mating are not important causes of aggression. Preferred models indicated that the risk of wounding increased monotonically with body size in males but not in females. Small males were less likely to be injured, suggesting that they employ a risk-averse strategy by avoiding direct mate competition. There was no evidence of asymptotic or decreasing wounding probability in the largest males, which is consistent with the hypothesis that large males compete most intensively to monopolize mates.

0393 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Bryan Keller¹, Jean-Sebastien Finger², Tristan Guttridge², Samuel Gruber²

¹Coastal Carolina University, Conway, SC, USA, ²Bimini Biological Field Station, Bimini, Bahamas, Bahamas

Energetic Savings During Group Participation and the Influence of Swimming Speed on Partner Preference in the Juvenile Lemon Shark, *Negaprion brevirostris*

Grouping in sharks is well-known, however, there are few quantitative analyses on the mechanisms that drive their formation. In this study we use controlled semi-captive behavioral experiments to assess the potential role that swimming speed and energetic efficiency plays in the group formation and social behavior of a large marine vertebrate. Juvenile lemon sharks, *Negaprion brevirostris*, in Bimini, Bahamas were captured, measured, tagged with external color codes for individual recognition, and housed in pens that exposed them to ambient conditions. Sharks were introduced into a social network pen while an overhead video system recorded behaviors for one hour. Tracking software transformed their movement patterns into a coordinate system. Multiple algorithms were used to analyze these coordinates, and a matrix of interactions was produced demonstrating when sharks were following or paralleling other individuals. When individuals were engaged in a following behavior, swimming speed was calculated for both animals while ensuring the distance between the two was constant. Similarly, an investigation was conducted to determine if interacting sharks select each other based upon swimming speed. Preliminary results suggest that juvenile lemon sharks show an active partner preference for animals with a similar swimming speed and that energy is conserved while closely following a conspecific. This research advances our understanding of the mechanisms driving group formation in lemon sharks, a model species for large marine predators.

0597 Fish Systematics II, Carson 3, Sunday 19 July 2015

Christopher Kenaley¹, William Ludt², Prosanta Chakrabarty², Alexandra Stote³

¹Boston College, Chestnut Hill, MA, USA, ²Louisiana State University, Baton Rouge, LA, USA, ³Harvard University, Cambridge, MA, USA

Phylogenetic and Morphometric Analysis of Hitchhiking: New Insights into the Morphological Evolution of Suction Discs in the Remoras (Percomorpha: Carangiformes: Echeneidae)

The percomorph family Echeneidae consists of eight species of marine fishes that hitchhike by adhering to a host via a dorsal sucking disc. Osteological components of this unique suction device are composed of serially arranged, hierarchically organized substructures. While recent studies have focused on the evolution and development of the modified dorsal-fin osteology that forms the specialized disc, very little work has

focused on the morphological basis of adhesion. In this study, we combine a new phylogenetic hypothesis for the family based upon analysis of ultraconserved elements with a detailed morphometric dataset based upon micro-CT analysis of all eight species of remora. The goal of this study was to identify axes of disc morphospace that vary among all remora species and to evaluate key morphological innovations that may be implicated in hitchhiking success. Through a comparative methods approach, correcting for phylogeny, we reveal that only a very few of the more than two dozen disc design variables evaluated contribute to significant morphological change in the group. These key morphological variables are discussed in terms of their ability to affect adhesion performance and hitchhiking behavior within the family.

0587 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Christopher Kenaley¹, Mikhaila Marecki², George Lauder²

¹*Boston College, Chestnut Hill, MA, USA*, ²*Harvard University, Cambridge, MA, USA*

Muscle-unit Force and Power Input of Lower-jaw Adduction: New Insights from Biorobotic and Computational Modeling in Deep-sea Fishes

The functional design of actinopterygian cranial musculoskeletal systems and its contribution to aquatic prey capture has been the subject of study for nearly two centuries. Even today, the complex kinematic basis and physiological determinants of fish feeding behavior remains an active and productive area of comparative research. Most fishes rely on inertial suction to overtake a prey item, a behavior reliant upon the rapid expansion of the oral cavity. While buccal expansion has been described as organizationally complex, models of buccal compression remain relatively simple. In particular, the musculoskeletal elements associated with jaw adduction in most fishes adheres to a third-order lever model. Accordingly, adductor muscles actuate jaw closing by applying force to an in-lever some distance from the jaw joint. In this study, we considered to what degree the organizational complexity of the adductor muscle system has in jaw closing performance. Through biorobotic and computational biomechanical modeling of jaw-adduction systems in dragonfishes (family Stomiidae), we reveal that the architectural design of adductor muscle-tendon units imparts an ability to dynamically alter the mechanical advantage of major inputs to the lower-jaw lever system. Specifically, we show that a division of adductor muscle system – the $A\omega$ – may play a role in applying adduction torques to more distal positions along the lower jaw, thus increasing mechanical advantage. The role of dynamic mechanical advantage brought on by this design is discussed in terms of behavioral responses to feeding requirements and the performance tradeoffs dictated by different prey types.

0205 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Steven Kessel¹, Alexander Hansell⁴, Samuel Gruber¹, Tristan Guttridge¹, Nigel Hussey², Rupert Perkins³

¹Bimini Biological Field Station Foundation, Bimini, Bahamas, ²University of Windsor, Windsor, Canada, ³Cardiff University, Cardiff, UK, ⁴University of Massachusetts, Fairhaven, MA, USA

Lemon Shark (*Negaprion brevirostris*) Catch Per Unit Effort (CPUE) Trends, Bimini, Bahamas, Derived from a Fishery Independent, 32-year Shallow Water Longline Survey

Long-term population assessments are necessary to determine species specific trends and inform management decisions. The waters surrounding the Bimini Islands, Bahamas, are rich in elasmobranch fauna. This study assessed three shallow water longline research campaigns at this location, 1982 - 1992, 1993 - 2003 and 2004 - 2014, with the aim to determine annual catch per unit effort (CPUE) trends for an IUCN listed near threatened species, the lemon shark (*Negaprion brevirostris*). A general additive model (GAM) was used to analyse the non-linear annual CPUE values over the entire 32 year research period. The GAM displayed high variability of annual CPUE, with a peak value of 0.026 in 2000. The 1982-1992 campaign saw highest portion of mature individuals (19.8%) and the smallest average pre-caudal length [PCL] (198 cm). The 1993 - 2003 campaign had the highest average annual CPUE (0.018) and percentage of total capture (32.3%). The 2004 - 2014 research period saw largest average PCL size (134.8 cm) and the lowest average CPUE values (0.009) of the entire research period. Long-term trends of this study highlight annual variability, and provide a baseline for future assessment of the Bahamas shark sanctuary relative to lemon shark abundance.

0573 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Ethan J. Kessler¹, Matthew C. Allender², Michael J. Dreslik¹

¹Illinois Natural History Survey, Champaign, IL, USA, ²University of Illinois at Urbana-Champaign, Champaign, IL, USA

Assessing Health Through Hematology in Head-started Alligator Snapping Turtles (*Macrochelys temminckii*)

Anthropogenic habitat loss and fragmentation have made translocation programs a necessary component of conservation plans for many species. Because young turtles have high mortality rates, many programs use head-starting to alleviate size-specific mortality. Assessing post-release survival is a common component of successful translocation programs however, hematological assessments are absent from the majority of chelonian programs. The Alligator Snapping Turtle (AST; *Macrochelys temminckii*) is state-endangered in Illinois with the last known free-ranging individual observed in 1984. A multi-institutional translocation program was undertaken to recover

the species in 2014 after a successful pilot release. Sixty-two head-started AST of mass 104-7300g and originating from Peoria Zoo (PZ) and Tishomingo National Fish Hatchery (TNFH) were fitted with radio-transmitters and released in July 2014 in a single riverine system. Individuals were recaptured in October 2014. Complete blood counts were performed upon release and recapture. TNFH turtles had increased WBC counts (WBC mean: 12,383.81; 95% CI: 11,293.99-13,473.62) with significantly higher heterophils, lymphocytes monocytes, and basophils, than PZ turtles (WBC mean: 3,967.51; 95% CI: 3,386.60-4,548.43). Turtles with higher mass displayed significantly lower PCV and TS values. Additionally, individual WBC counts decreased between samples (mean Δ WBC: -3,135.85), and heterophils, lymphocytes, monocytes, basophils, PCV, and TS were significantly lower within individuals between samples. Head-started AST of varying mass and origin have different initial health profiles and while individual hematology changes through time these changes are independent of mass and origin. Continued monitoring may elucidate changes in survival, behavior, or pathogen susceptibility that will aid this and future conservation plans.

0194 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Jin-Koo Kim, Soo-Jeong Lee

Pukyong National University, Busan, Republic of Korea

Evidence of Restricted Gene Flow Between Two Lineages of the Sand Lance, *Ammodytes personatus* (PISCES, Ammodytidae) Based on Larval Distributions in the Yellow and the East Seas, and Taxonomic Implications

To clarify the extent of the gene flow between two lineages of the sand lance, *Ammodytes personatus*, a larval survey was conducted at the Yellow Sea (YS), the Korean Strait (KS), and the East Sea (ES). In total, 8687.5 individuals/100 m³ of the sand lance larvae were collected in the YS and ES, but not in the KS. The larval individuals were the highest in the middle ES, followed by the middle YS. We identified the lineage status of 191 larval individuals using molecular methods. As a result, only south lineage (SOL) occurred in the YS, whereas SOL and the north lineage (NOL) occurred together in the ES. The average larval occurrence ratio for NOL and SOL was 2.6:1 in the ES, but that of NOL was much higher than that of SOL (4.5:1) in the middle ES, but the two lineages occurred at similar levels (1.5:1) in the southern ES. These results indicate that there is no gene flow between the two lineages in the YS, and restricted gene flow in the ES. We also identified a distinctive difference in the melanophore behind the isthmus between the two lineages in the ES (developed in NOL but absent or rudimentary in SOL). Therefore, our study suggests the potential of the two biogeographic barriers between the two lineages 1) at the thermocline and/or halocline between southern ES and KS, and 2) at the thermal front between middle and southern ES. We discuss the taxonomic status of the two lineages.

0193 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Jin-Koo Kim, Soo-Jeong Lee, Young-Sun Song, Se-Hun Myoung, Hyo-Jae Yu, Woo-Jun Lee, Sang-Yun Han, Seo-Ha Jang, Soo-Eun Ye, Ui-Cheol Shin

Pukyong National University, Busan, Republic of Korea

Introduction of Marine Fish Resources Bank of Korea (MFRBK)

Convention on Biological Diversity was adopted through international consensus for Biodiversity conservation, sustainable use and benefit-sharing of bio-resources in 1992. Thereafter, Nagoya Protocol for access to genetic resources and benefit-sharing was selected in 2010. Based on this, it needs to establish and operate the Bio-Resources Bank in order to effective exploitation of marine organisms in Korea. In this necessity, a total of 14 Marine Bio-Resources Bank were built under the direction of the Ministry of Maritime Affairs and Fisheries of Korea until 2014. Among them, Marine Fish Resources Bank of Korea (MFRBK) was established in Pukyong National University on December 2013, and is working on collection, deposition, registration, preservation and supply of diverse marine fish in Korea. Until today, we collected a total of 317 fish species and 4,106 collections, comprising 24 species of big sized fish (mainly sharks; 76 collections), 42 species of valuable candidate fish (mainly puffers; 716 collections), 15 species of deep sea fish (mainly zoarcoids; 232 collections), 106 species of subtropical fish (mainly damselfishes; 1104 collections), 42 species of regional fish (mainly broadly distributed fish; 728 collections), and 142 species of unexploited fish (mainly larvae or non-commercial fish; 1250 collections). The MFRBK is serviced at the web site: <http://myweb.pknu.ac.kr/org/user/pisces/>.

0351 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

David Kizirian¹, Maureen Donnelly²

¹*American Museum of Natural History, New York, NY, USA*, ²*Florida International University, Miami, FL, USA*

The Network Species Model

We argue that research in systematics and evolutionary biology would be strengthened if the model for species aligned with the models used in other scientific disciplines (e.g., physics, chemistry, other branches of biology) in their focus on the inherent **organization** of systems and the **processes** unique to those systems. The model proposed here, *species are any network of organisms integrated by reproductive mechanisms*, is focused on inherent organization of the system (i.e., network of organisms) and the processes unique to such systems (e.g., gametogenesis and syngamy). To further allineate with other disciplines, the new model excludes reproductive isolation, divergence, and other criteria incorporated in competing species

models. Fate is not an intrinsic property of systems; therefore, it is an inappropriate criterion in species models.

0020 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Peter Klimley¹, David Acuna², Randall Arauz³, Sandra Bessudo⁴, Eduardo Espinosa⁵, Hector Guzman⁶, Alex Hearn⁷, Mauricio Hoyos⁸, James Ketchum⁸, Cesar Penaherrera⁹, George Shillinger¹⁰, German Soler⁴

¹University of California, Davis, CA, USA, ²Charles Darwin Foundation, Puerto Ayora, Santa Cruz Island Galapagos, Ecuador, ³Programa Restauracion Tortugas Marinas, San Jose, Costa Rica, ⁴Fundacion Malpelo, Bogota, Colombia, ⁵Parque Nacional Galapagos, Puerto Ayora, Santa Cruz Island, Ecuador, ⁶Smithsonian Tropical Research Institute, Panama City, Panama, ⁷Turtle Island Restoration Network, Forest Knolls, CA, USA, ⁸Pelagios Kakunja, La Paz, Baja California Sur, Mexico, ⁹University of Tasmania, Hobart, Tasmania, Australia, ¹⁰Hopkins Marine Station, Stanford University, Pacific Grove, CA, USA

The Role of Geology and the Design of Marine Reserves for Sharks in the Eastern Pacific

Nine species of sharks are commonly present at "hot spots", at seamounts and islands in the Eastern Pacific. The movements of these species have been described at the Espiritu Santo Seamount and Revillagigedos, Cocos, Coiba, Malpelo, and Galapagos Islands by (1) shipboard tracking, (2) satellite tracking, and (3) coded beacon detection by autonomous receivers. The whitetip reef, silvertip, blacktip, and tiger sharks are seasonally insular, staying most of the time close to shore. The Galapagos, scalloped hammerhead, silky, and small-tooth sandtiger sharks are seasonally insular-pelagic, making daytime or nighttime foraging migrations into the pelagic environment. The whale shark is truly pelagic, moving widely throughout the ocean while only briefly visiting these hot spots. These sites are of volcanic origin, being formed by the extrusion of basalt containing single-domain particles of magnetite from the earth's lithosphere that align to the polarity of the earth's field as the basalt cools after eruptions. The polarity of the earth's main field rotates periodically over geological time so the lava flows contain magnetite aligned parallel and anti-parallel to the current earth's field forming maxima ("ridges") and minima ("valleys") in the earth's field to which sharks may orient using magnetic "topotaxis". It is suggested that these magnetic features limit extent of the feeding excursions of these species, and knowledge of their extent can be used to specify zones of enforcement of fishing prohibitions at these sites so that they can continue to generate revenue as "shark parks".

0463 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Matthew Kolmann, Nathan Lovejoy

University of Toronto Scarborough, Toronto, Ontario, Canada

Feeding Kinematics of the Ocellate River Ray, *Potamotrygon motoro*

Marine to freshwater incursions are comparably rare events, although several fish lineages have bridged the ecological and physiological boundaries inherent to these transitions. The South American river rays, Potamotrygonidae, invaded freshwater at least 14 mya and have subsequently diversified into nearly 30+ species. From a generalist invertivore ancestor, several instances of piscivory, mulloscivory, and insectivory have arisen independently in this clade of stingrays. For dietary generalists like *Potamotrygon motoro*, considerable behavioral modulation is assumed to be necessary to consume such a wide swath of prey taxa and prey materials. Here we present data on prey-handling in *P. motoro* filmed on bare-bottom enclosures using high-speed videography. We report the degree of asymmetrical jaw protrusion, relevant for processing large or tough prey as well as the general behavioral routines involving prey capture, prey processing, and overall handling time. We find that these rays utilize an initial "pounce" to apprehend prey, followed by repeated jaw protrusion and retraction, during which indigestible prey material is ejected from the spiracles. Prey-handling times increase for larger prey items as well as the degree to which jaw asymmetrical protrusion is observed. Based on prior myological studies, we hypothesize then that the coracohyomandibularis and levator hyomandibularis aid in hyoid depression and retraction (respectively), and when coupled with the coracomandibularis, protrude the jaws. These muscles in particular may be relevant to further study of functional feeding trait evolution in the Potamotrygonidae.

0389 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Peter Konstantinidis, Eric J. Hilton, Sarah K. Huber, Deborah K. Steinberg

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

**Antarctic Ichthyoplankton in the Virginia Institute of Marine Science
Nunnally Ichthyology Collection**

Investigation of larval fishes is important in taxonomy, systematics, morphology, fisheries science, and oceanography. Large and well-maintained ichthyoplankton collections, however, remain rare among museum collections, due in part to lack of training in ichthyoplankton identification, which often results in the neglect of those collections that are made. The VIMS Nunnally Ichthyology Collection contains a large uncatalogued collection of ichthyoplankton, which is currently the subject of a renovation and cataloging effort. Within this collection are an estimated 11,000 vials derived from the Palmer Antarctica Long-Term Ecological Research study, which has conducted annual plankton sampling during the austral summer since 1990. The sample area is along the Western Antarctic Peninsula from Anvers Island south to Charcot

Island, and covers coastal waters to approximately 200km offshore. This region is currently experiencing one of the fastest rates of warming on Earth, resulting in declines in sea ice extent and duration, and affecting the marine food web. We are in the process of sorting and identifying the ichthyoplankton from this program to make the specimens accessible for scientific study. Here we present a selection of larvae of nototheniids, channichthyids, artedidraconids, bathydraconids, microstomatids, paralepidids, myctophids, and muraenolepidids and discuss the potential of this ichthyoplankton collection for updating and augmenting larval fish identification keys, range expansion of taxa, studies of larval ecology and community structure, and as a character source for phylogenetic systematics.

**0232 ASIH STOYE AWARD PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY,
Carson 3, Friday 17 July 2015**

Kristin Kopperud, Michael Grace

Florida Institute of Technology, Melbourne, FL, USA

Circadian Rhythms of Retinal Sensitivity in the Atlantic Tarpon, *Megalops atlanticus*

Light is a critically important environmental variable in the lives of marine organisms. It affects physiology and behavior acutely, and can also have long-term effects on immune function, daily biological rhythms, seasonal reproduction and longevity. In unpolluted natural environments, the daily light-dark cycle is a reliable cue, but with today's rapid coastal development, light pollution is an increasingly serious threat to living things. This study aims to understand the effects of light at night in coastal marine ecosystems using an ecologically and economically important marine fish, the Atlantic tarpon (*Megalops atlanticus*), as a model. Electroretinography (ERG), an *in vivo* measure of retinal function, was used to quantify overall retinal sensitivity ($\mu\text{V}/\mu\text{W s}^{-1}\text{cm}^{-2}$) during light and dark hours. In tarpon subjected to a "natural" 12-hr light, 12-hr dark photocycle (LD) prior to testing, sensitivity was higher at night than in day. To investigate biological clock function, tarpon were held in constant darkness (DD) following synchronization to a light/dark cycle, and sensitivity was likewise higher in "subjective" night, though rhythms were damped. This continuance of rhythms in constant conditions (i.e. *without* the environmental stimulus) is a hallmark of biological clock operation. While extensive research has been conducted on circadian function in humans, rodents and migratory birds, comparable studies on marine fish are virtually non-existent. These fish are outstanding models for future studies on exposure to light at inappropriate times in order to link what we already know about retinal change with the reasons why change is important in the natural world.

0443 Fish Genetics, Carson 3, Saturday 18 July 2015

Trevor Krabbenhoft¹, Gerald Smith², Thomas Dowling¹

¹Wayne State University, Detroit, MI, USA, ²University of Michigan, Ann Arbor, MI, USA

Genome Evolution Following Whole Genome Duplication: Insight from Suckers (Catostomidae)

Whole genome duplications (WGD) are often assumed to be important evolutionary events because they provide raw material for adaptation. We assess patterns of gene silencing following WGD in suckers (Catostomidae). The Catostomidae originated as the result of WGD event 50-60 million years ago, making all members of the family tetraploid. Since then, sucker species have become partially diploidized through gene silencing, as evidenced by allozyme data. We sequenced the transcriptomes of six catostomins to assess genome-wide gene silencing and retention of duplicated genes in this clade for different groups of genes. For allozyme loci, we will test whether genes silenced at the protein level are also silent at the mRNA transcript level (i.e., pseudogenes) or whether they are transcribed but not detectable with allozyme methods (i.e., either neo-functionalization or post-transcriptional silencing). In addition, we will use gene ontology analysis to test the null hypothesis that duplicated genes are silenced at random with respect to function (e.g., adaptive immune response, glycolysis, etc.). Understanding patterns of gene silencing following WGD is key to determining whether WGD facilitates evolutionary diversification as some researchers have suggested.

0559 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Chelsea Kross, John Willson

University of Arkansas, Fayetteville, AR, USA

Post-breeding Movements and Habitat Use of Crawfish Frogs (*Lithobates areolatus*) in a Fragmented Landscape

Prairies and their associated wetlands have become one of the most endangered ecosystems due to land-use change. The loss of prairies and prairie wetlands has had a negative effect on a wide array of wildlife and several species that are considered prairie specialists (e.g. Crawfish Frog [*Lithobates areolatus*]). Many prairie species have experienced range-wide declines or local extirpations. However, there is little information on how prairie amphibians use wetland and upland habitats and the degree of connectivity necessary to maintain viable populations and metapopulations. Our objectives were to (1) determine the extent of upland habitat used by *L. areolatus* in a highly fragmented landscape and (2) locate hotspots of habitat use and microhabitat features preferred during the non-breeding season. We used radiotelemetry to monitor post-breeding (March - June) movement of adult *L. areolatus* breeding in a small section of restored wet prairie located within a matrix of degraded prairie, agriculture, and

urban land cover in Fayetteville, Arkansas. We recorded *L. areolatus* locations and microhabitat characteristics (e.g. vegetation, crayfish burrow use) to examine movement ecology and landscape-scale habitat use. Our research contributes to our understanding of ecology and habitat requirements of *L. areolatus* and will help guide conservation and management of prairies and their amphibian inhabitants.

0489 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kathy Krynak¹, Ron Oldfield¹, Pam Dennis², Mike Durkalec³, Claire Weldon³

¹Case Western Reserve University, Cleveland, OH, USA, ²Cleveland Metroparks Zoo, Cleveland, OH, USA, ³Cleveland Metroparks, Cleveland, OH, USA

**A Novel Field Technique to Assess Ploidy in Introduced Grass Carp
(*Ctenopharyngodon idella*, Cyprinidae)**

Invasions by Asian carps have become a high profile topic due to the threat they pose to native ecosystems and associated economies. One of four primary invasive Asian carp species, Grass Carp, *Ctenopharyngodon idella* (Cyprinidae), is commonly produced as triploid, sterile, individuals and stocked as a biological control for the suppression of unwanted aquatic vegetation. Illegal sale and transport of diploid fish can result in unwanted fertile populations. Current methods of determining ploidy of an individual require the use of laboratory equipment (Coulter Counter) and are not possible to perform under field conditions. Here we introduce a rapid, inexpensive technique to distinguish diploid fertile versus triploid sterile Grass Carp under field conditions using a compound microscope. We compared blood smears of known diploid and triploid Grass Carp individuals, finding that the frequency of abnormally shaped erythrocyte nuclei (dumbbell or teardrop shaped) is significantly higher in triploid animals. This difference is accompanied by larger cell and nuclear volumes and is significantly correlated with Coulter Counter values (the standard measure of ploidy used by the United States Fish and Wildlife Service). Additionally, we field tested our method on a managed, presumably triploid, standing stock of Grass Carp and found that all individuals tested exhibited proportions of abnormal nuclei typical of triploids. Finally, a blinded study was used to confirm diagnostic reliability of our visual assessment of ploidy. Examination of blood smears for abnormally shaped nuclei may become a powerful tool in the management of invasive Grass Carp.

0602 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kole Kubicek¹, Ralf Britz², Kevin Conway¹

¹Department of Wildlife and Fisheries Sciences and Biodiversity Research and Teaching Collections, Texas A&M University, College Station, TX, USA, ²Natural History Museum, London, UK

Ontogeny of the Catfish Stinger

Catfishes (Siluriformes) are characterized by an impressive number of skeletal autapomorphies, including the anteriormost pectoral-fin ray highly modified into a lockable spine, which in some species may be associated with a venom gland. Previous anatomical investigations of the catfish pectoral spine have focused largely on the adult stage and have clarified how the spine locks into place and how it grows via the addition of segments distally. Detailed information on the earliest stages in the development of the catfish pectoral spine is not currently available leaving a number of questions about the development of the catfish stinger unanswered (e.g., at which point in development do the hemitrichia of the anteriormost fin ray fuse to form a single element?). Using a combination of clearing and double staining and serial sectioning, we document the earliest stages of pectoral spine formation in two species of ictalurid catfishes (*Noturus gyrinus* and *Ictalurus punctatus*) and compare early pectoral-fin ray development in ictalurids to non-siluriform otophysans.

0338 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

Shawn Kuchta

Ohio University, Athens, OH, USA

Ancient River Systems and Phylogeographic Structure in the Spring Salamander, *Gyrinophilus porphyriticus*

The river drainages of the Appalachian Mountains have experienced a dynamic history as glacial cycles, stream capture, and other geological events have lead to the fragmentation and fusion of formerly isolated paleodrainages. We investigated the contribution of contemporary and historical drainages to patterns of phylogeographic structure in the Spring Salamander, *Gyrinophilus porphyriticus*. To do this, we collected mitochondrial DNA sequence data (cytochrome b) and nuclear sequence data (RAG-1) from individuals from throughout the range of *G. porphyriticus*. A time calibrated phylogeny was inferred from the mtDNA data, and a haplotype network was constructed to examine relationships among RAG-1 alleles. Contemporary and historical river influences on patterns of genetic diversity, as well as isolation by distance, were tested using mantel tests and distance-based redundancy analysis (db-RDA). For both mtDNA and RAG-1, we found that historical river systems explained more phylogeographic structure than did contemporary drainages or geographic distance.

These results indicate that extinct or re-modeled paleodrainages played a fundamental role in the accumulation of phylogeographic structure in *G. porphyriticus*. In particular, we documented the impacts of the former Teays River, which drained much of northern Appalachia prior to the Pleistocene, and found phylogeographic support for White's River, a postulated river that may have along the Blue Ridge Escarpment.

0522 Fish Conservation & Management, Carson 3, Saturday 18 July 2015

Bernard Kuhajda¹, Matthew Piteo², Paul Hartfield³, George Jordan⁴, Edward Heist⁵

¹Tennessee Aquarium Conservation Institute, Chattanooga, TN, USA, ²Citizen, Pleasanton, TX, USA, ³U.S. Fish and Wildlife Service, Jackson, MS, USA, ⁴U.S. Fish and Wildlife Service, Billings, MT, USA, ⁵Southern Illinois University Carbondale, Carbondale, IL, USA

Morphological and Genetic Variation in Lower Mississippi River *Scaphirhynchus* Part 1: Morphological Discrimination Among Pallid, Shovelnose, and Intermediate Sturgeon Phenotypes

The federally endangered Pallid Sturgeon (*Scaphirhynchus albus*) ranges from the upper Missouri River in Montana downstream in the middle and lower Mississippi River to Louisiana, as well as in large tributaries. Throughout its range it is sympatric with the wider-ranging and common Shovelnose Sturgeon (*S. platorhynchus*). Intermediate phenotypes have been reported in the lower Missouri River and Mississippi River since the early 1980s. A former study demonstrated that sheared PCA on morphometric characters and PCA on meristic characters separated known Pallid, Shovelnose, and F1 hybrid sturgeon propagated and raised in hatcheries using upper Missouri River broodstock. Qualitative characters were also identified as useful diagnostic traits. The current study utilized these analyses on 200+ specimens of *Scaphirhynchus* sturgeon collected in the lower Mississippi River where intermediate phenotypes are not uncommon. Genetic tissues were taken before specimens were preserved in formalin and transferred to 70% EtOH. Thirty seven morphometric and 12 meristic characters were used to assess specimen identification. PCAs on both datasets gave no separation between the vast majority of field identified Pallid, Shovelnose, and Intermediate phenotypes. Six qualitative characters were used to make the final assessment of specimen identification on potential Pallid and Shovelnose Sturgeon. Based on these data most of the lower Mississippi River specimens are identified as intermediate phenotypes, with low numbers of both Pallid and Shovelnose Sturgeon phenotypes present. The origin of the large number of Intermediate phenotypes in the lower Mississippi River and the impacts on the conservation of the endangered Pallid Sturgeon will be discussed.

0497 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Brian Lavin

Sonoma State University, Rohnert Park, CA, USA

Biogeography and Examination of Cryptic Diversity in the Northern Alligator Lizard (*Elgaria coerulea*)

The Northern Alligator Lizard (*Elgaria coerulea*) is a cold tolerant Anguid lizard with a broad range in Western North America. Despite this broad range in a well-studied area it is unclear how the species is structured genetically. Morphologically, two examinations came to differing conclusions placing the species into either four subspecies with intergrade zones or two species in pattern classes. I present an mtDNA phylogeny and preliminary nuclear data in order to examine biogeography and cryptic diversity in this species.

**0495 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Thursday 16 July 2015**

Brian Lavin

Sonoma State University, Rohnert Park, CA, USA

Breaking the Glass: Phylogeny, Divergence, and Cryptic Diversity in Glass Lizards (Anguinae)

Lizards in the family Anguinae occur primarily in the New World with one exception. The Glass Lizards are a radiation of legless anguids with a grass-swimming morphology and the only extant radiation of Anguid lizards to occur outside the New World being found in North America, Europe, and Asia. Relationships within the Anguinae are complicated by similar morphology. I examine twenty-one nuclear protein coding genes and specimens comprising all major lineages in order to examine phylogeny, divergence dates, cryptic diversity, and species delimitation of the major lineages in the Anguinae at the species level.

0486 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

Adam Leache¹, James Archie³, Nassima Bouzid¹, Jared Grummer¹, Roger Anderson²

¹University of Washington, Seattle, WA, USA, ²Western Washington University, Bellingham, WA, USA, ³California State University, Long Beach, CA, USA

SNP-Based Phylogeography and Ecological Niche Modeling of Western Fence Lizards

Ecological divergence plays an important role in generating phenotypic and genetic diversity, ultimately resulting in the formation of new species. Young species with large geographic distributions spanning diverse environments provide an opportunity to measure the strength of ecological divergence during the early stages of population divergence. We investigated the role of ecological divergence in shaping phylogeographic structure of the most widespread lizard in Western North America, *Sceloporus occidentalis*. We used single nucleotide polymorphism (SNP) data to obtain high-resolution estimates of population genetic structure and phylogenetic relationships. Our sampling includes 100+ individuals representing 80+ localities from throughout the geographic range of the species. We used tests of niche overlap in combination with ecological niche models to determine if the degree of ecological divergence separating populations scales with their phylogenetic divergence. Phylogenetic analyses partition *S. occidentalis* into at least 10 populations that can be partitioned into three major groups: (1) a paraphyletic assemblage of populations in Southern California, (2) a clade with a broad distribution along the Pacific Coast and the Sierra Nevada Mountains, and (3) a clade that extends from the Mojave Desert into the Great Basin. We discuss the roles of ecological and non-ecological divergence in shaping phylogeographic structure, and the evidence for partitioning populations into multiple species.

0143 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Daniel Leavitt, Ashley Grimsley

Arizona Game and Fish Department, Phoenix, AZ, USA

Reptile Community and Environmental Structure Associations on a Proposed Transmission Corridor

Habitat alteration and fragmentation are major threats to reptiles in the Sonoran Desert. Collecting baseline reptile community data before major development occurs will result in a greater understanding of the resilience of communities in those particular areas. In 2014, reptile trapping surveys were conducted along the 500kV transmission line being constructed in the vicinity of the Picacho Mountains, Arizona. Before construction of the transmission line began, we installed 50 trapping arrays, each with 4 box-funnel traps, to capture an assortment of reptile species. We trapped for 1600 trap nights (32 nights over

50 trapping arrays) and captured 995 reptiles representing 18 different species. To gain insight on the reptile community, we evaluated landscape level environmental characteristics within the transmission corridor. We separated the Arizona Upland and Lower Colorado River Valley subdivisions of the Sonoran Desertscrub biotic community to inform this comparison. The largest environmental differences detected between these subdivisions related to soils (rocky-sandy gradient) and vegetation (sparse-heavily vegetated gradient). We conducted gradient analysis using Principal Coordinates Analysis to determine if the reptile community assemblages were associated with any particular environmental feature or biotic subdivision. The clearest conclusions were that reptile diversity and the abundance of both Tiger Whiptails and Common Side-blotched Lizards were slightly higher in the Arizona Upland subdivision. Now that we have a reference point for reptile community and environmental structure in this area, it will be beneficial to repeat this study after construction of this transmission line is completed.

0096 Herp Conservation I, Carson 1, Saturday 18 July 2015

Daniel Leavitt¹, Robert Lovich², Lee Fitzgerald³

¹Arizona Game and Fish Department, Phoenix, AZ, USA, ²Naval Facilities Engineering Command, San Diego, CA, USA, ³Texas A&M University, College Station, TX, USA

The Bucket Brigade Went Pro but the Library is Still on Fire: Modern Challenges in Reptile Conservation

Conservation of reptiles in modern times is challenged by a host of problems. In some circumstances, organisms in peril have been monitored to extinction and nothing prompted action to alter the trajectory. Here we present data and discussion for three species of lizard that have received attention regarding their conservation status (St. Croix Ground Lizard, Dunes Sagebrush Lizard, and Flat-tailed Horned Lizard). We will review the strategy used to monitor populations and contrast these three species against each other in light of their local threats. Further, we will offer solutions to any perceived weak spots in the conservation of these species based on the best and most recent data available regarding their ecology and population biology.

0097 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Daniel Leavitt, Taylor Cotten

Arizona Game and Fish Department, Phoenix, AZ, USA

Multi-scaled Assessment of Lowland Leopard Frog (*Lithobates yavapaiensis*) Egg Masses in Three Watersheds

In order to determine the characteristics of the landscape that are most important for species of concern we need to consider multiple spatial scales. Here, we describe both the methodology used in and the results from a field study of egg-laying site selection in Lowland Leopard Frogs (*Lithobates yavapaiensis*). We conducted our surveys for egg masses in the Bill Williams, Verde, and Agua Fria watersheds in Arizona. When found we collected detailed environmental data on the exact position of an egg mass and a cluster of egg masses. Further, we compare landscape scale characteristics of watersheds to examine the potential contributors to their success. These data can and will be used to help reestablish this species in locations where they were extirpated from along the Lower Colorado River drainage.

0364 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4, Thursday 16 July 2015

Brenna A. Levine¹, Charles F. Smith², Gordon W. Schuett³, Marlis R. Douglas¹, Mark A. Davis⁴, Michael E. Douglas¹

¹University of Arkansas, Fayetteville, AR, USA, ²Wofford College, Spartanburg, SC, USA, ³The Copperhead Institute, Spartanburg, SC, USA, ⁴University of Illinois, Champaign, IL, USA

Reproductive Success and Sexual Selection in a North American Pitviper

Assessment of sexual selection in organisms with cryptic life histories is a challenge, but accurate parentage assignments can be obtained from genotypes, particularly when combined with behavioral data. This study employed 22 tetranucleotide microsatellite DNA loci to interpret mating and reproductive success in a population of Copperhead (Viperidae, *Agkistrodon contortrix*) in Connecticut, USA. DNA samples representing 114 adults (56 males, 58 females) and 137 neonates from known mothers were used to quantify Bateman gradients (β_{ss}), and sex-specific opportunities for selection (I) and sexual selection (I_s). Selection on male size (SVL: snout-to-vent length) was also determined, since this trait has been recognized as relevant for successful combat and subsequent copulations. Estimates of male I and I_s differed significantly from those of females when estimated with four different methods (i.e., with and without open population correction, and with and without observational data in addition to molecular data), and only males had a statistically significant Bateman gradient ($\beta_{ss} = 4.25$; $r^2 = 0.61$; $p < 0.0001$). As predicted, male reproductive success was positively correlated with increasing SVL ($r^2 = 0.50$; $p < 0.05$). These results contrast with those derived in another

study investigating the same population but based solely on observational data and without correction for open population bias. We thus argue that molecular analyses to quantifying reproductive success and strength of sexual selection provide more accurate results than do behavioral observations alone.

0474 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Nicholas Levis, Mitchell Schooler, Jarrett Johnson, Michael Collyer

Western Kentucky University, Bowling Green, KY, USA

Non-adaptive Phenotypic Plasticity: Morphology, but not Swim Speed, of Spotted Salamander Larvae is Affected by “Terrestrial” and “Aquatic” Herbicides

Apart from habitat loss, many factors have been implicated in contributing to global amphibian declines. Contaminants such as herbicides are among the most widespread potential contributors. Glyphosate-based herbicides (GBH; e.g., Roundup®) are the most widely used in the world and could potentially contribute to amphibian declines. Empirical research is needed to understand the toxicity of GBH for various amphibian taxa, especially to reconcile the physiological mechanisms that lead to population declines. A current hypothesis is that GBH exposure might retard larval amphibian “escape” swimming speed, making them more susceptible to predation. Using a “common garden” experiment, larvae of spotted salamander (*Ambystoma maculatum*) were reared in different environments based on varied GBH exposure to (1) determine if GBH exposure affects escape speed, (2) determine if different types of GBH produce varied effects, (3) determine if escape speed is correlated with morphological development, (4) and determine if GBH exposure increases direct mortality. We found no negative impacts of GBH exposure on mortality or swim speed; however, GBH significantly affected the morphological development of larvae. Compared to control larvae, exposed larvae had significantly faster overall growth rates but less change in head and tail shapes, suggesting a physiological response to increase growth in spite of development. However, GBH morphological changes varied among treatments, suggesting non-glyphosate chemicals in the solution might also affect amphibian development. Although further research is needed to understand the extensive consequences of exposure to GBH, our results indicate that such consequences are likely varied with different types of GBH.

0425 Herp Ecology, Carson 4, Saturday 18 July 2015

Mara Leyendecker², José Pedro do Amaral¹

¹University of Cincinnati Clermont College, Cincinnati, OH, USA, ²University of Cincinnati, Cincinnati, OH, USA

Thermoregulation of the Wall Lizard, *Podarcis muralis*: an Introduced Species

Thermoregulation is vital for the survival of ectotherms. Without proper thermoregulation, an ectotherm's enzymes may likely overheat and denature, or freeze and stop functioning. Throughout this experiment, we tested how thermoregulatory effectiveness of *Podarcis muralis* changed as the seasons progressed from spring to summer. Each lizard was individually noosed in Prospect Hill near Cincinnati, Ohio. It was hypothesized that the lizards' need to thermoregulate more carefully increases as the seasons progress, because the environmental temperatures become less favorable.

The results showed that the thermoregulatory effectiveness varied as the seasons progressed. From May to June the mean thermoregulatory effectiveness decreased, when from June to July the mean thermoregulatory effectiveness increased. Furthermore, it was shown that when the thermal quality of the environment was less favorable the lizards did thermoregulate more effectively. Therefore, the hypothesis was supported. It was concluded that as the weather worsened, the lizards became more accurate and effective at thermoregulating. For the future, it would be interesting to measure the lizards temperatures using both an infrared thermometer and noosing them in the field. We would also like to study the lizards in their native Italy and compare those results to the ones studied in Cincinnati.

0068 Herp Ecology, Carson 4, Saturday 18 July 2015

Craig Lind¹, Steve Beaupre², Douglas Rhoads², Brenda Flack²

¹Stetson University, DeLand, FL, USA, ²University of Arkansas, Fayetteville, AR, USA

The Mating System and Reproductive Life History of Female Timber Rattlesnakes in Northwestern Arkansas

Vertebrate mating strategies and life history patterns show great variation within and among species. Elucidating phylogenetic and environmental factors that produce variation in reproductive tactics requires detailed natural and life history data on diverse taxa. Collection of such data in secretive species can often only be accomplished through the use of long-term monitoring and molecular tools. We used a combination of long-term (17 years) monitoring via radiotelemetry and molecular tools (microsatellite DNA markers) to describe in detail the reproductive ecology of a population of Timber Rattlesnakes, *Crotalus horridus*, in northwestern Arkansas. Female *C. horridus* are smaller at maturity and produce small litters compared to most reliable estimates for other populations. Female snout vent length and not preparturient body condition is positively related to litter size and total litter mass. Both pregnant and attractive females

(individuals found engaged in mating behavior) were in better body condition compared to the general female population, suggesting a threshold body condition for female receptivity and reproduction. Behavioral monitoring of radiotagged females showed that 15% of females observed engaging in mating behavior with a male went on to associate with additional males that year. At least 44% of females found engaged in mating behavior definitely did not go on to produce a litter the following year, indicating that females will associate with males even when their chances of producing a litter the following year are low. Genetic analysis of eight microsatellite markers confirmed multiple paternity in three of the seven litters analyzed.

0197 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Luke Linhoff, Maureen Donnelly

Florida International University, Miami, FL, USA

A Toad that Has Never Seen Dirt: Increasing Success Rates for Reintroductions of Captive Bred Wyoming Toads (*Anaxyrus baxteri*)

The Wyoming Toad (*Anaxyrus baxteri*) is a critically endangered species found only in Albany County, Wyoming, USA. In 1993, the species was listed as extinct in the wild, but it has survived in captivity. After multiple reintroduction attempts of the Wyoming Toad between 1992 and 2012 had limited success, efforts to study the causes of failure and explore new methods were undertaken by the Wyoming Toad recovery team. Previous reintroductions of the Wyoming toad have typically utilized a *hard release* strategy for both translocation of larvae and adults. In contrast, allowing an animal to acclimate to the release site, often in an outdoor enclosure, is known as a soft release. In the summer of 2014, we performed a paired release of two groups of captive bred adult toads. The released toads had been reared in a typical captive breeding facility, and translocation to the wild is a massive change for the toads. For example, the toads had never been previously exposed to dirt. Twelve individuals were hard released and 12 individuals were soft released after acclimating in an outdoor enclosure for 14 days. All released toads were fitted with a custom harness allowing for the external attachment of a harmonic tracking device. We tracked all toads for up to eight weeks to compare activity patterns, site fidelity, survival and home range size in both groups. We will present results of the tracking study and describe acquisition rates of the pathogenic fungus *Batrachochytrium dendrobatidis* (Bd) in the released animals.

0477 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kevin Liska¹, Drew Corder¹, Amanda Ellis¹, Vasilyev Evgeny¹, Sarah Hazzard², Sam Liska¹, Mack Lunn¹, Joe Powell¹, Victoria Rice¹, Emily Samples¹, Stephanie Scarborough¹, Tara Shaffernocker¹, Stefanie Smithers¹, Ali Stephens¹, Thaddeus Taylor³, Anna George²

¹Tennessee Tech University, Cookeville, TN, USA, ²Tennessee Aquarium Conservation Institute, Chattanooga, TN, USA, ³Tennessee Aquarium, Chattanooga, TN, USA

Snorkeling Without Getting Wet: Using Virtual Reality to Bring Freshwater Education into the Classroom

While environmental education often results in greater awareness of conservation problems, recent conservation psychology research indicates that environmental knowledge does not exclusively lead to pro-environmental behavior. Other factors involved in increasing pro-environmental behavior include greater awareness of impact of personal actions on environmental issues, a stronger belief that personal actions can make a difference, pro-environmental attitudes, verbal pledges of an intention to behave in an environmentally friendly way, and a greater sense of personal responsibility.

Video games are a booming industry nationally, making twice as much annually as film and music combined, and new virtual reality (VR) technologies associated with the games may offer opportunities to create educational programs that move beyond environmental awareness. Previous studies using VR have documented increases in recycling behavior after participants either grew or cut down a tree. To harness this power, Tennessee Tech's iCube created a River Ecosystem Conservation VR program to enhance field trip visits to the Tennessee Aquarium. Participants use the VR mask to "snorkel" in the Conasauga River, Tennessee, allowing them to view different animals as they move through the river. As they explore the healthy ecosystem, different pollution events happen, changing the water from clear to murky as species begin to disappear. The students must then surface to identify the source of the pollution and corrective actions that restore the watershed. As we implement this program, we will evaluate whether this gives students greater agency in making changes to local actions that impact the conservation of freshwater animals.

0331 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Krista Little, Robert Weaver

Central Washington University, Ellensburg, WA, USA

Microhabitat Preference of Oregon Ensatina (*Ensatina escholtzii oregonensis*) Within Small Populations in Snohomish County, Washington State

The Oregon Ensatina (*Ensatina escholtzii oregonensis*) is one of the more abundant and commonly observed salamanders in central Snohomish County, Washington State. This species is often found among leaf litter and downed woody debris along riparian

corridors in mixed coniferous and deciduous forests. The purpose of my study was to conduct a preliminary investigation of microhabitat preference of *E. e. oregonensis* that I observed in 2 different forested areas at a site near Lake Stevens, Washington. The sampled microhabitats were divided into 4 categories: fallen bark from trees, rotten logs, artificial cover and other (under moss, leaf litter, rocks). Observed individuals from each category were recorded over the span of several days in mid-Summer through early-Spring. Of the 54 total individuals observed the highest frequency of individuals were found under alder bark (*Alnus* spp.) that had been sloughed off by woodpeckers (68%). The second highest frequency of individuals were found under rotten logs (22%) while few (7%) were found under artificial cover, and 2% of salamanders observed were found under moss. Based upon my observations it seems *E. e. oregonensis* show a preference towards fallen alder bark. Under much of the fallen bark I observed an abundance of possible arthropod prey, more so than in other microhabitats. Future research direction will focus on obtaining a larger sample size, as well as examining additional microhabitat parameters (insect type and abundance, soil pH, and moisture) that may be driving the occurrence and any possible preferences by salamanders.

0300 Fish Systematics II, Carson 3, Sunday 19 July 2015

Thiago Loboda, Marcelo Carvalho

Instituto de Biociências - USP, São Paulo, SP, Brazil

Morphological Diversity and Taxonomic Revision of *Paratrygon* Duméril (1865) (Chondrichthyes: Myliobatiformes: Potamotrygonidae): A Species Complex

Currently recognized as a monotypic genus, *Paratrygon* shows potential to increase the diversity of the family Potamotrygonidae. *Paratrygon* has as principal diagnostic characters a spiracular process present on posterior margin of spiracles, concave anterior margin of disc, slender tail with reduced lateral, dorsal and ventral tail folds, and a reduced caudal sting (smaller than *Plesiotrygon* and *Potamotrygon*, but greater than *Heliotrygon*). Recent molecular studies with ATPase 6 and Cytochrome Oxidase I point to a greater genetic diversity of *P. aiereba*, with distinct populations from the Xingu, Tapajós, Araguaia, Negro and Solimões-Amazonas rivers. Our morphological and taxonomic revision has revealed five to eight groups within *Paratrygon* besides *P. aiereba*. Two groups occur in the Orinoco basin and the others in the Amazon basin. Main differences between these groups are: dorsal and ventral coloration, disc and tail morphology, size of eyes and spiracles, morphology and size of spiracular processes, morphology and distribution of dermal denticles, distribution and morphology of ventral canals of lateral line, and morphology of some skeletal components such as the neurocranium. *Trygon stroglyopterus* Schomburgk, 1843 and *Disceus thayeri* Garman, 1913 well delimited as junior synonyms of *P. aiereba* in previous works, also will be revised due to the possibility in reuse them to some of these potential new species.

0263 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Jenny Loda¹, Collette Adkins²

¹Center for Biological Diversity, San Francisco, CA, USA, ²Center for Biological Diversity, Minneapolis, MN, USA

SWPARC - Using the Endangered Species Act to Protect Rare Amphibians and Reptiles in the Southwest

The Center for Biological Diversity works to secure a future for all species, great and small, especially those hovering on the brink of extinction. By petitioning the U.S. Fish and Wildlife Service to provide Endangered Species Act protection for imperiled amphibians and reptiles - and following up with lawsuits when necessary - the Center is working to obtain federal safeguards and protected habitat for herps in the Southwest and across the country. Through hiring its second full-time attorney and biologist dedicated to conserving amphibians and reptiles, the Center is expanding its campaign to address the amphibian and reptile extinction crisis. In this presentation, Jenny discusses the Center's work to protect turtles, snakes, frogs, lizards and salamanders in the Southwest. These efforts include filing the largest-ever Endangered Species Act petition focused on amphibians and reptiles, securing habitat protections and recovery plans for listed species, advocating for salamander import restrictions to prevent the introduction of Bsal into the United States, and litigating to secure restrictions on pesticide use in endangered species habitats.

0228 Fish Systematics II, Carson 3, Sunday 19 July 2015

Alejandro Londoño-Burbano, Roberto Reis

Pontificia Universidade Católica do Rio Grande do Sul (PUCRS), Porto Alegre, RS, Brazil

Taxonomic Revision and Phylogenetic Relationships of the Species of *Dasyloricaria* (Siluriformes, Loricariidae), with Description of a New Species

A taxonomic revision and phylogenetic analysis were carried out for *Dasyloricaria*. The genus was found to be composed of three valid species: *D. filamentosa* and *D. latiura* that were included previously in the genus, and a new species described herein. *Dasyloricaria* is found to have a fully trans-Andean distribution, with *D. filamentosa* occurring in the lower and middle Magdalena, lower Cauca, Sinu, and Catatumbo basins in Colombia, and Maracaibo basin in Colombia and Venezuela; *D. latiura* is distributed in both the Atrato and Tuyra basins in Colombia and Panama respectively; and the new species occurs in the upper and middle Magdalena basin in Colombia. New synonyms for *D. filamentosa* and *D. latiura* are proposed, and a lectotype is designated for the latter. A parsimony phylogenetic analysis was performed based on 91 morphological characters (osteology and external morphology) and 23 terminal taxa. A single most parsimonious tree of 412 steps, consistency index (CI) of 0.46, and retention index (RI) of 0.63 was found. *Dasyloricaria* is here recovered as a monophyletic unit presenting seven uniquely

derived synapomorphies. Within the genus, the new species was found to be sister group to a clade formed by *D. latiura* and *D. filamentosa*. Furthermore, *Spatuloricaria* was recovered as sister to *Dasylicaria*, supported by characters related to neurocranium, branchial arches and external morphology features. *Rineloricariina* sensu Isbrücker was not recovered as monophyletic; relationships between *Rineloricaria* and the *Spatuloricaria* + *Dasylicaria* group were not resolved, even when they were found related within the analysis.

0237 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Gary Longo, Giacomo Bernardi

University of California Santa Cruz, Santa Cruz, CA, USA

Signals of Genomic Selection in Surfperches (Embiotocidae)

Understanding the genomic factors that underlie local adaptation is a central interest in evolutionary biology. However studying local adaptation in marine fishes can be difficult due to generally high levels of gene flow, which can decrease potential for local adaptation. Surfperches (Embiotocidae) represent an ideal system for investigating selection in marine systems because of their viviparous (live bearing) reproductive strategy, which results in relatively low gene flow and increased potential for local adaptation. Here we investigate genomic signatures of divergent selection between disparate populations of four surfperch species with overlapping ranges. These temperate reef fishes inhabit kelp forest and rocky reef habitats in a wide latitudinal distribution. This range encompasses dissimilar biotic and abiotic conditions, which likely result in divergent selective pressures among populations. Notably, a well-documented biogeographic break occurs at Point Conception (near Santa Barbara, CA) where contrasting currents result in significantly different species assemblages and sea surface temperatures (SST). This study utilized thousands of genome wide restriction site associated DNA (RAD) markers sampled from populations north and south of the biogeographic break and identified candidate loci for divergent selection with F_{ST} outlier methods. Although many of the significantly divergent markers were in non-coding regions several markers BLAST to known genes involved in functions such as immunosuppression. Better understanding the genomic response of surfperch populations to selective pressures such as increased SST can inform us about what kind of genetic diversity may be under selection in other commercially important teleost fishes in response to rising global temperatures.

0239 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Sarah Longo¹, Matthew McGee³, Christopher Oufiero², Peter Wainwright¹

¹University of California, Davis, Davis, CA, USA, ²Towson University, Towson, MD, USA, ³University of Bern, Bern, Switzerland

Re-evaluating the Importance of the Ram-Suction Continuum in Diversification of Fish Feeding Behaviors

Suction feeding fishes use a combination of suction and ram to decrease the distance between themselves and their prey. While suction is used to draw prey into the mouth, ram includes all movements of the predator toward the prey and can be achieved by the fish swimming (body ram) or by extending the jaws toward the prey (jaw ram). Previous research found that ram distances vary more than suction distances between strikes and among species. The contribution of suction to prey capture distance appears to be physically constrained, and therefore variation in the type and amount of ram may be largely responsible for differences in prey capture strategies among suction feeding fishes. We collected a large dataset of high-speed videos of representatives from over 30 families of acanthomorph fishes feeding on live prey to explore broad diversification patterns. For each strike, we calculated suction, body ram, and jaw ram distances. We find that the contribution of suction to prey capture on live prey is limited even at these broad scales, with no species occupying the extreme suction area of prey capture space. A number of species do occupy the other extremes, although invading the high jaw ram area of prey capture space appears to require novel functional modifications. Instead of finding the classic trade-off between suction and ram as the major driver of diversity in prey capture strategy, we find that the major axis of variation is largely a trade off between the contributions of jaw ram and body ram.

0139 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Yer Lor¹, David Boseto², Frank Pezold¹

¹Texas A&M University-Corpus Christi, Corpus Christi, TX, USA, ²Ecological Solutions, Honiara, Solomon Islands

Deciphering the Species Diversity in the Goby Genus *Stiphodon* (Teleostei: Gobioidae: Sicydiinae)

Gobies greatly contribute to the diversity seen in oceanic island fish communities and have high levels of endemism. Fishes of the goby subfamily Sicydiinae are found in tropical freshwater worldwide. These gobies exhibit an amphidromous lifestyle which consists of adults spawning in freshwater, larvae going out to sea and eventually returning upstream as juveniles. Species in the genus *Stiphodon* are found from the eastern Indian Ocean to Polynesia in the eastern Pacific Ocean. Species are distinguished

from one another primarily by the diverse coloration of the males (females being relatively drab) and by the length of fin rays in males. Other useful differentiating factors are the slight differences in the number of fin rays and the size of scales on the body. Patterns of diversification within *Stiphodon* are not fully understood due to the subtle color differences between males of some species, overlapping ranges of scale and ray counts, and poor understanding of species distributions. Phylogenetic analyses of mitochondrial and nuclear genes are being used to clarify the relationships within this genus. Preliminary mitochondrial and nuclear gene phylogenetic analyses indicate that there are at least two distinct clades within *Stiphodon*. However, more work needs to be done to both refine and expand on the existing data, specifically by increasing the species sample sizes and incorporating all available species localities to be able to make more confident interpretations on *Stiphodon* species diversity.

0452 ASIH STOYE AWARD ECOLOGY & ETHOLOGY II, Carson 4, Friday 17 July 2015

Caleb Loughran¹, Daniel Beck², Debbie Lewis², Megan Linn², Robert Weaver²

¹University of New Mexico, Albuquerque, NM, USA, ²Central Washington University, Ellensburg, WA, USA

Innate Recognition of Chemical Cues by Neonate Northern Pacific Rattlesnakes (*Crotalus oreganus oreganus*)

When rattlesnakes are born, after a short period of maternal attendance, they must immediately be able to navigate and interpret their environment to survive. Because foraging, predator avoidance, and protection from lethal climatic extremes are of primary importance, the ability to recognize cues in the environment is a critical component of their survival. Northern Pacific Rattlesnakes (*Crotalus oreganus oreganus*), which are typically born in the late summer, have about 4-6 weeks before they must retreat to a suitable overwintering refuge. In that period, they will survive off endogenous yolk stores, and if possible, consume at least one prey before arriving at a communal hibernaculum. Because of the exposure to a wide range of scents during this period, we tested the hypothesis that neonate *C. oreganus* can innately discriminate between environmental scents. We used scented cotton swabs to observe tongue flicking behavior. For one experiment, we tested 10 captive-born and 9 wild-caught individuals with scents from conspecifics, as well as 3 other sympatric snake species. There was a significant effect of scent recognition, with no difference in tongue flick response between captive-born and wild-caught individuals. For the second experiment, we tested 20 captive-born and 11 wild-caught individuals with scents from potential endothermic prey and ectothermic prey. There was a significant effect of scent recognition between endothermic and ectothermic prey, with no difference between captive-born and wild-caught individuals. Our results suggest that neonate *C. oreganus* innately recognize different environmental scents. Additionally, we also present preliminary data on behavioral responses to different scents.

0537 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Kim Lovich¹, Chris Brown²

¹*San Diego Zoo Global, CA, USA*, ²*United States Geological Survey, CA, USA*

SWPARC - Collaborative Conservation Efforts for the Western Pond Turtle (*Actinemys marmorata*) in San Diego County

The Western pond turtle is an endemic species that has seen decreasing populations and increasing threats throughout its range. Habitat loss and invasive species are two common issues and now increasing drought is impacting populations in the Southwest. Native pond turtles have dwindled to only 120 in five locations in the San Diego region. Here we will discuss a multi pronged approach to conservation that incorporates public education, head starting young turtles for release, monitoring of young and adult turtles, invasive species removal and population relocation within regional watersheds utilizing the best available genetic data for helping make informed decisions. Included in this partnership is the California Department of Fish and Wildlife, the San Diego Zoo, United States Geological Survey, Western Ecological Center (USGS WERC) and support from the San Diego Association of Governments (SANDAG). In addition, this species is on display at the San Diego Zoo, an Association of Zoos and Aquariums (AZA) accredited institution, and most recently the AZA hosted a stakeholder meeting for Western Pond Turtle Conservation and this new "SAFE" program will briefly be discussed.

0525 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Robert Lovich¹, Chris Petersen²

¹*U.S. Navy, San Diego, CA, USA*, ²*U.S. Navy, Norfolk, VA, USA*

SWPARC - First Strategic Plan for Herpetofauna by the United States Government

The Department of Defense (DoD) in 2015 endorsed The Strategic Plan for Amphibian and Reptile Conservation and Management on Department of Defense Lands, thereby becoming the first department in the history of the United States to have a Strategic Plan for herpetofauna. This document is intended to help installation natural resource managers better address the conservation and protection of amphibians and reptiles and their habitats and to help Commanders comply with federal law (Endangered Species Act and the National Environmental Policy Act) to meet mission readiness. We present a history of the steps that led to the formation and acceptance of this plan, along with a description of the strategic goals and objectives, including those already completed and those yet-to-be accomplished. This strategic plan is intended to be beneficial to the United States Military mission in ways that preclude mission conflicts and loss of

training capabilities while at the same time protecting America's natural heritage in the form of resident herpetofauna and their habitats.

0144 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Christopher Lowe¹, Connor White¹, Diego Bernal²

¹*California State Univ. Long Beach, Long Beach, CA, USA*, ²*Univ. Mass. Dartmouth, Dartmouth, MA, USA*

Behavioral Thermoregulation in Elasmobranch Fishes: What Do We Know and Where Do We Go from Here?

There is a growing number of telemetry-based movement studies across a range of ectothermic elasmobranch species suggesting that individuals exhibit some form of behavioral thermoregulation. In addition, there is considerable speculation as to the benefits of this behavior and what potentially drives movements relative to changing water temperatures. Fewer studies have focused on quantifying the actual physiological cost/benefits of changing body temperatures and how these changes may influence behavior. Unfortunately, in a vast majority of cases there is little physiological and behavioral data for the same species to allow for realistic assessment of potential behavioral thermoregulation. Cases where there are comparable physiological and behavioral data have focused primarily on smaller species that are easier to keep in captive settings. As a result, our understanding of how behavioral thermoregulation scales with body size is sorely lacking. New technology, experimental designs, and modeling tools may allow for a better assessment of behavioral thermoregulation. New movement (accelerometer, temp and depth dataloggers) and tracking tools (VRAP, MAP600, AUVs) can allow for simultaneous, fine-scale assessment of movements relative to environmental conditions, especially if accompanied with internal body temperature sensors (e.g., gastric or IP temperature sensors). Use of field-based translocation experiments across thermal gradients may allow for experimental assessment of body temperature and movement predictions. Lastly, better physiological, behavioral and related environmental data will allow for more sophisticated modelling to predict movement patterns as ocean temperatures continue to warm.

**0231 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

William Ludt¹, Christopher BurrIDGE², Prosanta Chakrabarty¹

¹Louisiana State University, Baton Rouge, LA, USA, ²University of Tasmania, Hobart, Tasmania, Australia

**What, if Anything, is a Morwong? A Genomic Investigation of
Cheilodactylidae Using Ultraconserved Elements (UCEs)**

Fishes in the family Cheilodactylidae are found in both the northern and southern hemispheres in warm-temperate and temperate rocky habitats. They are part of the superfamily Cirrhitidae, along with Cirrhitidae, Aplodactylidae, Chironemidae, and Latridae, which is nested within Centrarchiformes (sensu Near et al. 2012). Previous studies have suggested that the 27 recognized species in this family are not monophyletic, yet no taxonomic changes have been made due to poor taxonomic resolution in these studies. Furthermore, the relationships among families within Cirrhitidae also remain contentious. Here we present a phylogenomic approach that includes all Cheilodactylid genera, and the majority of species. We included outgroup representatives from all families within Cirrhitidae, as well as species found across Centrarchiformes. Ultraconserved elements (UCEs) were used to generate more than 400 loci, exceeding 400,000bp of data in total. Here we present results using maximum likelihood, Bayesian, and coalescent-based methods. We have conducted all analyses using a complete data matrix, as well as an 85% complete data matrix. Our results support previous findings suggesting that Cheilodactylidae is polyphyletic. We discuss possible relevant taxonomic changes with reference to Latridae, and place our results in a global biogeographic framework. This study further supports the utility of using UCEs to gain better resolution to difficult phylogenetic questions.

0440 AES Morphology & Physiology, Carson 2, Sunday 19 July 2015

Carl Luer¹, Cathy Walsh¹, Laura Edsberg², Jennifer Wyffels²

¹Mote Marine Laboratory, Sarasota, FL, USA, ²Daemen College Center for Wound Healing Research, Amherst, NY, USA

**Experimental Wounding of Atlantic Stingrays, *Dasyatis sabina*: Role of
Epidermal Mucus in Protection of Early Stage Wound Beds**

Anecdotal reports of relatively rapid and infection-free healing of wounds in sharks and rays are common, yet controlled experimental wounding studies to characterize the healing process are rare. Experimental wounds were inflicted on pectoral fins of Atlantic stingrays, *Dasyatis sabina*, by excising the epidermal and dermal layers of skin and exposing the epaxial musculature. While the gross physical appearance suggests that wound beds are covered by blood and/or blood clots for at least the first 4 days, histology has shown that migration of epidermal cells from the wound margin onto the

bed is well underway by 16-24 hours. By 48 hours, the wound bed is completely covered with a thin epidermal layer containing mucus cells and a clearly identifiable basal layer. Wound biopsy samples were examined using scanning electron microscopy (SEM) and post-fixation to preserve secreted epidermal mucus. Resulting SEM images of 8, 16, and 24 hour wounds demonstrate that wounds are covered with mucus before re-epithelialization. The 24 and 16 hour wound beds are obscured almost completely by mucus, while much of the 8 hour wound bed surface, particularly near the wound bed margins, is also covered by mucus. Studies are underway to investigate the extent of mucus coverage on wounds at times earlier than 8 hours. Epidermal mucus secretions isolate the wound from the environment and may represent the first line of defense for wound healing in *D. sabina*.

0057 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

John Lundberg¹, Mariangeles Arce H.¹, Dean Hendrickson², Kyle Luckenbill¹, Maureen O'Leary⁴, Paula Mabee³, John Sullivan⁵

¹Academy of Natural Sciences, Philadelphia, PA, USA, ²University of Texas, Austin, TX, USA, ³University of South Dakota, Vermillion, SD, USA, ⁴Stony Brook University, Stony Brook, NY, USA, ⁵Cornell University Museum of Vertebrates, Ithaca, NY, USA

Ictaluridae 2015: Systematic Challenges, Opportunities and New Approaches

North America's favorite catfishes, our endemic Ictaluridae, offer more than most compatriotic fishes: tasty fried filets eaten with hushpuppies and much beer; thrills of angling their huge, snot-covered meat with hooks or bare hands; painful stings; stunning prehistoric skeletons; four, eye-less subterranean imps; and a genus named *Satan*. The nearly-complete inventory of living ictalurids totals 51 valid species among 137 available names. Some cryptic *Noturus* and Mexican *Ictalurus* may yet be named, with one languishing borderlands *Ictalurus* coming soon. Fossils represent 12 living and 16 extinct species; anticipate more. Distributions of modern ictalurids are mapped across the USA east of the western continental divide, into southern Canada and southward across nearly all of mainland Mexico to Guatemala. Neogene fossils extend the native realm of bullheads into the Great Basin and Pacific northwest, and *Ictalurus* onto the mid-Atlantic slope. *Astephus*, a plesiomorphic Paleogene ictalurid, is sister to all other confamilials. Cranoglanididae in China is sister to Ictaluridae. Independent phylogenetic analyses of Ictaluridae using morphological and molecular datasets recover well-resolved trees *but* conflicting relationships among genera and within *Ameiurus*. The four subterranean and several fossil species remain uncertainly resolved. This poster presents four cameos on coincidentally ongoing efforts that are advancing knowledge of ictalurid diversity and evolution. 1) Reinvestigating the phylogeny of Ictaluridae using the new phenomic tools of AVAToL and MorphoBank, and Phenoscape. 2) Description and conservation status of the Chihuahua catfish. 3) First shots at molecular sequencing *Trogloglanis*. 4) *Satan's* bony skeleton revealed by a high-res catscan.

0252 Fish Ecology I, Carson 3, Sunday 19 July 2015

Dustin Lynch, Daniel Magoulick

University of Arkansas, Fayetteville, AR, USA

Temporal Variation in Flow-Ecology Relationships in the Ozark Highlands

We examined flow-ecology relationships in fish communities in the Ozark Highlands over two years with contrasting environmental conditions, a drought year (2012) and a flood year (2013), using an IT multiple regression approach with a priori selected predictor variables incorporating hydrology, habitat, geomorphology, and water quality. Response variables included species richness, Simpson's diversity, percent intolerant species, percent centrarchids, and total density. In the drought year, we found positive relationships between species richness and RHA (rapid habitat assessment) score and between % centrarchidae and substrate size, and negative relationships between diversity and HDI (hydrologic disturbance index), % intolerant species and Total P, and total density and substrate size. In the flood year, we found positive relationships between % centrarchidae and substrate size and a negative relationship between total density and flow variability. There were fewer significant relationships during the flood year than drought year, and flow-ecology relationships differed between the two years. While hydrology was an important influence on community structure, it was often less important than other types of environmental variables, especially in a drought year.

0404 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kady Lyons¹, Douglas H. Adams²

¹*University of Calgary, Calgary, Alberta, Canada*, ²*Florida Fish and Wildlife Conservation Commission, Melbourne, FL, USA*

Maternal Offloading of Organochlorine Contaminants in the Pseudoplacental Scalloped Hammerhead

Elasmobranchs have a propensity to accumulate high contaminant levels, especially in species that occupy upper trophic levels. However, contaminant concentrations and the types of contaminants that marine fishes accumulate can vary with species, age, sex and environmental parameters. In addition, females have the ability to transfer contaminant to their young through reproductive processes. Therefore, contaminant concentrations and signatures can be used a tool for examining elasmobranch ecology. Organic contaminants (PCBs and chlorinated pesticides) were measured in livers of both female and male scalloped hammerheads (*Sphyrna lewini*) from several age classes that were collected from U.S. Atlantic waters, including two near-term pregnant females and their embryos. Adult female hammerheads were found to have lower levels of PCBs compared to the younger, adult male (mean \pm SD, 11.1 ± 1.0 versus $22.8 \mu\text{g g}^{-1}$ lw), but had substantially higher concentrations of pesticides (4.1 ± 0.9 versus $1.9 \mu\text{g g}^{-1}$ lw). While females were found to offload substantial contaminants to their offspring, females

were only able to depurate their total hepatic load by approximately 0.03 to 2.3%. Differences in standardized contaminant concentrations were observed between the adult male and females, with males having greater proportions of more chlorinated PCB congeners. These differences could be due to the ability of females to offload contaminants to offspring as well as sexual segregation in habitat use. Results from future contaminant studies with increased sample sizes from different localities will further our understanding of scalloped hammerhead health and ecology and aid in effective conservation.

**0402 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday
18 July 2015**

Kady Lyons, Matt Vijayan

University of Calgary, Calgary, Alberta, Canada

**Compromised Stress Response in Round Stingrays Exposed to PCBs along the
Southern California Coast**

Stress response impairment due to environmental contaminant exposure has been documented in a variety of organisms; however, little research has investigated these types of effects in elasmobranch fishes. The objective of this study was to examine the primary and secondary stress response in round stingrays (*Urobatis halleri*) that have been exposed to different levels of environmental organochlorine contaminants, primarily polychlorinated biphenyls (PCBs). Our hypothesis was that higher PCBs body burden would compromise the stress response in this species. To test this, stingrays were sampled from two locations (mainland California, Long Beach, and a nearby offshore island, Catalina) and subjected to two treatments (“stressed” and “unstressed”). Stingrays were collected by hook and line from these two locations and plasma was sampled either immediately (unstressed) or 15 min after handling and confinement (stressed) to examine changes in liver and plasma parameters. Stingrays sampled from Long Beach had significantly higher hepatic PCB levels compared to stingrays Catalina. Our results support the hypothesis that higher PCB body burden suppresses the highly conserved corticosteroid stress response in these animals. Also, liver glucose and glycogen content were lower in the stressed Long Beach stingrays compared to the Catalina rays. Overall, PCB contamination reduces the capacity to elicit a physiological stress response in the round stingrays.

**0301 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday
18 July 2015**

Paula Mabee

University of South Dakota, Vermillion, SD, USA

**Progress in Comparative Morphology Can Be Accelerated Through Semantic
Annotation**

Donn Rosen died before molecular data revolutionized phylogenetics, access to big open data was possible, and methods to make phenotypic data machine readable and linked had been developed. Assuming that the practice of comparative morphology could stay the same and yet contribute to its full potential in informing our understanding of evolution, inhibits scientific progress in comparative biology. By annotating morphological characters with ontology terms, machine reasoning can be used to readily aggregate relevant morphological character data from previous studies. A significant amount of anatomical knowledge is implied but not directly stated in comparative morphological treatments. This inhibits progress in comparative biology, because it is not available for direct use. Reasoning over annotated morphological data can be used to reveal “unknown knowns” such as developmental precursor of a feature or its presence or absence. For example, authors often do not state when an anatomical entity is present, though its presence is implied by the condition of a part, e.g., if pectoral fin rays are described as ‘curved’, the pectoral fin is present. Inferred data substantially reduces the missing data in synthetic supermatrices and further enables the isolation of conflicts in the data, i.e., cells where both presence and absence are indicated. Finally ontology-annotated morphology can be readily linked to genetic and developmental data, which enables a deeper understanding of evolutionary change.

**0361 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Daniel MacGuigan, Thomas J. Near

Yale University, New Haven, CT, USA

**Molecular and Morphological Species Delimitation in the Greenthroat Darter,
*Etheostoma lepidum***

Discovering and describing biodiversity is one of the primary goals of systematic biology. The Greenthroat Darter (*Etheostoma lepidum*) is distributed primarily in southern Texas, but with a disjunct population in southeastern New Mexico. The species exhibits variation in morphology and male nuptial coloration, which has been considered clinal in nature. We investigated phylogenetic structure among populations of *E. lepidum* using DNA sequences from a mtDNA gene and 14 nuclear DNA loci. We also investigated variation in meristic and male nuptial coloration traits in the context of the inferred molecular phylogeny to determine if *E. lepidum* comprises multiple undescribed species.

Based on patterns of morphological variation and results from widely used molecular species delimitation approaches such as bGMYC, BPP, and Bayes factor delimitation, we found that *E. lepidum* appears to contain three distinct evolutionary lineages: one in Pecos River in New Mexico, one in the upper reaches of the Colorado River in Texas, and one in the lower Colorado River, Guadalupe River, and Nueces River in Texas. When interpreted in a phylogenetic context, morphology and coloration both support recognition of three species and provide several diagnostic characteristics. This research effectively demonstrates that molecular and morphological data can be used in tandem to delimit and describe new species of darters. Additionally, our results suggest roles for headwater capture, aridification, and vicariance as drivers of allopatric speciation in the *Etheostoma lepidum* species complex.

0383 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Breanna Machuca¹, Kelley van Hees², David Ebert²

¹California State University, Monterey Bay, Seaside, CA, USA, ²Moss Landing Marine Laboratories, Moss Landing, CA, USA

Trophic Ecology of Coastal Elasmobranchs Using Stomach Content and Stable Isotope Analysis

Sharks and rays are apex predators that inhabit Elkhorn Slough, a tidally influenced estuary in Central California. These elasmobranchs use the Slough as a seasonal habitat and food source. These are upper trophic level predators that may be threatened by changes in their habitat, especially to their food source. Leopard sharks (*Triakis semifasciata*), bat rays (*Myliobatis californicus*), and thornback rays (*Platyrhinoidis triseriata*) were used to evaluate how trophic positions and food web relationships have changed over time, using a study by Barry et al. (1996) as a comparison. Stomach-gut Content Analysis (SCA) was used to visually analyze the stomach contents and ten replicates per species of liver and white muscle tissue were analyzed for trophic position using Stable Isotope Analysis (SIA). Additionally, whole frozen prey items underwent SIA for trophic position to provide a basis for the food web. Comparing the results from SIA and SCA identified whether the elasmobranchs were benthic or pelagic feeders and what percentage of their diet is dependent on prey items available within Elkhorn Slough. The results will determine if and how trophic relationships are changing in a key estuarine habitat, and assist with management decisions and conservation of these elasmobranch species.

0240 Chemical Ecology Symposium, Crystal 3 & 4, Sunday 19 July 2015

Stephen Mackessy

UNC, Greeley, CO, USA

Biochemical Ecology and Snake Venoms: Biological Roles, Phenotypic Plasticity and Venom Evolution

Many species of advanced snakes produce moderate to highly complex venoms which are used to subdue prey chemically and to facilitate prey handling and digestion. Advances in -omics technologies have accelerated the ability to probe deeply into the venom proteome and transcriptome, and many venoms have been analyzed in great detail. However, downsides to this sensitivity include confusion over what exactly constitutes a venom toxin, as opposed to gland housekeeping proteins and transcripts. Further, thousands of different proteins are expressed in cells, but only about 24 protein families constitute venom toxins. Using the venoms of rattlesnakes, elapids and several rear-fanged colubrids, and a transcriptomic analysis of Burmese Python tissues, we address the question of identifying toxins in venoms unequivocally. Orthologs of venom genes are widely distributed in non-gland tissues, and many potential venom toxins (transcripts) are absent from the suite of proteins present in the secreted venom. Although a single venom may contain 100 or more components, major venom constituents, can have a profound and over-arching effect on prey immobilization, regardless of the presence of other venom toxins. Venom analysis therefore is presented with a quandary: does more precise detection capability actually inform better on biological roles of venoms? It is argued here that the effects of minor venom constituents are currently irrelevant to the main biological roles of venoms as trophic adaptations. However, molecular diversification of venoms, particularly at the transcriptome level, could increase plasticity of phenotypic expression as well as facilitate more rapid evolution of the venom proteome.

0563 Cypriniformes Biology, Crystal 1 & 2, Sunday 19 July 2015

Richard Mahoney, Erik Halverson, Todd Huspeni, Justin Sipiorski

UW-Stevens Point, Stevens Point, WI, USA

Age, Growth, Body Condition and Spawning Phenology of *Luxilus cornutus* (Cyprinidae: Actinopterygii) in Wisconsin: A Statewide, 65-year Perspective

We are currently constructing a dataset comprising all specimens of the Becker Memorial Ichthyology Collection (University of Wisconsin- Stevens Point Museum of Natural History) for the Common Shiner (*Luxilus cornutus*). Specimens have been collected from throughout the state of Wisconsin over the past 60 years. Our accessioning and cataloging is ongoing, and to date we have currently gathered data from over 10,000 specimens. This represents approximately 30% of the total individuals in this collection. For each specimen cataloged, we have recorded total length (mm),

preserved mass (g), gonad mass (g), and estimated the age of each by counting scale annuli. Length-weight regressions and length-at-age analyses were performed to characterize the size and age structure of past populations of Common Shiners. The monthly gonadal somatic index (GSI) was also calculated and this metric had its highest value across Wisconsin populations in the month of June. This finding is consistent with the natural history observation that spawning for this species generally peaks in July in Wisconsin. We will design manipulative experiments to determine if otoliths provide a more accurate age estimate compared to scales. Ultimately we will use this dataset to explore long-term trends in age, growth, body condition, and spawning phenology patterns throughout Wisconsin. We will analyze how these patterns may correlate with ecological, land-use, and climatological variables. We will also resample historically collected sites to assess potential changes in the above life history parameters and how these vary within and among populations over time.

0566 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Richard Mahoney, Kevin Schmidt, Christopher Hartleb

UIW-Stevens Point, Stevens Point, WI, USA

LED Lighting Color Effects on Yellow Perch (*Perca flavescens*) Growth

Many different factors can contribute to growth and survival when raising yellow perch (*Perca flavescens*). Handling, netting, and even walking by the tank can startle the fish which halts feeding and suspends growth. By using in-tank lighting the startle response by fish can be reduced and previous studies have shown that the spectrum of light may also play a significant role. LED lighting is gaining popularity in aquaculture due to low running cost, high light output and longevity. This study will compare the growth and survival of yellow perch raised under five different spectrums of commercially available monochromatic LED lights installed in-tank. In this study, yellow perch will be placed into two recirculating aquaculture systems, with each system having ten, 38-gallon round Fiberglas tanks. Ten fish will be placed into each tank and four replicate tanks will be used for each color light: blue, green, red, yellow and white. Yellow perch will be fed 2-3% of their body weight per day using ST International auto feeders which distribute the food 6-8 times per day. Water temperature will be held constant at 21-22°C using an inline heater and pH, dissolved oxygen and temperature will be monitored daily, as well as Ammonia-N and nitrite-N weekly. Fish growth, length and wet weight will be recorded every two weeks. The predicted results, due to a few previous studies, indicate that fish may grow and survive more efficiently in lighting of the red spectrum.

0416 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Maria Malabarba, Priscilla Silva, Luiz Malabarba

Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil

**Molecular Systematics and Dating of the South American Cichlid
Genus *Gymnogeophagus***

Cichlids are teleost fishes found chiefly in fresh waters. They constitute one of the major vertebrate families with more than 1660 species, of which nearly 600 inhabit the neotropics. Among the Neotropical cichlids, *Gymnogeophagus* Miranda Ribeiro is a geophagin genus distributed in the río Paraguay, río Paraná and río Uruguay drainages and also in the coastal rivers of Uruguay and southern Brazil. Its monophyly is supported by two derived features: the absence of supraneurals and the presence of a forward spine in the first dorsal-fin pterygiophore. Besides a fossil species (*G. eocenicus*), the genus includes 11 recognized and five still undescribed living species so far. Herein, based on a comprehensive data sampling, we proceed to the first molecular phylogenetic and divergence timing analyses for this genus. Parsimony and Bayesian analyses sequences of two mitochondrial (Cytochrome c oxidase I and Cytochrome b), and two nuclear genes (Myh6 and S7) are performed to investigate the phylogenetic patterns among *Gymnogeophagus* species. In addition to developing concatenated multigene phylogenies, the timing of divergence of *Gymnogeophagus* using related molecular clocks and fossil calibrations methods will be discussed.

0067 General Ichthyology I, Crystal 3 & 4, Friday 17 July 2015

Lacey Malarky, Tracey Sutton

Nova Southeastern University, Dania Beach, FL, USA

Faunal Composition and Distribution of Pelagic Larval Flatfishes (Teleostei: Pleuronectiformes) in the Northern Gulf of Mexico: Connectivity Between Coastal and Oceanic Ecosystems

Pleuronectiformes (flatfishes) occur throughout the global oceans, and have high ecological and commercial importance in some areas. Though much is known regarding life history, abundance, and distribution for the benthic adult stages of flatfish species, much less is known about the pelagic larval and juvenile phases of flatfishes in the open ocean. Taxonomic uncertainty and limited sampling in the oceanic Gulf of Mexico have led to data gaps with respect to the distribution of early life history stage flatfishes in this region. Pleuronectiform specimens collected during six cruises in the northern Gulf of Mexico from 2010-2011, as part of the NOAA Offshore Nekton Sampling and Analysis Program, were quantified and identified to lowest taxonomic category. Results of the first large-scale distributional analysis of pleuronectiform larvae and juveniles in the northern oceanic Gulf of Mexico will be presented. During the M/V Meg Skansi 7 (April - June 2011) and NOAA FRV Pisces 10 (June - July 2011) cruises, 566 flatfish specimens

were collected, representing four families and ten genera. Species composition was dominated by *Bothus* spp. at 78%, *Trichopsetta ventralis* at 9%, and *Citharichthys* sp. at 5% - the remaining seven genera comprised less than three percent each. With respect to vertical distribution, discrete-depth sampling revealed that 56% of specimens occurred between 0 and 200 m, 15% between 200 and 600 m, < 10% between 600 and 1000 m, 15% between 1000 and 1200 m, and < 10% between 1200 and 1500 m.

0213 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Alejandro Marquez¹, Eugenia Errico³, Julia L. Tourinho², Alfredo N. Pereira³

¹Comisión Administradora del Río Uruguay, Paysandú, Uruguay, ²Facultad de Ciencias, UDELAR, Montevideo, Uruguay, ³Dirección Nacional de Recursos Acuáticos, Montevideo, Uruguay

Genetic Confirmation of the Presence of Hybrids of Sorubim

***Pseudoplatystoma coruscans* and *P. reticulatum* in the lower basin of Río de la Plata**

The sorubim are emblematic species in Uruguay and Parana rivers, constituting one of the main components of artisanal and recreational fisheries. The main objective of this work was to evaluate the genetic integrity of the two species of sorubim (*P. coruscans* and *P. reticulatum*) occurring in the lower basin of Río de la Plata. For the study, we analysed a fragment of approximately 500 bp of the mitochondrial control region of 95 adult individuals phenotypically identified as *P. coruscans* (n = 70) and *P. reticulatum* (n = 25), collected in four localities of the lower basin of Río de la Plata. The sequences obtained formed two monophyletic groups with robust support, confirming the existence of the two species described for the studied region. However, for nine individuals of both species, there was no correlation between phenotypic identification and mitochondrial genotype, indicating, for the first time, the presence of hybrids in the lower basin of Río de la Plata. The detection of hybrids of sorubim in the Río de la Plata basin is not new, as it was already detected in the upper basin by previous study, and it suggests that aquaculture could be contributing to the presence of such individuals in the whole basin of Río de la Plata, including lower and median Parana and Uruguay Rivers. This could pose a threat of degradation of the genetic diversity of both species, which in the long run, may pose a risk to the permanence of these as two distinct evolutionary units.

0314 Fish Genetics, Carson 3, Saturday 18 July 2015

Nicholas Marra^{1,2}, Minghui Wang¹, Paulina Pavinski Bitar¹, Qi Sun¹, Michael Stanhope^{1,2}, Mahmood Shivji^{2,3}

¹Cornell University, Ithaca, NY, USA, ²Save Our Seas Shark Research Center, Dania Beach, FL, USA, ³Nova Southeastern University, Dania Beach, FL, USA

Genome Sequence of an Apex Predator, the White Shark (*Carcharodon carcharias*)

The white shark, *Carcharodon carcharias*, is one of the most prominent species of the Lamnidae, achieving notoriety among biologists and the general public alike. Here we provide the first draft genome of a lamnid species and the first elasmobranch genome from a large apex predator. Using a mixture of single-end, paired-end, and mate-paired Illumina sequencing libraries, we obtained 309 GB of sequence data from a single individual caught off the coast of Delaware. Employing a K-mer counting method we determined the genome size of the white shark to be 5.03 GB, and from that we estimate our genome sequence coverage to be approximately 61X. We also assembled the white shark mitochondrial (mt) genome, adding a full mtDNA genome from an Atlantic individual to the existing mt genome data from the Pacific. Our draft assembly of the white shark nuclear genome yielded 14,317 scaffolds over 10 KB and 1,236 contigs greater than 1 MB; the longest scaffold was 10,508,623 bp and the scaffold N50 was 1.14 Mb. Using annotations of gene-sized scaffolds, we studied genes related to common questions in elasmobranch biology (e.g. evolution of adaptive immunity) and questions peculiar to the white shark and its predatory lifestyle (e.g., the presence of genes that play a role in vision, olfaction, and regional endothermy). The genome appears to lack the high levels of repetitive content or transposable element activity often associated with large genomes. In light of this, we attempted to identify the factors that drive large genome size in this species.

0136 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Ashley N. Marranzino, Jacqueline F. Webb

University of Rhode Island, Kingston, RI, USA

Novel Observations of Neuromast Receptor Organ Distribution in Stomiiform Fishes

The mechanosensory lateral line system in deep-sea fishes, especially in Stomiiformes, is relatively unknown. Unlike melamphoids and gadiforms, which have obvious widened lateral line canals and large neuromasts, stomiiforms appear to have less prominent lateral line canals and few superficial neuromasts. We examined two important stomiiform taxa: hatchetfishes (*Argyropelecus*: Sternoptychidae) and bristlemouths (*Cyclothone*: Gonostomatidae). Species of *Argyropelecus* and *Cyclothone* were collected at

sea (tucker trawl) or obtained from museum collections and examined using clearing and staining, whole mount hematoxylin staining, histology, μ CT imaging, and SEM. Contrary to Handrick (1901), who reported the presence of an unusually small number of neuromasts in *Argyropelecus*, we observed lines and clusters of densely placed superficial neuromasts above and below the eye, on the cheek, along the mandible, and in discrete vertical lines on trunk, reminiscent of some gobies. Canal neuromasts were identified in the unossified and partially enclosed supraorbital canals. In contrast, *Cylothone* has no cranial lateral line canals and small superficial neuromasts distributed in similar locations on the head and trunk; they were not as highly proliferated as in *Argyropelecus*. Our study revealed that the skin of these fishes is extremely thin and thus easily subject to damage during collection. Our novel observations of neuromast distributions were dependent upon our ability to obtain high-quality specimens of deep-sea fishes. This work was funded by an NSF Graduate Research Fellowship and an ANMH Lerner Grey Fund Award to A.N. Murraino.

0226 Fish Ecology I, Carson 3, Sunday 19 July 2015

Eddie Marsh-Matthews, William Matthews

University of Oklahoma, Norman, OK, USA

Stream Fish Community Dynamics: Confronting the Conventional Wisdom

We used data on 31 stream fish communities (each sampled at least four times) to compare community dynamics across a wide range of habitat types and environmental conditions at sites across Oklahoma and Arkansas (plus one site in Virginia). For each community we determined eleven emergent properties: number of families, total species detected, average number of species detected per collection, variation in number of species detected, number of core species, percent composition of the community made up of core species, variation in percent core, average diversity, variation in diversity, average evenness, and variation in evenness. We used these emergent properties to perform a Principal Components Analysis (PCA) of the 31 communities in community character space. PC-1 represented a gradient of species diversity and community variation, which were negatively correlated. PC-2 represented a gradient in the importance of core species versus the variation in the contribution of core species. We examined the effects of a number of intrinsic and extrinsic factors on the positions of communities in PCA space. Position of communities on PCA biplots were not related to geography or to the dominant family, except for those in the Neosho-Verdigris basin, all of which were dominated by mosquitofish and were characterized by high variability in community structure. Communities in intermittent habitats were more variable than those in perennial systems. Communities in smaller, shallower streams were more variable in their emergent properties and communities from higher elevation sites and with higher stream gradient were less variable.

0462 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

Heather Marshall¹, Diego Bernal², Gregory Skomal³, Richard Brill⁴, Peter Bushnell⁵, Nick Whitney¹

¹Mote Marine Laboratory, Sarasota, FL, USA, ²University of Massachusetts Dartmouth, North Dartmouth, MA, USA, ³Massachusetts Division of Marine Fisheries, New Bedford, MA, USA, ⁴National Marine Fisheries Service, NOAA, Gloucester Point, VA, USA, ⁵Indiana University South Bend, South Bend, IN, USA

The Importance of Physiology in Shark Mortality Assessments and Fisheries Management

The National Marine Fisheries Service recently released the Atlantic Highly Migratory Species Management-Based Research Needs and Priorities, with research needs including establishing post-release mortality rates for commercially caught sharks. Published at-vessel mortality rates indicate that capture-associated mortality is species-specific. Through assessments using various types of electronic tags (e.g., pop-up satellite archiving tags and accelerometer tags), such species-specific responses appear to carry over to post-release mortality rates as well, with rates ranging from 0% (*Galeocerdo cuvier*, and *Carcharhinus leucas*) to 75% (*C. brevipinna*). Research assessing interspecific mortality rates is critical, but it is also imperative to understand the physiology underlying such mortality events. The physiological upset sharks experience while captured on fishing gear can result in irreversible cellular damage, resulting in immediate or delayed mortality. Previous research on shark stress physiology has found that changes in various blood stress indicators (e.g., lactate) are correlated with magnitude of the capture stress, and that blood potassium levels are significant ($p < 0.05$) predictors of both at-vessel and post-release mortality. The future of such research lies in pointed physiological studies to understand how stress indicators and mortality are linked, and how such information can be used to understand the capture-related stress response in teleosts as well. The further elucidation of mortality indicators, and what is driving such mortality events, can be used on various scales in the future to predict mortality rates, and develop mitigation measures for fisheries management.

0372 Fish Conservation & Management, Carson 3, Saturday 18 July 2015

Karen Martin, Vincent Quach, Emily Pierce

Pepperdine University, Malibu, CA, USA

Population Trends in California's Original Surfers, the Beach-Spawning *Leuresthes tenuis*

Famous for unique spawning behavior, California Grunion *Leuresthes tenuis* surf onto sandy beaches to lay eggs out of water. This endemic silverside fish, found only off

California and Baja California, shares critical spawning habitat with millions of beachgoers along one of the world's most heavily populated coastlines. Spawning occurs during spring and summer, the times of heaviest human use. Although regulations offer some protection, anthropogenic impacts include a recreational fishery with bare-handed catching, and habitat loss from shoreline armoring and beach erosion. The stock cannot be assessed with traditional fisheries methods, so evaluation of population status and trends is difficult. For 13 years, spawning runs have been monitored across the habitat range with the help of citizen scientists Grunion Greeters. Greeters evaluate the runs and other ecological features, including incidence of animal predation and recreational fishing. Analysis of data over time shows a drop in the median strength of the runs, a decrease in the probability of an observer witnessing a significant run, and a decline in the number of moderately sized spawning runs. While large runs still occur, fisheries-independent data indicate that this species has never been common. Management of this species includes a brief closed season and gear restrictions, but no bag limits and little enforcement of illegal take in this midnight recreational fishery. Protection has been increased in 2015 by the enforcement of "no take" reserves in Marine Protected Areas. Additional efforts may be necessary in the future to conserve this iconic, charismatic California species.

0047 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Rene Martin, Matthew Davis

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

Evolution of Jaw Shape and Length Variation in Deep-sea Lanternfishes (Teleostei: Myctophiformes)

Lanternfishes (Myctophiformes; ~260 species) are one of the most species-rich groups of fishes endemic to deep sea and open ocean environments. They account for a large proportion of mid-water (200-1,000 meters) fish biomass worldwide, perform daily vertical migrations for the purpose of feeding, and play a major role in the oceanic ecosystem by transferring energy to deeper oceanic levels. Lanternfishes possess a number of hypothesized evolutionary adaptations (e.g., bioluminescent organs, variation in jaw size and shape, variation in dentition) that may have facilitated their high diversification in their open-ocean environment, which has few physical reproductive isolating barriers. There have been few studies on feeding structures in lanternfishes, and no studies that have quantitatively investigated variation in jaw shape and length. Previous studies have suggested that lanternfishes have tremendous variation in jaw length across their radiation. Coupled with other reproductive isolating mechanisms (species specific and sexually dimorphic bioluminescent structures), the variation in elongation of the jaws could be a potential diversification driver if it is allowing for niche differentiation in the open ocean. In this study we use geometric morphometrics and mensural measurements to investigate the amount of variation in

jaw shape and length within lanternfishes, and the evolutionary pattern of changes in jaw shape and length across the lanternfish radiation.

0145 Fish Morphology & Histology, Crystal 1 & 2, Saturday 18 July 2015

Christopher Martinez¹, F. James Rohlf³, Michael Frisk²

¹Department of Ichthyology, American Museum of Natural History, New York, NY, USA, ²School of Marine & Atmospheric Sciences, Stony Brook University, Stony Brook, NY, USA, ³Ecology & Evolution, Stony Brook University, Stony Brook, NY, USA

Sexual Dimorphism in Sister Species of *Leucoraja* Skate and Its Relationship to Reproductive Strategy and Life History

Instances of sexual dimorphism occur in a great variety of forms and manifestations. In some skates (Batoidea: Rajoidei), pectoral fins of mature males create a distinct bell-shaped body form not seen in females, although the pattern has never been evaluated in detail. This particular form of dimorphism is present in each of the sister species *Leucoraja erinacea* and *Leucoraja ocellata*, but differences between sexes are much greater in the former. In order to understand the nature and potential causes of pectoral dimorphism, we used geometric morphometrics to investigate allometry of fin shape in *L. erinacea* and *L. ocellata* and its relationship to the development of reproductive organs, based on previous work on the bonnethead shark, *Sphyrna tiburo*. We found that allometric trajectories of overall pectoral shape were different in both species of skate, but only *L. erinacea* varied significantly with respect to endoskeleton development. Male maturation was characterized by a number of sex-specific morphological changes, which appeared concurrently in developmental timing with elongation of cartilage-supported claspers. We suggest that external sexual dimorphism of pectoral fins in skates is an unintended product of skeletal growth needed for clasper development. Further, the magnitude of male shape change appears to be linked to the differential life histories of species. This work reports for first time that pectoral dimorphism is a persistent feature in rajoid fishes, occurring in varying degrees across several genera. Lastly, our results suggest that pectoral morphology may be useful as a relative indicator of reproductive strategy in some species.

0146 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Christopher Martinez, John Sparks

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

Morphological Diversity in the Cichlid Subfamilies Etroplinae and Ptychochrominae

Etroplinae and Ptychochrominae represent two subfamilies of the highly diverse family Cichlidae, with origins purportedly linked to Gondwanan vicariance. Occurring in Madagascar and South Asia, these groups are smaller and much less studied than their confamilial counterparts in the Neotropics and Africa. For this work, our goal was to better understand the morphological diversity of etropline and ptychochromine cichlids in the context of their current lifestyles but also their evolutionary histories. We used geometric morphometrics to quantify and compare morphological diversity of overall body shape and internal structure of oral jaws between the two cichlid subfamilies. In addition, we evaluated jaw variation in terms of a four-bar linkage, which has been used as a model for jaw mechanics in a number of teleosts. Variety of overall body form and jaw morphology was larger in the ptychochromines, although etropline cichlids also displayed interesting morphological patterns that appear to be habitat specific. This suggests different patterns of diversification in these closely related clades. Results from this work will be used for future research to develop a modeling procedure that explores hypothetical pathways in oral jaw morphospace to represent functional transitions from ancestral to derived forms. Overall, this research is critical for understanding the diversity exhibited in two groups that include a number of endemic Malagasy species, many of which are exceedingly rare or even recently extinct.

0259 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Ninon Martinez¹, Ryan Thoni¹, Hector Espinosa², Richard Mayden¹

¹Saint Louis University, Saint Louis, MO, USA, ²Universidad Autonoma de Mexico, Mexico DF, Mexico

New Species of *Gila* from the Upper Rio Mezquital, Durango, Mexico

The genus *Gila* has been one of the more taxonomically challenging groups of cyprinid fishes in North America. The rios Mezquital and Nazas are hypothesized to have had a historical connection, as indicated by similar aquatic assemblages. Recent collections from the region have allowed for more adequate analyses of *Gila* from these and other nearby drainages. While several species are identified in the arroyos and rivers of Northern Mexico, no samples were reported by Miller (2006) from the Rio Mezquital Drainage. Specimens of *Gila* have been taken from multiple localities in eastern and southern headwaters of this drainage, and materials were found from this area and in

small playas and arroyos NE of Durango in ichthyological collections. Morphological comparisons of Mezquital populations of *Gila* clearly indicate that divergent and diagnosable forms exist in the system, one in the eastern and southern headwaters and the second in the area NW of the City of Durango. Tissue samples exist for the former form but not the latter. Molecular analyses of this form clearly indicate that it is a distinct lineage from any species of *Gila* in Mexico. It is hypothesized that a vicariance event, linked with the headwater transfer of the Rio Tunal to the Rio Mezquital, resulted in the separation of these bodies of water, and permitted isolation for divergence, which has been observed in co-distributed species.

0086 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Katherine P. Maslenikov¹, James W. Orr², Nirupam Nigam³

¹University of Washington, Burke Museum of Natural History and Culture, and School of Aquatic and Fishery Sciences, Seattle, WA, USA, ²NOAA Fisheries Service, Alaska Fisheries Science Center, Seattle, WA, USA, ³University of Washington, School of Aquatic and Fishery Sciences, Seattle, WA, USA

Distal Radials in the Pectoral Fin of Snailfishes (Liparidae): A New Character for Phylogenetic and Alpha-level Systematics

The phylogenetics of snailfishes (Liparidae) are poorly understood. Over 350 species are presently described in the family and many undescribed species are known. The family comprises several genera, many of which contain single or very few species while three (*Liparis*, *Paraliparis*, and *Careproctus*) contain the bulk of known species. Reasons for the lack of a clear phylogenetic hypothesis include the early state of alpha-level taxonomy, the poor preservation of many specimens, the rarity of both morphological and genetic material, and a lack of phylogenetically informative morphological characters. Among morphological characters, those associated with the pectoral girdle have been invaluable in diagnosing species and putative clades. However, early efforts described methods using only alizarin red stain for bone to identify and describe components of the girdle. While allowing significant advances in species descriptions and leading to a better understanding of snailfish evolution, at least one set of cartilaginous components, distal radials, has thus been overlooked and was thought to be absent. Recently, however, by using standard counterstaining techniques with alcian blue for cartilage, we found distal radials to be present in nearly all species of snailfishes we examined from the eastern North Pacific. Moreover, numbers and sizes of distal radials exhibit little intraspecific variation but vary widely among species, providing a potentially useful character for alpha-level systematics as well as for higher-level phylogenetics.

0158 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Rui Matsumoto¹, Miwa Suzuki², Kiyoshi Asahina², Kiyomi Murakumo¹, Yosuke Matsumoto¹, Keiichi Ueda¹, Keiichi Sato³

¹Okinawa Churaumi Aquarium, Okinawa, Japan, ²Nihon University, Kanagawa, Japan,

³Okinawa Churashima Research Center, Okinawa, Japan

Long-term Observation of the Behavioral and Hormonal Trends in Male Whale Shark in the Okinawa Churaumi Aquarium

The maturation cycle of a male whale shark kept in the Okinawa Churaumi Aquarium for 20 years was recorded. This shark (total length [TL], 4.6 m) was accidentally caught by local fishermen in March 1995. In order to determine the exact size of this shark at maturation, we have monitored the clasper elongation; the elongation was defined as the ratio of the outer length (COL) of the clasper to the length of the inner pelvic margin (P2I). Analysis revealed that this ratio increased rapidly from 1.09 (August 2011) to 1.60 (July 2012), and the shark attained a length of 8.5 m TL. A high plasma testosterone level was maintained at 21.49 ng/mL (June 2011-June 2012) during rapid clasper elongation. Additionally, we observed a behavioral change where the whale shark began to rotate its entire body laterally, while crossing both claspers (April 2012) and simultaneously discharged white turbid fluid from its clasper tips (August 2012). We continued to monitor the behavioral and hormonal changes in the shark. In May 2014, the male began demonstrating sexual behavior by pursuing two immature female sharks (7.5 m and 7.4 m TL). In June 2014, we continued to monitor this pursuing behavior and began counting the number of clasper rotating actions as well as measured the hormone levels and water temperature. Current observations indicate that the clasper rotation and pursuing action increased in frequency at higher water temperatures (25-28°C) from June to early August and did not occur in lower temperature waters.

0397 Fish Ecology I, Carson 3, Sunday 19 July 2015

William Matthews, Edie Marsh-Matthews

University of Oklahoma, Norman, OK, USA

Traits of Individual Fish Species and Their Distributions across Environmental Gradients or Success under Adverse Conditions

There is growing interest in “trait based” research, using traits of a large number of species either known explicitly, or inferred from similar species. We review here a potpourri of specific examples from our previous work in which detailed information on traits helps explain distributions of fish across harsh or variable environments. Laboratory tolerance for high temperature (CTMs) or low oxygen relates directly to differences in distributions of fish species across gradients of environmental harshness in the Great Plains, or within individual stream systems. Limits of tolerance, and boom and bust reproductive tendencies, allow some species, like *Gambusia affinis*, to persist in

or rapidly repopulate highly variable local habitats. Flexible reproductive tactics by *Cyprinella lutrensis*, including maturing and reproducing during the first summer of life, production of young far into autumn, and successfully overwintering large numbers of small YOY, also provides this species an advantage in environments of the central United States. Finally, our results with *Etheostoma spectabile* and various other minnows and darters indicate that factors like thermal tolerance, food and habitat use, body size or life history traits can be highly variable across different habitats or in a given year, suggesting that general classifications of species in trait-based models that tacitly assume biological traits to be species-specific, may overlook interesting and important information on variability within species.

0112 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Jessica Maxfield, Kathleen Cole

University of Hawaii Manoa, Honolulu, HI, USA

Uncovering the Secret of Sex Change: Mapping the Sex Change Pathway in Gobiid Fishes

The ability to change sex (hermaphroditism) is a rare reproductive strategy found among teleost fishes. It has been documented in only 27 of 448 fish families. This study aims to understand the development, evolution and diversification of sex change in two species of marine fishes in the family Gobiidae, using a variety of molecular and histological techniques. We have created a developmental series for sex change in one species of goby, *Lythrypnus dalli*, in order to document the morphological changes that take place as a fish transitions from ova producing to sperm producing. We have also sequenced the whole transcriptome of one lobe of the gonad, brain and liver (RNAseq) from fish as they transitioned from ova producing to sperm producing. The RNAseq data will be used to construct coexpression networks, which will allow genes related to sex change and novel genes and splice variants to be identified. Connecting the histological data with the genetic data will elucidate the genetic pathway(s) that lead to a change in reproductive function. Finally, a comparison between *L. dalli* and a closely related species, the Hawaiian *Eviota epiphanes*, will be performed to evaluate the evolution of this characteristic in multiple fish lineages. This will provide key insights into how novel features and diversity arise.

0177 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Richard Mayden¹, Chia-Hao Chang², Wei-Jen Chen³

¹*Saint Louis University, St Louis, MO, USA*, ²*Department of Biological Science and Technology, National Chiao Tung University, Hsinchu, Taiwan*, ³*Institute of Oceanography, National Taiwan University, Taipei, Taiwan*

Relationships of Major Clades in the Order Cypriniformes, Derived from an Expanded Phylogenetic Analysis using Six-Nuclear Genes

Research and public awareness of the diverse Cypriniformes have escalated in the last decade as a result of multiple investigators focusing in on this once poorly known lineage. Cypriniforms are well known for the great diversity of habitats, life histories, adaptations, morphologies, distributions, etc., all of which makes this major group of great interest in comparative evolutionary biology. However, these inquiries demand a phylogenetic framework. The present study is an expansion of our previous analysis using six nuclear genes as phylogenetic markers (RAG1, RH, IRBP, EGR1, EGR2B, and EGR3) to now include at least 823 species. The resulting relations are supportive of and/or consistent with the more recent multi-gene and taxon-rich trees for the group. Many of the same monophyletic groups continue to appear, and the vast majority of relationships have remained consistent through over the last few years during efforts for continued increase in taxon and character sampling. In addition to relationships presented for these nuclear genes, there are many other hypotheses in recent years based on mitochondrial, mitochondrial/nuclear genes, and morphological characters. For the first time species relationships in this order are becoming very clear, opening up many hopeful possibilities for individual or joint adventures to expand the tree and use relationships to address evolutionary questions. A call for researchers around the globe to become involved with increasing the species diversity for these and mitochondrial genes to continue to advance our understanding of these fishes.

0434 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Logan McCardle, Clifford Fontenot

Southeastern Louisiana University, Hammond, LA, USA

The Influence of Thermal Biology on Road Mortality Risk in Snakes

Road mortality is a significant threat to terrestrial vertebrates in many areas, and the novel thermal environment of black-topped roads may represent ecological traps for some species and demographic groups. We investigated the relationship between ambient temperature and road entry in seven snake species in southeastern Louisiana by comparing observations of live snakes on a black-topped road, across measurements of air temperature and road temperature on survey days. Analyses indicated that the seven species could be separated into three significantly different groups based on the temperature conditions under which they were encountered on the road, and that road

temperature was the strongest driver of species differences. Additionally, we compared how air and road temperatures affected occurrence on the road between sexes in *N. fasciata*, *N. cyclopion*, *T. proximus*, and *P. obsoletus*. Males and females of the viviparous species *N. fasciata*, *N. cyclopion*, and *T. proximus* diverged significantly in temperature preferences while males and females of the oviparous species *P. obsoletus* did not. Road temperature was also the strongest driver of differences between sexes. Our results indicate that black-topped roads are an ecological trap that is heavily influenced by sex, reproductive condition, and species specific thermoregulatory requirements, particularly viviparous species.

**0600 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY,
Carson 3, Friday 17 July 2015**

Evan McCartney-Melstad¹, H. Bradley Shaffer¹, Peter L. Ralph⁶, Gideon S. Bradburd⁵, Jannet Vu¹, Erik Lundgren⁶, Franziska C. Sandmeier⁴, Bridgette E. Hagerty³, Chava L. Weitzman², C. Richard Tracy²

¹University of California, Los Angeles, Los Angeles, CA, USA, ²University of Nevada Reno, Reno, NV, USA, ³York College of Pennsylvania, York, PA, USA, ⁴Lindenwood University - Belleville, Belleville, IL, USA, ⁵University of California, Davis, Davis, CA, USA, ⁶University of Southern California, Los Angeles, CA, USA

Full-genome Conservation Genetics: Using Genomic Tools to Evaluate the Impacts of Alternative Energy Development on the Threatened Mojave Desert Tortoise (*Gopherus agassizii*)

Landscape-level planning of alternative energy installations is underway in the Mojave Desert, and several development alternatives are currently being considered. We sequenced and analyzed low-coverage full genome sequences of 270 Mojave desert tortoises (*Gopherus agassizii*) to determine the relative impacts of the five different development alternatives on gene flow across the range of the species. We used novel landscape genetic methods to create a high-resolution map of historical genetic connectivity tuned with the 1.2 trillion base pairs of genetic information that we sequenced for this project. We evaluated development alternatives by removing the proposed development areas from the landscape, calculating the estimated differences in commute times between points on the landscape with those areas removed, and summing the differences across the range of the desert tortoise. We found that removing 3.7% of desert tortoise habitat in the agency-preferred alternative led to an 18% reduction in gene flow across the range of *Gopherus agassizii*, and that the effects of developing individual regions were nonadditive when considered together. We discuss the advantages and pitfalls of working with low-coverage full genome data, as well as plans to incorporate the landscape genetic models into future population viability analyses.

0302 General Herpetology, Carson 1, Friday 17 July 2015

Ryan McCleary, Matthew Lim, R. Manjunatha Kini

National University of Singapore, Singapore, Singapore

Colorspace Modeling of the Whipsnakes (Genus *Ahaetulla*): Implications for Conspecific and Predator-Prey Interactions

Color patterns in snakes are generally categorized as aposematic or cryptic. From a human perspective, whipsnakes of the colubrid genus *Ahaetulla* have intense green coloration that appears similar to their habitat and assumingly provides an effective visual camouflage from predators and prey. These snakes are also known to inflate their nuchal regions when disturbed, thus effectively increasing their size to reveal a black-and-white checkerboard pattern in the skin between the scales. However, empirical data on these colors from both conspecific and interspecific visual perspectives are lacking as are natural history data concerning the primary predators of these species, which are currently undocumented. To improve our understanding of how two species of *Ahaetulla* appear to a range of predators, prey, and conspecifics, we conducted colorimetric studies using reflectance spectrometry and relevant colorspace modeling. We measured several color patches from *A. prasina* and *A. mycterizans* as well as the leaves of several plant species found in the same habitat. Using avian colorspace modeling, we found that the majority of the snake hues were similar to plants, with the exception being the UV-reflective white checkerboard patterns. Interestingly, although the greens of snakes and plants appeared similar to each other from an avian visual perspective, these same hues differed from a snake's perspective based on reptilian trichromatic colorspace modeling. Together, these results suggest that color in these snakes serves a triple function: crypsis from predators and prey (green), species-specific recognition (green), and defense against predators (checkerboard).

0407 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Eric McCluskey, Thomas Hetherington

The Ohio State University, Columbus, OH, USA

Role of Historical Land Use in the Distribution of Eastern Massasauga Rattlesnake Habitat in Northeastern Ohio

Historical processes play an important role in the patterns of biodiversity we observe today. Of particular interest to conservation biologists and ecologists are the roles of prior land use and land cover change in influencing the present day distribution of rare species and ecosystems. We used object-based classification techniques to analyze historical aerial photographs (covering ~75 years) in order to quantify anthropogenic land use and successional transitions in land cover to gain a better understanding of how these processes have influenced the present day distribution of a threatened

species, the eastern massasauga rattlesnake (*Sistrurus catenatus catenatus*) in northeastern Ohio. We compared these patterns of land use with habitat suitability maps generated from species distribution models based on current conditions. We found considerable overlap between prior agricultural areas and current suitable habitat. We also observed current massasauga populations residing in habitat patches that had previously been agricultural fields. In the absence of natural disturbance agents, agricultural fields that were allowed to go fallow represent an important source of early successional habitat vital to massasauga in this part of their range. These findings, coupled with observed increases in tree cover, which is detrimental to massasaugas, provide evidence for the role of agricultural land use as an important contributing factor to the distribution of massasaugas and their habitat in northeastern Ohio.

0317 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Hannah McCurdy-Adams¹, Jeff Hathaway², Jacqueline Litzgus¹

¹Laurentian University, Sudbury, Ontario, Canada, ²Scales Nature Park, Orillia, Ontario, Canada

Anthropogenic Influences on Chronic Stress and Patterns of Nest Predation in Freshwater Turtles

Turtles and their populations face many threats, both indirect and direct. Indirect threats affect physiology by re-directing resources from production to maintenance, while direct threats cause mortality. We are investigating the indirect and direct impacts of human development on turtles by examining chronic stress levels and nest predation patterns across an anthropogenic density index gradient. Animals near human-altered landscapes exhibit high levels of stress hormones that have been associated with decreased fitness. We hypothesize that if human presence increases the long-term stress levels of turtles, then turtles at field sites closer to anthropogenic structures will display higher levels of corticosterone in their claws than turtles from more pristine field sites. We collected claw samples from 260 turtles of 3 species from locations with varying human impacts, and these samples are currently undergoing enzyme immunoassay analyses. A number of studies have found that the highest predation risk to turtle nests is within the first week after the eggs are laid; however, other studies have found that predation occurs throughout the incubation period. We hypothesize that if human presence increases predator abundance, then the frequency of predation events on turtle nests will be greater at field sites closer to anthropogenic structures than at more pristine field sites. In summer 2014, we found 43 Snapping Turtle nests; we are currently examining predation frequency of these nests in relation to human impacts. Preliminary results will be presented and discussed. Understanding these effects will aid in the recovery and conservation of turtle populations.

**0521 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Matthew McElroy¹, Adrián Nieto Montes de Oca², Adam Leaché¹

¹University of Washington, Seattle, WA, USA, ²UNAM, Mexico City, Mexico

**Comparison of Time-Calibrated Phylogenies Reveals Historical Admixture in
Sceloporus.**

Discordant gene trees can obscure phylogenetic inference, but they may also provide the sole signatures of historical hybridization between species. For instance, deep nuclear divergence in concert with recent mitochondrial DNA (mtDNA) divergence may result from recent mtDNA introgression. Alternatively, nuclear genome conversion may result from extensive nuclear introgression, which may only be fully understood in the context of deeply divergent mtDNA genomes. We describe a new example of gene tree discordance in spiny lizards (*Sceloporus*) involving *S. exsul*, an elusive species that is restricted to a disjunct island of the Chihuahuan desert in the state of Queretaro. We differentiate recent and extensive nuclear gene flow from ancient mitochondrial introgression using two time-calibrated phylogenies. Phylogenies were estimated from mtDNA and from 500+ nuclear genes obtained using targeted sequence capture. These new data suggest gene tree discordance results from gene flow approximately 4-5 million years ago between the lineage leading to *S. exsul* and either *S. cautus* or an extinct *Sceloporus* species. We discuss our results within the context of the ecology and biogeography of *Sceloporus*.

0076 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Thomas McElroy¹, Lucianna Araujo¹, LeeAnn Fishback², William Ben Cash³

¹Kennesaw State University, Kennesaw, GA, USA, ²Churchill Northern Studies Centre, Churchill, Manitoba, Canada, ³University of Central Arkansas, Conway, AR, USA

**Genetic Structure in Wood Frogs (*Lithobates sylvaticus*) Near a Northern Edge
of Distribution**

We investigated the population genetic structure of wood frogs (*Lithobates sylvaticus*) collected in boreal and tundra habitats near Churchill, Manitoba, Canada, which approaches the northern edge of this species distribution. Previous studies in other regions on this species have revealed significant subdivision among populations at large (20 km) spatial scales and high gene flow within 5 km. We assayed a set of 15 microsatellite loci used in previous studies for 160 specimens collected for this study. Our study revealed extensive genetic diversity among the samples for all of the loci surveyed, but a significant reduction in heterozygosity compared to other studies. We detected significant population structure at smaller spatial scales than previously reported. Analysis using STRUCTURE revealed population genetic clustering associated with different habitat types found around Churchill, Manitoba. These data also suggest

that migration may be dominated by movement from boreal and transition habitats to tundra habitats. Understanding the genetic composition and ecology of edge populations can provide key information on the environmental and demographic factors shaping species' geographic ranges.

0577 Herp Behavior, Carson 4, Friday 17 July 2015

James McLister¹, Shane Conway², Sunny Boyd²

¹Indiana University South Bend, South Bend, IN, USA, ²University of Notre Dame, Notre Dame, IN, USA

Size-Dependent Male Phonotaxis in Grey Treefrogs, *Hyla versicolor*, in Response to Stimuli of Different Intensities

Male spatial distribution within a chorus may play an important role in male-male interactions and male reproductive success, but is not well studied in *Hyla versicolor*. One simple model of spatial distribution involves the use of sound intensity to gauge and regulate nearest neighbor distance, such that males would tend to move toward quiet stimuli but away from loud stimuli. To test this model, males (n = 37) were released inside an arena at a point 1.5 m in front of a speaker that was either silent (control) or continuously repeating the same pre-recorded *H. versicolor* call at an intensity of either 56, 68, or 90 dB (relative to the release point) and their movement within the arena was tracked for 15 minutes. Net preference (amount of time spent closer to the speaker relative to the release point minus the amount of time spent farther away) and final distance (from the speaker) were recorded for each trial. Body size (SVL) was found to be a significant covariate of both net preference and final distance, with smaller males tending to move towards the speaker and larger males tending to move away, when sound stimuli were used; SVL did not correlate with net preference or final distance in the silent control. ANCOVA, using SVL as a covariate, found no significant difference among the different dB levels. These results suggest larger males spread themselves out in a chorus while smaller males orient themselves closer to other males.

0546 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Caleb McMahan¹, Yue Li², Kyle Piller³, Prosanta Chakrabarty²

¹The Field Museum of Natural History, Chicago, IL, USA, ²LSU Museum of Natural Science, Baton Rouge, LA, USA, ³Southeastern Louisiana University, Hammond, LA, USA

Systematics and Taxonomy of *Awaous banana* (Teleostei: Gobiidae)

The diadromous goby *Awaous banana* is distributed along the Atlantic and Pacific slope from Mexico (and some localities in southern United States), throughout Central America, to northern South America. Additional species have been proposed within this taxon and the limits and validity of these species remain unresolved. The goal of this study was to assess phylogenetic structure within this widespread species, and use the results from this analysis to guide a re-examination of the morphological variation within *A. banana*. Comparisons will be made between this species and phylogeographic patterns observed based on other diadromous species in the region.

0043 Herp Conservation I, Carson 1, Saturday 18 July 2015

Lauren McPherson, Jim Anderson

West Virginia University, Morgantown, WV, USA

Comparing Amphibian Metamorphic Success Between Created and Natural Wetlands

Previous studies on the success of wetland mitigation indicate that created wetlands and natural wetlands differ in their ability to provide amphibian habitat. To isolate potential causative factors, we reared larval spring peepers (*Pseudacris crucifer*) and wood frogs (*Lithobates sylvaticus*) in twelve mesocosms containing water from three created wetlands and twelve mesocosms from three reference (natural) wetlands in West Virginia and evaluated effects of water quality on metamorphosis. Spring peepers experienced similar metamorphic success between created and natural wetland mesocosms ($P > 0.05$). Wood frog mass (created: mean = 0.59 g, SE = 0.02; natural: mean = 0.66 g, SE = 0.02) ($P = 0.052$) and body length (created: mean = 14.8 mm, SE = 0.17; natural: mean = 15.2 mm, SE = 0.12) ($P = 0.051$) upon completion of metamorphosis were greater in natural wetlands. Wood frog length of larval stage was shorter in natural wetlands (mean = 33.5 days, SE = 0.11) than in created wetlands (mean = 34.4 days, SE = 0.27) ($P = 0.011$). A shorter larval period and large body size at metamorphosis are ideal traits for amphibian life history. Water quality measurements of dissolved oxygen, pH, conductivity, temperature, and total nitrogen were similar between created and natural wetlands ($P > 0.05$) and were unable to explain the differences in metamorphic success of the wood frog. These results suggest that created wetlands may function similarly to natural wetlands in supporting spring peepers, but wood frogs experience higher metamorphic success in natural wetlands.

0122 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Emily Meese, Christopher G. Lowe

CSU Long Beach, Long Beach, CA, USA

Finding a Resting Place: How Environmental Conditions Affect the Spatial Distribution of Benthic Elasmobranchs at Big Fisherman's Cove, Santa Catalina Island

Ectothermic elasmobranchs are known to seek out habitats and environmental conditions to optimize their energetic requirements. Spatial distribution patterns of three species, bat rays (*Myliobatis californica*), shovelnose guitarfish (*Rhinobatos productus*), and round stingrays (*Urobatis halleri*) were used to determine resting habitat within Big Fisherman's Cove (BFC), Santa Catalina Island. Distribution patterns of individuals were determined via field observation surveys and related to detailed georeferenced habitat maps. All species were found associated with sand and vegetated/sand substrata; however, all three species selected their substrata disproportionately from what was available in the survey area within the cove ($p < 0.001$). Seafloor water temperatures were stratified by distance to the shoreline (range: 17-21 °C), and differed between two survey periods (fall 2013 and summer 2014). In the fall, there was a significantly higher density of all three species in areas with water temperatures ~18 °C (range: 17.0 - 20.75) ($p < 0.001$). Bat ray density increased in the summer around areas with temperatures between 20.25 - 20.75 °C in BFC, while they had a more random spatial distribution in the fall. All three species demonstrated a hierarchical habitat selection by prioritizing either substrata type or temperature ranges. Aggregating elasmobranchs can potentially be more susceptible to exploitation when at these sites. Therefore, understanding how individuals select their resting habitat and environmental conditions may provide managers with opportunities to provide better protection for these species.

0448 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Savannah Michaelsen, Kyle Piller

Southeastern Louisiana University, Hammond, LA, USA

Genetic Structure and Migration Patterns of Red Drum (*Sciaenops ocellatus*) across the Northern Gulf of Mexico

Understanding population structure is important and necessary in order to effectively manage fisheries. Although relatively little is known about the population structure of stocks of many important marine species, especially in the Gulf of Mexico, molecular technologies and bioinformatics allow for a more comprehensive assessment than

traditional approaches. The red drum (*Sciaenops ocellatus*) is a marine-estuarine fish that is of great recreational importance in the northern Gulf of Mexico. This study incorporated twenty microsatellite markers and a 370bp fragment of mitochondrial DNA (D-loop region) to examine spatial aspects of population structure for red drum populations across the major estuaries and offshore areas of the northern Gulf of Mexico from Texas to Florida. Data from both inshore (juvenile/subadults) and offshore (adult) populations were gathered, and migration patterns, genetic diversity, and genetic structure were evaluated and compared between the two populations. Offshore populations show lower genetic diversity, inbreeding, and pairwise F_{st} values in comparison to inshore populations. Inshore populations possess an isolation by distance pattern, which is similar to what has been recovered in previous studies.

0441 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Savannah Michaelsen, Diego Elias, Erica Rottmann, Ariana Rupp, Kimberly Foster, Kyle Piller

Southeastern Louisiana University, Hammond, LA, USA

Rounding Up Diversity within the Weed Shiner (Cyprinidae: *Alburnops texanus*)

The weed shiner, *Alburnops texanus*, has a long and chaotic taxonomic history. This is partly because of its wide distribution, which spans the Mississippi drainage system in Minnesota and Wisconsin down to the Gulf Coast, and stretching east-west from the Nueces River in Texas to the Coastal Plain drainage of the Suwannee River in Georgia and the Florida panhandle. Previous work indicated the occurrence of intraspecific variation for several morphological characters. We expanded this data set and examined additional characters to provide a comprehensive summary of morphological variation of this widespread species. Results indicate that several characters are variable and informative including chin-lip, anal ray, and lateral band pigmentation. This information, coupled with previous molecular and morphological data sets, suggest that the weed shiner may be more diverse than is currently recognized.

0335 Fish Ecology II, Carson 3, Sunday 19 July 2015

Alejandra Mickle, Ralph D. Grubbs, Jeffrey P. Chanton

Florida State University, Tallahassee, FL, USA

Trophic Structure, Feeding Ecology and Bioaccumulation of Hg in Gulf of Mexico Hagfishes

We investigated the trophic structure, feeding ecology and bioaccumulation of Hg in three species of hagfish from the Gulf of Mexico (GoM). Inter and intra specific variations as well as changes along important environmental gradients in trophic structure and feeding ecology of *Eptatretus springeri*, *Eptatretus minor*, *Myxine mcmillanae* were studied using nitrogen ($\delta^{15}\text{N}$), carbon ($\delta^{13}\text{C}$) and sulfur ($\delta^{34}\text{S}$) stable isotope analysis along with DNA analysis of stomach and fecal samples. Total Hg, Methyl-Mercury and Inorganic Hg concentrations in muscle tissues were measured via cold vapor fluorescent mass spectrometry and combined with stable isotope signatures to identify the influence of trophic structure in Hg accumulation and any potential effects of the DWH oil spill on Hg concentrations. *E. springeri* had the lowest $\delta^{15}\text{N}$ value (11.1‰), followed by *E. minor* (12.3‰) and *M. mcmillanae* (13.4‰). *E. springeri* also had the lowest $\delta^{34}\text{S}$ value (20.3‰) followed by *E. minor* (21.8‰) and *M. mcmillanae* (21.9‰). The only significant changes with depth were observed for *E. springeri* with an enrichment in $\delta^{15}\text{N}$ and a depletion of $\delta^{34}\text{S}$ suggesting a diet shift with increased depth. Despite having the largest mean body length (518.6 mm) and body mass (262.6 g) *E. springeri* had the lowest mean THg concentrations (1.1 $\mu\text{g g}^{-1}$), while *M. mcmillanae* had the smallest mean body length (74.2 mm) and the highest THg concentration (11.2 $\mu\text{g g}^{-1}$). Only *M. mcmillanae* had a significant increase in Hg concentrations with depth. Preliminary results indicate variations in trophic structure and diet composition and Hg concentrations in GoM hagfishes.

0002 Herp Ecology, Carson 4, Saturday 18 July 2015

Jessica Middleton, David Green

McGill University, Montreal, QC, Canada

Altered Adult Age-Structure as an Amphibian Population Declines

Populations of pond-breeding amphibians may normally fluctuate in size in response to stochastic environmental events and may suffer unsustainably high mortality rates when habitats are progressively lost or degraded. The population's age-structure should, consequently, be altered in predictable ways if increased mortality is age- or stage-specific. This decline in recruitment should result in a progressively older adult population whereas a decline in adult survivorship should be accompanied by a decrease in the average age of adults. We used skeletochronology to determine the chronological ages of adult Fowler's Toads in a population that, over a span of 20 years, went from a period of regulated population fluctuation to a period of sustained

population decline. Age structure was not significantly different between the sexes but was highly variable during both the pre-decline period (1992 - 2002) and the decline period (2002 - 2011). Although there was no temporal trend detected in average age among 420 toads sampled during the decade before the population began to decline, there was a significant increase in average age among 469 toads sampled during the decline, with no significant change in adult survivorship. This evidence of an aging population is consistent with a reduction in recruitment in the population, which has been related to the progressive loss of breeding habitat due to an invasive plant. This example demonstrates that amphibian populations may be threatened with decline even when mortal threats to adults have not increased.

0424 ASIH STOYE AWARD ECOLOGY & ETHOLOGY II, Carson 4, Friday 17 July 2015

Emily Miller¹, Michael Thomas¹, Gabriel Singer¹, Matthew Peterson¹, Eric Chapman¹, Ryan Battleson¹, Marty Gingras², A. Peter Klimley¹

¹University of California, Davis, Davis, CA, USA, ²California Department of Fish and Wildlife, Stockton, CA, USA

The Timing of Green and White Sturgeon Movements and Distribution in the San Francisco Bay, Delta, and Sacramento River

Green and white sturgeon are sympatric sister taxa found in the Sacramento-San Joaquin watershed that differ in their life history patterns. Understanding the distributional overlap of the two species while in the watershed can inform management decisions. The anadromous green sturgeon spends much of its subadult and adult life in nearshore marine waters along the northern Pacific coast while the semi-anadromous white sturgeon resides within the estuary throughout adulthood. However, subadult and adult green sturgeon are present in the estuary and delta during pre-spawning migrations in spring and post-spawning movements after holding upriver for the summer or through fall or winter. Both species spawn in the Sacramento River so juveniles reside in the lower river, delta and bay as they age and out-migrate. We acoustically tagged 160 white and 41 green sturgeon from 2010-2012 in San Francisco Bay. Tagged sturgeon included large juveniles, subadults, and adults. Green sturgeon adults previously tagged by our laboratory were also included in analyses. The array of monitors operated by our Laboratory, state, federal, and consulting agencies detected individual sturgeon movements from 2010-2014. Size-class distributions of each species and the timing of movements of spawning adults by watershed reach will be compared. Route selection through the delta by migratory adults will be compared pre- and post-spawn. Understanding how green and white sturgeon differ in their timing of seasonal movements and movement paths within the watershed can improve the management of each and help explain the mechanisms of coexistence of these two closely related species.

**0565 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Melissa Miller¹, John Kinsella², Ray Snow³, Bryan Falk⁴, Robert Reed⁴, Scott Goetz¹, Craig Guyer¹, Christina Romagosa⁵

¹Auburn University, Auburn, AL, USA, ²HelmWest Laboratory, Missoula, MT, USA, ³Everglades National Park, Homestead, FL, USA, ⁴US Geological Survey, Fort Collins, CO, USA, ⁵University of Florida, Gainesville, FL, USA

Are Invasive Burmese Pythons Impacting Native Snakes through Parasite Spillover?

Non-indigenous species (NIS) are a leading cause of biodiversity loss, with species decline occurring primarily through competition and predation. However, recent work has shown that introduced pathogens play a significant role in NIS impact. While NIS often carry only half the parasite load they contain in their native range, numerous studies have documented the co-introduction of pathogens with NIS and exotic pathogens of NIS have been shown to spillover to native taxa with adverse results. We examined invasive Burmese Pythons (*Python molurus bivittatus*) and native snakes collected in southern Florida for lung endoparasites to explore the potential for parasite spillover. Parasites were identified to species using both morphological and molecular analyses. We found pythons co-introduced a pentastomid parasite (*Raillietiella orientalis*) that is native to Asia. Furthermore, we found *R. orientalis* in several species of native snake (e.g. *Agkistrodon piscivorus*, *Thamnophis sirtalis*, *Pantherophis guttatus*, *Nerodia fasciata*, and *Nerodia clarkii*) collected from areas of sympatry with pythons. Our results indicate that Burmese Pythons have introduced an exotic parasite that is capable of infecting native snakes. As the effect of pathogens co-introduced with NIS are often more harmful in native versus co-introduced hosts, spillover of an exotic parasite from pythons to native snakes could negatively affect native snake assemblages.

**0224 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18
July 2015**

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The Redefinition of Cladistics – Are All Data Really Evidence?

Donn Rosen suggested that the assumption "redefining the problem can solve it" inhibited progress in comparative biology. Cladistic approaches have changed considerably since their introduction to North America almost 50 years ago. Some of those changes have redefined concepts of evidence and the role of congruence. These redefinitions have not solved previous questions; rather, they have changed the questions we are asking and have inhibited progress just as Rosen predicted. It is

generally agreed that cladistics is more than building trees and should include cycles of testing and re-testing of evidence where the identification and resolution of incongruence will lead to better-supported hypotheses of relationship (i.e., reciprocal illumination). Such cycles, however, are rarely applied; we are left comparing topologies and the methods by which they were produced rather than focusing on the evidence they summarize. Without that focus, the 'solutions' (topologies) are produced in intellectual and factual isolation from each other. This approach has promoted the congruence test as the sole arbiter of homology and has encouraged the use of all data, even misinterpreted data, as evidence. While important, congruence is not the only test for determining evidence and is itself incapable of resolving incongruence - it merely identifies it. Using examples from various fish taxa, we explore the role of reciprocal illumination in clarifying our understanding of characters and the topologies they support. We conclude that incongruent data are not evidence despite applications to the contrary.

0131 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Molly Morris¹, Ryan Frieberthausen¹, Oscar Rios-Cardenas², Melissa Liotta¹, Jessica Abbott³

¹Ohio University, Athens, OH, USA, ²Instituto de Ecología A.C., Xalapa, Veracruz, Mexico, ³Lund University, Lund, Skåne, Sweden

Selection on Growth Rates across Alternative Reproductive Tactics in the Swordtail Fish *Xiphophorus multilineatus*

Trade-offs are common across alternative reproductive tactics (ARTs), and yet the extent to which growth rates are a part of these tradeoffs has often been overlooked. The ARTs in the males of *Xiphophorus multilineatus* consist of two tactics with distinct life histories: one optimizes mating success by maturing later at larger size (courters), and one optimizes survival to sexual maturity by maturing earlier at a smaller size (sneakers). We detected a correlation between faster growth and adult mortality in laboratory-reared courter males, suggesting that growing faster as a juvenile generates a cost of shorter longevity. We present a simple model to suggest that given a difference between the ARTs in probability of surviving to sexual maturity, the increased probability of survival to sexual maturity gained through faster growth multiplied by the cost of faster growth will determine if there will be tactical disruptive selection on growth rate (positive selection for courters, negative selection for sneakers). We also detected a significant relationship between growth and appetite in laboratory-reared males, and a significant difference in appetite between wild-caught courter and sneaker males. We suggest that variation in the copies of melanocortin-4 receptor (Mc4r) gene could link faster growth with delayed sexual maturation through appetite. This link could explain the positive relationship between male size and growth rate, and potentially resolve intralocus tactical conflict on growth rates produced by tactical disruptive selection.

0083 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Joshua K. Moyer, William E. Bemis

Cornell University, Ithaca, NY, USA

Comparisons of Tooth Structure and Replacement in the Blue Shark (*Prionace glauca*) and the Great White Shark (*Carcharodon carcharias*)

Elasmobranchs exhibit two distinct arrangements of mineralized tissues in the teeth that are known as orthodont and osteodont histotypes. Traditionally, it has been said that orthodont teeth maintain a pulp cavity throughout tooth development whereas osteodont teeth are filled with osteodentine and lack a pulp cavity when fully developed. We used light microscopy, scanning electron microscopy, and high-resolution micro-computed tomography to compare the structure and development of elasmobranch teeth representing the two histotypes. As an example of the orthodont histotype, we studied teeth of the Blue Shark, *Prionace glauca* (Carcharhiniformes: Carcharhinidae). For the osteodont histotype, we studied teeth of the Great White Shark, *Carcharodon carcharias* (Lamniformes: Lamnidae). We document similarities and differences in tooth development and the microstructure of tissues in these two species and review the history of definitions and interpretations of elasmobranch tooth histotypes. We discuss a possible correlation between tooth histotype and tooth replacement and review the history of histotype differentiation in sharks. We find that contrary to a long held misconception, there is no orthodentine in the osteodont teeth of *C. carcharias*.

0608 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Alexsis Mross, Brook Fluker

Arkansas State University, Jonesboro, AR, USA

Phylogeography of the Slough Darter, *Etheostoma gracile*, across the Gulf Coastal Plain

Recent phylogeographic studies of darters distributed throughout the Gulf Coastal Plain in the southeastern United States have revealed unique patterns of diversification. However, concordant phylogeographic breaks among darters inhabiting this region have not yet been well identified. One obvious and well-tested phylogeographic break among coastal plain species is the division between populations east and west of the Mississippi River. For example, *Etheostoma proeliare* and *E. parvipinne* both have well supported clades falling east and west of the Mississippi. In this study, we analyzed mitochondrial and nuclear DNA sequence data from *E. gracile* throughout its range to evaluate concordance of the east-west Mississippi phylogeographic break observed in other darters, and to gain a better understanding of factors that shape genetic structure in darters across the Gulf Coastal Plain. Preliminary analyses reject a well-defined phylogeographic break east and west of the Mississippi River for *E. gracile*. However,

specimens from the Colorado River exhibit substantial levels of mtDNA divergence, suggesting previously unrecognized cryptic diversity within *E. gracile*. Ongoing work with additional nuclear DNA markers and increased sampling will be incorporated into this framework, shedding light on this unique phylogeographic pattern in the Gulf Coastal Plain.

0153 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Andy Mueller, Cole Spicer, Mattie Lewis, Kristoffer Wild, Mollie F. Cashner

Austin Peay State University, Clarksville, TN, USA

Initial Investigation of a Newly Discovered Population of *Chrosomus cumberlandensis* Using mtDNA Haplotypes

Chrosomus cumberlandensis, Blackside Dace, is a federally threatened minnow that typically inhabits pools of small, cool streams along the Cumberland River drainage in Tennessee and Kentucky. Recently, its range has been expanded by the discovery of additional populations throughout the Cumberland River system and tributaries of the North Fork Powell River system in Virginia. In 2013, a population was discovered in Maces Creek (Perry Co., Kentucky), part of the Kentucky River system. Whether this population represents a recent range expansion or was a previously undetected population is unknown. As an initial investigation into the affinity of the Maces Creek population, we compared their ND2 haplotypes (mtDNA) to those of individuals collected from a previously known population (Big Lick Branch). Haplotype frequencies, divergences and networks will be presented.

0059 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Alison Murray, Juan Liu

University of Alberta, Edmonton, Alberta, Canada

Eocene Cypriniform Fishes

Cypriniform fishes, based on ostariophysan relationships, are expected to have an equivalent age to Siluriformes or Characiformes. The fossil record of those two orders extends to the Late Cretaceous; however, the oldest known cypriniform is an isolated bone from the mid-Palaeocene. A greater diversity is found in the Eocene, leaving a significant gap between their expected minimum Late Cretaceous origin and the first known fossils. Within the Cypriniformes, the families are unevenly represented in the fossil record. The earliest forms are catostomids, cyprinids, and a new extinct family; there are no representatives of the algae eater and loach families prior to the Miocene. Eocene catostomids are known from Asia and North America, with the genus *Amyzon* found in both. A new species from Eocene deposits of Montana brings the number of

valid species in *Amyzon* to seven. A diversity of fossil cyprinids is known from Indonesia, with several species assigned to extant genera based on meristic characters and body form. With new studies on recent collections from Indonesia we expect most species will be placed in new genera. The age of the Indonesian deposits has been reported previously as anywhere from Cretaceous to Miocene; however, recent work suggests they are Eocene in age, placing these specimens among the oldest cyprinids known (others are from China). The third Eocene cypriniform family is based on a single species that was previously included in both Cyprinidae and Catostomidae. We now give it its own family based on osteological features and a phylogenetic analysis.

0481 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Chris Murray¹, Caleb McMahan², Brian Crother³, Craig Guyer¹

¹*Auburn University, Auburn, AL, USA*, ²*The Field Museum, Chicago, IL, USA*,

³*Southeastern Louisiana University, Hammond, LA, USA*

The Inhibition of Scientific Progress: Perceptions of Biological Units

There was considerable debate regarding species for two decades. Questions discussed assessed the ontological status of the most important biological unit; species. Are species real? Is the species level the only taxonomic level that exists outside of human perception? Or, are they artificial fabrications that we define, not diagnose? The lengthy debate regarding the ontology of species has waned, in our opinion. With numerous former strides in diagnosing the ontology of species and debating their purpose, use, and nature, we hypothesize that this critical discussion has fallen absent in current biological function and operation. With competing and exciting operational strides in math, technique, and data handling, biologists, perhaps, have lost sight of the fundamental unit on which they base their livelihoods. Here, we submit a voluntary survey to the members of the Society for Evolution and the Society for Systematic Biology to assess whether the debate on species ontology has been settled or simply given up on. This survey takes census of the current views in species ontology, taxonomic theory, and species concepts to assess differences in opinion among cohorts of biologists. We predict that the age of thinkers is over and since the species debate's premature disposal; theory on this fundamental unit has been lost. We find that opinions on species and knowledge of biological philosophy vary widely among biologists as well as among academic position and field of study.

0199 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Prachya Musikasinthorn

Faculty of Fisheries, Kasetsart University, Bangkok, Thailand

An Undescribed Species of Loach (Family Nemacheilidae) with Piscivorous Food Habits from the Inle Lake Basin, Myanmar

Nemacheilidae is the most species-rich family of the order Cypriniformes next to Cyprinidae and contains 46 genera with some 600 species. The majority of them are distributed in mountain streams of south and southeastern Asia. During an ichthyological survey of Inle Lake in Shan State, Myanmar, which is known for its highly specialized fauna, including fishes, I discovered a morphologically unique undescribed species of nemacheilid loach from a stream flowing to the lake. The species can be distinguished from all other nemacheilids by its remarkably large head (lateral head length 26.7–29.1% in standard length [SL]); elongated snout (length 10.3–12.4% SL); dorsally situated small eyes (diameter 3.2–4.7% SL); wide mouth (gape width 7.3–9.6% SL) with a median interruption on lower lip; numerous dark brown spots dorsally and laterally on head; and 5 to 7 large dark brown blotches along lateral midline of body. Examination of stomach contents by dissection and radiography revealed that the species feeds mainly on other nemacheilids. Piscivorous food habit is apparently rarely known for nemacheilids and even for members of the superfamily Cobitoidea to which the family belongs. The biology of the undescribed species, including generic status, possible relationship to other species and relation to the natural history of Inle Lake, will be discussed.

0374 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2, Thursday 16 July 2015

Edward Myers, Frank Burbrink

College of Staten Island, CUNY, Staten Island, NY, USA

Comparative Phylogeography of Snakes Across North America's Warm Deserts

The Western Continental Divide has been shown to be a phylogeographic break across a diversity of taxa within the warm deserts of North America. It is hypothesized that this region is a contact zone between closely related species that were previously isolated from one another during Quaternary glaciation in desert refugia. In spite of this barrier's importance in North American biogeography and biodiversity, no study has simultaneously examined multiple species spanning this region to investigate phylogeographic histories. We have generated Rad-seq data to test competing models of demographic history and speciation in three co-distributed species complexes, *Crotalus atrox* (4470 SNPs), *Lampropeltis getula* (3917 SNPs), and *Coluber flagellum* (6418 SNPs). These data corroborate population subdivisions detected with mtDNA and support non-

synchronous divergence times across these taxa at a shared vicariant barrier. We also test for simultaneous divergence across 12 co-distributed sister taxon pairs of snakes using a single locus. Results again suggest multiple waves of population divergence across these taxa, with divergence times ranging from the late Pleistocene to the late Miocene. We illustrate that the last glacial maximum has not been the driving force of diversification within this region.

0512 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Joshua Myers, Jade Keehn, Chris Feldman

University of Nevada, Reno, NV, USA

The Effect of Local Conditions on Activity Levels Associated with Extinction Risk in Desert Reptiles

Climate change has been associated with local extinctions in reptiles, especially lizards. The proposed mechanism of extirpation is an increase in midday temperatures which restrict the hours of lizard activity during the breeding season (hr). Lizards become unable to meet energy demands during the shortened activity period. However, this risk may vary across populations within a species. To better understand how local habitat conditions influence activity and local extinction risk, microclimate temperature data collected with iButton temperature loggers were used to estimate hr across 8 populations of *Uta stansburiana* (side-blotched lizard) in Palm Springs, CA. Hr estimates were correlated with elevation, human disturbance, and ground cover to determine how variation in the environment related to activity period length. Field trials were also conducted to test the accuracy of iButton temperature loggers as operative temperature models for lizards on different substrates. Correlations between lizard body temperature and iButton temperature (after both have stabilized to ambient temperature) ranged from $R^2 = 0.84$ to 0.90 . The majority of iButton temperature readings (± 2 SE) fell within $1.86 - 2.36$ °C of lizard body temperatures. Yet, measurements of lizard body temperature from field-captured individuals were not correlated with the temperatures of their substrates. The ability of lizards to move quickly across unsuitably hot substrate may play an important role in reducing susceptibility to local extinctions. Lizards can continue to forage during high-temperature periods by selecting microclimates (rocks, shrubs, etc.) which reduce exposure to temperatures above the preferred body temperature.

0192 Fish Systematics II, Carson 3, Sunday 19 July 2015

Se Hun Myoung¹, Jin-Koo Kim¹, Choon Bok Song²

¹Department of Marine Biology, Pukyong National University, Busan, Republic of Korea, ²College of Ocean Sciences, Jeju National University, Jeju, Republic of Korea

Preliminary Study on Three Morphotypes of *Pristiophorus japonicus* (PISCES, Pristiophoridae) from the Northwest Pacific

The family Pristiophoridae belonging to the order Pristiophoriformes, consists of about eight species and two genera in the world. Among them, only one species (*Pristiophorus japonicus*) inhabits the coastal waters of Korea and Japan. This family is characterized by having an elongated and flattened rostrum with laterally projecting sharp teeth. In order to understand morphological and genetic variations among the local populations of *P. japonicus*, we investigated 17 individuals collected from five locations in Korea and Japan [Jeju/Busan (n=7), Shikoku/Misawa (n=2), Okinawa (n=8)]. Morphological analysis indicated that there might exist three morphotypes, of which A-type (Jeju/Busan and Shikoku/Misawa, n=9) showed a short pre-oral length (25.9-28.4% of TL) and a moderate snout width (5.7-6.6% of TL), B-type (Okinawa, n=3) showed a long pre-oral length (31.9-32.2% of TL except one female) and a wide snout width (5.9-6.4% of TL), and C-type (Okinawa, n=3) showed a long pre-oral length (31.4-32.9% of TL except one female) and a narrow snout width (4.7-5.3% of TL). According to Ebert and Wilms (2013), *P. japonicus* has pre-oral length of less than 31% of TL. However, B- and C-type (Okinawa) are different from *P. japonicus* in having longer pre-oral length (more than 31% of TL). Molecular analysis using the mitochondrial cytochrome *b* DNA sequences showed that the Kimura-2-distance between A- and C-type was 2.2 %, whereas those within A-type ranged 0.3-0.5 %. Therefore, C-type would be a distinct species which differs from *P. japonicus* (type locality: Japan, A-type here) in both morphology and genetics.

0484 ASIH STOYE AWARD PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY, Carson 3, Friday 17 July 2015

Brianna Myre¹, Roldan Valverde¹, Michael Bresette²

¹Southeastern Louisiana University, Hammond, LA, USA, ²Inwater Research Group, Hutchinson Island, FL, USA

Ovarian Dynamics in Free-Ranging Loggerhead Sea Turtles

Vitellogenin is a yolk-precursor protein that serves as a nutrient source for developing embryos in oviparous vertebrates. The hormonal control of this protein has been studied in a variety of taxa, but there are still a lot of unknowns. Vitellogenin production is induced in several reptilian and fish species by estradiol, and inhibited by testosterone in freshwater turtle species. However, recent loggerhead sea turtle hormonal profiles have revealed that this may not be true for sea turtles. Oviparous vertebrates that lay

multiple clutches in a single nesting season (such as loggerhead sea turtles) must produce vitellogenin in very high concentrations in order to meet the needs of developing embryos. To investigate the hormonal control of vitellogenin in a multi-clutch species, I sampled 38 loggerhead females entrained in St. Lucie Nuclear Power Plant in Hutchinson Island, FL from May-August of 2014. I took ultrasound images of the gonads to determine sex and reproductive status. Additionally, I took blood samples to measure testosterone, estradiol and vitellogenin using an enzyme linked immunosorbant assay (ELISA). The results of ELISA showed that estradiol and vitellogenin declined over the course of the season, and varied significantly according to reproductive status (as determined via ultrasound). I expect that the results of this study will have implications for both comparative physiology and for the conservation of this threatened species.

0458 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Chloe Nash, Michelle Kraczkowski, Barry Chernoff

Wesleyan University, Middletown, CT, USA

Island Population Structure of Hardhead Silversides, *Atherinomorus stipes*, in the Caribbean

Little is known about the population-genetic structure of Hardhead Silversides, *Atherinomorus stipes*, a small schooling fish commonly found in the western Atlantic from Florida and Bermuda to Brazil. Because of its distribution, this species offers an excellent opportunity to investigate the isolation by distance model of evolution. The model hypothesizes that the greater the geographic distance between populations, the greater the amount of genetic differentiation if gene flow between populations has ceased. Early results show that there are observable genetic differences between populations of *A. stipes*, which may indicate isolation and possible speciation, as well as some continued gene flow among the Caribbean populations. Testing of this model has included over 150 samples collected from seven different island populations along the southern coast of Belize. Other locations around the Caribbean will be added in the future. The mitochondrial gene *nd2* was amplified from extracted DNA to assess each population for evidence of genetic differentiation. Specimens were vouchered for anticipated morphological analyses. Preliminary results show surprisingly high haplotype diversity within and among populations. These combined analyses will illuminate the population-genetic diversity of *A. stipes* within the Caribbean.

0603 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Kevin M. Neal, H. Bradley Shaffer

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

Nuclear-Mitochondrial Discordance of Distinct Phylogeographic Lineages within the Western Spadefoot Toad, *Spea hammondi*

Although there have been several attempts at determining the phylogenetic relationships of North American spadefoot toads (Scaphiopodidae) of the genus *Spea*, to date no study has taken a phylogeographic approach using both nuclear and mitochondrial DNA. Here I present a multi-locus nuclear phylogeny and a mtDNA phylogeny of the four *Spea* species: *S. bombifrons*, *S. hammondi*, *S. intermontana*, and *S. multiplicata*, with particularly abundant sampling throughout the range of *S. hammondi*. Both nuclear and mtDNA datasets reveal two distinct lineages within *S. hammondi*, split by the Tehachapi Mountains in south-central California. However, we find surprising discordance between the nuclear and mtDNA phylogenies in the placement of these lineages: the nuclear dataset shows *S. hammondi* to be monophyletic, while the mtDNA dataset shows the northern *S. hammondi* clade to be sister to *S. bombifrons*, *S. intermontana*, and the southern clade of *S. hammondi*. With *S. hammondi* already considered a Species of Special Concern in California due to extreme habitat loss throughout its range, the revelation of distinct northern and southern lineages may warrant the consideration of each lineage as a unique conservation unit with more urgent need of management.

0419 Fish Systematics II, Carson 3, Sunday 19 July 2015

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Ultraconserved Elements Resolve the Phylogeny of Spiny-rayed Fishes (Teleostei: Acanthomorpha)

One of the most enduring problems in the phylogeny of vertebrates is the untangling of relationships among the ~18,100 species of spiny-rayed fishes, or acanthomorphs. Recent molecular phylogenies identify several lineages of acanthomorphs not anticipated in traditional classifications. The prospect of resolving the relationships among these newly delimited lineages using DNA sequence data generated with traditional Sanger methods is diminished by short internodes that characterize the deepest parts of the acanthomorph phylogeny. In this study we use a designed capture array to enrich and sequence more than 1,000 ultraconserved DNA elements (UCE) from 112 species of Acanthomorpha. Our analyses provide a phylogeny of acanthomorphs that is fully resolved and strongly supported among the most ancient lineages to recent divergences

within genera. Our results provide an additional perspective to the debate regarding the relationships among the major acanthomorph lineages by resolving a clade that contains opahs (Lampriformes), beardsfishes (*Polymixia*), dories (Zeiformes), cods (Gadiformes), and the Tube Eye (*Stylephorus*), which is the sister lineage of Acanthoptergii, a clade containing the paraphyletic beryciforms and the hyper-diverse Percomorpha. Within percomorphs, the UCE-inferred phylogeny has a highly resolved backbone that supports many of the major lineages discovered in traditional molecular studies, but refutes previous hypotheses of their relationship to one another. The UCE array developed here holds enormous potential for developing a fully resolved phylogeny of all species of Acanthomorpha.

0568 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Melissa C. Nehmens, David A. Ebert

Moss Landing Marine Laboratories, Pacific Shark Research Center, Moss Landing, CA, USA

Age and Growth of Deep-Sea Sharks on Seamounts in the Southwestern Indian Ocean

Knowledge of deep-sea Chondrichthyan life histories is relatively limited given the difficulties in obtaining adequate sample sizes. Life history characteristics that are known of deep-sea Chondrichthyans include slow growth, increased longevity, and late maturation. Ageing studies on deep-sea sharks, such as Squaliformes, are limited and necessitate further investigation as fisheries expand to deeper waters. During a series of surveys in the spring of 2012 and 2014 on the Madagascar Ridge in the Southwestern Indian Ocean, vertebrae and dorsal fin spines were collected from a suite of deep-sea sharks for age and growth analysis. The species collected were *Centroscymnus coelolepis*, *C. owstoni*, *Centroselachus crepidater*, *Centrophorus granulosus*, *Dalatias licha*, *Deania calcea*, *D. profundum*, *Etmopterus granulosus*, and *Scymnodon plunketi*. These species will be aged using their vertebrae and spines. This study will provide crucial information as part of a broader project to characterize the Chondrichthyan fauna on this remote chain of seamounts and may be useful in developing better management plans for this and other remote seamounts around the world.

0033 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Emily Nelson¹, Neil Hammerschlag^{1,2}, Duncan Irschick³

¹Rosenstiel School of Marine and Atmospheric Science, Miami, FL, USA, ²Leonard and Jayne Abess Center for Ecosystem, Science and Policy, Coral Gables, FL, USA,

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Variation in Body Form Influences Broad Scale Movement Patterns and Ecological Locomotor Performance by an Apex Predator

Throughout the long evolutionary history of sharks, physical, hydro-dynamical, and ecological demands have created considerable selection pressure to create the most efficient design for locomotion. Variation in body shape can impact an individual's ability to move effectively through the water and variation in body condition can influence the timing, length, and nature of migrations. Here we present a functional approach toward movement. We integrate functional morphology, physiology, and ecology to determine how variation in body form influences broad scale movement patterns and ecological locomotor performance of a marine apex predator (the tiger shark, *Galeocerdo cuvier*). Fourteen tiger sharks, ranging in size from 180 cm to 357 cm (total length) were captured. For each individual, 13 morphological measurements were taken and sharks were tagged with satellite transmitters to track their movement patterns. Using these data we evaluated how variation among individuals in movement (maximum distance moved, dispersion rate, rate of movement, kernels density, activity space, and area used per day) is influenced by morphology (caudal fin area, caudal fin aspect ratio, total length, and body condition). Our results help to understand the mechanisms underlying of the ecological and evolutionary implications of variation in morphological adaptations on marine apex predator movement and behavior.

0079 Donn Rosen and the Assumptions Symposium II, Crystal 3 & 4, Sunday 19 July 2015

Gareth Nelson

University of Melbourne, Melbourne, Victoria, Australia

Donald Eric Rosen (1929-1986)

Donn's family home was on west 78th Street in Manhattan, a short distance from the American Museum of Natural History. He was a volunteer there from the age of eight, destined to find employment as a curator in the Department of Ichthyology. Early on he adopted, as his own, the ideas about evolution that prevailed in the Museum – the New Synthesis. In his own research on fishes he later came to reject the Synthetic Theory because of its “assumptions that inhibit scientific progress in comparative biology” (best summarized in his 1985 course given at the University of Miami). His changed outlook - - his progress -- resulted from his study of biogeography. This field has remained contentious ever since, but is still explored in the hope of finding illumination. There

Rosen became sensitive to the conflict between assumption and discovery, or in his terms “empirical evolutionary research versus neo-Darwinian speculation” (title of a 1980 paper). For him the outcome approached the motto of the Royal Society of London, *Nullius in verba*, or in plainspeak: “We take nobody’s word for it.”

0179 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Kyle Newton

Florida Atlantic University, Boca Raton, FL, USA

The Yellow Stingray, *Urobatis jamaicensis*, Has a Magnetic Sense but Can It Use the Geomagnetic Field to Derive a Sense of Location?

The strength and inclination angle of the geomagnetic field vary predictably with latitude and magnetically sensitive animals can use these cues to derive a sense of location during migrations. Our previous work has demonstrated that the yellow stingray, *Urobatis jamaicensis*, can detect magnetic fields from permanent magnets. However, it is unknown if elasmobranchs can detect changes in the strength or inclination angle of a magnetic field. Stingrays were placed into two treatment groups that experienced magnetic stimuli that were 2.5X the range of possible magnetic field values that this species might encounter across its distribution. Stimuli were generated by a Merritt four-coil electromagnet system and the initial response of naive rays to stimuli served as a control. Individual stingrays were trained to swim to a feeding station when the magnetic field strength was increased by 45 μ T or the inclination angle was shifted vertically by 75°. Once the rays learned the task the stimulus intensity was gradually reduced in order to determine the threshold for a behavioral response. Rays were then subjected to stimuli from the other treatment group to determine if the rays could discriminate between the two stimuli.

0334 Donn Rosen and the Assumptions Symposium II, Crystal 3 & 4, Sunday 19 July 2015

Kirsten Nicholson¹, Craig Guyer², John Phillips³

¹*Central Michigan University, Mt. Pleasant, MI, USA*, ²*Auburn University, Auburn, AL, USA*, ³*University of Tulsa, Tulsa, OK, USA*

Biogeography of Central American Anoles of the Genus *Norops*

One of Don Rosen’s lasting legacies is the notion that vicariance events shape geographic distributions of organisms, as evidenced by replicated historical relationships within each lineage of organism. We use anoles of the genus *Norops* to revisit the biogeography of a region used by Rosen to illustrate vicariance effects. Time-calibrated phylogenies document that mainland *Norops* represents a monophyletic

group that experienced an ancient divergence event separating a Central American lineage from a South American lineage. The Central American lineage, one of the most species-rich lineages of all anoles, appears to have expanded southward as the Chortis, Chorotega, and Choco blocks accreted sequentially to Central America, forming the Panamanian Portal. Our analysis supports diversification of Central American *Norops* on the Choco block and that this diversification represents an important component of the diversity of the entire group. We demonstrate that lineages present on the Choco block re-radiate northward, perhaps because of multiple separations and reconnections during the closure of the Panamanian Portal. This process requires consideration of more complex models of biogeography than the simple north-to-south or south-to-north models of the past.

0431 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Natasha Noble, Sean Boyle, Matthew G. Keevil, David Lesbarrères, Jacqueline D. Litzgus

Laurentian University, Sudbury, Ontario, Canada

Sex Bias in Juvenile Dispersal Assessed Using Sex-Ratios of Juvenile Turtles Killed on Roads in Ontario

Dispersal is a risky, costly behaviour, which individuals undertake for uncertain and deferred inclusive fitness benefits. Hypotheses about the evolutionary causes of dispersal make differing predictions about sex-biases among dispersers. In addition, the importance of dispersal and dispersal mortality for conservation are poorly known. Sex-biases in juvenile dispersal are largely unknown in freshwater turtles. Juveniles encountering roads are likely a subset of those dispersing between suitable habitats and can therefore be a source of information on dispersers. We tested predictions that juvenile dispersal is sex-biased in Snapping Turtles (*Chelydra serpentina*) and Painted Turtles (*Chrysemys picta*) by examining sex ratios of juveniles killed on roads in south and central Ontario. Sex was determined by inspecting gonads of dissected turtles. In total, 19 male and 19 female Snapping Turtles, and 9 male and 2 female Painted Turtles were identified. There was no bias in the sex ratio for Snapping Turtles, indicating dispersal is not biased. In Painted Turtles there was a trend toward a male-biased sex ratio, possibly indicating male-biased juvenile dispersal. Male biased dispersal in Painted Turtles could be favoured by the avoidance of kin competition for mates or inbreeding avoidance. Unbiased juvenile dispersal in Snapping Turtles suggests that dispersal in this species functions to lessen kin competition for resources. The sex ratio of disperser mortality is critical for understanding how roads and other threats affect populations because the sexes differ in their contribution to population growth and viability.

0070 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Andrew Nosal¹, Yuzo Yanagitsuru¹, John Hyde², Philip Hastings¹, Nicholas Wegner²

¹*Scripps Institution of Oceanography - UCSD, La Jolla, CA, USA*, ²*Southwest Fisheries Science Center - NOAA Fisheries, La Jolla, CA, USA*

The Effects of Simulated Catch-and-Release on Metabolism and Hypoxia Sensitivity in an Important Recreational Rockfish Species, the Bocaccio (*Sebastes paucispinis*)

Due to overexpansion of swim bladder gas, rockfishes (*Sebastes spp.*) suffer from barotrauma when brought from depth to the surface during capture. Although returning the fish to depth using descending devices can significantly increase survival rates, up to 20% of released fish do not survive. Given that much of the physical trauma should be alleviated by recompression, we hypothesized that seasonably variable hypoxia at depth exacerbates the stress incurred during capture and, when coupled with barotrauma, may lead to increased mortality. To examine this, we determined the resting metabolic rate (RMR), critical oxygen concentration, and near-lethal oxygen concentration in the Bocaccio (*S. paucispinis*) both before and after simulated capture. These values are compared to oxygen concentrations experienced by Bocaccio in the wild, as determined by passive acoustic tracking of individuals relative to fixed oxygen monitoring stations, as well as via fish-borne oxygen sensor tags.

0399 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Erika Nowak

Northern Arizona University, Flagstaff, AZ, USA

SWPARC - Using Field Research to Inform Captive Husbandry of the Federally-threatened Narrow-headed Gartersnake

The Narrow-headed Gartersnake (*Thamnophis rufipunctatus*) is a riparian-obligate piscivore which has suffered extensive declines across its former range in Arizona and New Mexico, due to a combination of factors, including habitat alteration and loss of native prey species. Recent wildfires which have burned across the species' range have exacerbated these issues, and the species was listed as federally threatened in 2014. The species is notoriously challenging to keep in captivity. Northern Arizona University is expanding captive husbandry and breeding facilities on campus to assist with future species recovery efforts, including introduction, augmentation, and repatriation. This thus-far successful program is rooted in 15 years of field research on the species, and more recent student investigations of captive conditions. The program involves extension collaboration with state and federal agencies, zoological institutions, veterinarians, and countless volunteers. I will discuss progress to date with captive husbandry and breeding, including how telemetry and mark-recapture research with

wild snakes is informing captive husbandry. I will also discuss opportunities for future collaboration, relative to important gaps in our knowledge of basic physiology and ecology.

0571 Herp Conservation I, Carson 1, Saturday 18 July 2015

Justin Nowakowski¹, Andrew DeWoody², Matthew Fagan³, Janna Willoughby², Maureen Donnelly⁴

¹*University of California, Davis, Davis, CA, USA*, ²*Purdue University, West Lafayette, IN, USA*, ³*Goddard Space Flight Center, Greenbelt, MD, USA*, ⁴*Florida International University, Miami, FL, USA*

Mechanistic Insights into Landscape Genetic Structure of Two Tropical Amphibians Using Field Derived Resistance Surfaces

Conversion of forests to agriculture often fragments distributions of forest species and can disrupt gene flow. We examined effects of prevalent land uses on genetic connectivity of two amphibian species in northeastern Costa Rica. We incorporated data from field surveys and experiments to develop resistance surfaces that represent local mechanisms hypothesized to modify dispersal success of amphibians, such as habitat-specific predation and desiccation risk. Populations of both species were structured at similar spatial scales but exhibited differing responses to landscape features. Litter frog population differentiation was significantly related to landscape resistances estimated from abundance and experiment data. Model support was highest for experiment-derived surfaces that represented responses to microclimate variation. Poison frog genetic structure was strongly associated with geographic isolation, which explained up to 45% of genetic variation, and long-standing barriers, such as rivers and mountains. However, there was also partial support for abundance and microclimate response derived resistances. Differences in species responses to landscape features may be explained by overriding effects of population size on patterns of differentiation for poison frogs, but not litter frogs. In addition, pastures are likely semi-permeable to poison frog gene flow because the species is known to use pastures when remnant vegetation is present, but litter frogs do not. Ongoing reforestation efforts will likely increase connectivity in the region by increasing tree cover and reducing area of pastures.

0248 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Robert J. Nowicki, Jordan A. Thomson, James W. Fourqurean, Michael R. Heithaus

Florida International University, Miami, FL, USA

Effects of Predation Risk from Tiger Sharks (*Galeocerdo cuvier*) on Resilience of an Iconic Seagrass Ecosystem Following a Widespread Climate Driven Disturbance

Ecological resilience will play an important role as anthropogenic ecosystem disturbance continues. Understanding how marine apex marine predators contribute to resilience is important in the context of global overfishing and increased disturbance potential from climate change. Here I present a 16 month field experiment to determine whether a dominant apex predator, the tiger shark (*Galeocerdo cuvier*), contributes to the stability of the recently disturbed seagrass community of Shark Bay, Australia. Shark loss was mimicked by simulating shifts in risk-sensitive habitat use and foraging patterns of dugong mega-grazers. Different levels of dugong excavation grazing, imitated by divers, were applied to plots to characterize these shifts. Excavation is energetically profitable to dugongs but destructive to seagrass beds, removing both target and non-target seagrass; it also increases risk of predation and is rarely used when predators are abundant. Mixed effects modeling was used to determine the importance of grazing treatments to the change in percent cover of the dominant climax seagrass (*Amphibolis antarctica*) and an herbivore-preferred pioneer seagrass (*Halodule uninervis*). *A. antarctica* cover declined with shark loss and subsequent increased grazing, though the effects were site-dependent. *H. uninervis* also declined but was more variable. Results indicate the current, fragile state of Shark Bay and the likelihood for a phase shift to an *A. antarctica* depauperate ecosystem if tiger sharks were removed from the ecosystem. This work highlights the contribution apex predators can make to the resilience of marine ecosystems, as they become exposed to more frequent and intense disturbances through climate change.

0055 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Glynn O'Neill¹, Valerie Douren¹, Mike Stegall², Aaron Francois², Prosanta Chakrabarty¹

¹*Museum of Natural Science, Louisiana State University, Baton Rouge, LA, USA,*

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One Fish? Two Fish? Three Fish? How Many Species Compose the Longear Sunfish (Centrarchidae: *Lepomis megalotis*)?

The Longear Sunfish, *Lepomis megalotis*, is a brightly colored member of Centrarchidae. It is found in freshwater regions from the Great Lakes throughout much of the Mississippi

River basin and the south. Its characteristic feature, an elongated opercular flap, is found on both sexes, but for males, it serves as a way to attract females: the longer the flap, the more attractive the mate. Morphological variation across its range leads us to hypothesize that this taxon may represent two or more species. The samples collected for this study include 54 ingroup taxa collected from 29 regions across Alabama, Kansas, Louisiana, Mississippi, Oklahoma, and Texas. Five outgroup species *L. marginatus*, *L. cyanellus*, *L. gibbosus*, *L. auritus*, and *Micropterus salmoides* were also examined. Two mitochondrial genes (16S and CO1) and one nuclear gene (CAM) were examined in the analysis, yielding a well-resolved phylogenetic tree. The phylogenetic tree shows three major lineages of *Lepomis megalotis*, but they do not correspond to distinct geographic areas nor do they correspond to distinct ecomorphotypes. This leads to the conclusion that *L. megalotis* is a single species with high morphological variability.

0596 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Minki Oh¹, Jong-Young Park²

¹California Academy of Sciences, San Francisco, CA, USA, ²Chonbuk National University, Jeonju, Jeollabuk-do, Republic of Korea

Taxonomic Review of Korean Mud Loach, *Misgurnus mizolepis* (Cobitidae)

Loaches (Pisces; Cobitidae) are widely distributed freshwater fishes across Eurasia region consisting of 21 genera and 171 species (Kottelat, 2012). Among them, the genus *Misgurnus* as one of the most confused taxonomic group has been found in South Korea, which is comprised of two species, namely *M. anguillicaudatus* and *M. mizolepis* (Kim et al., 2006). *M. mizolepis* was firstly described by Günther (1888), it was reviewed and reidentified as a junior synonym of *Paramisgurnus dabryanus* by Vasil'eva (2001) due to the priority with well coincidence of the taxonomic characters, which is a closely related taxon to *Misgurnus*. When *M. mizolepis* has been still used in Korea, we have taxonomically reviewed this group upon 5 populations (n=80; 70.3~167.5 SL) collected from around Korea and on the basis of Hubbs and Lagler (2004) for measurements and counts. As a result, Korean population has 104~132 (116±6.1) lateral scale rows, well developed keel at the caudal peduncle region, deep body depth, elongated and distinctive lamina circularis at the base of 1st pectoral fin ray which are well distinguished from *M. anguillicaudatus* easily, and as a consequence, Korean *M. mizolepis* is considered as a junior synonym of *Paramisgurnus dabryanus* so far. But there are still doubts between Korean *M. mizolepis* and *P. dabryanus*, because other morphological characters (e.g. barbel length, head part and overall shape, etc.) are not well agreed each other and mitochondrial cytochrome b gene sequence analysis is showing separated cluster. Further studies are needed to determine their taxonomic relationship.

0570 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Ron Oldfield

Case Western Reserve University, Cleveland, OH, USA

Alternative Male Mating Behavior in a Clade of Typically Monogamous Cichlid Fish Species

The Cuatro Ciénegas cichlid, *Herichthys minckleyi*, occurs in a clade of sexually monochromatic monogamous species. However, recent observations have revealed that males of this species are polygynous, with large males guarding large territories that may include multiple females. Compared to the closely related monogamous Rio Grande cichlid, *H. cyanoguttatus*, males of *H. minckleyi* are present at their nests less often and perform lower rates of aggressive offspring defense. Furthermore, males and females of *H. minckleyi* have dramatically different reproductive color patterns. Here I will show in *H. minckleyi* photographic evidence that male body color is associated with intrasexual competitive behavior and videographic evidence of alternative mating behavior (sneaking) performed by smaller, less competitive males. Polygynous mating in *H. minckleyi* evolved after it colonized Cuatro Ciénegas, and the increased competition among males for mates was accompanied by evolution of body color and alternative male mating behavior.

0110 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Lauren Oliver¹, Elizabeth Prendini², Fred Kraus³, Christopher Raxworthy¹

¹American Museum of Natural History, New York, NY, USA, ²Rutgers University, New Brunswick, NJ, USA, ³University of Michigan, Ann Arbor, MI, USA

A Systematic and Biogeographic Evaluation of the *Hylarana* Frog (Anura: Ranidae) Radiation Across Tropical Australasia, Southeast Asia, and Africa

Hylarana (Ranidae) is a speciose lineage with a vast distribution spanning tropical Africa, Asia, and Australasia that has often been considered a morphologically difficult group for species identification due to paucity of consistent external diagnostic characters. Previous phylogenetic studies have also been taxonomically limited due to a research focus on resolving relationships within targeted species complexes or between *Hylarana* s.l. and closely related genera. Here, we present an inclusive molecular phylogeny for *Hylarana* across its global distribution, utilizing two mitochondrial and four nuclear gene regions for 68 of the 97 currently described species. We use phylogenetic methods to test monophyly of *Hylarana*, determine relationships among ten putative subgenera, identify major clades, reconstruct biogeographic history, and estimate continental dispersal dates. Results support *Hylarana* as a monophyletic lineage comprised of eight clades that partly correspond to currently described subgenera but that support the recognition of two new groups. The African and Australasian species are represented by a single clade each, both embedded within a paraphyletic Southeast

Asian group. We estimate that Africa and Australasia were colonized by *Hylarana* s.l. from SE Asia approximately 18.7 and 10.8 MYA, respectively. Biogeographic reconstructions also support three separate colonization events in India from Southeast Asia. Examination of museum specimens identified morphological characters useful for delineating subgenera and species. We herein elevate all supported subgenera to genus rank and formally describe two new genera to produce a revised taxonomy that is congruent with our new phylogenetic and biogeographic findings.

0324 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Jason Ortega, Steven Beaupre

University of Arkansas, Fayetteville, AR, USA

The Effect of Prey Type on SDA Response in the Western Cottonmouth (*Agkistrodon piscivorus leucostoma*)

A predator's seemingly wide diet breadth may not coincide with the scope of its digestive performance when fed a wide array of prey. In our continued efforts to examine the interplay between prey preference and digestive physiology, specific dynamic action (SDA) was examined in the Western Cottonmouth (*Agkistrodon piscivorus leucostoma*). Snakes were fed meals of varying prey types (crayfish, fish, frog, and mouse) and their SDA responses were measured. To reduce variation in meal size and ensure meal ingestion, meals were administered as gavaged homogenates. Whole animal feeding runs were also incorporated to examine the effect of meal hominization on SDA response. Metabolic rates (VCO_2 and VO_2) were measured using open-flow respirometry. A total of 14 animals were measured for all meal types and forms (whole and homogenized). Target meal size for all runs was 25% of snake fasted mass. In addition to SDA response, respiratory quotient was recorded from all fasted pre-fed animals. Variation in SDA response due to prey type not only corresponds with the metabolic cost of digestion, but also gives insight to the snake's ability to maximize growth potential based on prey type.

0420 Fish Genetics, Carson 3, Saturday 18 July 2015

Megan Osborne¹, Joshua Perkin², Keith Gido³, Thomas Turner¹

¹University of New Mexico, Albuquerque, NM, USA, ²Tennessee Technological University, Cookeville, TN, USA, ³Kansas State University, Manhattan, KS, USA

Comparative Riverscape Genetics Reveals Reservoirs of Genetic Diversity for Conservation and Restoration of Great Plains Fishes

We used comparative landscape genetics to examine the relative roles of historical events, intrinsic traits, and landscape factors in determining the distribution of genetic

diversity of river fishes across the North American Great Plains. Spatial patterns of diversity were overlaid on a patch-based graphical model, and then compared within and among three co-occurring species across five Great Plains watersheds. Species differing in reproductive strategy (benthic vs. pelagic spawning) were hypothesized to have different patterns of genetic diversity, but the overriding factor shaping contemporary patterns of diversity was the signature of past climates and geological history. Allelic diversity was significantly higher at southern latitudes for *Cyprinella lutrensis* and *Hybognathus placitus*, consistent with northward expansion from southern Pleistocene refugia. A similar trend was seen in *Notropis atherinoides* but it was not statistically significant. In an historical context, all species exhibited lowered occupancy and abundance in heavily fragmented and drier upstream reaches, particularly *H. placitus*; a pelagic-spawning species, suggesting rates of extirpation have outpaced losses of genetic diversity in this species. Within most basins, genetically diverse populations of each species persisted. Hence, reconnecting genetically diverse populations with those characterized by reduced diversity (regardless of their position within the riverine network) would provide populations with greater genetic and demographic resilience.

0428 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Olga Otero

UPoitiers - CNRS, Poitiers, France

Diversification of the African Fish Fauna: The Question of the Driven Factors Addressed Through a Review of Modern and Fossil Data in Their Environmental Context

High level of endemism and presence of archaic fish are some of the striking features of the African fish fauna. In a preliminary correlative approach to link the diversification events that shape this diversity with the various potential extrinsic controls, I depict the evolution of the African freshwater fish replaced in its palaeoenvironmental context along the Tertiary. The evolution of the African fish fauna is described from the fossil record considering four groups on the basis of the phylogeny, of the modern distribution and of the habitat: each group has probably its diversity driven, at least partially, by similar or close environmental conditions. (I) The Archaics, belong to old depauperate lineages. They were close to extinction at some point during the Tertiary and saw a recent radiation that I link to the advantage of breathing the air in the Neogene contrasted climatic context. (II) The Archaeolimnics are far the more diverse: they belong to primarily freshwater endemic families that diversify after the Western Gondwana dislocation. Geological events appear to constraint greatly their diversity pattern, particularly tectonics and the related topographical modifications of the hydrographical divide. (III) The Invaders are freshwater fish from Eurasia that mostly invade Africa at the plate collision 18Ma ago, and then at the favour of further tectonic events. (IV) The Neolimnics invade the waters from the sea at different times and knew various success such as the cichlids and the latids. Tempo of "conquest events" and "key role" of certain regions are also proposed.

0422 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Olga Otero¹, Diogo Mayrinck²

¹*UPoitiers - CNRS, Poitiers, France*, ²*UFRJ, Rio Janeiro, Brazil*

When and Where Fossils Enlighten Cypriniform and Cyprinid Diversification and Dispersion Path and Timing

Current developments in phylogenetics, in evo-devo and in ecology greatly enhance our knowledge on cypriniform and cyprinid evolutionary history and also carry promising perspectives. However, some grey areas remain poorly elucidated. In some respect at least, fossil study brings original information and allows testing independently existing hypotheses. Here, we focus on three questions on cypriniform evolution that can be addressed by including palaeontological study as illustrated by our current and past works. First, fossils document main clade origin and diversification. Indeed, only a few Cretaceous freshwater fossils from Bolivia and some marine Tethysian ones were described as basal otophysans including stem cypriniforms. Their current revision opens new perspectives on the evolution of key structures such as the Weberian apparatus. This might help to understand deep relationships among otophysans. Moreover, new systematic attributions are proposed and the exclusion of certain marine fossils from extant orders weakens the hypothesis of a primary marine origin. Second, fossils can document paleobiogeographical events and their dating. For instance, fossils allow dating the cyprinid primary entrance in Africa at about 18Myr ago which is just after the first continental connection with Eurasia. Moreover, certain fossil distributions do not fit with the modern and suggest palaeobiogeographical scenario more complex than expected from the modern. Third and more prospective, a very peculiar fossil tooth morphology with smooth cusps and a cylindrical crown described in Arabia was also observed in archeological deposits: this makes me suggest to test together driving geographical, environmental and phylogenetical factors for morphologies.

0325 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Dustin Owen¹, Matthew Holding², Emily Taylor³, M. Rockwell Parker⁴, C.M. Gienger¹

¹*Austin Peay State University, Clarksville, TN, USA*, ²*The Ohio State University, Columbus, OH, USA*, ³*California Polytechnic State University, San Luis Obispo, CA, USA*, ⁴*Washington and Lee University, Lexington, VA, USA*

A Comparison of Commonly Applied Body Condition Indices in Snakes

Body condition indices (BCI) are commonly used surrogate measures for estimating relative amounts of stored energy reserves, especially fat, in vertebrate taxa. These

measures are assumed to provide ecologists and management biologists with a useful, non-lethal metric for assessing the “health” of free-ranging organisms. However, most BCIs lack empirical validation, and their usefulness is thought to vary among taxa. While comparative evaluations for BCIs have been conducted in many taxa (i.e. birds, mammals, and amphibians); reptiles have received considerably less attention with regards to evaluating current BCI methodologies. We evaluated the performance of eight of the most commonly applied BCIs to data on known fat pad masses from eleven snake species, *Boiga irregularis*, *Crotalus atrox*, male *C. oreganus*, *Hierophis viridiflavus*, *Nerodia fasciata*, *N. rhombifer*, *N. sipedon*, *Natrix natrix*, *Python bivittatus*, female *Thamnophis sirtalis*, and *Vipera aspis*. Our results provide a critical evaluation for the usefulness of BCIs in snakes. These results will aid in future conservation and ecological research employing BCIs as metrics for assessing organismal health.

0362 Fish Biogeography, Carson 3, Saturday 18 July 2015

Hannah Owens¹, Kale Bruner²

¹University of Florida, Gainesville, FL, USA, ²University of Kansas, Lawrence, KS, USA

Holocene Pacific Cod (*Gadus macrocephalus*) Distributional Changes: Ecological Niche Models and Archeological Evidence

Deglaciation in the Northern Hemisphere at the end of the Last Glacial Maximum (~19 kya) led to dramatic alterations in North Pacific Ocean ecosystems. Reductions in the geographical extent of permanent and seasonal sea ice and fluctuations in temperature and salinity patterns, among other factors, likely forced marine species to alter their distributions to follow favorable habitat. In this study, we used ecological niche modeling to infer effects of late Holocene environmental changes on the distribution of suitable habitat for Pacific cod, *Gadus macrocephalus*, a species native to the temperate North Pacific continental shelves. Present-day locality data were collected from databases of georeferenced museum vouchers and observations and integrated with present-day observed environmental data on bathymetry, average surface temperature and salinity, and maximum and minimum sea ice concentration using the correlative maximum entropy algorithm Maxent. The resulting ecological niche models were projected using 500-year climatologies at 1000-year intervals derived from the TRaCE-21Ka transient climate simulation run in the CCSM 3 coupled atmosphere-ocean climate model. Time-structured estimates of suitable habitat distributions were then compared with dated sub-fossil material recovered from 14 georeferenced prehistoric archeological sites occupied by hunter-gatherers across the Aleutian Islands and dated between 300 and 6500 ya. Our study demonstrates the utility of archeological evidence as a means of independently assessing ecological niche model projection performance, and considers the implications of historical patterns of suitable habitat distribution on the population structure of Pacific cod.

0538 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Michael Packer¹, Jesse Breinholt², Robert Murphy³, Catherine Stephen¹

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Phylogeography of Desert Iguanas (*Dipsosaurus dorsalis*)

Dipsosaurus consists of two desert dwelling iguana species: *D. dorsalis*, distributed throughout the southwestern United States, Northern Mexico, and the Baja California Peninsula; and *D. catalinensis* on Isla Santa Catalina. On the Baja peninsula, north-south divisions (morphological and genetic) are exhibited by multiple mammalian and herpeto fauna, without the current presence of any physical barriers. We examine the genetic structure of *Dipsosaurus*, and whether this species exhibits a similar north-south division on the peninsula and/or differentiation among mainland populations and whether the current taxonomy of *Dipsosaurus* is reflective of evolutionary relationships. To address these questions, blood samples from 100 individuals were collected across the entire geographic range of this species from various sources; field and museum specimens found in six distinct phylogeographic regions. DNA was extracted from the samples, and DNA sequence data collected from three loci: nuclear loci MLH3 (~850bp), NT3 (489bp), and mtDNA locus ND4 (~850bp). Numbers of haplotypes per locus ranged from 4 to 42. Haplotype network reconstructions for each locus were constructed to examine the distribution of genetic variation across the range and assess levels of differentiation between phylogeographic regions. According to these networks, the genetic variation seen in S. Baja populations is distinct from all other regions for all three loci. Additionally, differentiation of the Southern California-North Baja population is distinct from adjacent regions. Populations in southern Arizona and Sonora Mexico have the highest amount of gene flow between them. These patterns of genetic differentiation are examined in light of past geologic events.

0032 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Larry M. Page

Florida Museum of Natural History, Gainesville, FL, USA

An Overview of the NSF- funded All Cypriniformes Species Inventory, an International Project

The NSF-funded All Cypriniformes Species Inventory was initiated in 2010 and will be completed in 2015. It has accelerated the rate of discovery and description of cypriniform fishes, expanded our knowledge of the phylogenetic relationships of cypriniforms, increased the capacity for systematic research in other countries through student training and establishing long- term collaborations, including conferences in Thailand, Brunei, Malaysia, Burundi, and China, led to the formation of the Asian Society of Ichthyologists, and made available large numbers of specimens and tissues of

freshwater fishes, including many species never before collected, in permanent collections in US and foreign institutions. This symposium will report on the varied and important products resulting from global inventories and phylogenetic studies of diverse clades of organisms.

0476 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

E.W. Misty Paig-Tran¹, Lara Ferry¹

¹CSU Fullerton, Fullerton, CA, USA, ²Arizona State University West, Phoenix, AZ, USA

Integrative Elasmobranch Biology for the 21st Century

The current climate at granting institutions requires new research proposals to be truly interdisciplinary between two or more fields to be competitive for funding. NSF now has an entire division (Integrative Organismal Systems) dedicated to supporting research that is inherently integrative and asks us to identify "Grand Challenges in Organismal Biology". We argue in this symposium that elasmobranchs are excellent candidates for integrative research for numerous reasons, the most compelling of which are that: 1) they are ideal for asking large scale evolutionary questions (ex. evolution of endothermy) as they are a basal vertebrate on the tree of life and have survived with essentially the same features as they had 450 million years ago; 2) they are ecologically unusual in that they are the apex predators in nearly every system where they are present and thus play an important and possibly unmatched role in most trophic systems; and, 3) they are functionally important in that they possess an entirely cartilaginous skeleton, they are the first lineage to develop a true set of jaws, and they have the complex sensory system we typically associate with all vertebrates. Here we present a review of the history of integrative elasmobranch research and touch upon how the future of elasmobranch research is driving a variety of scientific fields of study highlighting how elasmobranchs were an essential part of the research, that elasmobranchs were the ideal organism for the research, and how the research is truly interdisciplinary between two or more fields of study.

0031 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

Yannis Papastamatiou

University of St Andrews, St Andrews, UK

A Day in the Life: Combining Biologging and Modelling to Understand Shark Behaviour and Physiology

Sharks represent an important ecological group as many species are meso or upper level predators. They are also an excellent study animal for ecological and behavioural studies as their larger size allows them to retain and carry a variety of sensors that record behavioural and physiological data in real time. With the current iterations of sensors we can measure the horizontal and vertical movements, activity, habitat selection, digestive physiology, and biomechanics of free-ranging animals. However, these tools are producing large datasets, and we need the appropriate statistical and modelling tools to appropriately analyse them. Analytical tools such as Hidden Markov Models allow us to identify switching behaviours and determine the covariates that drive these switches, and can be applied to a variety of time-series data including animal step lengths and turning angles, swimming depths, and activity. I will illustrate these methods using tracking data from white sharks, and behavioural/physiological data from reef (grey reef and blacktip reef sharks) and pelagic (oceanic whitetips) sharks. By combining these methods we can start to move beyond just describing shark movements, but also focus on the drivers of these movements.

0520 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Sebastian Pardo¹, Marc Dando², Nick Dulvy¹

¹Simon Fraser University, Vancouver, BC, Canada, ²FlukeArt, Plymouth, UK

Can Fin Shape Explain Variation in Somatic Growth Among Shark Species?

Across vertebrate taxa, morphology is related to function. An example from fishes is that caudal fin shape relates with swimming speed and activity level, with more elongated fins indicative of fast, active species and rounded fins slower, inactive ones. There is evidence that activity levels correlate with food consumption (more active fish eat more prey), and given that food consumption is relative to somatic growth rate (the more you eat the faster you grow), it might be possible to explain observed variation in growth among species based on a simple measure of fin morphology: caudal fin aspect ratio. Here we present a framework for exploring the relationship between somatic growth rate, maximum size, ocean temperature, and aspect ratio among a range of shark species, and discuss preliminary findings.

**0114 Donn Rosen and the Assumptions Symposium II, Crystal 3 & 4, Sunday
19 July 2015**

Lynne Parenti

National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

**Raising Cain: On the Assumptions that Inhibit Scientific Progress in
Comparative Biogeography**

Donn Eric Rosen (1929-1986) spoke and wrote extensively about biogeography. He was critical of biogeographic analyses that treat assumptions about age and dispersal ability as more informative than distribution patterns. He emphasized that the oldest fossils give a minimum age estimate rather than the maximum age of the groups to which they belong. He dismissed attempts to identify the center of origin of a group because they too required numerous assumptions and often gave ambiguous results. Stanley Adair Cain (1902-1995) was a botanist and ecologist who led development of the modern field of conservation biology in the United States. His influential book, *Foundations of Plant Geography* (1944), focused on the geography of plants but included general principles that apply to all biological distributions. In his critique of the criteria used to recognize a center of origin for a group, he explicitly called for assumptions to be reduced and for distributional hypotheses to be based on empirical data. Rosen and Cain each had a comparative approach to biogeography that did not depend on a particular distribution mechanism (dispersal or vicariance) but, instead, used the empirical data of plant and animal distributions, and their relationships, to reveal patterns to be explained. Both worked before the extensive use of molecular clocks to arbitrate between vicariance and dispersal explanations, but that new approach would likely not have changed theirs. Minimizing assumptions allows us to discover, not generate, biogeographic patterns, as demonstrated for select members of the Southeast Asian/western Pacific biota.

**0499 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Elyse Parker¹, Thomas J. Near^{1, 2}

¹*Yale University, Department of Ecology and Evolutionary Biology, New Haven, CT, USA,* ²*Peabody Museum of Natural History, New Haven, CT, USA*

**Molecular Phylogenetics and Morphometrics Support a Dramatic Reduction of
Recognized Species Diversity in *Pogonophryne* (Notothenioidei:
Artedidraconidae).**

Over the past decade molecular phylogenetics have increasingly played a role in species delimitation. One common critique of DNA-based species delimitation is that the use of genetic data could result in oversplitting of lineages, where sub-clades are misinterpreted as distinct species. But far less common are cases in which genetic data results in the recognition of fewer species than previously described using morphology.

Pogonophryne, a clade of benthic Antarctic plunderfishes that currently comprises 28 valid species classified into five species groups, may exemplify such a situation. *Pogonophryne* species are primarily distinguished by the appearance of the mental barbel, which, even within a single species (e.g. *P. scotti*), can vary widely from long and elaborately-branched to short and unbranched. This intraspecific phenotypic variation in a structure used to diagnose the majority of *Pogonophryne* species, as well as a lack of variation in meristic traits among species, warrants examination of species delimitation in the clade. In this investigation, Bayesian phylogenetic analyses performed under the general mixed Yule-coalescent (bGMYC) model using mtDNA sequence data supports the recognition of only five species of *Pogonophryne* that correspond to the recognized species groups. Furthermore, a principal components analysis of morphological character data reveals very little morphological differentiation among the newly delimited five species of *Pogonophryne*. We discuss the implications of the dramatic reduction of 28 to 5 species of *Pogonophryne* in reconstructing patterns of lineage diversification within the Antarctic notothenioid adaptive radiation.

0535 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

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Modulation of Pheromone Expression in Brown Tree Snakes via Hormonal Manipulation

Sex pheromones are potent signals mediating mate choice, and the manipulation of pheromone production in natural populations serves as a powerful management strategy for pest and invasive species. A particularly successful invasive reptile, the brown tree snake (*Boiga irregularis*), is known to use pheromones for locating and choosing between potential mates, especially in its invasive range on Guam. The brown tree snake pheromone has previously been isolated and identified, but nothing is known about whether the pheromone expression responds to steroidal manipulation. Previous work in garter snakes demonstrated that both estrogen implantation and testosterone removal (castration) could induce female pheromone expression in males. It was thus the goal of this study to use estrogen implantation to manipulate pheromone expression in male brown tree snakes and determine the effect of implantation on male attractiveness. We have implanted males (n=7) with silastic implants (1 cm) containing estradiol and are currently determining the effects on pheromone composition using hexane extraction, column fractionation, GC-MS and multidimensional scaling. Next, we plan to test the pheromone extracts in bioassays to assess attractiveness of the isolates. If male brown tree snakes can be induced to express female pheromone, it may be possible to generate abundant amounts of pheromone that could be used in trapping efforts currently in place on Guam.

0533 Herp Physiology & Reproduction, Carson 4, Friday 17 July 2015

M. Rockwell Parker¹, Jennifer Zachry¹, Saumya Patel¹, Michael S. Grace², Michael L. Avery³

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Possible Sex Pheromones in Burmese Pythons: Isolation, Identification and Behavioral Testing

Burmese pythons (*Python bivittatus*) are an invasive species of concern in the Florida Everglades and pose a significant threat to native vertebrates, especially birds and mammals. Their reproductive ecology is poorly understood in their invasive range, and successful management strategies could be derived from establishing fundamental knowledge of sexual signaling in pythons. Thus, this project is designed to determine the role and identification of chemical signals in Burmese python reproduction. We have been collecting and processing shed skins from wild caught male and female pythons and have extracted total skin lipids from these sheds. Sex pheromones in other species of snakes are abundant in both the exposed surface of intact snake skin and in shed skins, with the latter accurately reflecting the native composition of skin lipids while being much easier to collect. We isolated different components of the skin lipids via fractionation and then chemically analyzed whole skin lipid samples and fractions of those samples with GC-MS. Similar to other species of snakes, Burmese pythons produce abundant amounts of long chain methyl esters, but there were no sexual dimorphisms in their relative abundance. However, we have seen sexually dimorphic differences in cholesterol metabolites in the extracts and are quantifying expression differences between sexes, seasons and individuals. Next, we hope to determine whether the whole extracts and their composite fractions are biologically relevant in behavioral assays (Y-maze). By testing male trailing responses to these extracts, we hope to identify attractive components of the skin lipid milieu of the Burmese python.

0279 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

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¹Colorado Mesa University, Grand Junction, CO, USA, ²U.S. Fish and Wildlife Service, Colorado River Fishery Project, Grand Junction, CO, USA

Predicting Fish Movement Through Two Selective Fish Ladders in the Grand Valley, Colorado

Though poorly understood, fish movement patterns are ecologically important and are associated with reproduction, habitat selection, or possibly for other unknown reasons. Cues that initiate fish movement include flow, temperature, photoperiod, and barometric pressure. The U.S. Fish and Wildlife Service has operated two fish ladders

with traps on the Colorado River (9 years) and the Gunnison River (18 years) that capture fish moving upstream. To understand fish movement patterns, we used multiple linear regression modeling to predict fish movement, and selected the best models using Akaike Information Criterion (AIC). Multiple regression models will include the metrics: species, stream discharge (mean flow, minimum flow, maximum flow, and coefficient of variation), atmospheric conditions (temperature and barometric pressure), and photoperiod (date). This study may have important implications for the management and conservation of native fish species in the Colorado River Basin, four of which are federally listed as endangered and three species are considered of conservation concern. An improved understanding of the movement behavior of Colorado River fishes will add to the general understanding of the ecology of these fishes, and provide important insight into how barriers to fish movement, such as low head dams, may affect the ecology of these fishes.

0446 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Emily Peele

University of North Carolina at Wilmington, Wilmington, NC, USA

Genetic Diversity, Population Structure and Movements of the Bonnethead (*Sphyrna tiburo*) in North Carolina

The bonnethead shark (*Sphyrna tiburo*) inhabits coastal ecosystems and estuaries from North Carolina to Brazil. Some aspects of the genetic population structure of this species have been documented, including substantial variation between the Atlantic Ocean and Gulf of Mexico. *S. tiburo* that migrate to NC are primarily found in specific estuaries each year, yet genetic variances related to their site fidelity are unknown. This study will quantify genetic heterogeneity and detail population structure of bonnetheads along the NC coast. We are particularly interested in whether site fidelity reported previously for this species is associated with genetic population structure. Tagging efforts will help to reveal bonnethead migratory routes leaving NC estuaries and to identify overwintering grounds to the south. In conjunction with studying genetic differences, the mating system of this species will also be studied. Bonnetheads have been shown to exhibit a high percentage of genetic monogamy in Florida, contradictory to the expectation of polyandry seen in most shark species. Female specimens and their embryos collected as incidental bycatch from NC estuaries will be studied using microsatellite DNA profiling to determine numbers of males contributing to each litter. The oviducal gland will also be sampled for remaining sperm and profiled for number of paternal genotypes. Implications of this study include determining susceptibility of local populations to loss of genetic diversity in the event of population declines. Furthermore, a better understanding of the movement patterns of this highly migratory shark may lead to a reevaluation of conservation status.

0280 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Brian Peña, Larry Allen

California State University, Northridge, Northridge, CA, USA

Variation in Age and Growth of Vermilion Rockfish, *Sebastes miniatus*, Along the U.S. Pacific Coast

Among recreationally caught rockfish, the vermilion rockfish (*Sebastes miniatus*) is the most commonly harvested in southern California and is the third statewide. A recent discovery of a cryptic species, named sunset rockfish, within the vermilion rockfish complicates the assessment and management of this species due to life history discrepancies. As a species complex with the sunset rockfish, vermilion rockfish populations have shown declines in size and age frequencies since the 1980s due to fishing pressure. The “true” vermilion rockfish exhibit significant genetic differences across biogeographic barriers along the northeast Pacific coast, presumably because of high site fidelity and limited larval dispersal. This study will investigate differences in the life histories of “true” vermilion rockfish among these regions separated by these genetic barriers. Vermilion rockfish will be sampled by hook and line at depths <100 m to avoid catching the deeper-living cryptic species. Fish will be collected in five regions along the U.S. Pacific coast corresponding to current management zones (i.e. Northern, Central, and Southern). Differences in the growth parameters among the sites and between the sexes will be assessed using fish lengths and otoliths. The von Bertalanffy growth function will be used to model somatic growth. Further exploitation of vermilion rockfish could reduce genetic diversity and shift demographics of this species. If differences in life history among the subpopulations are detected, regional-scale management of this species may help ensure the persistence of healthy and sustainable populations of vermilion rockfish.

0319 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

David Penning, Schuyler Dartez, Brad Moon

University of Louisiana at Lafayette, Lafayette, LA, USA

The Big Squeeze: Scaling of Constriction Pressures in Two of the World's Giant Snakes (Genus: *Python*)

Constricting snakes usually kill their prey by exerting pressure through body coils around the prey. However, the specific cause of death remains uncertain. Constriction has been hypothesized to kill by suffocation, circulatory arrest, or spinal dislocation. Few studies have addressed constriction performance, and to our knowledge, no study has evaluated intraspecific scaling of constriction performance in any species. We studied the ontogeny of peak constriction pressure in two giant pythons, the reticulated

python (*Python reticulatus*) and the Burmese python (*Python bivittatus*). Constriction pressures were similar in the two species. In both species, peak constriction pressure increased significantly with snake diameter, but with a significantly lower slope than that of interspecific data. In contrast to previously published results, the number of loops in the constriction coil did not impact maximum constriction pressure. Constriction pressures were typically higher than both the systolic and diastolic blood pressures in their prey, suggesting that these pressures are not only capable of arresting circulation but may also be capable of killing rapidly by over-pressurizing the brain via forced blood flow to the head.

**0318 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Friday 17 July 2015**

David Penning, Baxter Sawvel, Brad Moon

University of Louisiana at Lafayette, Lafayette, LA, USA

Is There Always a Need for Speed? How Fast Can Ratsnakes (*Pantherophis obsoletus*) Strike?

To survive, organisms must avoid predation and acquire nutrients and energy. Their sensory systems must correctly differentiate between potential predators and prey. Many organisms use this sensory information to maintain or close distances accordingly. For snakes, striking is an important behavior that can serve both purposes. However, strike performance is known for very few species. Vipers have received considerable attention, and are thought to have the fastest strikes among snakes. We evaluated strike performance in the Texas Ratsnake (*Pantherophis obsoletus*) in defensive and offensive (feeding) trials, and compared their performance to that of vipers. High-speed video analyses showed that ratsnakes struck defensively at significantly greater distances than during encounters with prey. However, strike times were not significantly different, leading to snakes who struck from greater distances (defensive strikes) having higher maximum velocities. In many cases, ratsnake strike performance (e.g., maximum velocities and accelerations) was similar to or greater than values reported for vipers. Strike times were so short that they were similar to or less than mammalian startle-response times. These strikes are so rapid that ratsnakes may be capable of circumventing their target's senses by striking faster than the target can detect and evade.

0169 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

William Perez-Doria, José G. Mestra-Ricardo, Charles W. Olaya-Nieto

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

Reproductive Ecology of Mayupa *Sternopygus macrurus* in the Sinu River, Colombia

The reproductive ecology of Mayupa *Sternopygus macrurus* in the Sinu River was evaluated. Individuals collected between January and December 2004, with lengths ranging 39.6-112.0 cm of total length (TL) and 132.0-1748.0 g of total weight were analyzed. The gonads were placed in Gilson solution, the Vazzoler scale was applied and sexual proportion, sexual maturity index, spawning season, the length at first maturity, oocyte diameter and fecundity were estimated. 161 females, 162 males and 12 undifferentiated were studied, with sexual proportion female: male of 1:1. The length at first maturity was estimated in 74.6 cm TL for combined sexes; oocyte average diameter was 2490 μ m and fecundity was estimated in 7632 oocytes, with better equation $F = 1911.8 WG^{0.36}$, $r = 0.65$, $n = 62$. The Mayupa is a fish with partial spawnings, with prolonged spawning season that extends throughout the year, with large oocytes and medium fecundity.

0219 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Cheston Peterson¹, R. Dean Grubbs^{1,2}

¹Florida State University, Tallahassee, FL, USA, ²FSU Coastal and Marine Laboratory, St. Teresa, FL, USA

Investigating Trophic Relationships Between Sharksuckers (*Echeneis naucrates*) and Their Elasmobranch Hosts Using Stable Isotope Analysis

Despite the ubiquity of the symbiotic relationships of diskfishes (Echeneidae) and their hosts in marine ecology, the nature of the symbioses between individual species and their hosts is poorly understood - especially among the facultative symbionts (*Echeneis* sp.). We used carbon and nitrogen stable isotope analysis of white muscle biopsies from both free-living and commensal sharksuckers (*Echeneis naucrates*), as well as their hosts, to evaluate the suggestion that commensal sharksuckers feed heavily on scraps of their hosts' prey. We also used these data to evaluate among-host differences in pairwise similarity of individual sharksucker and host isotopic signatures, which we hypothesize could be indicative of long-term commensalism or high quality hosts. Mean pairwise differences of both $\delta^{13}C$ and $\delta^{15}N$ were lowest in bull (*Carcharhinus leucas*) and lemon (*Negaprion brevirostris*) sharks, and highest in nurse (*Ginglymostoma cirratum*) and tiger sharks (*Galeocerdo cuvier*). There was no effect of host taxon on pairwise $\delta^{13}C$ differences, but there was a significant effect of host taxon on pairwise $\delta^{15}N$ differences. Similarly, there was not an effect of commensalism on $\delta^{13}C$, accounting for variation in

sharksucker size and collection location; however, there was an effect of commensalism on $\delta^{15}\text{N}$, accounting for variation in sharksucker size and collection location. Despite being larger in size, free-living sharksuckers had lower $\delta^{15}\text{N}$ values, and therefore relative trophic position, than commensal sharksuckers. Our results suggest relative trophic levels of sharksuckers drop when they are free-living and that there may be an ontogenetic shift in both dependency on commensalism and trophic level.

0098 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Robert Peterson¹, James Walker², Robert Weaver¹

¹Central Washington University, Ellensburg, WA, USA, ²University of Arkansas, Fayetteville, AR, USA

Ecology and Behavior of the Colorado Checkered Whiptail (*Aspidoscelis neotesselata*) in Grant County, Washington State

The purpose of our study was to begin a long term investigation on the ecology and behavior of an introduced population of Colorado Checkered Whiptail Lizards, (*Aspidoscelis neotesselata*) near Lind Coulee in Grant County, Washington state. We collected lizards by hand from late June to late August 2014, while post capture laboratory analysis of stomach contents and egg size in mature individuals took place from July to early December. We took photographs and video footage of the behaviors of the lizards, as well as recorded GPS positions, body, soil and air temperatures for each lizard observed. The mean egg length in mature individuals was 14 mm, and the average clutch size was 3.75 (mean clutch mass = 3.25 g). It was found that 94% of captured individuals had prey items in their stomachs. Analysis also indicated that introduced population's diet consists primarily of Coleoptera (26%), Hymenoptera (21%) and Lepidoptera (14%), as well unidentifiable organic material (19%). Other prey items, such as invertebrate orders Aranea, Odonata, and Orthoptera, comprised up to 20% of the population's diet. On site observations determined that the introduced population is expanding outward along the banks of Lind Coulee This expansion was verified through the presence of burrows with tail drags, as well as observed individuals, south of the original site of introduction.

0261 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Mariah O. Pflieger¹, R. Dean Grubbs², Toby S. Daly-Engel¹

¹University of West Florida, Pensacola, FL, USA, ²Florida State University, Tallahassee, FL, USA

The Dogfish Formerly Known as Mitsukurii: A New Deep-water Shark Species from the Gulf of Mexico

The shortspine spurdog shark (*Squalus mitsukurii*) is a putative circumglobal deep-water shark that was originally described from Japanese waters. Sharks of the genus *Squalus* are easily misidentified due to the high degree of morphological similarity with their congeners. Recent taxonomic research on this species from the Pacific has indicated that *S. mitsukurii* may actually comprise a species complex, a group of separate but closely related species. Using approximately 680 bp of mitochondrial cytochrome c oxidase 1 (barcoding gene) we found 99.61% bootstrap support for the separation of the Gulf of Mexico *Squalus cf mitsukurii* from *Squalus mitsukurii* in Japan. We found similar support using 595 bp of mitochondrial NADH dehydrogenase 2 (ND2), as well as morphological characters. The new species in the Gulf of Mexico is named *Squalus clarkae* in honor of Dr. Eugenie Clark.

0588 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Catarina Pien, David Ebert, Jessica Jang, Paul Clerkin, Justin Cordova, Matthew Jew, Breanna Machuca, Melissa Nehmens, Amber Reichert, Victoria Vasquez, Kristin Walovich

Moss Landing Marine Laboratories, Moss Landing, CA, USA

Looking for "Lost Sharks"

Sharks, and their relatives the batoids and chimaeras, come in a variety of sizes and shapes, from the whale shark (*Rhincodon typus*), the world's largest fish, to the dwarf pygmy sharks (*Squaliolus* spp.), and occupy most marine, and some freshwater, habitats. There are more than 500 species of sharks, along with nearly 650 batoid and 50 chimaera species, bringing the overall total to about 1200 species of sharks and shark-like fishes. The diversity of sharks and their relatives has increased exponentially over the past decade with more than 230 new species having been described over the past decade. This represents nearly 20% of all shark species that have been described. Most of these new discoveries have come from the Indo-Australian region, followed by the western Indian Ocean and western North Pacific regions. However, a review of the Red List status of Chondrichthyans indicates that 17.4% are threatened and nearly half (46.8%) are Data Deficient or have not been assessed. Despite such a rich and diverse fauna, the majority of sharks and their relatives have largely been "lost", having been overshadowed by a few large charismatic media mega-stars, such the Great White Shark

(*Carcharodon carcharias*). In an effort to highlight and assess these little known, or unknown, species we have initiated a global program "Looking for Lost Sharks" to find and discover these lost sharks.

0275 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Emily Pierce, Vincent Quach, Karen Martin

Pepperdine University, Malibu, CA, USA

Effects of Human and Animal Predators on the Spawning Runs of the California Grunion, *Leuresthes tenuis*

California Grunion, *Leuresthes tenuis*, form aggregations along the coast of Southern California, then emerge from the ocean to spawn on sandy beaches. Many predators follow the aggregations in the water, including sharks, marine mammals, and larger fishes. Terrestrial predators await them on shore, with shorebirds picking fish off one by one as they emerge. However, a more effective predator lurks on these beaches. During open season, humans of all ages collect grunion by the handful and basketful for bait, food, and sport. Some nights, nearly every fish that appears is taken, and no spawning occurs. Because of their vulnerability to overharvest, *L. tenuis* have been protected by unique regulations since 1927, including gear restrictions and a closed season. Originally from April through June, the closed season was shortened to just April and May in 1949, the last time regulations were changed. Data collected by citizen scientist Grunion Greeters show that grunion runs have decreased in recent years over the habitat range, suggesting a population decline. According to our data, humans chasing the fish have a negative effect on spawning run success, while bird predation has no effect. The pressure on this species is exacerbated by loss of critical spawning habitat from coastal development and sand erosion along the coast. With the increasing human population in Southern California, *L. tenuis* face challenges greater than the predators of the sea, air and land.

0367 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Josh Pierce¹, Craig Rudolph¹, Steve Reichling², Emlyn Smith³, Beau Gregory⁴, Michael Sealy⁵

¹USDA Forest Service, Southern Research Station, Nacogdoches, TX, USA, ²Memphis Zoo, Memphis, TN, USA, ³USDA Forest Service, Kisatchie National Forest, Bentley, LA, USA, ⁴Louisiana Department of Wildlife and Fisheries, Lake Charles, LA, USA, ⁵U.S. Fish and Wildlife Service, Lafayette, LA, USA

Louisiana Pine Snake (*Pituophis ruthveni*) Reintroduction in Grant Parish, Louisiana

Ongoing surveys suggest that the Louisiana Pine Snake (*Pituophis ruthveni*) is rapidly declining; and currently occupied habitat is limited to a few small blocks of degraded and highly fragmented habitat. Research suggests that the species requires frequently burned sites with a well developed herbaceous understory capable of supporting populations of its primary prey, Baird's Pocket Gopher (*Geomys breviceps*). Recent changes in management practices on U. S. Forest Service lands have resulted in restoration of substantial blocks of suitable habitat, which are now available for reintroduction. A captive population consisting of approximately 60 individuals has been established from wild-caught snakes from Bienville Parish, LA. A reintroduction site was established in 2010 which is located on the Catahoula District of the Kisatchie National Forest. Forty-five individuals have been released to date. The current protocol is to continue to breed captive snakes and release 50% of available animals as neonates immediately following post-natal shed, while the remaining snakes will be head-started and released the following April. Currently, automated pit tag recorders and trapping are the primary monitoring techniques, however canine detection and radiotelemetry, may be used in the future. To date, nine snakes have been detected the year following release, and four of those snakes are known to have survived at least two years. Production of neonates and release of young will be repeated annually until a viable population is established or it is concluded that further releases are not likely to result in establishment of a population.

0308 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Theodore Pietsch¹, Tracey Sutton²

¹University of Washington, Seattle, WA, USA, ²Nova Southeastern University Oceanographic Center, Dania Beach, FL, USA

A New Species of the Ceratioid Anglerfish Genus *Lasiognathus* Regan (Lophiiformes: Oneirodidae) from the Northern Gulf of Mexico

A new species of the deep-sea ceratioid anglerfish genus *Lasiognathus* Regan (family Oneirodidae) is described on the basis of three female specimens collected in the northern Gulf of Mexico. Not especially similar to any one of the five previously

described members of the genus, the new species is unique in having a cylindrical, internally pigmented, anterior esca appendage and a pair of elongate distal esca appendages. The new species is diagnosed and described, and a revised key to the species is provided.

0473 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Tyler Pilger¹, Keith Gido², David Propst¹, James Whitney², Thomas Turner¹

¹University of New Mexico, Albuquerque, NM, USA, ²Kansas State University, Manhattan, KS, USA

Demography and Genetic Diversity are Correlated in a Desert River Fish Metacommunity.

Demographic history, environmental, and ecological factors all play a role in shaping patterns of genetic variation and diversity. We evaluated relative influences of life history and metapopulation dynamics on genetic variation using a comparative data set of nine co-occurring fishes from the Gila River, NM, USA. Global F_{ST} , Mantel's r (a measure of the correlation strength between genetic distance and stream distance), and contemporary genetic effective size (N_e) were estimated for each species using microsatellite DNA. We compiled life history data for each species and estimated contemporary abundance (average density) along with long-term metapopulation probabilities (occupancy P_o , extirpation P_e , colonization P_c) from a 27 year data set. Although populations were not strongly differentiated for most species (global $F_{ST} < 0.05$ all species), landscape genetic patterns and diversity were associated with life history and metapopulation variables. Fecundity explained significant variation in Mantel's r across species (adj. $r^2 = 0.50$, $P < 0.05$) indicating species with low fecundity were genetically structured with respect to distance but high fecundity species were not. Probability of extirpation was negatively associated with N_e (adj. $r^2 = 0.37$, $P = 0.048$) and contemporary abundance was positively associated with N_e (adj. $r^2 = 0.33$, $P < 0.061$), suggesting a trade-off between temporal stability (low P_e) and abundance (high density). Demography appeared to account for differences in N_e across co-occurring species with different life history characteristics.

**0488 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Helen Plylar, Clifford Fontenot

Southeastern Louisiana University, Hammond, LA, USA

Shining a Light on Snake Eyes: A Photorefractive Study of Visual Accommodation in Colubrid Snakes

The vertebrate eye utilizes a multi-lens system (composed of the cornea, aqueous humor, crystalline lens, and vitreous body), and the refractive properties of visual media (i.e. air and/or water) to facilitate vision. In terrestrial vertebrates, differences in refractive indices between the air and cornea are necessary for the production of a clear image. Semi-aquatic vertebrates face a unique challenge when transitioning from terrestrial to aquatic environments: the refractive index of the cornea is similar to that of water, resulting in a loss of corneal refractive power, and defocus of the optical system. However, some vertebrates (including at least one species of snake, *Thamnophis melanogaster*) are able to overcome this defocus. I used photorefractometry to compare refractive state and accommodative ability in air versus water between five sympatric colubrid snake species (*Nerodia cyclopion*, *N. rhombifer*, *N. fasciata*, *Pantherophis obsoletus*, and *T. proximus*), representing three ecotypes (aquatic specialist, aquatic generalist, and terrestrial generalist). Additionally, for each species I examined the pupillary response when submerged under water. A change in pupil size causes a corresponding change in the amount of light entering the eye. Decreasing the pupillary opening increases the depth of focus (and vice versa). Thus, a dilation of the pupil when submerged represents a potential mechanism for enhanced underwater visual acuity in some species. Results of this study will be presented and interpreted in terms of air versus underwater visual acuity, and how these relate to ecotype.

0398 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Daniel Portik¹, David Blackburn²

¹*University of California, Berkeley, Berkeley, CA, USA*, ²*California Academy of Sciences, San Francisco, CA, USA*

Molecular Systematics and Trait Evolution of the Afrobatrachia, an Extensive Radiation of African Frogs

Sub-Saharan Africa contains over 800 species of amphibians, and remarkably over 400 of the anuran species belong to a single clade referred to as the Afrobatrachia. This extensive radiation of frogs is composed of four families (Arthroleptidae, Brevicipitidae, Hemisotidae, Hyperoliidae), and species across these families are diverse in terms of ecomorphology, reproductive mode, and male secondary sexual traits. Here, we present the most comprehensive phylogenetic analysis of genus-level relationships of the Afrobatrachia. We sampled 52 species from 25 genera, and sequenced five nuclear loci

for a total of ~3,000 bp. Using these data, we estimated divergence timings and performed ancestral state reconstructions for several key traits. Our results support the monophyly of Afrobatrachians and resolve the phylogenetic placement of key genera. Several lineages of Afrobatrachians are quite ancient (~40-50 Ma), however diversification of the most species-rich genera began in the Early Miocene and resulted in the formation of over 250 species. In this framework, we discuss the evolution of reproductive modes and other relevant ecological traits across Afrobatrachians. Finally, we highlight ongoing systematic and evolutionary studies focused on specific clades of Afrobatrachians.

0273 AES Genetics, Carson 2, Friday 17 July 2015

David Portnoy¹, Jonathan Puritz², Christopher Hollenbeck², John Gold²

¹Texas A&M University - Corpus Christi, Corpus Christi, TX, USA, ²Harte Research Institute, Corpus Christi, TX, USA

Adaptive Genetic Variation and Male-mediated Gene Flow in the Bonnethead

The combination of male-biased dispersal and female philopatry, common in sharks, is expected to homogenize genetic variation in nuclear sequences across geographic space relative to variation in mitochondrial (mt)DNA sequences. However, when site-fidelity occurs across a heterogeneous environment, local selective regimes may add complexity to this pattern and on a genome-wide scale. We examined this possibility in bonnetheads, a species known to exhibit site fidelity. We obtained samples of bonnetheads from three areas along the west (Gulf) coast of Florida and one area off North Carolina on the U.S. Atlantic coast. We assessed patterns of variation in each sample in sequences of mtDNA and in 5,914 nuclear-encoded single nucleotide polymorphisms (SNPs). Sequences of mtDNA and putatively neutral SNPs revealed male-mediated gene flow and female philopatry among the samples from the Gulf. A total of 45 'outlier' SNPs (O-SNPs) were identified, and allele frequencies for 20 O-SNPs were correlated significantly with latitude, suggesting localized adaptation. There were no fixed differences in allele frequencies at any O-SNP locus; combinations of alleles common in one sample were present in low frequencies in other samples. There also was a significant correlation between estimates of genetic divergence based on O-SNPs and mtDNA sequences, but not between mtDNA sequences and either O-SNPs or putatively neutral SNPs. These results indicate that localized adaptive variation may sort primarily through the philopatric sex (females), with the dispersing sex (males) facilitating movement of potentially adaptive variation among locations and/or environments.

0073 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Gregg Poulakis, Philip Stevens, Rachel Scharer

Florida Fish and Wildlife Conservation Commission, Port Charlotte, FL, USA

A Comparison of Movement Patterns in Two Smalltooth Sawfish, *Pristis pectinata*, Nursery Areas

Movements of endangered juvenile (<3 yr old) Smalltooth Sawfish (*Pristis pectinata*) were monitored in the highly human-altered, freshwater inflow-managed Caloosahatchee River (2005-2013) and in the more natural Peace River, Florida (2010-2013) using 63 acoustic listening stations. A total of 133 sawfish (76 in the Caloosahatchee River; 57 in the Peace River) were monitored in main-stem river habitats and non-main-stem habitats (i.e., natural mangrove-lined creeks, semi-natural creeks, seawall-lined canals) of both river systems. Sawfish used all of the habitats available to them in both rivers, but tended to reside in specific regions of the nurseries. In the Caloosahatchee River, sawfish were usually associated with five hotspots that contained natural shoreline habitats along a 25 river kilometer (rkm) stretch of the nursery. They moved upriver during dry, low freshwater inflow conditions and downriver during wet, high inflow conditions. In contrast, in the Peace River, sawfish tended to remain in only a 6 rkm portion of the nursery during all freshwater inflow conditions. This portion of the nursery includes the only hotspot that has been identified in the Peace River. Possible reasons for these observations relate to differences in geomorphology and freshwater inflow regimes between the rivers.

0305 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kikuzawa Preslie, Ryan McCleary, David Bickford

National University of Singapore, Singapore, Singapore

Microhabitat Use by Homalopsid Snakes in Pasir Ris Park Mangrove, Singapore, and Its Implications for Management

Coastal development in Singapore has resulted in a loss of approximately 91.2% of original mangrove habitats. These habitats are essential for many species of wildlife including homalopsid snakes that can be abundant even in small mangrove fragments. In order to understand how microhabitat characteristics influence the numbers and types of species found within mangrove fragments, we measured habitat characteristics in the immediate vicinity where snakes (N = 245) were found, including root and shoot densities, substrate characteristics, and potential prey at Pasir Ris Park mangrove (PRPM). We also took morphometric measurements of all snakes that were captured. For comparison, we measured the same habitat characteristics in random locations (N = 100) throughout the mangrove where snakes were absent. A generalized linear modeling (GLM) approach was used to predict microhabitat preference. The snake assemblage at PRPM was dominated by the piscivorous *Cerberus schneiderii* (91%) with

two crab-eating species (*Gerarda prevostiana* and *Fordonia leucobalia*) also present. *C. schneiderii* were found mostly in habitats with open water (streams or pools), whereas *F. leucobalia* were generally associated with mudflats and mud mounds ($P \ll 0.001$). *C. schneiderii* presence was positively correlated with fish density and negatively correlated with crab density and water depth, whereas *F. leucobalia* was negatively correlated with both root density and turbidity. Overall, our results suggest that mangrove replantation may have negative short-term impacts on homalopsid snake presence, and that managing for the presence of mudflats and mud mounds (created by the mud lobster *Thalassina*) may increase snake diversity.

0125 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Bianca Prohaska, R. Dean Grubbs

Florida State University, Tallahassee, FL, USA

Stress Physiology of Deep Demersal Sharks in the Gulf of Mexico

Prior to the Deep Water Horizon oil spill, little research effort was focused on studying the physiology of deep demersal sharks inhabiting the Gulf of Mexico. While the physiology of these fishes remains virtually unknown, they are still routinely captured in commercial fisheries, both as targeted catch and as bycatch. In the absence of basic biological data, effective management plans cannot be formulated, making populations highly susceptible to declines. Potential effects the oil spill has had and will continue to have on these organisms are also unknown. Blood chemistry analysis can be used as a method of assessing physiological stress in elasmobranchs, and using this method three main questions will be addressed in the present study: 1) What are the baseline blood chemical parameters in deep demersal elasmobranchs? 2) Are the stress responses in these species ecologically-mediated or taxonomically-mediated? 3) Are there significant differences in blood chemical profiles between elasmobranchs potentially affected by the oil spill and those captured in less affected areas? Preliminary results suggest that stress responses are relatively similar among seven elasmobranch species sampled thus far, including *Mustelus sinusmexicanis*, *M. canis*, *Squalus cubensis*, *S. c.f. mitsukurii*, *Centrophorous c.f. uyato*, *C. granulosus*, and *Hexanchus griseus*. However, lactate and $p\text{CO}_2$ concentrations in *M. sinusmexicanis*, *M. canis*, and *S. cubensis* are relatively higher than that of the other species sampled, potentially suggesting a depth mediated stress response.

0515 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Catherine Purcell¹, Andrew Severin², Mark Drawbridge³, Kevin Stuart³, John Hyde¹

¹Southwest Fisheries Science Center, NOAA Fisheries, La Jolla, CA, USA, ²Genome Informatics Facility, Iowa State University, Ames, IA, USA, ³Hubbs-SeaWorld Research Institute, San Diego, CA, USA

Applying Genomic Tools to Help Improve Yellowtail (*Seriola dorsalis*) Aquaculture

Yellowtail aquaculture (*Seriola* spp.) is established globally with an estimated annual value of \$1.3 billion. Of these species, the native California *Seriola dorsalis*, is considered a prime candidate for aquaculture development in southern California. While genetic resources have been used to improve aquaculture practices for several marine species, few have been developed for *S. dorsalis*. We are working to develop genetic resources for *S. dorsalis* to help improve aquaculture techniques, and to gain a better understanding of the early life-stages of this species. In a collaborative effort, the Southwest Fisheries Science Center, the Genome Informatics Facility at Iowa State University, and the Hubbs-SeaWorld Research Institute have created a de novo draft assembly of the genome for *Seriola dorsalis*. DNA sequencing was conducted using the Illumina HiSeq 2500, resulting in approximately 1.2 billion raw reads, for estimated 160X coverage of the 685Mb genome. CEGMA analysis indicated that the MaSurCA assembly contained 93% of the Core Eukaryotic genes. Transcriptome analyses were also conducted to characterize physiological system development and examine growth heterogeneity. Gene expression was measured in three replicates of pooled larval samples at 2, 7, and 17 days post hatch. Sixty million reads, on average, were obtained per replicate. Genes of related function were sorted into clusters; those found at high frequency in the differential gene expression set were identified. This presentation will summarize highlights from these projects, and discuss results of these analyses, to date.

0435 Fish Genetics, Carson 3, Saturday 18 July 2015

Catherine Purcell¹, Andrew Severin², Mark Drawbridge³, Kevin Stuart³, John Hyde¹

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Using Transcriptomics to Investigate Development in California Yellowtail Larvae (*Seriola dorsalis*)

Seriola species (*S. dorsalis*, *S. dumerili*, *S. lalandi*, *S. rivoliana*, *S. quinqueradiata*), collectively known as amberjacks, are fish of particular interest to the growing aquaculture industry due to their high value, forming a billion dollar plus component of the sashimi industry.

The Pacific yellowtail, *Seriola dorsalis*, is a strong candidate for future development of offshore commercial aquaculture in southern California. Larval rearing methods for this and other *Seriola* species are still unreliable, resulting in highly variable survival and physical malformation rates that reduce market value of cultured fish. We are working to develop genetic resources for *S. dorsalis* to help improve aquaculture techniques, and to gain a better understanding of the early life-stages of this species. In a collaborative effort between the Southwest Fisheries Science Center, the Genome Informatics Facility at Iowa State University, and Hubbs-SeaWorld Research Institute, we are conducting transcriptome analyses of larval yellowtail to characterize physiological system development and examine growth heterogeneity. Gene expression, using RNAseq on an Illumina HiSeq 2500, was measured in three replicates of pooled larval samples at 2, 7, and 17 days post hatch for both slow- and fast-growing larvae. Sixty million reads, on average, were obtained per replicate. Genes of related function were sorted into clusters; those found at high frequency in the differential gene expression set were identified. This presentation will summarize highlights from these projects, and discuss results of these analyses, to date.

**0154 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Breanna Putman, Rulon Clark

San Diego State University, San Diego, CA, USA

**The Fear of Hidden Predators: Ground Squirrels Honestly Signal Vigilance
Toward Undetected Rattlesnakes**

Predators must evaluate several aspects of their prey before mounting an attack. Predators are less likely to attack prey that is vigilant, is aware of their presence, or may easily escape. Prey often exhibit conspicuous displays that advertise these qualities; such advertisements are termed "pursuit-deterrent signals" and benefit both predator and prey. When confronted with rattlesnakes (*Crotalus oreganus*), California ground squirrels (*Otospermophilus beecheyi*) use a tail-flagging signal that advertises predator detection. However, squirrels also signal in the absence of snakes, which could either dishonestly advertise predator detection or honestly advertise prey vigilance. Yet no study has tested these hypotheses experimentally. We tested the vigilance advertisement function of tail flagging by simulating snake strikes and quantifying strike-avoidance behaviors in signaling and non-signaling squirrels. We removed the effect of snake presence on signaling by simulating strikes 1) in the presence of a rattlesnake, 2) with no snake present, or 3) in an area where squirrels had recently encountered a snake that was no longer present. Squirrels tail flagged most when interacting with snakes, and rarely signaled when snakes were not present. In areas of recent snake encounters, squirrels also signaled, responded faster to simulated strikes, and were more likely to flee using aerial leaps. Tail-flagging rate was also related to flight speed and modality. Displays in the absence of predators can thus honestly signal vigilance, or the readiness for an

attack, even if predators are undetected. Rattlesnakes should avoid striking tail-flagging squirrels as their likelihood of a successful attack would be low.

0155 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Breanna Putman, Rulon Clark

San Diego State University, San Diego, CA, USA

The Potential for New Discoveries in Snake Ecology and Behavior Using Fixed Videography: A Case Study on the Rattlesnake *Crotalus oreganus*

Traditional observational studies of free-ranging snake behavior are difficult to conduct because of snakes' cryptic nature and because humans have difficulty maintaining attention toward infrequent behavioral events. Thus, in recent years, researchers have turned to using fixed videography to overcome these issues. Just as radio-telemetry revolutionized the study of snake ecology and behavior, fixed videography has the potential to do the same. Rattlesnakes in particular are easily studied using fixed videography due to their ambush-hunting behavior, tolerance of human disturbance, and their relatively large body size which facilitates the use of radio-telemetry to track individuals over time. Over the course of two summer field seasons (2011-2012), I used fixed videography to record the behavior of free-ranging northern Pacific rattlesnakes (*Crotalus oreganus*) in central coastal California. In just 2268 recorded hours of 18 adult individuals (11 male, 7 female), I gathered data on behaviors that would be too difficult to study without videography. This research has advanced our knowledge on rattlesnake hunting behavior, providing quantitative data on key aspects of this species' foraging ecology. In addition, I recorded several unique behaviors including intentional manipulation of the ambush site, the use of a non-rattling tail display, and interactions with conspecifics outside of reproduction. As the use of fixed videography to study free-ranging snakes grows, we will likely find that their behaviors are more complex than currently thought.

0390 ASIH STOYE AWARD ECOLOGY & ETHOLOGY II, Carson 4, Friday 17 July 2015

Thomas Radzio, Michael O'Connor

Drexel University, Philadelphia, PA, USA

Behavior and Short-term Survival of Captive-reared Yearling Gopher Tortoises Following Hard Release

Captive-reared animals often exhibit difficulty adjusting to life when released into the wild. This can impede research or conservation efforts that depend upon raising animals

in captivity. We collected hatchling gopher tortoises from natural nests in southwest Georgia and raised them in the laboratory for physiology experiments that required having animals in controlled environments for prolonged periods. Upon completing the lab work, we outfitted 30, one-year old individuals with radio transmitters and hard-released them in late summer at their nest sites to determine post-release behavior and survivorship. Most yearlings constructed burrows soon after release, and, like wild tortoises, released tortoises disproportionately placed burrows under deadwood. Video cameras located at tortoise burrows indicated normal activity patterns. Tortoises slept in burrows at night, emerged during warm daylight hours, basked extensively at burrow entrances, and limited time spent foraging away from the safety of burrow areas. Importantly, simulated predator approaches revealed that released tortoises showed normal antipredator responses by reliably hiding inside their burrows in response to potential threats. Released yearling tortoises exhibited survivorship similar to that of wild yearlings, 63-77% survived until the following spring. All known mortalities were due to predators. Despite having been raised inside plastic boxes and having daily contact with laboratory personnel for the first year of their life, captive-reared yearling tortoises retained critical traits necessary for success in the wild. These findings indicate that young gopher tortoises used in lab studies or captive-reared in efforts to augment wild populations may be successfully hard-released back into nature.

0581 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Thomas Radzio, Michael O'Connor

Drexel University, Philadelphia, PA, USA

Behavioral Thermoregulation and Thermal Constraints on Growth in Juvenile Gopher Tortoises

Many reptiles behaviorally regulate their body temperatures to increase energy assimilation and growth. However, some reptiles may limit thermoregulation due to increased predation risk associated with basking or other thermoregulatory activities. We investigate behavioral thermoregulation in juvenile gopher tortoises (*Gopherus polyphemus*), burrowing reptiles of the southeastern United States, and predict how thermoregulation and thermal environment influence growth. Since young tortoises are difficult to observe undisturbed, we used video cameras at burrows to quantify tortoise activities. Juveniles limit most basking activity to directly in front of their burrows from where they can quickly hide below ground to avoid predators. Juveniles shuttle in and out of burrows at predictable intervals to maintain preferred body temperatures. While juveniles generally only bask in front of burrows, they take advantage of most thermal opportunities available at these locations. In the lab, food intake and growth rate are highly temperature dependent across a narrow range of ecologically relevant temperatures and are greatest at the preferred body temperatures of fed tortoises. Therefore, by maintaining preferred body temperatures, juveniles can presumably increase their growth rates. Since young tortoises limit most basking to directly in front

of their burrows, increased shading of their environment, stemming from fire suppression and other poor land management practices, may reduce tortoise growth rates and potentially result in adverse population-level consequences.

0366 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Noelikanto Ramamonjisoa¹, Harisoa Rakotonoely², Yoshihiro Natuhara¹

¹Nagoya University, Nagoya, Japan, ²Hokkaido University, Sapporo, Japan

Tadpoles Differentially Use Visual Cues for Detecting Predators

Prey survival and fitness directly depend on their ability to detect predators. Chemical cues have been suggested to be the main cues for predator detection in aquatic environments but the role of visual cues remains controversial. We tested the changes in behavior and growth rate of *Rhacophorus arboreus* tadpoles when exposed to chemical, visual and the combined chemical-visual cues originating from dragonfly larvae (*Anax parthenope julius*) and newt (*Cynops pyrrhogaster*) predators. Tadpoles differentially responded to the presence of predators. Tadpoles reduced their activity in response to chemical cues of both predators. Chemical cues from dragonfly larvae reduced tadpole activity more than chemical cues from newts. Visual cues from dragonfly larvae did not induce a reduction in activity in tadpoles, whereas visual cues from newts did. The greatest reduction in tadpole activity was recorded in the combined visual and chemical cues from dragonfly larvae. Tadpoles' growth rates did not change in the presence of any of the cues from newt but increased in response to chemical and combined cues from dragonfly larva. These findings suggest that investment in defense is predator-specific and varies in response to cues from different predators with potential consequences on fitness.

0377 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Noelikanto Ramamonjisoa¹, Harisoa Rakotonoely², Yoshihiro Natuhara¹

¹Nagoya University, Nagoya, Japan, ²Hokkaido University, Sapporo, Japan

Learned Recognition of Alien Predators through Association with Heterospecific Prey in a Tadpole

Many prey species express defense against predation, usually reduced activity, which is suggested to be one of the most effective defense strategies in aquatic systems. Alien predators are often the major causes of the extinction of local biodiversity, in part because the defense repertoire of native preys has not evolved yet to the new ecological context. We tested the behavioral responses of two coexisting anuran tadpoles *Rhacophorus schlegelii* (RS) and *Pelophylax nigromaculata* (PN) to the presence of a non-lethal invasive alien predator *Procambarus clarkii*. The two species were raised

individually or together in the absence or the presence of caged predators in the laboratory. We hypothesized that either both or neither species would behaviorally respond to the presence of the alien predator. Interestingly, we found that PN reduced its activity level in the presence of predators both in monospecific and heterospecific treatments. Surprisingly, RS did not reduce its activity when reared alone in the presence of predators but only when reared together with PN in the presence of predators. We suggest that RS may have learned to recognize the alien predator through association with the heterospecific species that has already evolved an adaptive recognition to the predator. Our findings suggest first, that the evolution of adaptive defense plasticity in prey to novel predators can differ even in closely related species. Second, social learning may contribute to reduce tadpole vulnerability to alien predators and alleviate the impact of invasions in natural populations.

0386 Fish Ecology I, Carson 3, Sunday 19 July 2015

Sarah Ramsden, Mary Carla Curran

Savannah State University, Savannah, GA, USA

**Seasonal Patterns in Residency and Distribution of the Atlantic Stingray
Dasyatis sabina in Two Tidal Creek Systems near Savannah, Georgia**

The Atlantic Stingray *Dasyatis sabina* is found in freshwater, estuarine, and saltwater habitats along the Atlantic and Gulf coasts of the United States. It is a predator of commercially important blue crabs. Additionally, this species is an ecosystem engineer that disturbs meiofaunal species when excavating feeding pits in the benthic substrate. There are discrepancies about whether *D. sabina* is a seasonal or year-round resident of coastal habitats along its entire geographic range. Thus, the purpose of this study was to determine the effect of season on the residency and distribution patterns of the Atlantic Stingray in two creek systems near Savannah, Georgia. Forty stingrays were passively tracked using acoustic telemetry (Vemco) in Romerly Marsh Creek and the Herb River systems. Seasonal residence was calculated for each stingray. Usage was calculated for each receiver station during each season. The Atlantic Stingray was present year-round in Georgia estuaries, although monthly residence was positively correlated with bottom-water temperature in both study sites. Stingrays were present in the creeks most often (>60% of days) during the summer months when water temperatures were >20°C. Most rays left the creeks during winter when water temperatures were <15°C, using them for <20% of days. We conclude that Atlantic Stingrays remained in a Georgia estuary during all seasons. Thus, acoustic telemetry may be a more suitable technique than historically utilized methods that may have underestimated Atlantic Stingray presence, thereby misinterpreting seasonal patterns in residence.

0227 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Zachary Randall, Lawrence Page

Florida Museum of Natural History, Gainesville, FL, USA

Revision of the Hill-stream Gecko Loaches, *Homalopteroides* Fowler 1905 (Teleostei: Balitoridae)

Homalopteroides geographically is one of the most widely distributed balitorid genera, occurring in northeastern India, Myanmar, Thailand, Laos, Cambodia, Vietnam, Peninsular Malaysia, Sumatra, Java, and Borneo. The genus currently consists of 11 species with several populations exhibiting a large amount of morphological variation that may constitute new species. A molecular phylogeny of *Homalopteroides* is presented and the morphological diversity and relationships are discussed as well as the geographic structuring of the widespread species of the genus.

0185 Herp Conservation II, Carson 1, Saturday 18 July 2015

Brendan Reid, Richard Thiel, Zach Peery

University of Wisconsin-Madison, Madison, WI, USA

If You Build It, They Will (Slowly) Come: Population Dynamics of Endangered Blanding's Turtles (*Emydoidea blandingii*) in a Restored Area

Habitat protection and restoration are often used to promote recovery in endangered reptile species, yet the long-term consequences of these efforts can be difficult to assess. Measuring the effects of habitat restoration on turtles can be especially difficult due to long generation times and consequent time lags between restoration activities and population-level responses to these activities. Here, we collected 24 years of data on a population of IUCN-Endangered Blanding's turtles (*Emydoidea blandingii*) inhabiting a large restored wetland-upland complex in Wisconsin, USA. We used these data to examine survival and recruitment in the population as a whole as well as the response of individual aggregations of nesting females to recent restoration of an extensive upland prairie-savanna nesting habitat. The population exhibited positive growth over time ($\lambda = 1.03$). Mark-recapture data also supported increased recruitment of nesting females in the recently restored prairie-savanna nesting area. Females nesting in recently restored prairie-savanna habitat were smaller and decreased in size over time compared to females using two older nesting areas, indicating increased recruitment of young breeding females in recently restored habitat. Nest depredation probability decreased with increasing distance from forest edges, suggesting that the recent clearing of woody vegetation in recently restored habitat increased reproductive success. Collectively, our results highlight the potential benefits of habitat restoration to turtles and identify upland habitats as a key to promoting population growth in turtles with complex habitat requirements such as Blanding's turtle.

**0062 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Sean Reilly, Jimmy McGuire

University of California, Berkeley, CA, USA

Biogeographical History of Flying Lizards (Genus: *Draco*) from the Lesser Sunda Islands, Indonesia

Flying lizards of the genus *Draco* are known to have originated and diversified in Southeast Asia. Populations occupying islands within the biogeographic region of Wallacea, which lies to the east of the Sunda shelf, have colonized these islands by overwater dispersal. The Lesser Sunda Islands make up the southern portion of Wallacea, are poorly studied, and are home to two described species of Flying Lizards (*Draco boschmai* and *D. timorensis*). We obtained tissues from over 300 flying lizards from the Lesser Sunda Islands of Bali, Lombok, Sumbawa, Flores, Lembata, Pantar, Alor, Wetar, Sumba, Rote, and Timor. These samples were sequenced for the ND2 gene to provide an initial glimpse into the biogeographic history of this monophyletic group. We then used an exon-capture approach to collect sequence data for 1,200 nuclear genes from 93 lizards. We used this genomic dataset to estimate a phylogeny, species tree, and population structure. We infer that flying lizard biodiversity within the Lesser Sunda Islands is underestimated, and that there has been an unexpectedly complex pattern of colonization that is related to the tectonic history of the archipelago. Conservation of the biodiversity within the Lesser Sunda Islands is dependent on an accurate understanding of species diversity and its spatial organization. We believe that genomic studies of this and other widely distributed species in the archipelago will reveal that they in fact represent species complexes, which will prove crucial for conservation planning in the region.

0036 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Qiu Ren¹, Lei Yang², Chia-Hao Chang¹, Richard Mayden¹

¹*Saint Louis University, Saint Louis, MO, USA*, ²*Hollings Marine Laboratory, SC, USA*

Molecular Phylogenetic and Geometric Morphometric Analyses of Asian Barbs in the *Puntius* (*sensu lato*) Complex (Teleostei: Cypriniformes)

"*Puntius*" Hamilton *sensu lato* is one of the largest of the genera in the family Cyprinidae. There are around 120 valid species widely distributed in Southeast Asia, Nepal, India, Bangladesh and China. "*Puntius*" has long been known as an artificial assemblage and "catch-all" genus in which a large number of small, unrelated cyprinids have been placed. With new species and genera being described each year, obtaining detailed knowledge of the phylogenetic relationships of this complex is critically important in the

assessment of a natural classification. In the present study, we use two mitochondrial and four nuclear genes to examine the interspecific relationships of the "*Puntius*" complex and test the monophyly of the current genera. Geometric Morphometrics is used as a complementary data set to investigate the shape variation between or within groups. The molecular analysis identified nine clades and this tree was used to explore the origin, evolution and divergence of Asian and African diploid barbs using a molecular evolutionary time calibration approach. Genera *Puntius s.s.*, *Systemus*, *Pethia*, *Dawkinsia*, *Haludaria*, *Desmopuntius*, and *Puntigrus* are monophyletic with high support; however, monophyly of *Oliotius*, *Striuntius* and *Sahyadria* is not supported in this study. The inclusion of *Puntius semifasciolatus* and *P. snyderi* from China and Taiwan made *Puntius s.s.* paraphyletic. Inferences of divergence time analysis indicate that *Puntius s.l.* likely dates to early Miocene.

**0501 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Friday 17 July 2015**

Rachel Rhymer, Jeanne Robertson, Gilberto Flores, Robert Espinoza

California State University Northridge, Northridge, CA, USA

Testing the Benefits of Maternal Care in a Viviparous Lizard

Parental care has evolved independently in many lineages, indicating that it can play an important role in fitness. However, this trait is considered rare in squamate reptiles. *Phymaturus extrilidus* (Liolaemidae) is a recently described herbivorous and viviparous lizard inhabiting the high-elevation desert (Puna) of San Juan, Argentina. Females and neonates have been observed interacting in the weeks after birth. Our study goals were to (1) test whether grouped individuals are related, and (2) identify the likely evolutionary pressures selecting for these presumed maternal behaviors. Such pressures likely include reducing predation risk and/or the need to socialize to transfer vital microbial endosymbionts from one generation to the next. First, we determined relatedness via kinship analyses of microsatellite data. Predation pressure was assessed by conducting predator-approach experiments with models of two known predators. Hindgut microbes, which are required for digesting plant material, were compared among groups to test whether microbes are transferred from one generation to the next. Grouping was most commonly observed in neonates and adult females, suggesting that these associations improve fitness. Flight-initiation distance was not different between groups and individuals, suggesting that grouping is not related to predation pressure, perhaps because neonates do not benefit from maternal cues in the presence of predators. Microsatellite-based pedigrees and microbiome analyses are underway. Our study will be the first to elucidate the pressures selecting for the evolution of this behavior in this lineage, which appears to be shared by other species of *Phymaturus*.

0322 SWPARC Symposium, Carson 4, Sunday 19 July 2015

Jonathan Richmond¹, Dustin Wood¹, Michael Westphal², Robert Fisher¹

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SWPARC - Population Genetic Connectivity Patterns in the Endangered Blunt-nosed Leopard Lizard *Gambelia sila* Reveal Clues about the Former Landscape of California's San Joaquin Desert

Since the late 1800s, California's San Joaquin Desert has become an infamous hotspot of threatened and endangered species due to the rapid and near complete transformation of this ecoregion's natural landscape. Much of the Desert encompasses the San Joaquin Valley, an area historically partitioned by a series of westward draining rivers and creeks that emptied out of the Sierra Nevada and into three large lakes on the Valley floor. These lakes, their surrounding wetlands, and riparian areas along the rivers that fed them, may have presented barriers to gene exchange for a number of xeric-adapted vertebrate species like the endangered blunt-nosed leopard lizard *Gambelia sila*, a San Joaquin Valley endemic that inhabits open, sparsely vegetated desert scrub habitat. We used mtDNA sequences, microsatellite allele frequency data, and restriction-associated digest sequences from 18 locations covering the range of *G. sila* to test the extent to which population structuring and gene exchange were shaped by mesic habitat or other barriers within this otherwise desert ecoregion. Our results suggest that wetland and riparian areas did little to impede historical movement across the Valley floor, and instead point to precipitation patterns owing to topographic effects as a more cogent factor in determining population structuring and directionality of gene flow. This work identifies areas that were important dispersal corridors for *G. sila* prior to humanity's major alteration of the landscape, and can be used to guide habitat restoration efforts for this and numerous other xeric-adapted species of conservation concern in the San Joaquin Desert.

0234 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Hayley J. Roberts¹, Marc J. Mazerolle², Stephen C. Lougheed¹

¹Queen's University, Kingston, Ontario, Canada, ²Université du Québec en Abitibi-Témiscamingue, Rouyn-Noranda, Québec, Canada

Comparing Male and Female Breeding Phenology in Gray Treefrogs

Phenology is a key facet of organismal response to environmental variation, both in terms of seasonality and, over the longer term, climate change. Breeding phenology has obvious implications for individual fitness, local adaptation and population persistence.

Despite its importance, many aspects of breeding phenology are poorly known in many temperate frogs. Therefore, our research investigated differences in within-season temporal trends and abundance between male and female Gray Treefrogs (*Hyla versicolor*). We predicted asynchronous chorus attendance, with males arriving first and showing peak numbers early but with a sustained chorus, followed by female arrival and quick diminution in numbers after breeding. I conducted nightly transect searches at two breeding sites in eastern Ontario, Canada during the breeding season of 2014. We used models accounting for imperfect detection probabilities to estimate the abundance of male and female Gray Treefrogs throughout the season. In contrast to my predictions, I found that the sexes have synchronous peaks and similar patterns of chorus attendance. This result suggests that males and females respond to similar environmental conditions, rather than females responding to male chorusing. My research highlights the importance of detailed studies of phenology both to increase our understanding of mating systems and how individual populations might vary in response to environmental change.

0254 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Alexandre B. Roland¹, Juan C. Santos², Luis A. Coloma³, Elicio Tapia³, Bella Carriker¹, Lauren A. O'Connell¹

¹Harvard University, Cambridge, MA, USA, ²University of British Columbia, Vancouver, BC, Canada, ³Centro Jambatu for Research and Conservation of Amphibians, Quito, Ecuador

Hybridization and Expansion of the Polymorphic Little Devil Poison Frog *Oophaga sylvatica*

Aposematism is a deterrent signal displayed to warn potential predators of danger or unpalatability. The evolution of such signals is assumed to favor a unique model under predator selection pressure. However, some species in the poison frog family Dendrobatidae have extreme variability in aposematic traits. Such color pattern polymorphisms, likely at the early basis of speciation processes, could result from a multi-component natural selection processes ranging from geographical isolation, predators selection, and mate choice. To better understand the origin of these color and pattern polymorphisms in poison frogs, we studied the Little Devil poison frog *Oophaga sylvatica*, which has homogeneous populations with “stable” color pattern as well as highly variable populations. Using PCR and Sanger sequencing, we amplified 3 mitochondrial genes (12S rRNA, 16S rRNA and Cytochrome Oxidase 1 subunit) and 3 nuclear genes (Recombination Activating Gene 1 (RAG-1), Sodium-calcium Exchanger (NCX) and Tyrosinase), to assess relationship between more than 200 frogs of 13 populations sampled throughout their distribution range in the western slope of Ecuadorian Andes. Our data show that these populations follow a north-south gradient, where northern populations have high genetic and phenotypic diversity probably arising from hybridization of adjacent populations in an admixture zone, while southern populations have relatively low genetic diversity and likely expand more recently. Here

we show a striking example of an ecologically important trait (aposematism) evolving through natural hybridization between phenotypically divergent populations, after putative migration events.

0269 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Nicole Roman-Johnston¹, Kayla Anatone¹, Julio Angel¹, Alexandra Fireman¹, Abrial Meyer¹, Chloe Nash¹, Michelle Kraczkowski², Barry Chernoff¹

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Over the Falls: The Effect of Waterfalls on the Genetic Structure of the Eastern Blacknose Dace, *Rhinichthys atratulus*, in Connecticut

Following the retreat of the Wisconsinan glaciers, approximately 22,000 years ago (Hewitt 2000), the new hydrologic regime in Connecticut resulted in many waterfalls once glacial meltwaters receded. These waterfalls created fragmented habitats that stranded populations of freshwater fishes above the falls, thereby impacting gene flow of fish species, such as the Eastern Blacknose Dace, *Rhinichthys atratulus*. Other studies, based on salmonids, have shown that waterfalls act as barriers to gene flow. Populations above and below the falls have been shown to diverge genetically, while below-falls populations exhibit greater genetic diversity. We test these hypotheses with data from 15 nuclear microsatellites of which seven were polymorphic. We tested populations above and below three independent waterfalls in the Connecticut River basin. Based on the molecular analyses, we found that waterfalls are acting as leaky barriers to gene flow. Populations of *R. atratulus* above and below the falls each evolved unique (private) alleles, supporting the theory. However, populations above the falls exhibited equal or higher genetic diversity than populations below the falls. Furthermore, populations either above or below the falls that were not separated by the waterfall barrier, exhibited limited gene flow among populations. Overall, the population-genetic structures observed for *R. atratulus* at these three waterfalls in CT contradict theory.

0320 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Thursday 16 July 2015

Jonathan Rose, Brian Todd

Department of Wildlife, Fish, and Conservation Biology, University of California, Davis, Davis, CA, USA

Designing Effective Eradication Strategies for Non-native Watersnakes (*Nerodia*) in California Using Integral Projection Models

Effectively managing invasive species requires knowledge of the population biology of invaders. Population models can simulate the effect of management actions on the rate

of population growth and spread of invasive species, but the models' usefulness depends on how accurately its structure reflects the biology of the target species. Age based matrix models are difficult to implement for many amphibians and reptiles. Integral Projection Models (IPMs) present a promising tool for modeling amphibian and reptile populations because they model vital rates such as survival, growth, and fecundity as continuous functions of size. We demonstrate the use of IPMs to model the population growth rate of two incipient invasive species in California, *Nerodia fasciata* and *Nerodia sipedon*, which are potential competitors with *Thamnophis gigas*, a threatened, native species. By combining data from populations in the native and invasive range of these species, we create stochastic IPMs that account for uncertainty in the estimation of vital rates. Based on diagnostic criteria such as the stable size distribution and age at sexual maturity, our IPMs accurately model the demography of watersnake populations. Model results indicate that eradication efforts will be most effective if trapping occurs in spring and early summer, before parturition. Elasticity analyses show that to maximally depress the population growth rate, eradication efforts should target removal of females smaller than 400 mm SVL, followed by newly mature females, which have the greatest reproductive value. We also use population viability analysis to estimate the trapping effort necessary to eradicate non-native watersnake populations.

0204 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Nicholas Rosso, Brad Coupe

Castleton State College, Castleton, VT, USA

Mate Attraction by Female Sidewinder Rattlesnakes: An Individual-based Spatially-explicit Computer Simulation

Snake mate location through non-volatile pheromone tracking is understudied due to the difficulty of mapping actual movement paths. In order to research these behaviors, a spatial model was written in the computer programming language Python that simulated female movements to attract mates. Female movements were varied by both distance and meander ratios (actual distance moved/straight-line distance) using previously collected telemetered data from sidewinder rattlesnakes to parameterize the model. We hypothesized that a straight-line movement strategy would be the most successful in attracting males because it would most effectively broadcast female pheromones. Modeled snakes that used attraction movements with lower meander ratios (closer to a straight line) were more successful than movements that modeled a random walk, which has a high meander ratio. However, a straight-line movement strategy did not differ significantly in attraction success from a strategy that modeled natural movements. Truly straight lines would be unexpected in nature, and these data suggest that selection has favored female movements to approximate the straight-line ideal. If long-distance, straight-line movements increase the probability of attracting a mate, then females moving much longer distances than other females should further enhance their probability. We tested this by adding a single female to the model who moved considerably farther than others in that model run. This female dramatically

outperformed others in her cohort, but experienced diminishing returns on her movement investment. Despite these diminishing returns, the data suggest that females that can afford, energetically, to make long attraction movements should do so.

0479 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Erica Rottmann, Kyle Piller

Southeastern Louisiana University, Hammond, LA, USA

Expanding Detection Capabilities of Fishes in Louisiana: An Integrative eDNA Approach

Environmental DNA (eDNA) techniques have proven to be valuable monitoring tools for the detection of invasive and imperiled aquatic organisms. However, the usefulness of this approach in the southern United States may be impacted by more rapid DNA degradation due to higher water temperatures and other chemical and physical characteristics of southern waters. Southeastern Louisiana has many imperiled aquatic species that are in need of study from a conservation perspective. A cost-effective, non-invasive monitoring approach is needed to assess the conservation status of many aquatic species in the region. In previous studies, there has yet to be standardization of the methodology for eDNA sampling. This project had two objectives. First, we conducted laboratory and field experiments on a locally abundant fish, the blacktail shiner, *Cyprinella venusta*, to test the efficiency of several common extraction and amplification methods in an effort to shed light on the most reliable protocols for eDNA sampling in this region. Second, we used both eDNA and traditional field sampling techniques in a seasonal sampling approach to assess the conservation status of two imperiled taxa in the Lake Pontchartrain Basin, the gulf logperch, *Percina suttkusi*, and the flagfin shiner, *Pteronotropis signipinnis*. Both species are known to occur historically in a limited number of localities in the basin making them ideal candidates for field-testing of the eDNA method. Each species was detected at a greater number of sites based on eDNA samples in comparison to traditional sampling techniques, further supporting the usefulness of this technique.

0034 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Sara Ruane¹, Chris Raxworthy¹, Alan Lemmon³, Emily Lemmon³, Frank Burbrink²

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Estimating a Malagasy Snake Phylogeny: A Comparison of Small and Large Molecular Datasets

Despite comprising over 80% of the ophidian diversity in Madagascar (~81 species), the pseudoxyrhophiines are a poorly known subfamily from both an ecological and systematic perspective. Previous phylogenetic studies including these snakes have been depauperate with respect to locus number, species diversity, or both. Here we use datasets which differ in both species number and locus number to determine how varying the number of molecular markers and species affects the results using a variety of phylogenetic methods for tree estimation. With ~700 pseudoxyrhophiine samples available representing 90% of described genera and 87% of described species, plus additional undescribed species diversity, we estimate phylogenies using multiple methods (full coalescent models, summary statistics approaches, and concatenation) with datasets generated using Sanger-sequencing for 5 frequently used markers in squamate phylogenetics and compare this with a dataset of ~400 loci generated using anchored phylogenomics. We find that many of the relationships between genera are stable regardless of which phylogenetic method is used and that many of the subgroups based on earlier morphological work are confirmed by the molecular analyses. Furthermore, we find that under certain circumstances, all methods recover the same topology, but that the only the full coalescent model is consistent when using <50 loci. Our results illustrate that while hundreds of loci may not always be necessary for species-tree estimation, this is dependent on both the number of taxa and method utilized.

0222 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Cassandra Ruck¹, Fabio Hazin², Rima Jabado³, Mahmood Shivji¹

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Global Genetic Connectivity in a Shark of High Conservation Concern, the Oceanic Whitetip, *Carcharhinus longimanus*

The oceanic whitetip shark, *Carcharhinus longimanus*, is globally distributed in warm waters and has suffered drastic declines in recent history due to high bycatch in diverse pelagic fisheries and demand for its large fins in international trade. Due to these

declines, the once common oceanic whitetip is now listed as "Critically Endangered" in the Western North and Western Central Atlantic and "Vulnerable" to extinction globally by the IUCN Red List. Thus, there are urgent calls for improved data collection and management strategies to conserve this enigmatic species. However, there exist no data on the population genetics of oceanic whitetip sharks. We report an assessment of the global population structure and demographic history of this shark based on analysis of two mitochondrial DNA region sequences (entire control region (1067 bp) and part of the NADH dehydrogenase subunit 4 gene (682 bp) and nuclear microsatellite markers. Pairwise analysis of concatenated mitochondrial data with ARLEQUIN v. 3.5.1.2 indicates significant differentiation between the western Atlantic (n=93) and Indo-Pacific (n=72) populations ($\Phi_{ST} = 0.0757$, $P < 0.001$). Furthermore, analysis of only the 682 bp ND4 fragment, a more variable locus than the control region in this species, indicates differentiation between all three ocean basins: Atlantic vs. Pacific (n=40) ($\Phi_{ST} = 0.0804$, $P < 0.001$), Atlantic vs. Indian (n=32) ($\Phi_{ST} = 0.0508$, $P = 0.0108$), Indian vs. Pacific ($\Phi_{ST} = 0.0509$, $P = 0.033$). Despite the global distribution and presumably high vagility of *C. longimanus*, significant population structure exists and effective management strategies must take this into consideration.

0196 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Ariana Rupp, David Sever

Southeastern Louisiana University, Hammond, LA, USA

Histology and Ultrastructure of Mental Glands and Caudal Courtship Glands in Three Genera of Plethodontid Salamanders

Salamanders in the family Plethodontidae exhibit a unique tail-straddle walk during courtship that can include the use of sexually dimorphic mental glands and caudal courtship glands, which are thought to increase female receptivity during courtship. Mental glands are found in the skin of the lower jaw and caudal courtship glands are found in the skin at the dorsal base of the tail. The presence of mental glands and caudal courtship glands has been observed in some species of plethodontid salamanders, but a limited number of studies exist on the seasonality and ultrastructure of these glands. While there are many light microscopy studies of mental glands that have observed intergeneric morphological variation, only four histological studies of caudal courtship glands exist. Ultrastructural studies using transmission electron microscopy are even less available, with only two previous studies on mental glands, and one study on caudal courtship glands. The data available for mental gland characters can be optimized on a phylogeny to learn about evolution of these glands, but more data must be collected on caudal courtship glands before optimization would be useful for studying their evolution. This study will use light microscopy and transmission electron microscopy to describe the histological and ultrastructural seasonal intergeneric variation of these glands in the three genera *Plethodon*, *Eurycea* and *Desmognathus*, focusing on native Louisiana species that have not been extensively studied for these

glands. Preliminary light microscopy results on *Plethodon mississippi* and *Eurycea quadridigitata* have shown that caudal courtship glands exhibit intergeneric morphological variation.

0195 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Jung-Hwa Ryu, Jin-Koo Kim, Soo-Jeong Lee, Young-Sun Song, Se-Hun Myoung, Hyo-Jae Yu, Sang-Yun Han, Yoo-Jun Lee

Pukyong National University, Busan, Republic of Korea

Community Structure of Marine Fish in the Korean Waters During 2006-2013

In order to clarify the community structure of marine fish around the Korean peninsula, we collected fish four times a year from the Yellow Sea (2006-2008), Korea Strait (2009-2010), Jeju Island (2011), and East Sea (2012-2013), using set net or gill net. During the survey, a total of 283 fish species was collected, of which *Engraulis japonicus* (63.8%), *Collichthys lucidus* (9.8) and *Trachurus japonicus* (8.9) were dominant. The number of fish species was the highest in the East Sea (140 spp.), and followed by the Yellow Sea (139 spp.), the Korea Strait (137 spp.), and Jeju Island (86 spp.), but the species diversity index was the highest in Jeju Island (2.90), and followed by the Korea Strait (2.05), Yellow Sea (1.81) and the East Sea (1.25). The main dominant species by each seas were *Collichthys lucidus* (37.6%), *Engraulis japonicus* (19.3) and *Collichthys niveatus* (13.5) in the Yellow Sea; *Engraulis japonicus* (41.6%), *Leiognathus nuchalis* (6.6) and *Trachurus japonicus* (6.3) in the Korea Strait; *Trachurus japonicus* (32.8%), *Sebastiscus marmoratus* (8.4), *Scomber japonicus* (5.7) in Jeju Island; *Engraulis japonicus* (82.9%), *Trachurus japonicus* (12.0) and *Clupea pallasii* (0.8) in the East Sea. UPGMA cluster analysis showed that Korean marine fish species were largely separated into four groups as follows; 1) the Yellow Sea group, 2) the western Korea Strait group, 3) the middle East Sea group, 4) Jeju Island, the eastern Korea Strait and the southern East Sea group. This grouping may be associated with the characteristics of the sea currents or water masses.

0099 NEOTROPICAL ICHTHYOLOGICAL ASSOCIATION, Carson 3, Friday 17 July 2015

Mark Sabaj Pérez¹, Daniel Fitzgerald², Leandro Sousa³

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Where the Xingu Bends: Exploring Volta Grande by Land, Air and Water

In a stretch of 130 river kms, the Xingu falls 90 meters and changes course by about 90° in each of three major bends known as “Volta Grande”. The first bend is at Altamira below which the Xingu is briefly a singular channel two kms wide. As it enters Volta

Grande, the Xingu unravels into countless braids loosely woven through lenticular islands and shoals. At Volta Grande's southern limit, the Três Palmeiras greenstone belt redirects the entire river to the northeast. The river's planform remains extremely woven throughout the lower Volta Grande, but the braids are more intricate with linear straits following fractures in the basement rock. The result is a complicated labyrinth of watery channels, powerful rapids and low waterfalls formed and bounded by granitic outcrops. The most spectacular cascades are cachoeira do Jericoá where much of the Xingu tightly zigzags through a narrow Z-shaped channel in the broken bedrock. At Volta Grande's downstream limit, three major braids coalesce into a singular channel that is about a half kilometer wide. Here the Xingu completes its departure from the Brazilian Shield, and gradually widens into a long estuary-like ria through sedimentary rocks of the Amazonas basin. Rapids occur in many large rivers, but rarely if ever achieve the scale and complexity of Volta Grande. Aerial photos and footage shot during the iXingu Project (NSF DEB-1257813), alongside ground level photography and physicochemical measurements, help us explore and appreciate the Xingu's complex geomorphology, collage of water chemistries and drastic hydrological cycle.

0467 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Daniel Saenz¹, Cory Adams¹, Josh Pierce¹, Toby Hibbitts²

¹*Southern Research Station, Nacogdoches, TX, USA*, ²*Texas A&M University, College Station, TX, USA*

Predators Influence Amphibian Communities in Artificially Constructed Wetlands

A generally accepted paradigm in aquatic ecology suggests communities are structured by hydroperiod and predation. This theme is prevalent in the literature regarding amphibian communities. We attempted to look for patterns of amphibian species co-occurrence and community structure associated with predator regime in artificially constructed wetlands. We sampled, using dip nets, 51 ponds in the Angelina and Davy Crockett National Forests in eastern Texas. These ponds, which typically hold water year-round, provide an excellent opportunity to study amphibian pond use and community assembly. We recorded 18 different species of amphibians in the ponds and various predators. In general, fishless ponds tended to have higher species richness than ponds with fish; however the species of fish present was also important. Ponds dominated by green sunfish (*Lepomis cyanellus*) tended to have the lowest amphibian richness while ponds dominated by largemouth bass (*Micropterus salmoides*) were intermediate with regard to amphibian richness. Initial analyses indicate that the primary predator is a main driver influencing amphibian species richness and community composition. Further, amphibian community structure may not show a generalized response to the presence of fish, rather a specific response to different species of predatory fish.

0065 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kenji Saitoh

National Research Institute of Fisheries Science, Yokohama, Japan

Reconciliation of Taxonomy with Laboratory Fish Communities

Advancement of phylogenetic systematics sometimes gives rise to changes of scientific names and placement in higher ranks of widely used model fishes. These changes affect computer retrieval systems. From a standpoint at which we should avoid changes if avoidable, I will review past changes for model fishes widely used by non-taxonomists and non-ichthyologists, and give a feasible solution especially on the zebrafish whose family name could be changed. Genus transfer of zebrafish from *Brachydanio* to *Danio* in 1993 could be unnecessary because this change was based on an incomplete molecular phylogeny. Reversion will make, however, another confusion nowadays. Changes of scientific names for fugu and rainbow trout were unavoidable because of nomenclatural priority. Recent change of the family name of medaka was among a couple of historical changes, and its impact was not bigger than past such changes. The specific name of goldfish not having been applied to its wild type impinged only a little as far as the captive goldfish is concerned. Dividing the Cyprinidae into a number of families to resolve paraphyly of the family will change the family name of zebrafish. Another solution may be to put a minor family (Psilorhynchidae) with long being unclear placement in the inclusive Cyprinidae. I prefer the latter solution with smaller impacts.

0064 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Kenji Saitoh¹, Tetsuya Sado², Mutsumi Nishida³, Richard Mayden⁴, Masaki Miya²

¹*National Research Institute of Fisheries Science, Yokohama, Japan*, ²*Natural History Museum and Institute, Chiba, Chiba, Japan*, ³*University of the Ryukyus, Nishihara, Okinawa, Japan*, ⁴*Saint Louis University, MO, USA*

Mitogenomic Phylogeny of Cypriniformes

Fishes of the order Cypriniformes are almost completely restricted to freshwaters and comprise over 4000 species in six to 13 families. Monophyly, interrelationships and classification of these families/subfamilies/tribes have historically been poorly resolved. Recent years of varied studies on the group are progressing towards a stable classification except for some enigmatic taxa. Following our previous mitochondrial phylogenomic study based on the 60 sequences (Saitoh et al 2011), we have determined over 400 additional whole mitogenome sequences for cypriniform species. The combined data worked for phylogenetic analysis in an effort to continue to move forward with a stable classification. This study is the most comprehensive molecular phylogeny of the world's largest freshwater-fish clade based on more extensive taxon sampling from over 600 cypriniform species (including phylogenetically enigmatic *Psilorhynchus*, *Ellopostoma*, *Paedocypris*, etc). Unambiguously aligned, concatenated mitogenome sequences from 13 protein coding, two rRNA and 22 tRNA genes,

representing over 15kb, were divided into five partitions (1st, 2nd, and 3rd codon positions, rRNA and tRNA). Maximum likelihood phylogenetic analyses based on the partitioned dataset gave phylogenetic relationships that are largely congruent with the previous findings (Saitoh et al 2011), although with the addition of over 500 sequenced/published species it provides a much more detailed picture of relationships. The major relationships of monophyletic groups and enigmatic taxa are revealed. While this is the most extensive taxon and nucleotide site sampling, some branches remain not well supported.

**0572 NEOTROPICAL ICHTHYOLOGICAL ASSOCIATION, Carson 3, Friday
17 July 2015**

Norma Salcedo

College of Charleston, Charleston, SC, USA

**Finding the Holotype of *Chaetostoma marmorescens* (Siluriformes:
Loricariidae)**

The Irwin Expedition (1918-1919), conducted by Carl Eigenmann and Ray Allen, resulted in the collection of many fish specimens in Peru, Bolivia, and Chile. One particular work, that included species descriptions based on material collected during the Irwin Expedition, is the volume that Ray Allen compiled after Eigenmann's death. This volume, published in 1942, includes the description of *Chaetostoma marmorescens*, the holotype of which is, to date, considered to be lost. Eigenmann's material was transferred from Indiana University (IU) to the California Academy of Sciences (CAS) in 1938. The morphology (including meristics, and morphometrics) of all the *Chaetostoma* material at CAS was studied, as well as the entries in the original catalog ledger (Indiana University) where Eigenmann assigned numbers to the types-to-be of *Chaetostoma marmorescens*. A total of 81 *C. marmorescens* specimens were found at CAS identified as *C. taczanowskii*. None of the specimens at CAS matched the total length reported by Eigenmann for the holotype of *C. marmorescens*. A lot of *C. marmorescens* (10 specimens), collected by Allen during the Irwin Expedition, was recently discovered at the National Museum of Natural History, Smithsonian Institution (USNM). This lot includes the holotype of *C. marmorescens*.

0285 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Emily Sanchez, Christopher Tracy

California State University, Fullerton, CA, USA

Thermoregulatory Behaviors in Common Chuckwallas (*Sauromalus ater*): Do Males and Females Use Thermal Activity Windows Differently?

Climate change may decrease the time that environmental temperatures are suitable for ectotherm activity such as energy acquisition, territorial displays, and reproduction. Male common chuckwallas (*Sauromalus ater*) do not use all of the time where temperatures are suitable for activity outside of rock crevices, suggesting that climate change will have minor effects on their ability to perform such activities. However, sex differences in the use of suitable activity time could result in reduced reproductive output of populations in the face of climate change, so we measured female thermoregulatory behavior for comparison. To determine how chuckwallas used the thermal environment in the summer, we compared body temperatures of 5 females and 1 male in a semi-natural enclosure to environmental temperatures (T_e), measured with copper models that mimic heat exchange of chuckwallas. The proportion of time females were active relative to the time with suitable T_e (0.54 ± 0.061) did not differ from that of the male (0.64) in the enclosure ($t = -3.67$, $p = 0.021$). The proportion of time the male was active (0.78) relative to the time with suitable T_e was greater than wild males (0.45 ± 0.21) from the previous study ($t = -3.85$, $p = 0.012$). Although this suggests that chuckwalla populations may not be greatly affected by minor reductions in suitable activity time as a result of climate change, the use of suitable activity time may vary across seasons, which may reveal season specific sex differences, so female thermoregulatory behavior will be investigated during spring.

0337 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Franziska Sandmeier¹, Chava Weitzman², Nichole Maloney³, C. Richard Tracy², Christopher Gienger⁴

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Comparison of Current Methods for the Detection of Chronic Mycoplasmal UR TD in Wild Populations of the Mojave Desert Tortoise (*Gopherus agassizii*)

Chronic, nonlethal pathogens are notoriously difficult to quantify in wild populations. Mojave desert tortoises (*Gopherus agassizii*) have been the focus of much research aimed at measuring the presence of upper respiratory disease (URTD), and the presence of the two species of pathogens associated with UR TD (*Mycoplasma agassizii* and *M. testudineum*). Past surveys of wild populations have found relatively low prevalence in

natural populations (0-15 % positive) and positive animals tend to show only moderate, intermittent signs of morbidity (local inflammation and nasal discharge). Therefore, multiple tests have been developed to quantify different aspects of URTD: genetic detection of *M. agassizii* and *M. testudineum*, detection of specific antibodies via serology, as well as standardized quantification of signs of mucal discharge and body condition indices. To date, these techniques have only been compared in semi-captive animals. Here we compare these techniques in more than 200 wild animals – sampled across NV and CA in 2010 and 2011. All animals appeared generally healthy (via body condition indices) and the majority of animals with signs of URTD did not exhibit severe disease. Our work agrees with the recent suggestions that multiple measures of health should be used for diagnosing any one individual, as different techniques do not always correlate. In some populations, antibody results may over-estimate current disease but serve as an indicator of long-term presence of the pathogens in those host populations.

0184 AES Reproduction, Carson 2, Friday 17 July 2015

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Nourishment of White Shark Embryos with Uterine Milk during the Early Gestation Period

The white shark, *Carcharodon carcharias*, demonstrates viviparous and oophagous modes of reproduction. Morphological and histological observations of a 4,950mmTL gravid female accidentally caught by fishermen in the Okinawa Prefecture, Southern Japan revealed that the shark had conceived six embryos (543-624 mm), and also contained copious amounts of yellowish viscid uterine fluid as well encased nutrient eggs and broken egg cases in both uteri. Although ruptured, the six embryos had large stomachs, and the mean volume of the stomachs was approximately 197.9mL. About 20 rows of potentially functional teeth were present in the upper and lower jaws. Periodic Acid Schiff-positive substances were observed on the surface and in the cytoplasm of the epithelial cells, and large, secretory, OsO₄-oxidized lipid droplets of various sizes were distributed on the surface of the villous string epithelium on the uterine wall. These histological observations demonstrated that the uterine wall was comprised of villous structures, similar to the trophonemata of nourishing embryos of dasyatid rays, thereby suggesting that the large amount of fluid found in the uterus of the white shark was required for embryo nutrition. Hence, the following conclusions were drawn: (1) the uterine fluid is secreted from the uterine villi, (2) the embryos are able to use abundant uterine fluid and encased nutrient eggs for nutrition at this stage, and (3) the uterine fluid is the major source of embryonic nutrition before oophagy onset.

0315 Chemical Ecology Symposium, Crystal 3 & 4, Sunday 19 July 2015

Alan Savitzky¹, Shabnam Mohammadi¹, Hirohiko Takeuchi², Tatsuya Yoshida², Naoki Mori², Akira Mori²

¹Utah State University, Logan, UT, USA, ²Kyoto University, Kyoto, Japan

Sequestered Chemical Defense in a Lineage of Asian Natricine Snakes

Species belonging to three nominal genera of Asian natricine snakes possess defensive glands in the dorsal skin, either in the neck (nuchal glands) or along the entire trunk (nucho-dorsal glands). Recent studies have clarified several attributes of these glands but have raised additional questions that are presently being addressed. A recent phylogeny confirms that gland-bearing members of these genera (*Rhabdophis*, *Macropisthodon*, and *Balanophis*) belong to a monophyletic group, although a few species appear to have lost the defensive glands secondarily. Intraspecific variation in the glands has been found in two nominal species. The ancestral distribution of the glands (along the entire trunk or only the nuchal region) is ambiguous. In the best-studied species, *Rhabdophis tigrinus*, the nuchal gland has been shown experimentally to deliver bufadienolide toxins (BDs) sequestered from toads (*Bufo*) consumed as prey. Furthermore, female snakes can provision their embryos with toxins in proportion to their own levels of chemical defense. Consumption of toads appears to be ancestral to the gland-bearing clade. BDs are lethal to most predators, but natricine snakes in general exhibit mutations of the gene encoding Na⁺,K⁺-ATPase (NKA), the molecular target of the toxins, which appear to confer resistance. Enlargement of the adrenal glands in *Rhabdophis* suggests endocrine involvement in the response to BDs, and early results suggest that species with mutations to NKA exhibit a reduced stress response to the toxins. A group of earthworm-eating *Rhabdophis* also possess BDs, but some of those BDs appear to be structurally distinct from the toxins of toad-eating species.

0405 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Jillian Sawyna, Kelly Radecki, Weston Spivia, Marika Gotschall, Deborah Fraser, Christopher Lowe

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Establishing Baseline Parameters for Assessment of Immunological Effects of Organochlorine Exposure in Elasmobranchs

To evaluate the effects of chronic organochlorine (OC) exposure on elasmobranch immunity, a baseline of immunological parameters including complete blood counts, leukocyte counts, and phagocytosis was established. Round stingrays (*Urobatis halleri*) were collected from Santa Catalina Island, CA, which is considered a low contamination reference site for toxicology research off California. The genetically isolated population of rays from Catalina exhibit a low mean summed OC tissue concentration of 0.90 ± 0.98

ng/standardized liver sample compared to the mainland population, 15.7 ± 11 ng/standardized liver sample. Leukocytes obtained from lymphomyeloid tissues and peripheral blood were assayed for phagocytic activity *in vitro*. Using flow cytometry, % phagocytosis and phagocytic activity were evaluated by assessing % leukocytes positive for, and relative amounts of ingested fluorescent *E. coli* BioParticles. Cells isolated from splenic tissue, had a higher percentage of phagocytes in the sample cell population, with a mean % (\pm SE) phagocytosis of 18.85 ± 4.59 , compared to peripheral blood, 8.58 ± 1.53 , and epigonal tissue, 13.11 ± 4.93 . Blood demonstrated a higher measure of the phagocytes' activities, with a mean fluorescence intensity (\pm SE) of 2244.90 ± 265.63 , whereas cells isolated from spleen and epigonal were calculated as 1568.65 ± 211.87 and 796.15 ± 174.27 , respectively. Using microscopy, the same trend in % phagocytosis was found, but percentage values were higher, suggesting flow cytometry was a more conservative approach. These values can now be compared to those from the heavily OC contaminated southern California coastal mainland to determine if immunosuppression is correlated with OC exposure.

0088 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Scott Schaefer

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

Uncertainty and Decision in Revisionary Systematics

Taxonomic revisions and monographic research forms the fundamental basis for our understanding of biological diversity and its evolutionary history. Despite efforts to deploy novel approaches and tools, the practicing taxonomist typically faces difficult decisions about such issues as taxonomic status, species boundaries, diagnosis, variation, type status, nomenclature, and priority. Levels of uncertainty in the face of limited information and conflicting observations pose obstacles to progress in comparative biology. Work toward a revision of the Astroblepidae (Siluriformes) is presented as illustration of the challenges posed by uncertainty and its consequences. The case of *Astroblepus praeliorum*, described by Eigenmann & Allen in 1942 on the basis of a large series of syntypes from five distinct localities in central Peru, is used to illustrate some of the challenges faced in reaching taxonomic decisions involving broader comparisons in a group beset by substantial variation, limited material, and cursory original descriptions. While uncertainty may persist, Rosen's assumption #6— discovering that your conclusions were wrong— need not inhibit progress in revisionary systematics.

0072 AES Ecology & Behavior, Carson 2, Sunday 19 July 2015

Rachel Scharer, Philip Stevens, Gregg Poulakis

Florida Fish and Wildlife Conservation Commission, Port Charlotte, FL, USA

A Comparison of Abiotic Affinities and Spatiotemporal Distribution Patterns in Two Smalltooth Sawfish, *Pristis pectinata*, Nursery Areas

Research on the endangered Smalltooth Sawfish (*Pristis pectinata*) in the Charlotte Harbor estuarine system in southwest Florida has been ongoing for about a decade and we have begun to understand the life history, ecology, and habitat use patterns of this species. Sawfish are known to use multiple southwest Florida estuaries during the first 2-3 years of life and preliminary genetics analyses have indicated that adult females are returning to the same regions (e.g., major rivers) for parturition. Thus, understanding region-specific habitat use patterns has become important for effective management. Our initial research (2005-2009) was focused in the Caloosahatchee River; a highly human-altered river system within the federally designated Critical Habitat for juveniles. Most recently (2010-2013), we continued research in the Caloosahatchee and expanded sampling into a more natural area, the Peace River. A total of 135 juveniles ranging from 708 to 2,640 mm stretch total length were captured, tagged, and released between February and September. Annual recruitment peaked during April and May in both river systems. Logistic regression models identified combinations of water depth, water temperature, dissolved oxygen, and salinity as influencing the probability of catching a sawfish. Electivity analyses showed that sawfish in both rivers had affinities for water <1 m deep, water >24°C, moderate to high dissolved oxygen levels (>4 mg l⁻¹), and salinities between 12 and 27. Possible reasons for differences in dissolved oxygen and salinity affinities between the rivers relate to differences in their geomorphology and freshwater inflow regimes.

0391 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Mackenzie Schimpf, Joe Milliano, Chad Montgomery, Philip Ryan

Truman State University, Kirksville, MO, USA

Factors Affecting Metabolic Scaling in Vertebrates

Resting metabolic rate (RMR), the rate at which organisms use energy for maintenance, is an important component of the energy budget of living organisms. As RMR is largely affected by body size, there has been much debate about how metabolic rate scales with animal mass. The relationship between mass and metabolic rate is allometric, but there is controversy over whether a universal scaling exponent exists across all phylogenetic groups and, if such an exponent exists, what the value of that exponent is. Some argue that the scaling exponent is 2/3, based on the ratio of surface area to volume, while most argue it is 3/4 due to fractal splitting of biological systems. Additionally, the metabolic law may be dependent on phylogenetic lineage or not exist at all. Factors that could influence metabolic rate include endothermy vs ectothermy, phylogeny, foraging mode,

sex, and body temperature at which the metabolic rate was recorded. Along with body size, these factors were also accounted for in our analysis. In our experiment, we used flow-through respirometry to measure CO₂ production in *Diadophis punctatus* and combined our data with metabolic data from the literature to explore the allometric relationship between metabolic rate, mass, and phylogenetic relationship. Our data does not support an allometric scaling relationship across groups, but does support the possibility of a universal scaling exponent within endotherms and ectotherms, respectively. The difference in scaling exponent between endotherms and ectotherms is likely related to the increased energetic expenditure due to heat production in endotherms.

0084 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Susana Schonhuth¹, Lourdes Lozano-Vilano², Anabel Perdices³, Hector Espinosa⁴, Richard Mayden¹

¹*Saint Louis University, Saint Louis, MO, USA*, ²*Universidad Autonoma de Nuevo Leon, Nuevo Leon, Mexico*, ³*Museo Nacional de Ciencias Naturales, Madrid, Spain*, ⁴*Universidad Nacional Autonoma de Mexico, Mexico D.F., Mexico*

Phylogeny, Genetic Diversity and Phylogeographic Perspective on the Endemic Mexican Genus *Codoma* (Teleostei, Cyprinidae)

This study represents a thorough analysis of the monotypic cyprinid genus *Codoma*, endemic to north-western Mexico. A previous morphological analysis of the species identified diversity in *Codoma* as being underestimated. Genetic diversity across the range of *Codoma* has never been examined to test this hypothesis and identify possible independent lineages. We present a phylogeographic analysis using one mitochondrial and two nuclear genes, and specimens across the nine major drainages occupied by *Codoma* in both the Chihuahuan Desert and the Sierra Madre Occidental in western Mexico. All genes and analyses recovered populations of *Codoma* in a well-supported clade sister to *Tampichthys*, and both genera sister to *Cyprinella*. Analyses of both mitochondrial and nuclear genes recovered four/five genetically distinct lineages within *Codoma*, consistent with the prior morphological study for these populations. Composition and distribution of these major lineages is also consistent with prior biogeographic hypothesis for other fishes in the region, supporting an ancestral Rio Grande system extending south toward central Mexico. Fragmentation of this paleosystem was followed by allopatric speciation in the Chihuahuan Desert. These results suggest a scenario of long-term isolation in four major regions (upper Conchos, lower Conchos, Nazas, upper Mezquital).

0267 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Hayley Schroeder, Kevin Tang

University of Michigan-Flint, Flint, MI, USA

Phylogeny of Siganidae (Teleostei: Perciformes)

There are 28 species of rabbitfishes (Siganidae), in the genus *Siganus*. The family is a well-known group of fishes. Most commonly found in Indo-Pacific waters, these fishes have since migrated and become established in the Eastern Mediterranean, typically occur in shallow waters and are associated with coral reef communities. Rabbitfishes are named for their small, rabbit-like mouths, and are also equipped with unique features such as spiny pelvic and anal fins with venomous spines. The focus of this study is to reconstruct a phylogenetic tree of this family, building upon previous results. Relatives of the rabbitfishes from other percomorph families will be used for comparison in order to determine the relationships within Siganidae and their relationships to other families. Nuclear and mitochondrial genes will be used to construct a phylogeny of Siganidae, determining which groups are monophyletic. With this newly generated data, this study has the capacity to revise the current classification of Siganidae and provide some insight into these fishes concerning their higher-level relationships and evolutionary patterns.

0171 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Fredys F. Segura-Guevara, Edith A. Beltrán-Ortega, Charles W. Olaya-Nieto

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

Reproductive Biology of Barbul *Pimelodus blochii* in the Sinu River, Colombia

The reproductive biology of Barbul *Pimelodus blochii* in the Sinu River was studied. 328 individuals with total length (TL) ranged between 16.0 and 28.0 cm and total weight (TW) ranged between 32.0 and 238.0 g were collected. The gonads were placed in Gilson solution, the Vazzoler scale was applied and sexual proportion, sexual maturity index, spawning season, the length at first maturity, oocyte diameter and fecundity were estimated. 165 females, 144 males and 19 undifferentiated were found, with sexual proportion female: male of 1:1. The length at first maturity was estimated in 19.7 cm TL for combined sexes; oocyte average diameter was 787 μ m and average fecundity estimated was 15264 oocytes, with better equation $F = 2716.67 WG^{1.13}$, $r = 0.95$. The results achieved in this study suggest that Barbul is a rheophilous fish whose spawning season extends from March to October, with annual spawning in the rainy season and high fecundity, which is strongly associated to the weight of the ovaries.

0172 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Fredys F. Segura-Guevara, Katia M. Díaz-Lara, Charles W. Olaya-Nieto

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

Multiannual Length-Weight Relationship of Mojarra amarilla *Caquetaia kraussii* in the Ciénaga Grande de Lorica, Colombia

The length-weight relationship of Mojarra amarilla *Caquetaia kraussii* in the Ciénaga Grande de Lorica, Colombia, was estimated. The size ranged between 11.4 and 28.0 cm TL, the total weight between 28.0 and 346.0 g and the mean length in the catch was 18.4 cm TL. The length-weight relationship was $TW = 0.02 (\pm 0.03) TL^{3.01 (\pm 0.03)}$, $r = 0.96$, $n = 3802$, with isometric growth coefficient, ranging between 2.97 (2000, 2002) and 3.02 (2001), without statistically significant differences. The condition factor ranged from 0.017 (2001) to 0.020 (2000), without statistically significant differences. A correlation between the condition factor, hydrological cycle of Ciénaga Grande de Lorica and the spawning season of the Mojarra amarilla was observed. The results achieved in this study suggest that the body proportions of yellowfin Mojarra remained unchanged in the study period, and that the species has adapted its growth in size and weight to the new conditions of the Ciénaga Grande de Lorica after the Urra hydroelectric became operational and began generating electricity.

0018 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

Ronald Seidel¹, David Knoetel², Merlind Schotte², Daniel Baum², Daniel Huber³, Michael Blumer⁴, James Weaver⁵, Mason Dean¹

¹Max Planck Institute, Potsdam, Germany, ²Zuse Institute, Berlin, Germany,

³University of Tampa, Tampa, FL, USA, ⁴Medizinische Universität, Innsbruck,

Austria, ⁵Wyss Institute for Biologically Inspired Engineering, Cambridge, MA, USA

Interdisciplinary Approaches to Skeletal Biology and Mechanics: Design Lessons from Shark Skeletons

Fish skeletal tissues are far more diverse than those of mammals, providing unique windows into skeletal biology, development and form-function relationships in general, but also the evolutionary and environmental pressures that shape anatomy. We investigate the materials, structure and mechanics of elasmobranch cartilage, comprised of unmineralized cartilage wrapped in a layer of geometric, sub-millimeter, mineralized tiles (tesserae). Our interdisciplinary collaboration ties together high-resolution material and ultrastructure data with analyses of skeletal form to build bio-realistic and bio-inspired 3d-printed models for hypothesis testing and comparison with native tissues. We've learned that tesserae begin from isolated mineralization zones, employing a similar mineralization regulation pathway to bone, but being patterned on a wider

diversity of collagens. As tesserae grow into contact, striking patterns of structural reinforcement appear, developing mineral density and tissue stiffness comparable to (and sometimes higher than) mammalian mineralized cartilage or bone. Using custom, quantitative shape analyses of high-resolution CT scans, we map the massive network of tesserae on skeletal elements, allowing derivation of tissue growth and tiling laws and comparison with theoretical tilings. These data act as inputs into physical and theoretical models of tessellated cartilage, developed using new multi-material 3D printing techniques for high-resolution model fabrication. Combined with quantitative shape and mechanics analyses of whole jaws from shark species with different diets, we draw together multiple size scales to build holistic understandings of skeletal biology, learning fundamental design rules for this and other skeletal tissues, as well as layered, low-density composite materials in general.

0344 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Jason Selwyn¹, David Portnoy¹, Daniel Heath², J. Derek Hogan¹

¹Texas A&M University - Corpus Christi, Corpus Christi, TX, USA, ²University of Windsor, Windsor, Ontario, Canada

Kin Aggregations Explain a Commonly Observed Genetic Pattern in a Marine Fish Species

The phenomenon of chaotic genetic patchiness is a widespread population genetic pattern commonly seen in marine organisms, particularly those with demersal adults and pelagic larvae. This ubiquitous pattern has been attributed to a number of different biological mechanisms including selection, gene flow and genetic drift. Rarely has chaotic genetic patchiness been attributed to relatedness among individuals because such a condition is unlikely to be found in adult populations of species with highly dispersive larvae. The masked goby (*Coryphopterus personatus*) shows tell-tale signs of chaotic genetic patchiness, driven by the formation of related groups. We present two distinct mechanisms driving the formation of family groups, both with dramatically different impacts on the evolutionary trajectory of the species. The first mechanism involves larvae travelling together during the pelagic larval stage and settling onto a new reef as a related unit. The second involves either the complete or facultative loss of the pelagic larval stage altogether; with larvae simply moving out of the reef crevices they were spawned in and joining the group which spawned them. The first mechanism would allow for long dispersal but reduce the probability of finding a suitable habitat. The second mechanism dramatically increases the likelihood of finding suitable habitat, but reduces the ability to disperse and increases the risk of inbreeding and genetic isolation. Understanding the factors leading to patterns of chaotic genetic patchiness is important for understanding how gene flow occurs between isolated populations.

0013 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

David Sever

Southeastern Louisiana University, Hammond, LA, USA

Ultrastructure of Male Courtship Glands of the Red-Backed Salamander, *Plethodon cinereus*

The most prominent sexually dimorphic glands in male plethodontid salamanders are the mental glands, caudal courtship glands, and cloacal glands. Mental glands are present in most male plethodontids, but absent in some taxa in disparate clades. The absence of mental glands has been hypothesized to be the ancestral condition for plethodontids. The widespread occurrence of caudal courtship glands is unknown, as they have been investigated in few species. These glands apparently function in the tail straddle walk, however, which is stereotypic for plethodontids. All male plethodontids have five to six clusters of cloacal glands involved in spermatophore formation, and the vent glands that have been hypothesized to function in pheromone production. In only one species, the Red-Backed Salamander, *Plethodon cinereus*, have sexually dimorphic glands from all three areas been studied at the ultrastructural level. These results are reviewed in this presentation, with the conclusion that little similarity exists in cytology among putative pheromone producing glands from these three regions.

0339 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Brian Shamblin¹, Dean Bagley², Katherine Mansfield², Llewellyn Ehrhart², Mark Dodd³, Kristen Hart⁴, Campbell Nairn¹

¹*University of Georgia, Athens, GA, USA*, ²*University of Central Florida, Orlando, FL, USA*, ³*Georgia Department of Natural Resources, Brunswick, GA, USA*, ⁴*U.S. Geological Survey, Davie, FL, USA*

The Promise and Pitfalls of Mitochondrial DNA Repeat Markers in Marine Turtle Population Studies

Genetic studies have elucidated many aspects of marine turtle life history. Nonetheless, widespread sharing of dominant haplotypes defined by short mitochondrial DNA (mtDNA) control region sequences is common and can lead to poor resolution of demographic and migratory connectivity. One marker with potential utility to improve resolution is a mtDNA short tandem repeat (mtSTR) present in all marine turtle species. We explored the utility of this marker in green turtles (*Chelonia mydas*) nesting in Florida and loggerhead turtles (*Caretta caretta*) nesting in Georgia. Sequencing of the imperfect dinucleotide mtSTR in 299 green turtles carrying a common control region haplotype from 10 rookeries yielded 10 mtSTR variants that were strongly structured geographically. Whereas control region haplotypes had resolved two subpopulations in Florida, the mtSTR distinguished at least four different subpopulations. Given success with green turtles, we set out to optimize amplification of the perfect pentanucleotide

mtSTR in loggerhead turtles. We tested this marker on biological and technical replicates of DNA derived from skin biopsies and eggshells from respective females through genotyping. Marked stuttering was present for most individuals, although it is unclear whether this was due expression of heteroplasmy or PCR artifact. Only the dominant haplotype with respect to peak height was assigned. Several mismatches were detected for individual haplotype calls, particularly across different tissue types. This marker does not appear suitable for loggerhead studies without further optimization. Robustness of the markers is likely affected by structure of the repeat array, potentially limiting their utility in all species besides green turtles.

**0281 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

James Shelley¹, Stephen Swearer¹, Tim Dempster¹, Peter Unmack², Martin Gomon³

¹University of Melbourne, Melbourne, Victoria, Australia, ²University of Canberra, Canberra, ACT, Australia, ³Museum Victoria, Melbourne, Victoria, Australia

The Kimberley Ark: Assessing and Conserving Freshwater Fish Biodiversity in Australia's Last Pristine River Systems

Freshwater ecosystems worldwide are experiencing a period of unprecedented biodiversity loss. Effective biodiversity conservation requires accurate estimates of biodiversity and knowledge of species' threat of extinction. The Kimberley region in remote north-west Australia, which now faces imminent expansion of mining and agricultural operations, is both a biodiversity hotspot and a black hole in scientific knowledge. At least 18 (~40%) of the region's diverse freshwater fish species are found nowhere else and many of these endemics are extremely range-restricted. However, a dearth of surveys, and ecological and genetic studies means that current biodiversity estimates are not robust and the risk of extinction these species face is unknown. This project will help to establish the true biodiversity of the Kimberley freshwater fishes and assess their extinction risk using a combination of molecular techniques and ecological analyses. Hypotheses on the causes of diversity in fish communities will be tested by constructing phylogenies for two of the regions major families (Terapontidae and Melanotaeniidae). Furthermore, microsatellite data will be used to assess gene flow, population connectivity, and population genetic structure within species to evaluate their extinction risk in the face of future impacts. Finally, reproductive and early life-history ecology will be investigated to assess their contribution to the range-restriction and evolution of the Kimberley's endemic species. I will present my project ideas and design and the results of my phylogenetic analysis, which provides evidence for a suite of undescribed freshwater fish species and highlights the unique conservation challenges this region presents.

0042 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

David Shiffman, Catherine Macdonald, Harry Ganz, Neil Hammerschlag

University of Miami, Miami, FL, USA

Initial Assessment of the Scale, Practices and Conservation Implications of Land-Based Shark Fishing in South Florida

Angling for sharks from beaches is a popular recreational activity in Florida, but the scale, practices, and conservation implications remain unknown. Here we analyze thousands of posts made by land-based shark anglers on the public online discussion board of a local fishing club in order to assess angler attitudes, perceptions and practices. We found that land-based shark anglers are generally young (under 30) and male, a demographic different from most recreational anglers. These anglers enjoy land-based shark fishing because it is more affordable than boat-based fishing, but still allows people to catch and interact with large and exciting fish. Though there is some skepticism of government-led scientific population estimates, land-based shark anglers are aware of and concerned by global shark population declines. Conflicts between beach stakeholders (swimmers and anglers) are frequently discussed. These anglers believe that regulations which restrict recreational angling for overfished species are unjust because they believe commercial fishing is what caused the population declines. Land-based shark anglers also frequently discuss how laws that restrict land-based fishing, but not boat-based fishing (including beaches that ban fishing, and restrictions within state waters but not adjacent Federal waters), discriminate against lower income anglers. Land-based shark fishing raises some conservation concerns because of the increased physiological stress caused by the sharks being brought onto land. Additionally, there are numerous interactions with protected species like the physiologically sensitive great hammerhead. Potential policy and education solutions that minimize these conservation concerns and stakeholder conflicts while still allowing recreational anglers to fish are proposed.

0567 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Thursday 16 July 2015

Spencer Siddons, Jacob Kerby

University of South Dakota, Vermillion, SD, USA

Effects of *Batrachochytrium dendrobatidis* and an Herbicide on Larval Woodhouse's Toads (*Anaxyrus woodhousii*)

Amphibians around the world have been experiencing severe population declines in recent decades due to numerous factors including habitat destruction, pollution, over-exploitation, and infectious diseases. In the central United States, pesticides from agricultural runoff into water bodies and the presence of the pathogenic fungus, *Batrachochytrium dendrobatidis* (Bd), are considered to be important factors for decline in

abundance of larval amphibians. However, little is known regarding how these two factors specifically impact native amphibian species. This study investigated the individual and interactive effects of the herbicide 2,4-dichlorophenoxy acetic acid (2,4-D) and Bd on Woodhouse's toad (*Anaxyrus woodhousii*) tadpoles. We exposed tadpoles to one of four contaminant concentrations (0 µg/L, 1 µg/L, 10 µg/L 100 µg/L), with or without Bd present, for 11 weeks. Changes in mass, length, and Gosner stage were measured and Bd infection was confirmed via qPCR. Results showed that increasing herbicide concentration resulted in a significant reduction in mass over time ($p < 0.05$). Effects of Bd alone and interactions of Bd and contaminant were not significantly different for mass or other measured response variables. These results highlight the importance of understanding the effects of 2,4-D on native fauna, as 2,4-D is a commonly used pesticide in the central U.S.

0412 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Brian Sidlauskas

Oregon State University, Corvallis, OR, USA

When Has Convergence Really Occurred?

Donn Rosen claimed provocatively that by assuming that "convergence really occurs," we "inhibit scientific progress in comparative biology." His statement seems to challenge the immense literature on convergence and may reflect a perception that apparent convergence actually results from character coding errors during phylogenetic analysis. Once we truly understand the phylogeny of our organisms and the evolutionary history of our characters, will most apparent convergences be revealed as misperceptions? Analysis of anostomoid fishes suggests that morphological convergence occurs in discrete and continuous characters dealing with the oral jaws, gill arches, pigmentation and other systems. Many homoplastic characters contribute substantially to phylogenetic resolution, and the hindsight afforded by their reconstruction on molecular or morphological phylogenies does not always reveal obvious morphological dissimilarities that would suggest errors in the original coding. Analysis of morphometric data in a phylogenetic context using new tools like SURFACE similarly suggests shape convergence throughout the evolutionary radiation of these fishes. However, one must exercise caution when applying these new approaches, which relax the definition of convergence, abstract morphology substantially, employ relatively few evolutionary models, and sometimes seem prone to infer convergence between lineages that share only limited similarities. The morphometric models provide a statistically sophisticated means to identify potential convergences and adaptive peaks, but still require the context afforded by detailed study of morphology, function and ecology. As Rosen would have likely agreed, only by understanding organisms as fully as possible can we evaluate whether any particular claim of convergence holds biological reality and meaning.

0029 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Dustin Siegel, Brian Rabe

Southeast Missouri State University, Cape Girardeau, MO, USA

Renal Corpuscles of the Red-spotted Newt (*Notophthalmus viridescens*)

Salamanders possess a bipartite kidney: a caudal portion contains nephrons that primarily function in urine formation (pelvic kidney nephrons) and a cranial portion where nephrons also serve as sperm conduits (genital kidney nephrons). Spengel (1876) hypothesized that genital kidney nephrons were still involved in urine formation, as these nephrons possessed all the same functional regions found in pelvic kidney nephrons. Recent studies on *Ambystoma maculatum* and *Notophthalmus viridescens* provided high-resolution microscopy of genital and pelvic kidney nephrons. These studies demonstrated that although comparative regions could be found between both sets of nephrons, the epithelial linings of genital kidney nephrons possessed unique aspects; i.e., ciliation in the proximal tubule and lack of basal membrane folding in the proximal and distal tubules. Renal corpuscles from *N. viridescens* were analyzed for the current study. No microstructural differences were observed between renal corpuscles of the pelvic and genital kidney nephrons. However, pelvic kidney renal corpuscles were significantly larger than genital kidney nephrons and possessed a much more developed, and vascularized, glomerular structure. Furthermore, whereas filtrate was easily observable in the Bowman's space of pelvic kidney nephrons, the Bowman's space of genital kidney nephrons bound to no stains through examination with transmission electron microscopy. This finding corresponds with the previous lack of filtrate observed in the proximal tubules of genital kidney nephrons in comparison to copious filtrate in the pelvic kidney proximal tubules. These results may indicate a lack of urine forming function in the genital kidney nephrons.

0211 General Ichthyology I, Crystal 3 & 4, Friday 17 July 2015

João Pedro Silva¹, Marcelo Carvalho⁰

¹*University of Toronto Scarborough, Toronto, ON, Canada*, ²*Universidade de São Paulo, São Paulo, SP, Brazil*

Brain Morphology in the Family Potamotrygonidae, with Observations on the Evolution of the Brain in the Order Myliobatiformes

A characterization and description of the gross morphology observed in the brain of the four valid genera of potamotrygonids has been made as part of an effort to produce new data to be used in taxonomic and systematic studies of this family. Specimens were dissected manually and the general morphology of species of each genus was described and compared to each other, allowing inferences about how this character is informative

for the family systematics. In addition, the brain of representatives from three other stingray families were analyzed, as well as a literature review engaging anatomical, taxonomical and ecological hypothesis, in order to infer possible evolutionary patterns within the order Myliobatiformes and within chondrichthyans in general.

0470 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Priscilla Caroline Silva¹, Udson Santos², Luiz Malabarba¹

¹Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil,

²Universidade Federal de Campina Grande, Cajazeiras, Paraíba, Brazil

Rediscovery of *Deuterodon pedri* Eigenmann 1907 and Its Impact on *Deuterodon* Phylogeny

Deuterodon is a neotropical fish genus composed of 10 species mostly distributed on south and southeastern Brazilian coastal Atlantic river basins. Three synapomorphies define the genus: the anterior region of the toothed portion of the maxilla deeper than the posterior region of the toothed portion; ventral margin of toothed portion of maxilla arching toward the ventral margin of the premaxilla; posterior region without teeth of the maxilla smaller than anterior toothed region. *Deuterodon pedri* has been considered a species endemic from a small drainage of the rio Doce basin in Minas Gerais State, Brazil. Several expeditions have been made in this locality aiming to capture new specimens of *Deuterodon pedri*, but all have failed. We have surveyed the type locality and captured a singular species that we found to be *Deuterodon pedri* after comparison to the lectotype and paralectotype. Parsimony and Bayesian analyses with sequences of two mitochondrial and tree nuclear genes and parsimony analysis with 392 morphological characters were performed to investigate its relationship with related characids. The captured specimens lack the three synapomorphies of *Deuterodon*, having in common with *Deuterodon* species only the gradual decrease in size of dentary teeth from the symphysis. The species is redescribed based on new specimens and its relationship discussed based on morphological and molecular data.

**0531 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Raymond Simpson¹, Thomas Near², Steven Rider³

¹*Yale University, New Haven, CT, USA*, ²*Yale University, New Haven, CT, USA*,

³*Alabama Department of Conservation and Natural Resources, Montgomery, AL, USA*

A Taxonomic and Systematic Analysis of the Walleye, *Sander vitreus* (Percidae: Luciopercinae)

There was long thought to be two widespread species of the popular gamefish genus *Sander* in the New World: the Walleye (*Sander vitreus*) and the Sauger (*S. canadensis*). With the use of molecular techniques, it was discovered that there are at least three unique evolutionary lineages of the Walleye that correspond to distinct geographic areas of its range. These include a nominate race living in the northern tier drainages of North America and Canada, another lineage in the Mobile River basin, and a third lineage in the Cumberland River basin. The primary aim of this study is to gather meristic and morphological data from specimens sampled from the Mobile Basin to determine if they are divergent from the nominate species. Comparative material included specimens sampled from the type locality of *Sander vitreus*. In addition, we expanded the molecular dataset to include DNA sequences from ten nuclear and three mitochondrial genes. The molecular phylogenies resolve three distinct lineages currently recognized as *S. vitreus*. Hybridization between the Mobile Basin species and introduced, stocked *S. vitreus* was examined using microsatellite markers. Our work will result in a taxonomic reassessment of *Sander vitreus*.

**0129 ASIH STOYE AWARD GENERAL ICHTHYOLOGY, Carson 3, Thursday
16 July 2015**

Randy Singer^{1,2}

¹*iDigBio, Gainesville, FL, USA*, ²*Florida Museum of Natural History, Gainesville, FL, USA*

Telepresence as an Important but Underutilized Tool for the Modern Biologist

Telepresence, or the act of simulating presence through the use of high resolution video, facilitates collaboration among biologists. In contrast with a number of other professions, relatively few biologists appear to use the technology to its full potential. Video conferencing to communicate at meetings is not uncommon in biology, but unlike other fields, telepresence for collaborative and interactive work is rarely used. Real-time communication between researchers on a global scale facilitates methods of holistic data collection and can lead to novel research through the formation of "dream teams" that bring diverse backgrounds and expertise to participate in research projects from the field to the lab. Similar projects run by NOAA are prime examples of the power of telepresence where as many as 50 scientists are able to participate in research cruises

without leaving their offices. Telepresence even provides outlets for education and outreach through live streaming. With something as simple as a camera and an internet connection, we are able to participate in global studies of biodiversity, innovative education and outreach initiatives and far more complex research projects than were previously possible.

**0516 ASIH STOYE AWARD GENERAL HERPETOLOGY I, Crystal 1 & 2,
Thursday 16 July 2015**

Phillip Skipwith¹, Paul Oliver²

¹*University of California, Berkeley, Berkeley, CA, USA,* ²*Australian National University, Canberra, ACT, Australia*

Morphological Convergence in Diplodactyloid Geckos

The evolution of morphological diversity within clades is a complex topic that has been the focus of many studies in the various fields of evolutionary biology. A number of factors can influence morphological diversity ranging from the environment to constraint due to phylogenetic history. Using phylogenies in conjunction with ecological data and biogeographic history can allow us to elucidate how patterns of morphological diversity appear in certain clades. We use the Australasian diplodactyloid geckos as a case study to investigate convergence. This is a diverse clade (~200 species in three families) that encompasses much of the phenotypic diversity seen in gekkotan lizards, ranging from fully limbed arboreal forms with toepads to those that are limbless and fossorial. We use preexisting molecular data along with newly generated sequence data to reconstruct the phylogenetic relationships of pygopodoids. We use external morphological data in the form of 24 linear measurements and geometric morphometrics of toepads for 130 species to assess morphological convergence. Our results indicate that, after correcting for phylogenetic history, most forms fit within a general, arboreal grouping. However, unrelated Australian rupicolous lineages cluster together, showing a trend towards longer limbs and larger heads. Another clustering of arboreal forms including the New Caledonian and New Zealand forms was recovered. These data suggest that environmental factors have led to superficially similar phenotypes in multiple lineages.

0478 Fish Biogeography, Carson 3, Saturday 18 July 2015

Gerald Smith

University of Michigan, Ann Arbor, MI, USA

Causes and Consequences of Bad Divergence-Time Estimates

Sewall Wright's (1932) discovery that evolution can be fast in small populations caused authors to seek to test rapid evolution. Hubbs and Miller (1948) postulated rapid evolution of scores of small, divergent populations of Great Basin minnows since the last glaciation and pluvial stages, 11,000 years ago. Many authors fail to consider the 20+ glaciations that preceded the last one or the history of Pliocene climate changes before that. The consequences are unrealistic estimates of divergence times, mistaken environmental hypotheses about causes of speciation, and reification of assumed generality of rapid rates. Seven better practices can avoid these problems: (1) Base age estimates on dated apomorphies of taxa, not names attributed to epochs in lists of fossil taxa. (2) Correct for numbers of appropriate geological horizons following Marshall's equations to estimate the oldest occurrence, accurately estimate age, identify more plausible evolutionary causes, and more accurate rates. (3) Test a generous range of alternative ages of splits, not only the most recent one. (4) Beware of an unchanging fossil ancestor of a budding event that produced a changed descendant (sister); consider the nullifying effect of a static ancestor before and after the split. (5) Avoid reliance on time of initiation or elimination of a geographic barrier for calibration: those will usually underestimate divergence time. (6) Watch for genetic and morphological evidence of introgression, which may have erased molecular distance, reset the molecular clock, and underestimated time. (7) Control for dependence of DNA substitution rate on body size, temperature, and generation time.

0519 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Leo Smith

University of Kansas, Lawrence, KS, USA

Convergent Evolution of a Hinged Premaxilla in Benthic Percomorphs

During a character survey of scorpaenoid fishes, a hinged premaxilla was identified in a diversity of benthic families (e.g., Bembridae, Hoplichthyidae, and Platycephalidae). This feature had been previously characterized in platycephalids and relatives as the separation of the ascending process from the remainder of the premaxilla. This osteological specialization and related connective tissue modifications are described and shown to allow the rostral component of the upper jaw to extend its gape dorso-caudally, a potential benefit to benthic predators. As this anatomical survey was expanded, a hinged premaxilla was found in several additional benthic percomorph families. Using a new phylogenetic hypothesis based on anatomical and molecular data, the evolution of this feature will be explored. The repeated evolution of a hinged

premaxilla in benthic percomorphs will be discussed in light of Donn Rosen's view that the occurrence of convergence inhibits scientific progress.

0447 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Megan Snetsinger¹, Jeffrey R. Row², Megan E. Hazell³, Stephen C. Loughheed¹

¹Queen's University, Kingston, Ontario, Canada, ²University of Waterloo, Waterloo, Ontario, Canada, ³Amec Foster Wheeler, Mississauga, Ontario, Canada

Landscape Genetics of Butler's Gartersnake, *Thamnophis butleri*, in Ontario

The Endangered Butler's Gartersnake (*Thamnophis butleri*) has declined in its Canadian range due to habitat loss and fragmentation. Little is known about the resulting diminished distribution, population isolation, and reduced connectivity among populations in Southwestern Ontario, nor have their specific habitat preferences been well-described. DNA samples and geographical coordinates were obtained from 141 *T. butleri*. We genotyped the samples for 16 microsatellite loci (developed in existing studies) using PCR duplex reactions. Bayesian clustering revealed two genetic clusters: one centered on Windsor and one encompassing Sarnia and Aamjiwnaang, the adjacent First Nations reserve. We found departures from Hardy-Weinberg equilibrium at two of three localities with $n > 20$, Windsor (for 4 loci) and Aamjiwnaang (for 3 loci), potentially caused by undiagnosed population substructures. There were no departures in Sarnia. To characterize habitat preferences we supplemented the locations of sampled individuals with recent Natural Heritage Information Centre records (for a total of 1149 recorded observations), and from these developed a species distribution model to predict *T. butleri* distribution across their range. Greater amounts of open undeveloped habitat (31.4%) and shorter distances to developed habitat (32.6%) increased occurrence probability, though the latter's importance is likely exaggerated by having most collection sites situated near suburban areas (an exclusionary model gives similar results). Further analyses will incorporate additional landscape variables for greater predictive power. Future sampling will augment our power to delineate genetic structure. We will use our findings to make recommendations on *T. butleri* conservation, to increase its likelihood of persistence in Ontario.

0336 Herp Conservation II, Carson 1, Saturday 18 July 2015

Sarah Snyder¹, C. Richard Tracy¹, Ken Nussear¹, Lesley DeFalco²

¹University of Nevada, Reno, Reno, NV, USA, ²USGS, Henderson, NV, USA

After the Smoke Clears: The Effect of Wildfire on Desert Tortoise Body Temperature and Vegetative Cover Use

Wildfires in the Mojave Desert are consequential to desert tortoises (*Gopherus agassizii*) because they alter the microhabitats that tortoises use in behavioral thermoregulation. Here we evaluated vegetative cover use by tortoises in comparison to cover availability and compared body temperatures among tortoises using burned and unburned habitat. Tortoises in burned and unburned habitat were outfitted with GPS loggers, radio transmitters, and temperature-sensing data loggers to record body temperatures. Tortoises were tracked to record vegetative cover use, and to determine the ways in which body temperature varied with habitat use. Perennial plant cover and composition were estimated from plots in burned and unburned habitat. Tortoises in both burned and unburned habitat chose vegetative cover sites non-randomly. Tortoises in unburned habitat selected vegetative cover according to thermal quality while tortoises in burned habitat selected living shrubs over dead shrubs even when dead shrubs provided microhabitats of higher thermal quality. In burned habitats, tortoises exploited a novel shade shrub, which colonized the burned habitat after fire and attained large size and coverage. The only body temperature metric that varied between habitat types was minimum body temperature, which was slightly lower in burned habitat. Our study suggests that burned habitat is of comparable thermal quality to unburned habitat for tortoises, and that burned habitat does not impose constraints on tortoise thermoregulation. However, shrub species that are preferred by tortoises may be absent or rare in burned habitat, forcing tortoises to travel longer distances or switch cover species.

0191 Fish Systematics II, Carson 3, Sunday 19 July 2015

Young-Sun Song¹, Jin-Koo Kim¹, Jung-Ha Kang²

¹Pukyong National University, Busan, Republic of Korea, ²National Fisheries Research and Development Institute, Busan, Republic of Korea

Cryptic Diversity of *Atractoscion aequidens* (Perciformes: Sciaenidae) and a Description of a New Species from the Oman Sea

The genus *Atractoscion* Gill 1862, family Sciaenidae, contains two valid species worldwide, *Atractoscion aequidens* (Cuvier, 1830) and *A. nobilis* (Ayres, 1860). *Atractoscion aequidens* was reported as a new species in southwestern Africa (type locality: Cape of Good hope) and then in Australia, eastern Africa, the Persian Gulf, and Oman, whereas *A. nobilis* was reported as a new species in western America and has not been reported in other areas. We collected 15 specimens of *Atractoscion* (269.0-355.0 mm standard

length) from Oman in 2013-2014, and identified them as undescribed species, differing from the congeneric valid species. To clarify the taxonomic status of these fish, we compared our specimens with other local populations of *A. aequidens* (10 individuals in morph., 11 individuals in mol.). The neighbor-joining phylogenetic tree based on mitochondrial COI sequences identified four lineages, three of which (Australia, Benguela+South Africa, and other areas of Africa) were distinguished well with K2P distances of 4.5%-5.6%, although no morphological differences were identified. Our findings suggest that cryptic diversity may exist in *A. aequidens*. The specimens we collected from Oman were distinguished from other local populations, including at the type locality, not only by their genetic distance (3.9%-6.9%), but also by morphological characteristics, such as the number of lateral line scales (77-82 in *Atractoscion* sp. vs 70-75 in *A. aequidens* from South Africa). Therefore, we report that our specimens collected in Oman are a new species compared with several local populations, based on morphological and molecular evidence.

0370 Fish Biogeography, Carson 3, Saturday 18 July 2015

Timothy Sosa^{1,2}

¹University of Chicago, Chicago, IL, USA, ²Field Museum, Chicago, IL, USA

Characoidei: Timing and Number of Colonizations Across the Isthmus of Panama

A new molecular data set suggests that the Characoidei (tetras, pencilfishes, hatchetfishes, and others) colonized North America more times than is generally recognized, which has interesting consequences for our understanding of invasion biology and the ichthyofauna of the Americas.

0225 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

John Sparks

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

Assumptions of Convergence, So-called Regressive Evolution, and Dispersal Have Inhibited Progress in our Understanding of the Evolution of Subterranean Biotas.

Using cave faunas as examples, and focusing on the relationships of obligate cavefishes in particular, I will examine several of Rosen's assumptions that inhibit scientific progress in comparative biology. Cave systems are ideal in that they have generally been considered evolutionary dead ends, characterized by the loss of features in their inhabitants, so-called "regressive characters", and widespread convergence. Darwin

even went so far as to refer to their inhabitants as “wrecks of ancient life.” The general paradigm has been that cave ecosystems are ephemeral, evolutionary dead ends, characterized by losses and a lack of diversity. On the contrary, recent molecular phylogenetic work and a renewed interest in cave exploration have revealed that caves are quite dynamic systems, more crucibles of evolution than evolutionary dead ends. Not only do cave systems facilitate diversification, but so called “ecomorphological adaptations” to subterranean life can be reversed, permitting re-colonization of epigeal habitats. Whereas the general assumption has been that cave biotas are derived from the dispersal of proximate epigeal ancestors into hypogean habitats, recent studies of obligate freshwater cave organisms indicate that these systems can be quite ancient, such that their biotas reflect the Mesozoic fragmentation of Gondwana.

0323 Herp Conservation II, Carson 1, Saturday 18 July 2015

Ricky Spencer

University of Western Sydney, Sydney, Australia

Freshwater Turtle Declines: A Global Problem

Globally, freshwater turtles are one of the most threatened animal groups, with many species already listed as critically endangered (Buhlmann 2009). The principal threats are harvesting for human food and the pet trade, habitat loss and degradation (TCF 2002). However, climate change is emerging as an additional hazard to freshwater turtles, because of the effects of warming on temperature-dependent sex determination (Mitchell & Janzen 2010) and habitat loss from increasing frequency and severity of drought (Roe & Georges 2010). Turtle longevity masks the extent of the threat, because adults can persist with extreme mortality and reduced recruitment for decades before a decline becomes evident. However, large biomasses of turtles (100K tonnes- Thompson 1993) are threatened by chronic reproductive failure, exotic predators, disease, habitat modification and habitat loss over past decades. Here I critically review the true conservation status of freshwater turtles throughout the world, as well as, determine likely impacts on wetland ecosystems services if declines are likely to occur rapidly.

0601 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Brenton Spies, David Jacobs

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

Status, Habitat Impacts, and Management of the Tidewater Goby (*Eucyclogobius newberryi*): A Federally Endangered California Coastal Endemic

The federally endangered tidewater goby (*Eucyclogobius newberryi*) is a small annual fish species endemic to California. This species exhibits local genetic divergence at a finer geographic scale than any other Pacific coast vertebrate, and may be predisposed to local extirpation due to its preference for seasonally variable coastal lagoonal settings. The proposed reclassification of the tidewater goby from endangered to threatened is currently in review, despite the lack of management plans, and shortage of thorough population surveys and presence/absence data needed to conduct the appropriate metapopulation viability analysis listed in the USFWS Recovery Plan for reclassification. Given these circumstances, and the impacts of California's recent drought, we conducted spring/fall population surveys in 94 estuaries to assess the current health and status of the tidewater goby in five of the six recovery units, spanning from Bodega Bay to San Diego, CA. Surveys revealed a high degree of endangerment of this species, mainly in southern California due to habitat desiccation and the presence of invasive species. Endangerment is especially high in the southern unit of San Diego County. This unit is an undescribed, and unequivocally endangered, distinct species in the genus *Eucyclogobius* that is currently being managed as *E. newberryi*. Therefore, we feel at this time the reclassification of the tidewater goby is premature and risky, and should not be done until the appropriate metapopulation viability analyses are completed, and individual management plans are in place.

0251 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

C. Tristan Stayton

Bucknell University, Lewisburg, PA, USA

Patterns of Morphological and Mechanical Evolution in Terrestrial Turtle Shells

The evolution of a primarily terrestrial lifestyle has occurred approximately 8 times during the diversification of extant turtles. These multiple evolutionary transitions into a new habitat provide an excellent opportunity to test hypotheses concerning the evolution of morphology and functional performance in response to changed functional demands. The shells of aquatic turtles are likely subject to a number of selective pressures: to increase shell strength, to reduce drag during locomotion, to optimize the rate of heat transfer with the environment, and to facilitate righting when the turtle is

overturned, for example. Terrestrial turtle shells likely experience all of those same pressures but one: drag reduction. The shared reduction in functional demands on terrestrial turtles is predicted to lead to shared changes in both morphology and mechanics. Geometric morphometrics and finite element analysis were used to assess patterns of evolution among all terrestrial turtles and their relatives. Surprisingly, no evidence of any common patterns of morphological evolution was found among all terrestrial turtles - terrestrial turtles are not convergent, and do not differ from their aquatic sister taxa in a consistent way. However, terrestrial taxa do largely show common patterns of mechanical evolution towards stronger but less streamlined shells. Thus, there is more than one way to evolve a stronger shell shape. Shared patterns of evolution among certain terrestrial groups suggest that additional functional demands, such as crypsis or kinesis, may be responsible for channeling the morphological evolution of terrestrial clades into one of many alternate pathways.

0253 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

C. Tristan Stayton

Bucknell University, Lewisburg, PA, USA

The Turtle Shell as a Model System in Evolutionary Functional Morphology

Turtles and their shells are an ideal system for investigating macroevolutionary questions regarding morphology, functional performance, and the interactions between the two. The turtle shell is morphologically complex, and provides a rich source of data that is readily captured by traditional or geometric morphometrics. Turtles also span an impressive range of body sizes (over three orders of magnitude in mass) within a body plan that stays fairly consistent across species and over ontogeny. Despite its morphological complexity, the shell is mechanically fairly simple. In most species, the shell is a rigid structure; kinetic shells typically involve simple hinges with a single degree of freedom. This simplicity facilitates rigorous modeling, through finite element modeling, computational fluid dynamics, or other techniques, of performance for a variety of functions. A relationship between form and function has been established for certain functions - force resistance, drag reduction, heat exchange with the environment, or righting ability if the turtle is overturned, for example - and could be established for more. But not all shells perform all of these functions: terrestrial turtles do not need to maintain low-drag shells, for example. Turtles are found worldwide in a variety of climates and environments. Multiple evolutionarily independent transitions between environments and shell functions, within a large but manageable taxonomic diversity (~330 extant species), provide a robust sample size for comparative analyses. The virtues of the turtle shell as a model system are illustrated by a multi-factor comparison between eight evolutionarily-independent terrestrial turtle clades and their aquatic relatives.

0284 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

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¹Calvin College, Grand Rapids, MI, USA, ²Ohio State University, Columbus, OH, USA,

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Miocene Char and Char-like Diversity from Lacustrine Basins in the Western North American Cordillera

Miocene-age sediments provide a record of diverse chars or char-like forms occupying lakes in a series of basins in the western North American Cordillera. In the Great Basin region, these basins were transtensional, resulting from the disassembly of the Paleogene Nevadaplano. Others were in lava-dammed intermountain valleys. The Western Snake River Plain held long-lived rift lakes. Five char localities are, from north to south, the Clarkia Lake in northern Idaho, circa 15 Ma; the western Snake River Plain, 11-6 Ma; the Desert Peak locality, Churchill County, Nevada, between 13 and 10 Ma; Stewart Valley, Mineral County, Nevada, 15 Ma; and Coaldale, Esmeralda County, Nevada, 13-11 Ma. The Desert Peak taxon possesses many synapomorphies of extant *Salvelinus*, but the other forms are plesiomorphic chars assigned to other genera or yet under study. The Snake River Plain char, *Paleolox*, Kimmel 1975, includes numerous specimens that reify the validity of separate generic status. The Clarkia form shares features with the Eurasian genus *Hucho*. The Stewart Valley fossil salmonine is a plesiomorphic char sharing some but not all synapomorphies of extant *Salvelinus*. These fossils testify to a radiation of archaic chars in 1 km high valleys during a warm climatic interval. Other common members of these ichthyofaunas include centrarchids and large and small cyprinids; and in the case of the western Snake River Plain, ictalurids and catostomids.

0111 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Melanie Stiassny¹, Elizabeth Alter²

¹American Museum of Natural History, New York, NY, USA, ²York College, City University of New York, New York, NY, USA

The Evolution of Phenotypic Convergence in Fishes of the Lower Congo River

Phenotypic convergence provides powerful insight into how morphological diversity is shaped by selection. A striking instance of multi-trait convergence is found across a broad phylogenetic spectrum of fishes endemic to the lower Congo River (LCR), a complex, high-energy hydrological system characterized by some of the most extensive and powerful rapids on Earth. In this extreme selective environment, representatives of distantly related fish lineages have independently evolved complex suites of convergent traits including depigmentation, microphthalmia or eye loss, body depression with metameric increase, enhanced latero-sensory anatomy, and hypertrophied jaw

musculature. To better understand the evolution of these phenotypes, we developed a molecular phylogenetic framework for one of the groups - spiny eels of the genus *Mastacembelus*. Our analysis demonstrates that a series of traits have independently evolved multiple times within the group, representing distinct colonizations of the LCR by both lacustrine and riverine lineages. These convergent phenotypes arose within a narrow time window, concurrent with newly available habitat in the LCR. This study represents one piece of a novel comparative framework for the system, as we move toward the goal of understanding the evolutionary context of phenotypic convergence across multiple levels of biological organization.

0130 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Rochelle Stiles¹, Vanessa Kinney Terrell², Michael Lannoo³

¹Indiana State University, Terre Haute, IN, USA, ²University of Georgia, Athens, GA, USA, ³Indiana University School of Medicine, Terre Haute, IN, USA

Survivorship Estimates Across Life History Stages Suggest a 1000-m Upland Buffer is Key to Keeping Crawfish Frogs from Being Federally Petitioned.

Crawfish Frogs (*Lithobates areolatus*) are state endangered in Indiana and have declined across much of their historic range. In the past, their fossorial nature and scarcity has made detailed natural history and life history investigations difficult. Crawfish Frogs are a grassland-dependent species, and at our study site are obligate crayfish burrow dwellers. Seven years of continuous monitoring of breeding wetlands at Hillenbrand Fish and Wildlife Area (Greene County, IN) has given us reliable estimates of survivorship by life history stage as follows: eggs, 98%; larvae, < 1%; juveniles (in general 2 years to first breeding for males, 3 years for females), 3%; and interannual adult, 69%. A subset of frogs has been captured as adults the entire seven years of this study, making them at least nine years old. Abnormally low larval survivorship appears to be compensated by abnormally high adult longevity, facilitated by burrow dwelling. Head-starting programs for tadpoles increase larval survivorship to 80-90% (compared to < 1% naturally) and provide a way to bolster existing populations or provide a supply of animals to re-establish extirpated populations. Provided crayfish burrows are not limiting (in Indiana 40% of burrows are unoccupied by crayfish), the key to preserving populations is to ensure adult longevity. We recommend a 1000-m no-plow buffer zone around each breeding wetland, while mowing, herbicide application, and burning do not appear to affect populations. Our management recommendations, if implemented, could help prevent a consideration of federal listing for this species.

0349 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Carla Stout, Milton Tan, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Phylogeography of Leuciscinae

Members of Leuciscinae account for a vast majority of the freshwater fish diversity in North America, but representatives are also found in Asia and Europe. Members of this clade include minnows, shiners and chubs. While the clade as a whole has been supported as monophyletic across many studies, relationships among the genera within have had differing results. Certain clades have been recovered in multiple studies, and these include: (1) Eurasian phoxinins, (2) open posterior myodome (OPM), (3) creek chub - plagiopteran (CC-P), (4) western North America (WNA), and (5) leuciscins, but relationships among these clades has varied. The most recent analyses have resulted in conflicting topologies with low to moderate support for nodes among the major subclades. In an effort to understand biogeographical patterns within the Leuciscinae, we first established a highly resolved phylogeny using anchored enrichment that resulted in the following relationships: (leuciscins + (Eurasian phoxinins + (OPM + (CC-P + WNA))))). These relationships were then used to estimate divergence times and ancestral areas in an attempt to make inferences about their biogeographic history.

0507 One Special Talk, Crystal 1 & 2, Sunday 19 July 2015

Adam Summers

University of Washington, Friday Harbor, WA, USA

Want a Job in Academia? Join a Society.

Many scientific societies are suffering a decline in membership driven in part by a lack of new student members joining. Other factors are important-the age structure of societies leads to more retirements than new members. The lamentably low funding for basic science also squeezes out members at all career stages as they make spending decisions within a very limited budget. It is worth asking whether there are measurable benefits from joining a scientific society. I have tracked down 153 of 182 student members of the American Elasmobranch Society from 2004. 46% of them have jobs in academia with 20% being tenure track faculty. 15% are in government employment and 18% in the private sector. Belonging to this particular society appears to be a good predictor of success in academia. An equal number of male and female students were members in 2004 but 56% of men got Ph.D.s compared to 40% of women. More women got M.S. and B.S. degrees. This shows lamentable leakage in the academic pipeline. I also examined the award winners from the society since its founding-equal numbers of men and women won awards. Award winners were twice as likely to have tenure track jobs than the 'class of 2004'. There are many obvious reasons why it behooves students to join scientific societies. Here I present some data on the advantages if a student is

interested in an academic career. AES devotes more resources to students than ASIH, so possibly the effect of membership is different.

**0426 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4,
Thursday 16 July 2015**

Chad Sundol¹, Janis Bush¹, Cathryn Greenberg², Christopher Moorman³, Jerry Jacka¹

¹University of Texas at San Antonio, San Antonio, TX, USA, ²USDA Forest Service, Asheville, NC, USA, ³North Carolina State University, Raleigh, NC, USA

Comparison of Herpetofaunal Communities in Areas Disturbed by Oak Regeneration Silvicultural Treatments

Reptile and amphibian communities are crucial components of hardwood forests and could be impacted by disturbance from silvicultural practices in the Southern Appalachian Mountains. From May to August 2013 and 2014, herpetofauna were trapped to evaluate the impacts of silvicultural practices. Silvicultural treatment (midstory herbicide, shelterwood-burn, repeated prescribed fire) and control (no treatment) consisted of five-ha units with four replicates each. Herpetofauna were trapped using eight drift fences with two pitfall and two funnel traps at each fence in each treatment. Total abundance (animals caught over two years) by treatment was determined for reptiles and amphibians. Effects of silviculture treatment (4 levels) and year of sampling (2 levels), and their interaction, on abundance were determined using two-way ANOVA's. Abundance varied among treatments, but year and the interaction between treatment and year were not significant. Reptile abundance was greater in shelterwood-burn treatments (8 ± 3 , ± 1 SD) than prescribed burn (1 ± 1 , $P = 0.0187$). Amphibian abundance was lower in the shelterwood-burn treatment (7 ± 4 , $P = 0.0024$) than the prescribed burn (21 ± 8) and midstory herbicide (18 ± 8), but similar to the control (12 ± 6). Decreases in canopy cover in the shelterwood-burn may allow for more thermoregulatory opportunities and could also lead to an increase in prey availability for reptiles. The converse would be expected for amphibians as they depend on cool, moist microclimates promoted by heavy overstory cover.

0265 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Tracey Sutton¹, April Cook¹, Kevin Boswell², Heather Bracken-Grissom², David Wells⁵, David English⁴, Ron Eytan⁵, Dante Fenolio⁶, Tamara Frank¹, Chuanmin Hu⁴, Matthew Johnston¹, Heather Judkins⁷, Chad Lembke⁴, José Lopez¹, Jon Moore⁸, Martha Nizinski⁹, Isabel Romero⁴, Jay Rooker⁵, Mahmood Shivji¹, Mike Vecchione⁹, Brad Penta³, Marsh Youngbluth¹⁰

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DEEPEND: Deep-Pelagic Nekton Dynamics of the Gulf of Mexico

The *Deepwater Horizon* Oil Spill (DWHOS) was primarily a deep-pelagic event. Variable amounts of discharged hydrocarbons reached the ocean surface and/or seafloor, whereas 100% occurred within the water column. Understanding this pelagic habitat is important because about half of all fish species that occur in the Gulf of Mexico (GoM) spend all or part of their lives in the open ocean. Most mesopelagic (200-1000 m depth) species of fishes vertically migrate each night to feed in epipelagic (0-200 m) depths and return to deep water during the day. This behavior affects rapid cycling of natural and anthropogenic material in the water column. Deep-pelagic fishes are prey for gamefishes, seabirds, and marine mammals. Given the steady growth of oil exploration and operations, the likelihood of future spills emphasizes the need to document acute and chronic effects on pelagic fauna. The DEEPEND (Deep-Pelagic Nekton Dynamics) Consortium will conduct a 3-year sampling and analysis program that builds on two intensive NOAA-supported surveys during 2010-11. DEEPEND will focus on short-term and long-term timescales to appraise the dynamic nature of communities using a suite of integrated approaches. These investigations include: 1) a direct assessment of GoM deep-pelagic community structure including the physical and biological drivers of this structure; 2) a time-series analysis/comparison of biophysical data from the years 2010-2011 and 2015-2017; 3) a time-series examination of differences in genetic diversity among key species; and 4) a biogeochemical analysis of the effect of DWHOS on pelagic biota.

0268 Fish Ecology II, Carson 3, Sunday 19 July 2015

Tracey Sutton¹, April Cook¹, Tamara Frank¹, Heather Judkins², Jon Moore³, Martha Nizinski⁴, Theodore Pietsch⁵, Mike Vecchione⁴, Marshall Youngbluth⁶

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What Have We Learned about the Diversity of Oceanic Fauna of the Gulf of Mexico after *Deepwater Horizon*? Initial Results of the NOAA Offshore Nekton Sampling and Analysis Program

The *Deepwater Horizon* Oil Spill (DWHOS) necessitated a whole-water-column approach for assessment of disturbance in the epipelagic (0-200m), mesopelagic (200-1000m) and bathypelagic (>1000m) biomes. The deeper regimes collectively form the largest integrated habitat in the Gulf of Mexico (GoM). This habitat received the initial oil/methane discharge, plus millions of liters of dispersant, and contained persistent deep (~1100m) plumes of oil and dispersant. By some estimates, only half of the discharged oil and none of the methane reached the ocean surface. This demonstrated that DWHOS had an extensive and persistent deep-pelagic component. Before the DWHOS we had only a basic knowledge of the deep-pelagic GoM. Consequently, the large-scale, NOAA-supported Offshore Nekton Sampling and Analysis Program (ONSAP), was implemented as part of the natural Resource Damage Assessment process. Here we provide preliminary results of ONSAP field campaigns in 2011 that sampled the pelagic fauna that inhabit the uppermost 1500 m. During these campaigns a minimum of 717 fish species were represented from the 328,560 specimens collected via midwater trawling. Ongoing analyses are likely to discover and define additional species, as hard-to-identify taxa are resolved. This diversity encompasses one-half of the fish species currently known for the GoM. Also, 60 of the species are new records for the GoM, including numerous undescribed taxa. Fish species richness by functional group and numerical dominance will be presented. These data emphasize that the diversity of the deep-pelagic GoM fauna, like the World Ocean proper, has been historically underestimated.

0307 Fish Ecology II, Carson 3, Sunday 19 July 2015

Tracey Sutton¹, Kevin Boswell², Heather Bracken-Grissom², April Cook¹, Sergio deRada³, David English⁴, Eytan Ron⁵, Dante Fenolio⁶, Tamara Frank¹, Chuanmin Hu⁴, Matthew Johnston¹, Heather Judkins⁷, Jose Lopez¹, Jon Moore⁸, Brad Penta³, Isabel Romero⁴, Jay Rooker⁵, Mahmood Shivji¹, Michael Vecchione⁹, David Wells⁵

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Dynamics of Epi-, Meso-, and Bathypelagic Fish Assemblages: A Gulf of Mexico Case Study and New Research Initiative (DEEPEND)

The *Deepwater Horizon* oil spill (DWHOS) demonstrated a worst-case scenario oil disaster at great depths, while also highlighting the paucity of baseline data for deep-ocean ecosystems in the Gulf of Mexico (GoM) and elsewhere. Here we discuss recent oceanic fish surveys in the GoM and introduce a new research initiative, DEEPEND (Deep-Pelagic Nekton Dynamics of the Gulf of Mexico). The mission will characterize the biophysical conditions in the water column and utilize modeling approaches to increase understanding of the dynamics of deep-pelagic (0-1500 m) fish assemblages in time and space. The DEEPEND Consortium is a 3-year (2015-2017) initiative will expand the synergy developed during two intensive NOAA-supported investigations during 2010-11. DEEPEND will appraise biophysical variability on short-term (sub-generational) and long-term (evolutionary) timescales using a suite of integrated approaches: 1) a direct assessment (taxonomic and genetic) of deep-pelagic fishes, with simultaneous measurements of physical and biological drivers in this regime; 2) acoustic documentation of diel changes in sonic scattering layers in response to shifts in oceanographic factors; 3) time-series analysis/modeling of metadata from the years 2010-2011 and 2015-2017; 4) a time-series examination of differences in genetic diversity; 5) biogeochemical (otolith microchemistry and whole-body hydrocarbon analyses) assays of prominent taxa; and 6) traditional and isotope-based trophic scrutiny of principal foodweb vectors. DEEPEND Outreach/Education partners include the ten consortium institutions, the San Antonio Zoo, the Guy Harvey Research Institute, Save Our Seas Foundation, and the BBC. We enthusiastically invite collaboration with other fish researchers. Please see www.deependconsortium.org for more information.

0135 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Brendan Talwar¹, Edward Brooks², Alp Gokgoz², John Mandelman³, Dean Grubbs¹

¹Florida State University, St. Teresa, FL, USA, ²Cape Eleuthera Institute, Rock Sound, Eleuthera, Bahamas, ³New England Aquarium, Boston, MA, USA

Stress Physiology and Post-release Survivorship of Cuban Dogfish and Gulper Sharks Caught on Longlines

Cuban dogfish (*Squalus cubensis*) and gulper sharks (*Centrophorus cf. uyato*) are common bycatch in deepwater longline fisheries, yet their fate after release is entirely unknown. Given the highly variable nature of a deepwater longline haul and the documented interspecific differences in the elasmobranch stress response, this research investigates (i) the 24hr post-release survivorship rates of *S. cubensis* and *C. cf. uyato*, (ii) the potential factors contributing to mortality, and (iii) the suitability of caging as a method to address these aims. To meet these objectives, individuals were caught on longlines in Exuma Sound, The Bahamas, and lowered to their respective capture depths (450-900m) in a video-monitored cage. *Squalus cubensis* experienced a $43.8 \pm 0.73\%$ 24hr post-release survivorship rate whereas *C. cf. uyato* experienced 100% mortality. A logistic regression analysis showed that at-vessel blood pH and release condition could predict survivorship for *S. cubensis*, whereas glucose and lactate could not. Caging had no significant effect on *S. cubensis* mortality; in comparison, *C. cf. uyato* commonly lost the ability to orient within the cage prior to mortality. The exact drivers of this trend are unclear. This study greatly improves our understanding of discard mortality for deep sea sharks and offers a first characterization of the stress response for two common bycatch species. It also suggests that containment studies may not be appropriate for the genus *Centrophorus*.

0209 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Milton Tan, Jonathan Armbruster

Auburn University, Auburn, AL, USA

The All Cypriniformes Tree of Life: A Resource for Comparative Studies Applied to Diversification and Evolution of Body Size

Understanding patterns and processes underlying diversity is one of the core motivations of evolutionary biology. The order Cypriniformes is the most diverse monophyletic order of vertebrates with over 4000 species, and presents a potential model clade to study evolution. However, studying the origins of this diversity in relation to its morphological evolution and biogeography depends on a robust phylogenetic hypothesis to provide a comparative framework. Many recent studies have collected sequence data to infer phylogenetic relationships among cypriniform taxa, including phylogenomic-scale data. This has resulted in approximately 2000 species

with relatively few sequenced loci, as well as relatively few taxa with hundreds of sequenced loci. We integrate phylogenetic-scale and phylogenomic-scale data to infer a time-calibrated phylogeny for the order Cypriniformes. We demonstrate the utility of this tree for comparative phylogenetic analysis by applying this phylogeny to studying diversification and body size evolution across Cypriniformes.

0216 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Milton Tan, Jonathan Armbruster

Auburn University, Auburn, AL, USA

Transcriptome Evolution of Paedomorphic Cyprinids

The order Cypriniformes includes multiple genera of paedomorphic fishes. Recent phylogenomic analyses indicate these genera do not form a clade, and likely have independently evolved their paedomorphic phenotype. RNA-Seq is a convenient method to sequence the transcriptome, which includes thousands of expressed genes (ie. functionally-relevant genes), and thus is a powerful tool to sequence many genes for phylogenetic reconstruction and to gain insight into phenotypic evolution. To investigate the evolution of paedomorphism, we used RNA-Seq to sequence the transcriptomes of three species belonging to the paedomorphic genera *Paedocypris*, *Sundadanio*, and *Danionella*, and compare these sequences to those of non-paedomorphic species of Cypriniformes. We perform a phylogenomic investigation of cypriniform relationships. Furthermore, we infer genes that have evolved under selection or have convergent sequence evolution among paedomorphic taxa relative to non-paedomorphic taxa.

0092 Cypriniformes Biology, Crystal 1 & 2, Sunday 19 July 2015

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Taxonomic Revision and Phylogeny of the Cyprinid Genus *Saurogobio* (Gobioninae: Cyprinidae: Cypriniformes)

The cyprinid genus *Saurogobio* is endemic to East Asia, inhabiting the bottom of streams, rivers, and lakes as well, exhibiting high morphological and genetic diversity. Previous studies have shown that this genus is monophyletic. However, some taxonomic problems and interspecies phylogenetic relationships still remain unresolved. In this study we described a new species *Saurogobio punctatus* sp. nov., with a suspicious

species *Saurogobio lissilabris* re-described. The new species *S. punctatus* can be diagnosed from congeners by lots of blackish spots scattered on all fins except for anal fin. *S. lissilabris* differ from *S. gymnocheilus* by having longer paired fins and an obvious notch in front of nostril. The morphological differences among all eight valid *Saurogobio* species were also summarized. Based on cytochrome *b* gene sequences, three phylogenetic analysis methods (NJ, BI, and ML) consistently showed that *Saurogobio* species were divided into two reciprocally monophyletic clades, four species owning 7 branched dorsal fin rays grouped as Clade A, and those owning 8 clustered as Clade B. Within Clade B, widespread species *S. dabryi* included three subgroups: one individual from Korea formed an independent subgroup with 7.0% genetic divergence from other two subgroups; samples from the other two subgroups showed a genetic divergence of 2.1%, separately inhabiting fast-flowing and slow-flowing habitats, which might be in an early stage of speciation. So currently, the species diversity within *Saurogobio* might have been greatly underestimated, and further studies are needed to test this hypothesis.

0069 Herp Behavior, Carson 4, Friday 17 July 2015

Jessie Tanner¹, Jessica Ward², Mark Bee¹

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Multivariate Selection on the Advertisement Call of *Hyla chrysoscelis*, Cope's Gray Treefrog

Across animal taxa, signaling facilitates the identification of appropriate, high-quality mates, and signals are shaped by mate choice. In many systems, selection on males imposed by female preferences for individual traits is well documented. However, surprisingly few empirical studies have investigated multivariate selection with enough power to detect it; even fewer focus on behavioral traits. Thus, we still know little about how selection operates on complex signals. In order to address this gap, we measured multivariate selection on the multicomponent advertisement signal of *Hyla chrysoscelis*, Cope's gray treefrog. We generated synthetic advertisement calls that varied simultaneously and independently with respect to five call characteristics with known univariate preference functions: call duration, call rate, dominant frequency, relative amplitude, and pulse rate. Using a no-choice experimental design, female *H. chrysoscelis* were sequentially presented with two synthetic male calls. One call had trait values that matched the population mean, and the other had trait values drawn randomly from the distribution of values in the population. Linear, quadratic, and correlational selection gradients were estimated from the data. Our preliminary results indicate that significant directional selection is acting on call rate, relative amplitude, and pulse rate in this species. Canonical rotation analysis also shows stabilizing selection on two major axes; one is heavily influenced by call rate and relative amplitude, while the other is loaded primarily by call duration and relative amplitude. These results suggest that sexual selection promotes particular combinations of both temporal and spectral call properties.

0176 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Jordan Taylor

College of Charleston, Charleston, SC, USA

The Chondrichthyan Fauna from the Upper Eocene, Upper Oligocene, and Lower Oligocene Formations in the Coastal Plain of South Carolina

The coastal plain in southeastern South Carolina is composed of the Eocene, Miocene, and Oligocene strata, which are characterized based on sedimentary deposits. These stratigraphic layers contain the isolated remains of Chondrichthyan teeth. While the stratigraphy of the coastal plain of South Carolina has been studied extensively, a detailed study of Chondrichthyan fauna distribution and abundance present in these strata has been neglected. Here, I intend to identify and report a detailed taxonomic study of the Chondrichthyan fauna and distribution using isolated teeth present in the southeastern formations in South Carolina. Teeth of identified Chondrichthyan fauna and the presence of other microfossils in these stratigraphical layers can suggest certain ecological niches, species diversity, and marine systems from these time periods. Not only is this study vital to understanding South Carolina marine history, it is also useful for recreational fossil collectors interested in properly identifying Chondrichthyan teeth.

0148 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Friday 17 July 2015

Rory Telemeco¹, Eric Gangloff², Gerardo Cordero², Timothy Mitchell³, Brooke Bodensteiner², Kaitlyn Holden², Sarah Mitchell², Rebecca Polich², Fredric Janzen²

¹*University of Washington, Seattle, WA, USA*, ²*Iowa State University, Ames, IA, USA*,

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Thermal Taxis by Turtle Embryos: Behavioral Thermoregulation or Play?

Thermal taxis by egg-bound embryos has recently been observed in multiple reptiles and might allow embryos to behaviorally thermoregulate similar to post-hatching individuals. Because temperature affects development in fitness-relevant ways, such thermoregulation could allow embryos to control their fate far more than historically assumed. We assessed the opportunity for embryos to behaviorally thermoregulate in nature by examining thermal gradients within natural nests and eggs of the common snapping turtle (*Chelydra serpentina*), a species that displays embryonic thermal taxis. We observed little spatial thermal variation within nests, and thermal gradients were poorly transferred to eggs. Moreover, natural thermal gradients switched direction every 12 hours: substantially faster than embryos can shift position. Thus, *C. serpentina* embryos have little opportunity to behaviorally thermoregulate. We suggest that embryonic

thermal taxis instead represents a play behavior, and results from the mechanisms for behavioral thermoregulation in free-living stages "coming online" prior to hatching.

0161 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Kenneth Thompson

Lock Haven University of Pennsylvania, Lock Haven, PA, USA

Adventures in Africa (1974 - 75): A Graduate Student in Paradise

As a new graduate student in ichthyology at The University of Texas in the early 1970's I was offered the adventure of a life time. When my major professor, Dr. Clark Hubbs, asked if I would like to work on one of his projects to be carried out in Lake Tanganyika in East Africa I couldn't wait to get started! We were going to evaluate three endemic *Lates* or "Tanganyika Perches" for possible introduction into artificial reservoirs in Texas. Lake Tanganyika is home to an amazing array of fishes. Since my dissertation was an evolutionary study of the Cichlidae the 250 species of cichlids in the lake were just frosting on the cake! The scientific results of this study are documented elsewhere. This report concentrates on techniques of specimen collection. It concerns the results of a number of collection trips carried out in 1975. During March and April the UNDP-FAO ran a series of experimental open water purse seining trips in Lake Tanganyika near the Tanzanian/Burundi border. While most such trips were undertaken at night using traditional light attraction techniques, one trip was carried out during daylight for catch comparison purposes and to provide better photographs. In July an exploratory collection trip was conducted with a local tropical fish exporter 60 - 80 miles south of our base in Kigoma along the east coast of Lake Tanganyika in search of *Lates* and a fabled red cichlid that would be worth its weight in gold to the hobby industry.

0162 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kenneth Thompson

Lock Haven University of Pennsylvania, Lock Haven, PA, USA

Collecting *Lates* and Cichlidae in Lake Tanganyika: The University of Texas Expedition (1974 - 75)

When reservoirs are created by damming rivers the shift to a lacustrine environment often causes trophic imbalances among the fishes with various "rough" fish populations expanding beyond the control of indigenous predators. In 1974 - 75 a joint project sponsored by The University of Texas and the Texas Parks and Wildlife Department was undertaken to evaluate various species of the genus *Lates* for possible introduction into artificial reservoirs in Texas as a possible solution to this problem. The project was based in East Africa in Kigoma, Tanzania where it was carried out in cooperation with

the UNDP-FAO Lake Tanganyika Fisheries Research and Development Project. The scientific results of this study are documented elsewhere. This report will concentrate on telling the story of specimen collections. This poster is a report of the results of a number of collection trips carried out in 1975. During March and April the UNDP-FAO ran a series of experimental open water purse seining trips in Lake Tanganyika near the Tanzanian/Burundi border. While most such trips were undertaken at night using traditional light attraction techniques, one trip was carried out during daylight for comparison purposes and to provide better photographs. In July an exploratory collection trip was conducted with a local tropical fish exporter 60 - 80 miles south of Kigoma along the east coast of Lake Tanganyika in search of *Lates* and the fabled red cichlid.

0051 ASIH STOYE AWARD ECOLOGY & ETHOLOGY II, Carson 4, Friday 17 July 2015

Michelle E. Thompson, Maureen A. Donnelly

Florida International University, Miami, FL, USA

Amphibian and Reptile Diversity and Composition in Riparian and Upland Habitats in a Chronosequence of Secondary Forest

Riparian zones are important landscape features for wildlife and often harbor high species diversity and a distinctive assemblage of species from neighboring upland habitats. For amphibians and reptiles, riparian habitats are important thermal refugia, they provide breeding habitats, and can serve as important corridors for movement. In harsh landscapes, such as those generated as a result of land-use change, riparian zones may be especially crucial to maintaining amphibian and reptile populations by serving as a refuge for a variety of species. While riparian zones have been shown to be fundamental to maintaining amphibian and reptile populations in matrix habitat, there has been little research on the riparian-upland gradient of species diversity over the course of secondary forest succession. In our study, we examine the differences in species richness and community composition among riparian and upland habitats in a chronosequence of secondary forest in two tropical lowland wet forest regions of Costa Rica.

0298 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Ryan Thoni

Saint Louis University, Saint Louis, MO, USA

Garra of Bhutan: An Introduction to the Diversity, Taxonomy, and Ecology of Bhutan's Most Speciose Genus

The first internationally led ichthyofaunal expedition in Bhutan yielded several new records for the country, including four new records of described species of *Garra*: *G. arupi*, *G. lamta*, *G. lissorhynchus* and *G. stenorynchus*, as well as one new species, *Garra bimaculacauda*. *Garra bimaculacauda* is most notably different from its congeners by the presence of two dark spots on the lobes of the caudal fin. This, in addition to two previously recorded species, *G. annandalei* and *G. gotyla*, brings the diversity of *Garra* in Bhutan to seven known species. A phylogeny of *Garra* from Bhutan based on two mitochondrial genes, COI and Cytb, reveals the monophyly of these species groups, corroborates our identifications, suggests that the diversity is greater than currently recognized, and that some cryptic species may exist. The oral disc possessed by nearly all species of *Garra* provides suction for adhering to the substrate, allowing them to persist in torrential streams and headwaters. I hypothesize that isolation in headwater torrent streams and rivers provides opportunities for adaptation, genetic drift, and speciation and that the evolution of this disc may be a key innovation responsible for the high species diversity in lineages of *Garra* throughout the Himalayas.

0030 Herp Conservation II, Carson 1, Saturday 18 July 2015

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¹*UC Davis, Davis, CA, USA*, ²*University of Kentucky, Lexington, KY, USA*, ³*Davidson College, Davidson, NC, USA*

Citizen Science Data Shows Species' Sensitivities to Human Land Use

Conservation organizations and management agencies are increasingly seeking ways to leverage public involvement in data collection to address modern conservation challenges. A common example is the use of citizen scientists to report species occurrences to help understand patterns of decline and species distributions. We used the Carolina Herp Atlas (Davidson College Herpetology Lab) to solicit georeferenced occurrences of reptiles and amphibians in North Carolina and South Carolina, USA. We accounted for sampling biases in 21,048 occurrences of 143 native reptiles and amphibians submitted since 1990 to identify how species distributions are associated with human land use. Within each taxon, several species were found more often in highly natural landscapes than were other species. Examples include *Aneides aeneus*, *Aspidoscelis sexlineata*, *Clemmys guttata*, *Crotalus horridus*, and *Lithobates virgatipes*. Other species exhibited no apparent sensitivity to human land use and were equally likely to be found across a range of both human-modified landscapes and natural landscapes.

Finally, several species were found more often in human-dominated landscapes compared to others in their taxon. Examples include *Anaxyrus fowleri*, *Chelydra serpentina*, *Desmognathus fuscus*, and *Storeria dekayi*. Our approach provides a quantitative means for assessing conservation status of species on the basis of their sensitivity to human land use and can be used to anticipate which species are at greatest risk of decline in the face of ongoing habitat conversion. Our work also demonstrates the value of citizen science data collection in helping natural resource managers confront species declines and extinctions.

0217 AES Morphology, Ecology, & Physiology, Carson 2, Sunday 19 July 2015

Takeeru Tomita¹, Masaru Nakamura², Keiichi Sato², Hiroko Takaoka³, Minoru Toda², Junro Kawauchi⁴, Kazuhiro Nakaya⁴

¹Florida State University Coastal and Marine Laboratory, St Teresa, FL, USA, ²Okinawa Churashima Research Center, Motobu, Okinawa, Japan, ³Okinawa Churaumi Aquarium, Motobu, Okinawa, Japan, ⁴Hokkaido University, Hakodate, Hokkaido, Japan

Changes in Catshark Embryo Respiratory Mode During Mid-embryonic Period

Elasmobranchs are unique among fishes in producing extremely large embryos. Such a large embryo, with low body surface-volume ratio, may present respiratory challenges in utero. This is because gas diffusion solely through the body surface does not meet the oxygen demand for large embryos. Thus, some specific respiratory mechanisms are expected. Morphological and kinematical observations on captive catshark embryos have suggested that the embryo switches its respiratory mode just before the respiratory slits open on the egg capsule. During the pre-opening period, the embryo acquires oxygen mainly via diffusion in the external gill filaments. After slit opening, embryo starts buccal pumping to pass water over the internal gills. Some structural modifications (e.g., development of blood vessels in internal gills, development of oral valve, and establishment of pharyngeal skeletons and associated muscles) occur at the same time. It is known that the oxygen tension in the egg capsule is quite unstable after slit opening. The ability of buccal pumping is possibly advantageous for embryos to regulate oxygen intake by changing pumping frequency in an unstable oxygen environment.

0410 Fish Systematics I, Carson 3, Saturday 18 July 2015

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Little Fish in a Deep Dark World: Evolutionary Origins of Deep-reef Caribbean Gobies (Teleostei: Gobiidae: Gobiosomatini)

Mesophotic and other tropical deep reefs (> 50 m) represent one of the most diverse unexplored habitats on earth. At these pivotal depths, light becomes scarce for many photosynthetic reef-building corals, yet the benthos still harbor a robust assemblage of hard and gorgonian corals, sponges and algae, which in turn provide habitat for a diverse fish community. Unfortunately reef habitats below 50 m are too deep to sample with traditional SCUBA gear, and deep-diving submersibles rarely make stops at depths above 300 m. However, recent explorations of deep reefs in the Caribbean by the Smithsonian Deep Reef Observation Project have led to remarkable discoveries. Collections from the manned submersible Curasub have led to the discovery of more than 30 new species in just four years of limited sampling. Several of these new species belong to the American seven-spined gobies (Gobiidae: Gobiosomatini) - a group that represents one of the best known cases of adaptive radiation in the marine environment. Comprising more than 200 species of marine fishes endemic to the western Atlantic and Eastern Pacific Oceans, American seven-spined gobies have rapidly diversified both taxonomically and phenotypically to fill an impressive variety of niches in tropical and subtropical coastal waters. Here we investigate the phylogenetic origins and of these new deep-reef gobies relative to their ecologically divergent shallow-water relatives, and estimate the timing of shallow-to-deep transitions. Our phylogenetic hypothesis will serve as a framework to study the evolution of key morphological and genomic adaptations to life on deep reefs.

0544 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Cameron R. Turner

University of Notre Dame, ecoSystem Genetics LLC, South Bend, IN, USA

It's Contamination! Reducing Uncertainty in Environmental DNA Monitoring of Fishes and Amphibians

Genetic analysis of environmental DNA (eDNA) provides site occupancy inferences for rare fishes and amphibians that are often easier to obtain than direct observations of organisms. Research on the origin, state, transport, and fate of environmental DNA (eDNA) from aquatic macrofauna is needed to describe the spatiotemporal context for eDNA-based occupancy inferences, and to guide eDNA sampling design. One often

underestimated origin is lab contamination. Contamination sources, primarily PCR product and tissue, are abundant in most laboratories with interest and capacity to analyze eDNA. Unfortunately, standard precautions (i.e., autoclaving) are inadequate for destroying DNA contamination. Even worse, standard negative controls (i.e., water blanks) are inadequate for observing contamination occurrence and abundance. Having learned these old lessons the hard way, I present several case studies involving eDNA data that I ultimately concluded were best explained by contamination. These conclusions are supported by data from other fields making organismal inferences based solely on indirect genetic evidence from environmental samples: microbiology, forensics, paleogenetics, fecal source tracking, and environmental biosafety. Finally, I suggest a framework for accurately estimating contamination occurrence and abundance.

0454 Fish Conservation & Management, Carson 3, Saturday 18 July 2015

Thomas Turner¹, Megan Osborne¹, David Propst¹, Wade Wilson²

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²*Southwest Native Aquatic Resources and Recovery Center, Dexter, NM, USA*

Drought and Wildfire Compromise Genetic Diversity and Recovery in Gila Trout

Gila trout maintains a tenuous presence in highland desert streams of the Upper Gila River basin in the southwestern United States. Beginning in 2011, a series of catastrophic wildfires negatively impacted nearly all remaining populations, with local effects ranging from reduced abundance to extirpation. We assessed genetic responses by assessing variation in 13 microsatellite loci and a gene critical for immune function (MHC). In addition to severe demographic losses, levels of genetic diversity changed radically over a 10-year period of extensive drought preceding the wildfires. Two distinct lineages (Spruce and Whiskey), both with behavioral characteristics that complicate large-scale hatchery rearing, experienced extensive losses of heterozygosity and allelic diversity at all loci, including MHC. Spruce also exhibits reduced viability consistent with inbreeding depression. Lineages more amenable to hatchery rearing (Main Diamond, South Diamond) maintained diversity at microsatellite loci and MHC. Marker-assisted crosses with other Gila trout lineages will likely be necessary to restore diversity and viability to the Spruce lineage. Restoration of genetic connectivity across multiple lineages in complex watersheds could also ameliorate negative demographic and genetic effects of drought. Catastrophic fires and extensive drought will increase in frequency and geographic scale in coming decades, and we expect similar losses of diversity in other native trout populations. Gila trout serves as a case study in efforts to preserve other inland trout species.

0430 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

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¹University of West Florida, Pensacola, FL, USA, ²Florida State University, Tallahassee, FL, USA

Microsatellite Applications for Multiple Paternity in *Squalus clarkae*, a Novel Shark Species from the Gulf of Mexico

Squalus (Squalidae) is a genus of small, slow-growing sharks with long gestation periods. A new species, *Squalus clarkae*, was recently described from the Gulf of Mexico after being genetically and morphologically distinguished from Japanese *Squalus mitsukurii*. As a newly described species, little is known of *S. clarkae*'s reproductive behavior. Thus far, multiple paternity in members of the genus *Squalus* has been understudied, and the degree to which shark species exhibit this behavior varies greatly. Eight species-specific microsatellite loci previously developed for congeners *S. mitsukurii* and *S. acanthias* and are being cross-amplified with *S. clarkae* to assess for their suitability in testing for paternity and kinship. These microsatellites will be applied to litters of *S. clarkae* to determine the presence and frequency of multiple paternity in this species using 13 litters with an average of 6.7 pups per litter. This study will offer the first genetic insight into the reproductive behavior of this species, and will provide life-history data necessary for future conservation efforts.

0038 Herp Physiology & Reproduction, Carson 4, Friday 17 July 2015

James Van Dyke¹, Jessica Dudley², Oliver Griffith², Christopher Murphy², Michael Thompson²

¹University of Western Sydney, Richmond, NSW, Australia, ²University of Sydney, Sydney, NSW, Australia

How to Make a Baby Skink: The Evolution of Placental Nutrient Transport

Mechanisms of reproductive allocation are major determinants of fitness because embryos must receive sufficient nutrition from their parents in order to complete development. Although viviparity (live birth) has evolved frequently in vertebrates, most viviparous animals still rely on yolk for embryonic nutrition, and transfer only inorganic ions and incipient quantities of organic nutrients (ie, proteins, fats, and carbohydrates) across simple placentas. In contrast, placental transport of substantial quantities of organic nutrients has evolved only once in therian mammals and at least six times in skinks. Although the complex placentas of mammals and these skinks are homologous in embryological origin, they differ widely in morphology and it is unclear whether similar nutrient transport mechanisms have evolved concomitant with complex placentation. Our experiment examines how solute carriers (SLCs) transport amino acids to developing offspring in the placental southern grass skink, *Pseudemoia entrecasteauxii*. Transcriptomic results suggest that a number of SLCs are upregulated in the uterus of *P.*

entrecasteauxii during pregnancy. We used Western blotting to quantify the abundance of four of the most-highly upregulated SLC transporters (SLC7A7, SLC7A8, SLC38A4, and SLC38A5) in the uterus of *P. entrecasteauxii* at successive stages of pregnancy to determine whether these SLCs increase in abundance as pregnancy progresses. Although transporter abundances do not appear to change over time, they vary considerably at given stages of pregnancy. Forthcoming analyses will show whether placental transport of four separate ¹⁵N-labeled amino acids are correlated with the abundances of these transporters, and where they are localised in the placenta.

0380 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Rebecca Varney¹, Dean Grubbs², Kevin Feldheim³, Toby Daly-Engel¹

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A Novel Panel of Microsatellite Loci for the Gulf of Mexico Hagfish *Eptatretus springeri*

Hagfishes (Myxiniiformes, Myxinidae) are keystone marine detritivores as well as fishery species in much of the world. In spite of this, they are relatively unstudied relative to most fishes. In the Gulf of Mexico there are three co-occurring species: *Eptatretus springeri*, *E. minor*, and *Myxine mcmillinae*. Genetics has recently been demonstrated as an effective identification tool for these species, particularly between *E. springeri* and *E. minor*, which are morphologically difficult to distinguish. A novel panel of microsatellites has been developed for *E. springeri*, the most common of the three species in the Gulf of Mexico. Microsatellites will be applied to individuals from more than 20 collection sites in the Gulf of Mexico. Additionally, as microsatellites frequently cross-amplify at the genus level, these tools can potentially be applied to other species in the future. Resulting information will provide the first look at genetic connectivity among species in this genus, offering insight into the ecology and dispersal of this little-known group.

0313 AES Ichthyology, Carson 2, Thursday 16 July 2015

Victoria Elena Vásquez¹, David A. Ebert¹, Douglas J. Long²

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A New Lanternshark (Squaliformes: Etmopteridae: *Etmopterus*) from the Eastern Central Pacific Ocean

A new species of lanternshark shark, genus *Etmopterus* is described from specimens collected off the Pacific coast of Central America. The new species is placed in the '*Etmopterus spinax*' clade by a lack of flank markings and small hook-like conical dermal denticles distributed throughout the body. This new species can be separated from its congeners based on: proportional body measurements, meristic measurements of spiral valve and vertebral counts, arrangement of dermal denticles, and dark fin margins that contrast with other species in the '*E. spinax*' clade, which typically possess white fin margins. The dorsal fins in the new species are much similar in size compared with its congeners while the second dorsal spine is significantly larger than the first, as is typical for the genus. The dark coloration of this new species makes photophore markings difficult to identify. However, the dorsal portion of the head is unique from other *Etmopterus* in possessing parallel linear markings with a light brown patch in between. The head portion is also distinct from other members of the '*E. spinax* clade' in having a dense concentration of dermal denticles closely surrounding the eyes, mouth, gills and spiracles. This is the only *Etmopterus* species presently known from the Pacific coast of Central America.

0200 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Chavalit Vidthayanon

Mekong River Commission, Vientiane, People's Democratic Republic of Lao

Cypriniforms as Bioindicators in the Mekong Basin: How Systematic Research Impacts Monitoring

The Mekong River Basin is recognized as a global biodiversity hotspot, comprised of 12 habitat types from highlands to coastal waters, including peat swamps, subterranean streams and crater lakes. Mekong fish biodiversity, mainly Cypriniformes, plays an important role as Key Environmental Assets and provides important ecological services to over 60 million people. Of the more than 400 species of cypriniforms known in the basin, at least 200 are endemic, and over 30 are still undescribed or taxonomically unresolved. Most cypriniforms are sensitive to water quality and habitat degradation. Species composition and indicator species can be used to monitor aquatic ecosystem health and the impact of fisheries on fish stocks. Our knowledge of cypriniform diversity within the Mekong basin is limited, and some parts of the basin are under-surveyed. Large-scale development of water resources is underway throughout the

region with current and potential impacts on biodiversity. There is an immediate need to collate and make freely available existing knowledge on freshwater species distributions, ecological sensitivities, and habitat requirements for input into the decision making processes and in designing actions to mitigate impacts to aquatic ecosystems. Without such information, development is unlikely to proceed in a sustainable way, and the impact on freshwater species will be severe. More inventories, systematic studies based on anatomical, biogeographic, and ecological research are needed.

0272 ASIH STOYE AWARD GENETICS, DEVELOPMENT, & MORPHOLOGY, Carson 3, Friday 17 July 2015

Kirill Vinnikov, Kathleen Cole

University of Hawaii at Manoa, Honolulu, HI, USA

De Novo Transcriptome Sequencing and Genetic Marker Discovery for Goby Fishes (Teleostei: Gobiiformes)

High-throughput sequencing methods offer a unique opportunity to investigate genome-wide DNA polymorphism with a functional annotation, in non-model organisms lacking reference genome information. Using these approaches, we are able to solve complex biological problems such as: revealing phylogenies of rapidly diverged taxa; recovering population structures on a small geographic scale; finding genes under selection; and investigating character evolution. All the above are highly relevant to gobies. This taxon constitutes the second largest order of fishes with more than two thousand described species, with phylogenetic relationships and population structures being mostly unknown due to the lack of informative molecular markers. In this study, we are carrying out the first deep transcriptome sequencing of two amphidromous gobies, *Stenogobius hawaiiensis* and *Awaous stamineus*. Nearly 170M of 150 bp paired-end reads have been sequenced using Illumina HiSeq 2500. After quality trimming, adapter and bacterial contamination removal, all reads of *S. hawaiiensis* were assembled with Trinity and ABySS. The redundant assemblies contained 240-280K contigs. Annotation revealed over 15K contigs having unique matches with swiss-prot database, and subsequently, over 10K matches were recovered by comparing contigs against uniref90 fish protein datasets. Finally, nearly 10K polymorphic nucleotide sites were recovered by comparing orthologs within species lineages, and over 20K variable sites were identified from comparing the two species. The results of this study provide, for the first time, an annotated transcriptome of a gobioid species, *S. hawaiiensis*, and a set of genetic markers which can now be used as a reference for genomic studies on all gobies.

0299 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Liz Vinyard¹, Walter Buble², Bryan Frazier²

¹University of Charleston, South Carolina, Charleston, SC, USA, ²South Carolina Department of Natural Resources, Charleston, SC, USA

Age, Growth, and Maturation of the Finetooth Shark, *Carcharhinus isodon*, in Coastal Waters of the Western North Atlantic Ocean

Age, growth, and maturation are crucial fishery dynamics to understand, as they provide vital information that can be used for stock assessments of fishes. Because ontogenetic changes occur across the life history of many marine organisms, including elasmobranchs, an effort should be made to obtain specimens across entire size ranges for both sexes to accurately represent a given population structure. This study proposes three main objectives: 1) examine size at age while validating seasonal periodicity of increment formation used in age estimation, 2) estimate size and age of sexual maturation and 3) compare growth models to published growth models from the western North Atlantic and Gulf of Mexico. Samples will be collected from April 2014 through October 2015 from estuaries and nearshore waters off of South Carolina. Additional vertebral samples from a 2003 study and ongoing sampling with South Carolina Department of Natural Resources (SCDNR) will increase the sample size to approximately 500 vertebrae. Results of this study will provide accurate information regarding growth and maturation for the Finetooth Shark population along the southeastern United States.

0555 Fish Morphology & Histology, Crystal 1 & 2, Saturday 18 July 2015

Dylan Wainwright, James Weaver, George Lauder

Harvard University, Cambridge, MA, USA

The Surface Structure of Fish Scales

Fish scales are morphologically diverse and have been studied for hundreds of years, yet we still have little information about their function. We present a new imaging technique that allows us to investigate the 3 dimensional surface structure of fish scales – a necessary first step before determining hydrodynamic function. Using a new surface imaging process, we are able to make use of many surface metrology parameters such as roughness and skew, while also developing our own simple morphological measurements. We use this technique in conjunction with μ CT scanning to investigate how scales may change on different areas of the body of the bluegill (*Lepomis macrochirus*). We use discriminant function analysis to show that bluegill scales do change across the body - scales are cycloid on the opercle, ctenoid on the body and tail, and the proportion of ctenii coverage increases ventrally on the fish. We also investigate the surfaces of other teleosts using these new techniques.

0363 General Ichthyology II, Crystal 3 & 4, Friday 17 July 2015

Peter Wainwright, Samantha Price, Sarah Friedman

University of California, Davis, Davis, CA, USA

The Evolution of Spines Affects Body Shape Diversification in Teleosts

Spines are a conspicuous feature of many fishes. While they appear to function primarily as defensive structures, their impact on teleost diversification is not well understood. We were interested in how spines have impacted the evolution of teleost body shapes. Many aquatic predators exhibit gape limitation: the dimensions of the predator's mouth and pharynx limit prey size. It has been shown that, because fish are normally swallowed head first, it is the length of their dorsal-ventral axis that determines whether they fit in the predator's mouth. Spines in the dorsal and anal fin may work synergistically with deepening of the body to discourage predators. Predicting that lineages of teleosts with these spines show a tendency toward the evolution of deep body shapes, we measured the length of the first major spine in the dorsal and anal fins, and body shape in one species from each of 349 families of teleosts. Using a time-calibrated phylogeny to study evolutionary interactions we found a strong positive correlation between the length of fin spines and body depth, after correcting for body size. Lineages with spines were significantly deeper-bodied than lineages without spines and showed greater variability in body shape. Although many factors influence body shape, these results show that the evolution of spines biases lineages toward the invasion of deep-bodied regions of morphospace and suggests that protection from gape limited predators has been a major driver of body shape evolution in teleosts.

0498 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Margarete Walden, Nancy Karraker

University of Rhode Island, Kingston, RI, USA

Environmental Correlates of Hibernation Behavior of the Eastern Box Turtle, *Terrapene c. carolina*

The population of Eastern Box Turtles (*Terrapene c. carolina*) at the William Floyd Estate on the southern coastline of Long Island, NY, USA, represents the longest-studied population of *T. c. carolina* known, with turtles systematically marked since 1915, and is thus both a remarkable cultural and scientific resource. Mowing activities impact box turtle populations from direct mortality from the mower's blades and tires. Conservation measures to prevent injuries and mortalities to turtles at the William Floyd Estate have in part consisted of restricting mowing to between November and March, when it is believed the turtles are inactive. However, it would be more beneficial for both invasive

plant species control and habitat maintenance for meadow-nesting birds to mow earlier in the year. Efforts have been made to determine environmental correlates of the timing of hibernation in *T. carolina*; however, the results of such studies have not been definitive or are inconsistent between populations. The objectives of this research study are to test whether the environmental variables of air temperature, precipitation, soil moisture, soil temperature, relative humidity, solar radiation, and barometric pressure are correlated with the timing of hibernation in adult *T. c. carolina* in order to better inform the National Park Service as to the ideal mowing window for a particular year at the William Floyd Estate.

**0464 ASIH STOYE AWARD PHYSIOLOGY & PHYSIOLOGICAL ECOLOGY,
Carson 3, Friday 17 July 2015**

Whitney Walkowski

Southeastern Louisiana University, Hammond, LA, USA

**Courting CORT: Glucocorticoid Concentrations in Calling and Non-Calling
*Lithobates grylio***

Circulating glucocorticoid concentrations have been measured in a number of taxa to make inferences about mobilization of energy reserves during breeding season. Anuran vocalization is one of the most energetically expensive behaviors recorded in vertebrates, with energy costs being up to 25 times more than animals at rest. *Lithobates grylio*, the pig frog, is a fully aquatic frog distributed in freshwater marshes and swamps in the southeastern United States. They are considered prolonged breeders, calling from March to September. During the breeding season males exhibit a decline in foraging behavior and decline in body mass. This study measures corticosterone concentrations, the primary glucocorticoid in anurans, in calling and non-calling male *L. grylio*. Blood samples were obtained from specimens (n=38) collected from a freshwater marsh in St. Tammany Parish, Louisiana over the 2014 calling season. Behavioral observations and microhabitat selection were recorded upon capture. Corticosterone concentrations in blood plasma were analyzed using an enzyme linked immunosorbent assay. It was found that non-calling males had significantly higher CORT concentrations than calling males (p=.04). Because of the nature of corticosterone to suppress calling activity and increase gluconeogenesis, it can be inferred that elevated corticosterone concentrations in *L. grylio* during the breeding season influences calling and non-calling behavior.

0411 Poster Session I, STORER HERPETOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Whitney Walkowski¹, Erica Rottman¹, John Tupy², Brian Crother¹, Kyle Piller¹

¹*Southeastern Louisiana University, Hammond, LA, USA*, ²*Western Carolina University, Cullowhee, NC, USA*

Ponds of Plenty: A Comparison of *Lithobates sevosus* eDNA from Sites of Known Densities

Environmental DNA (eDNA) monitoring is a technique in which free DNA in water samples can be used to test for a species' presence. This non-invasive approach is particularly useful for surveying imperiled species. Factors such as high temperature or low organismal densities could be considered potential limiting factors of this new technology. The dusky gopher frog, *Lithobates sevosus*, is a critically endangered, fossorial amphibian that exploits ephemeral pools for breeding. Ephemeral ponds are extremely susceptible to temperature fluctuations because of their shallow nature. Three sites inhabited by tadpoles of *L. sevosus* were sampled in Harrison County, Mississippi. These sites had known high, medium, and low densities of *L. sevosus* tadpoles. Water samples were collected from these localities and were filtered. Environmental DNA was extracted from the water samples and recently developed mitochondrial primers of the sister species, *L. capito*, were used for amplification. *Lithobates sevosus* was successfully detected at all three known densities with eDNA sampling. The density of the tadpoles was found to have a direct effect on the eDNA detection success of *L. sevosus*. The implications of these results and the efficacy of this approach will be presented.

0529 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Rachel H L Walls, Nicholas K Dulvy

Simon Fraser University, 8888 University Drive, Burnaby, BC, Canada

A Tale of Two Seas: The Contrasting Status of Europe's Elasmobranchs

The International Union for Conservation of Nature's (IUCN) Red List Assessments provide the motivation and foundation for global and regional conservation and fisheries management efforts. Some of the earliest assessments were done in Europe, which led to improved fisheries management measures specific to elasmobranch protection in the Northeast Atlantic. Conversely in the Mediterranean Sea, there has been little scientific or management progress. The IUCN Shark Specialist Group recently reassessed all elasmobranchs in European waters, which allows us to review status changes since 2005 for both the Northeast Atlantic and Mediterranean regions. Our comparison revealed striking differences in the overall status of elasmobranchs since the previous assessments and between regions. While the status of elasmobranchs in the Northeast Atlantic has improved, the Mediterranean status has actually worsened. Approximately 35% of Northeast Atlantic elasmobranchs are considered "safe"

compared to only 10% of Mediterranean species. Similarly, 31% of Northeast Atlantic species are threatened with an elevated risk of extinction, compared to almost 50% in the Mediterranean: the highest proportion of threatened species in any region globally. It is likely that the lack of appropriate management measures implemented in the Mediterranean specific to elasmobranchs since the previous Red List assessment is the primary reason for these differences, and this will be explored in greater detail.

0466 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Kristin A. Walovich, David A. Ebert

Moss Landing Marine Laboratories, Pacific Shark Research Center, Moss Landing, CA, USA

A Revision of the Short-nose Chimaeras (Genus *Hydrolagus*) from Southern Africa: Conservation and Management Implications of an Enigmatic Fish Group

A lack of taxonomic clarity has negative implications for many facets of chondrichthyan research including proper identification, acquisition of basic life history information, and the implementation of fishery management and conservation efforts. The Order Chimaeriformes, also known as ghost sharks or chimaeras, is an enigmatic and understudied group of fishes particularly vulnerable to impacts of deep-sea fisheries. This vulnerability is compounded by taxonomic uncertainties and a paucity of life history information, especially for chimaeras of the genus *Hydrolagus* (Family Chimaeridae) from the southern African region. Given historical and current taxonomic ambiguity and its impacts on management and conservation, the main objective of this study is to provide a qualitative, quantitative and genetic assessment of the diversity of the genus in the Southern African region. Full elucidation of species composition will enable the development and dissemination of reliable identification material and range maps to improve fisheries statistics, initiate ecological research and facilitate appropriate conservation efforts.

0471 Poster Session I, AES CARRIER AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Kristin A. Walovich, David A. Ebert

Moss Landing Marine Laboratories, Pacific Shark Research Center, Moss Landing, CA, USA

'SPOT A BASKING SHARK': How Citizen Scientists Can Help Save an Enigmatic Shark

The distribution and trans-equatorial migrations of the basking shark (*Cetorhinus maximus*) have been well documented in the Northern Atlantic, yet seasonal patterns of distribution have not been fully elucidated in the eastern North Pacific. Filling in vital knowledge gaps will help inform the best recovery plan to rebuild the basking shark population in this region, which has been designated a 'Species of Concern' by NOAA's National Marine Fisheries Service and 'Endangered' by the International Union for the Conservation of Nature (IUCN). The 'Spot a Basking Shark' Project, ongoing since 2010, is a collaborative effort to investigate the abundance, distribution, and population status of basking sharks in the eastern North Pacific. The project employs a web-based reporting system for the public to record sightings, utilizes satellite tags to improve understanding of essential habitat and geographic range, and obtains additional information on life history and patterns of occurrence by data-mining existing records. Have you seen a basking shark? Report your sighting on our website:

<http://psrc.mlml.calstate.edu/current-research/basking-shark/>

0496 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Friday 17 July 2015

Danielle Wasserman

Southeastern Louisiana University, Hammond, LA, USA

Examining Variation of the Hyoid Apparatus in Varanid Lizards

In varanids, the hyoid apparatus is widely regarded to be a highly derived structure that functions during the swallowing of food and possibly during the inflation of the throat during threat displays. Previously, the morphology and function of the apparatus was characterized at the familial level and descriptions existed for four species. This study characterizes and describes the interspecific and intra-specific morphological variation that was observed in a sample of twenty-nine species of varanids and three out group taxa. In short, a tremendous amount of interspecific variation exists and intraspecific variation is identifiable. This study includes extensive morphological description and illustrations, a suite of new characters and a parsimony based hypothesis of twenty seven species of *Varanus*. Data was collected via dissection and by examining cleared and stained, osteological, and digitally scanned specimens. The hyoid bears synapomorphies that are intrinsic to both shallow and deep ancestral nodes. Overall, the

hyoid apparatus appears to carry a strong phylogenetic signal. This is the first in-depth systematic study of hyoid evolution at the sub-familial level in a tetrapodian clade.

0483 General Herpetology, Carson 1, Friday 17 July 2015

James Watling, Nicole Koballa, Ian Reider

John Carroll University, Cleveland, OH, USA

Using Agar Models to Assess Desiccation Risk of Amphibians among Vegetation Types in a Fragmented Tropical Forest Landscape

Conservation physiology is an emerging discipline focused on understanding physiological responses of organisms to human-mediated environmental change. For amphibians and reptiles, abiotic conditions such as temperature and/or humidity play a key role in determining activity times on diurnal and seasonal time scales. Often, abiotic conditions restrict activity of poikilothermic organisms to a limited subset of habitats or microhabitats for a small portion of the day. Physiological constraints can restrict dispersal to new habitat patches and exploitation of otherwise-suitable patches, limiting distributions of species in human-modified landscapes. Because of constraints to working with real organisms, there is a long history of using models to understand ecophysiological patterns of amphibians and reptiles. The use of ecophysiological models in a conservation physiology context is increasing, particularly with respect to our understanding of how physiology influences landscape distributions of amphibians and reptiles. We conducted a series of studies using agar models in the lab and field to examine how desiccation rates vary as a function of temperature and vegetation density. Agar models consistently maintain temperatures approximately 5-7 degrees Celsius below ambient conditions, although thermal relationships vary as a function of desiccation and vegetation cover. By understanding how temperature and desiccation risk covary across a gradient of vegetation density, we can better predict species responses to landscape and climate change.

0583 Herp Behavior, Carson 4, Friday 17 July 2015

Robert Weaver¹, Will Clark²

¹*Department of Biological Sciences, Central Washington University, Ellensburg, WA, USA,* ²*Department of Math and Science, Western Wyoming College, Rock Spring, WY, USA*

Intraguild Competition Between Ring-necked Snakes (*Diadophis punctatus*) and Desert Nightsnakes (*Hypsiglena chlorophaea*)

Resource partitioning due to competition between similar species is a well documented ecological phenomenon among vertebrates. Within snakes it is less well known, with

few studies carried out on an even fewer number of taxa (Australian elapids). Here we present data on intraguild (IG) competition between two ecologically and morphologically similar species, the Ring-neck Snake (*Diadophis punctatus*) and the Desert Nightsnake (*Hypsiglena chlorophaea*). Data were gathered with regard to habitat use, activity patterns, diet, and responses to chemosensory cues of each other. Field data were collected from 2000-2014, while behavioral trials were conducted between 2008-2010, and 2012-13. With regards to habitat use both utilize rocky areas within shrub-steppe and oak woodland habitat. However, in some areas especially in the shrub-steppe, and high elevation (>800 meters) oak woodland, these species were not found in sympatry. We saw high levels of sympatry only in low (< 200 meter) oak woodland, which also had the highest abundance of available prey. Within this habitat, both species utilized similar microhabitats (flat rocks, basalt outcrops and talus slopes), and fed on similar prey (sceloporine, anguid and scincid lizards). Adult *D. punctatus* were also found to consume small and large *H. chlorophaea*, while the reverse was not true. Laboratory trials showed *D. punctatus* larger than 200 mm responding with increased tongue-flicks to the odor of *H. chlorophaea*, while *H. chlorophaea* showed a weak response to odors of *D. punctatus*. In all trials individuals responded by backing away, and acting in an erratic, at times defensive manner.

0548 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Alison Webb, Lori Neuman-Lee, Eleanor Watson, Susannah French

Utah State University, Logan, UT, USA

Innate Immune Function in Juvenile Green Iguanas (*Iguana iguana*): A Longitudinal Assessment

To assess innate immunity following exposure to a novel antigen, juvenile green iguanas (n = 15, 11 males and 4 females) were injected with a weight dependent dose of sheep red blood cells and blood samples were collected at 0, 6, 13, and 20 days post immunization. A bacterial killing assay, hemolysis assay, and differential leukocyte counts were used in evaluating an individual's innate immune performance during an active infection. Mean bacterial killing capacity peaked at 6 days post immunization and mean hemolysis titers peaked at 13 days post immunization, both returned to near baseline values by 20 days post immunization. Differential counts of circulating leukocytes showed a decrease in percent lymphocytes and an increase in percent heterophils and monocytes post immunization. Since the complement pathway and natural antibodies can be involved in both the bacterial killing and hemolysis assays, the peak in bactericidal capacity 1 week prior to the peak in hemolysis titers could indicate increased performance for other components of the bacterial killing assay at that time, such as phagocytic cells and opsonizing proteins. The timeline of the innate immune response is not well studied in reptiles, nor is the concurrent assessment of these commonly used immune metrics but additional studies such as this could provide

insight into the mechanisms and performance trade-off's of specific components of the reptilian immune system.

0541 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Jacqueline F Webb, Oliver Bender

University of Rhode Island, Kingston, RI, USA

Post-Embryonic Ontogeny of the Lateral Line System on the Trunk of Two Cichlid Fishes

The lateral line (LL) system of the trunk (the posterior LL system) typically includes a lateral line canal comprised of a linear series of tubed LL scales (a important meristic character in bony fishes) in which neuromast receptor organs are found, and superficial neuromast receptors on the skin. Variation in the posterior LL system among teleosts is defined by the configuration (number, extent of development) of the trunk canal and the distribution of superficial neuromasts. We used fluorescent staining (4-di-2-ASP), SEM, and histology to describe the post-embryonic ontogeny of the posterior LL system in two Lake Malawi cichlids (*Aulonocara stuartgranti*, *Tramitichromis* sp.), thus complementing our earlier work on the ontogeny of their cranial LL system. We determined the pattern (order) and timing of the differentiation of neuromasts along the length of the trunk in larvae and juveniles in order to explore two important aspects of the posterior LL system: 1) how the spatial patterning of canal neuromasts (CNs) can explain the establishment of adult LL scale number (meristics) as well as the development of the unusual disjunct (two-part) trunk canal of cichlid fishes, 2) how differences in the ontogeny of superficial neuromasts (SNs) and CNs (re: size, shape, number) and the physiological orientation of their sensory hair cells may reveal their origins in one or more LL primordia, given what is known about the correlation of the physiological orientation of hair cells in neuromasts with different primordial origins in zebrafish (*Danio rerio*). Funded NSF grant IOS-0843307 to JFW.

0500 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

Nicholas Wegner

NOAA Fisheries, La Jolla, CA, USA

The Elasmobranch Gill: A Window into Evolution and Physiology

Due to its multiple functions in respiration, osmoregulation, pH balance, and nitrogenous waste excretion, many comparative physiologists consider the fish gill one of the most complex animal organs. Although the functional unit of the fish gill (the gill filament) has remained structurally and functionally intact throughout the course of fish

evolution and diversification from lampreys to teleosts, the elasmobranch gill has a number of largely unique features. Perhaps most notably is the connection of the gill filaments to interbranchial septa, which affects not only the flow of water through the gills, but may provide specific advantages and disadvantages to elasmobranch respiration. Thus, in many ways, the elasmobranch gill provides unique insight into the evolutionary factors that sculpt gill morphology and function. Because many elasmobranchs (and other fish groups) are large, live in remote or inaccessible habitats, and/or have high activity levels, direct physiological studies conducted in the laboratory or under controlled conditions may not be feasible. For such groups, examination of branchial morphology can provide significant insight into metabolic requirements and other important aspects of a species physiology.

0504 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Nicholas Wegner, John Hyde

NOAA Fisheries, La Jolla, CA, USA

Sustainable Swimming Speed and Metabolic Rate as Indicators of Fitness in Aquaculture-Raised California Yellowtail, *Seriola dorsalis*

In order to assess the health and fitness of juvenile aquaculture-reared California yellowtail, *Seriola dorsalis*, maximum sustainable swimming speed (U_{crit}) and oxygen consumption (Mo_2) were determined in comparison to wild-caught individuals using a variable speed swim tunnel respirometer. Wild-caught yellowtail were capable of swimming over one body length per second faster than aquaculture reared fish (6.72 ± 0.72 FL/s vs. 5.30 ± 0.89 FL/s). In addition, extrapolation of oxygen consumption over a range of swimming speeds revealed that the standard metabolic rate of wild-caught yellowtail (5.51 ± 1.33 mgO₂ min⁻¹ kg⁻¹ at 18°C) was approximately 30% lower than that of aquaculture-reared fish (7.75 ± 1.48 mgO₂ min⁻¹ kg⁻¹). Both slower swimming speeds and higher oxygen requirements indicate the reduced fitness of yellowtail reared in captivity. We hypothesize that rearing young juveniles under constant flow regimes to force continuous swimming may increase their health and fitness. An increase in the fitness of aquaculture-reared yellowtail (and associated reduction in metabolic demand), could substantially decrease rearing costs.

0229 Fish Ecology I, Carson 3, Sunday 19 July 2015

Stuart Welsh¹, Joni Aldinger²

¹West Virginia Cooperative Fish and Wildlife Research Unit, Morgantown, WV, USA,

²West Virginia University, Morgantown, WV, USA

Periodicity and Timing of Upstream Migration of Yellow-phase American Eels, Potomac River Drainage, USA

The American Eel (*Anguilla rostrata*) is a migratory species of ecological and economic importance, as well as a species of conservation concern. While studies have examined upstream migration of nocturnal yellow-phase American Eels, little is known about the diel periodicity of upstream migration. For example, although American Eels are active during low light conditions, few studies have examined the periodicity and chronology of upstream movements relative to time of night. Using American Eel passage data (2008-2014) from an eel ladder on the Shenandoah River, we found chronological patterns in the timing of upstream migration. Most eels (98%) used the ladder at night, between sunset and sunrise. The majority (69%) of individuals passed through the ladder closer to sunrise than sunset across all dates. The modal passage time (29%) was two hours before sunrise. Further research will focus on the association of movement patterns with environmental variables, including lunar illumination and river discharge.

0180 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Thursday 16 July 2015

Rachel Welt, Christopher Raxworthy

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

The Cryptic Diversity of Madagascar's Ground Gecko (Genus: *Paroedura*)

Paroedura (Madagascar's ground gecko), a genus of nocturnal gecko found on the islands of Madagascar and the neighboring Comoro archipelago, has experienced many taxonomic changes in the recent literature. Due to the highly cryptic nature of this genus, several new species of *Paroedura* have been described based on molecular analyses, and/or surveys of isolated habitats. Here we apply molecular and GIS techniques to a widely distributed sample of *Paroedura* to uncover cryptic diversity. We begin with preliminary species delimitations of several *Paroedura* groups to reveal potential independently evolving lineages. We then estimate population genetic parameters to describe the overall structure existing between candidate new species. Finally, we assess these findings within a geographical framework to determine if these independently evolving lineages are located in distinct or isolated habitats, such that niche specialization or barriers to gene flow might maintain the independent evolutionary trajectories of these lineages. Our analyses to date have uncovered high levels of cryptic diversity. Preliminary species delimitations of four currently recognized *Paroedura* species recovered 30 distinct lineages based on the substitution rate of the

barcoding gene, Cytochrome Oxidase I. A continuation of these analyses incorporating additional markers, as well as geographic and ecological information of these candidate species will allow for a validation of species limits within *Paroedura*, as well as an assessment of the conservation threats to this unique, diverse group.

0589 General Ichthyology I, Crystal 3 & 4, Friday 17 July 2015

Michael Westphal¹, Michael Izumiyama², Gary Longo³, Karen Crow², Giacomo Bernardi³, Ken Oda⁴, Steve Morey⁵

¹US Bureau of Land Management, Hollister, CA, USA, ²San Francisco State University, San Francisco, CA, USA, ³University of California Santa Cruz, Santa Cruz, CA, USA, ⁴California Department of Fish and Wildlife, Monterey, CA, USA, ⁵US Fish and Wildlife Service, Portland, OR, USA

Life History of the Livebearing Calico Surfperch, *Amphistichus koelzi* (Teleostei: Embiotocidae)

The calico surfperch, *Amphistichus koelzi*, is a sister species to two economically important gamefish, the barred surfperch (*A. argenteus*) and redbelt surfperch (*A. rhodoterus*). *A. koelzi* widely overlaps the other two amphistichine species in range, exists in close sympatry with them at the microhabitat scale and is roughly the same size. Whereas its sister amphistichines have received attention from ecologists, virtually no data has been published on *A. koelzi*. Here we present new data on the life history of *A. koelzi* in a comparative framework to examine the apparent paradox of how closely related species with such apparent similarities in feeding ecology can so intimately coexist.

0472 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Michael Westphal¹, Dustin Wood², Jonathan Richmond², Bradford Hollingsworth³, Robert Fisher², Amy Vandergast²

¹US Bureau of Land Management, Hollister, CA, USA, ²US Geological Survey, San Diego, CA, USA, ³San Diego Natural History Museum, San Diego, CA, USA

A Secretive Snake in a Secret Desert: Molecular Genetics of the California Glossy Snake, *Arizona elegans occidentalis* in the San Joaquin Desert of Central California

The San Joaquin Desert is a newly-named biotic community of the southern Central Valley of California known for its endemic and endangered fauna. The California glossy snake, *Arizona elegans occidentalis*, occupies a narrow strip of relict habitat along the western edge of the San Joaquin Valley and is thus subject to habitat fragmentation from ongoing agricultural conversion. To better understand the within-species population

structure of this species we collected tissue from individuals from across their known range within the San Joaquin Valley and adjacent foothill valleys, as well as individuals from throughout the range in Southern California. We sequenced two mitochondrial loci [NADH4, NADH1] and reconstructed a tree showing relatedness of populations encompassing the range of currently recognized subspecies in Southern California. Similar to other desert species that show significant population subdivision across the same landscape, we recovered genetic breaks among two major clades: Mojave/San Joaquin Desert clade and a Sonoran Desert Clade. These clades appear to contact one another along the western portion of the Mojave/Sonoran ecotone and therefore contrast with the currently recognized subspecies within Southern California. The California Glossy snake therefore appears to be restricted to the northern deserts, rather than extending southward in to Baja California. Throughout this restricted distribution the subspecies is subject to increasing habitat conversion from agriculture and renewable energy development. Future work will focus on fine-scale population differentiation and contemporary gene flow in order to provide for the preservation and long-term viability of the subspecies.

0575 AES Conservation & Management, Carson 2, Thursday 16 July 2015

Bradley Wetherbee¹, Michael Byrne⁵, Jeremy Vaudo², Guy Harvey³, Mahmood Shivji⁴

¹University of Rhode Island, Kingston, RI, USA, ²Guy Harvey Research Institute, Ft Lauderdale, FL, USA, ³Guy Harvey Ocean Foundation, Ft Lauderdale, FL, USA, ⁴Save Our Seas Foundation Shark Center, Ft Lauderdale, FL, USA, ⁵Warnell School of Forestry and Natural Resources University of Georgia, Athens, GA, USA

Orientation of Mako Sharks (*Isurus oxyrinchus*) to Environmental Conditions in the Open Ocean

Mako sharks (*Isurus oxyrinchus*) are frequently captured in long line fisheries and are heavily targeted by recreational anglers in many parts of the world. Given the fishing pressure on mako shark populations there is a great deal of interest in management of their stocks. However, information about movements and migrations of mako sharks that would enable comprehensive understanding of interactions with fisheries and delineation of distribution patterns in waters under the jurisdiction of numerous countries is sparse. We tagged 45 mako sharks with satellite transmitters and tracked their movements over the span of several years. A state space model was used to construct continuous tracks for sharks and to categorize their locations into two behavioral states - searching and transiting. Remote sensing databases were used to determine environmental conditions of sea surface temperature, chlorophyll, productivity, upwelling and frontal index at each location and values in areas searched were compared with those for locations when sharks were transiting. Environmental conditions of specific water temperature and productivity were associated with the searching behavioral mode indicating that mako sharks orient towards a specific set of water conditions for presumably engaging in foraging behavior.

0024 Poster Session I, Reno Ballroom & Tahoe Room, Friday 17 July 2015

John Whalen, Jim Gelsleichter

University of North Florida, Jacksonville, FL, USA

Multibiomarker Evaluation of Pollutant Effects in Atlantic Stingray (*Dasyatis sabina*) Populations in Florida's St. Johns River

The goal of this study was to examine the potential health effects of polychlorinated biphenyl (PCB) and polycyclic aromatic hydrocarbon (PAH) exposure on Atlantic stingray (*Dasyatis sabina*) populations in Florida's St. Johns River (SJR). Special emphasis was placed on identifying PAH- and/or PCB-related effects in stingrays from areas of the lower SJR basin that have been shown to possess elevated levels of these compounds, as well as characterizing baseline levels of pollutant exposure in other areas that may be subjected to dredging in the near future, potentially resuspending contaminated sediments and increasing pollutant associated effects. To accomplish this, we measured PCB and PAH biomarker levels in *D. sabina* collected from contaminated sites and reference locations. Animals were collected using seine nets and trotlines. We specifically examined the biomarkers cytochrome P4501a1 (CYP1a1), a Phase I detoxification enzyme; Glutathione-S-Transferase (GST), a Phase II detoxification enzyme; and fluorescent aromatic compounds (FACs), PAH bile metabolites. Enzymatic activity of CYP1a1 and GST was measured using the EROD assay and a commercially available GST Assay Kit, whereas FACs were measured using fixed wavelength fluorescence. Biomarker levels of individuals collected from contaminated sites were compared to individuals collected from reference sites. Previous research in our lab has detected elevated biomarker levels in *D. sabina* and bony fish from known contaminated areas in the St. Johns River. Expecting parallel results, we anticipate that the pollutants in the St. Johns River are negatively affecting *D. sabina*, and that dredging has the possibility to create a broader source of contamination.

0023 AES Morphology & Physiology, Carson 2, Sunday 19 July 2015

John Whalen¹, Jim Gelsleichter¹, Dean Grubbs²

¹*University of North Florida, Jacksonville, FL, USA*, ²*Florida State University Coastal and Marine Laboratory, St. Teresa, FL, USA*

Using DNA Adducts to Examine Polycyclic Aromatic Hydrocarbon Exposure in Shark Populations Affected by the Deepwater Horizon Oil Spill

The Deepwater Horizon oil spill (DWH) released 5 million barrels of crude oil into the Gulf of Mexico (GOM) between April and July of 2010, posing significant health risks to deepwater shark species because of the high concentration of oil and its most toxic components, polycyclic aromatic hydrocarbons (PAHs). Exposure to PAHs results in

increased expression of metabolic enzymes necessary for the biotransformation and excretion of these compounds. Occasionally, metabolites resulting from this process can bind to DNA, forming adducts and creating the potential for mutagenic effects. The objective of this study was to determine if increased PAH-DNA adduct formation occurred in two abundant and ecologically important Gulf of Mexico shark species: *Squalus cf. mitsukurii* and *Centrophorus granulosus*. Animals were collected using demersal long lines from the Northeast GOM at varying distances from the origin of the DWH in 2011 and 2014. The presence of DNA adducts was determined in peripheral blood cells using immunofluorescence. Adduct formation was examined in relation to relative levels of oil exposure. A total of 52.5% of individuals examined possessed DNA adducts, ranging from 0 to 19 per 500 cells. The proportion of *C. granulosus* with adducted cells increased from 0.273 to 0.875 while the proportion of *S. mitsukurii* remained constant at 0.571, suggesting possible oil-related effects in the former. This is the first study to examine and detect the presence of PAH-DNA adducts in sharks, suggesting that they may provide a useful tool for assessing PAH effects in these fishes.

0330 AES GRUBER AWARD, Carson 2, Friday 17 July 2015

Connor White¹, Yukun Lin², Jerry Hsiung², Christopher Clark², Christopher Lowe¹

¹California State University Long Beach, Long Beach, CA, USA, ²Harvey Mudd College, Claremont, CA, USA

Habitat Selection of the Leopard Shark, *Triakis semifasciata*, Using Fine Spatio-Temporal Movement and Temperature Data

Environmental conditions are largely considered to be drivers of elasmobranch movements and behaviors. However, conditions are in constant flux and can be highly variable over small spatial extents. Thus to understand how individuals interact with surrounding environmental conditions, researchers must be able to measure the movements of individuals and environmental conditions at high spatio-temporal resolutions. We developed an autonomous underwater vehicle (AUV) designed to actively track an acoustically tagged elasmobranch, providing better spatial accuracy than a human (AUV: 6.1 ± 4.8 m, Researcher: 16.6 ± 9.7 m, $F = 31.1$, $p = 0.005$), while generating significantly more localizations (AUV: 45.2 ± 10.5 detection/min, Researcher: 12.2 ± 9.1 detections/min, $t_{2,41} = 3.96$, $p = 0.04$). These positions were further refined by integrating magnetic heading of the animal provided by animal-borne inertial measurement units (IMU). Using this system 5 leopard sharks were tracked in Big Fisherman's Cove (BFC), Catalina Island. Seafloor temperature was collected every 5 min from 20 locations in the cove to derive interpolated temperature maps. Comparing the fine-scale shark movements with the fine-scale temperatures availability in the cove, showed leopard sharks disproportionately utilized warmer areas of the cove ($\chi^2 = 432.3$, $p < 0.001$). By utilizing tools that provide fine-scale information on the movement and behaviors of animals, researchers will be able to begin to tease apart how elasmobranchs

interact with their environment, and ultimately, how these interactions structure the distributions of species.

0215 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Macaulay White

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

The Impact of a Variable Marine Larval Stage on the Extent of Endemism in a Group of Amphidromous Fishes from Indonesia (Gobiidae: Sicydiinae: *Stiphodon*)

Sicydiine gobies are a diverse group of fishes belonging to the family Gobiidae. They inhabit rivers on oceanic islands and are highly adapted for island living due to their amphidromous life history (adults spawn in freshwater and larvae are carried to the open ocean to feed, grow, and later return to freshwater). Oftentimes, freshwater gobies make up the only native fish fauna in island streams. The subfamily Sicydiinae currently consists of nine genera and the genus *Stiphodon* exhibits the most diversity and is found throughout the Indo-Pacific. Many species of *Stiphodon* have very large distributional ranges, while others are found only in localized regions. Because of the high levels of endemism in *Stiphodon*, they are threatened by habitat destruction due to deforestation, mining, and damming of rivers. It is currently unclear as to why *Stiphodon* species have such varying distributional ranges. Otolith microchemistry analysis can aid in determining if all individuals go to sea as larvae. This variation in the percent of individuals traveling to the sea may influence dispersal capabilities, which may ultimately dictate the geographic range size for a given species. This study will be helpful in understanding the amphidromous life history of *Stiphodon* and whether or not there are a percentage of individuals that do not spend time in the marine environment. This information is critical for understanding the mechanisms that promote endemism, and thus is vital data for managing and conserving island stream gobies that may be at risk of local and global extinction.

0264 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

Mary White

Southeastern Louisiana University, Hammond, LA, USA

Developmental Macromutations and the "Hopeful Monster"

Donn Rosen's 1985 list of assumptions that inhibit scientific progress in comparative biology includes, "Goldschmidt's ideas must be wrong because they conflict with

neodarwinism.” Richard Goldschmidt proposed two very different ideas to explain the leap from microevolution to macroevolution. His first idea rejected the classical gene model and argued for what he termed “systemic mutations” such as chromosomal rearrangements to give variation for macroevolution. His forceful defense of this scenario often overshadowed his proposal suggesting that “developmental macromutations” might be an important agent of evolution at the level of speciation. While neoDarwinists were focusing on accumulation of small mutations over long periods of time, Goldschmidt recognized that mutations in controlling genes early in developmental pathways could lead to large-scale body plan alterations. Current research in evolutionary developmental biology, including the importance of regulatory genes such as hox genes in formation of body pattern, supports the idea that “hopeful monsters” may exist after all.

0102 AES Integrative Elasmobranch Biology Symposium, Carson 2, Saturday 18 July 2015

Lisa B. Whitenack¹, Matthew Kolmann²

¹Allegheny College, Meadville, PA, USA, ²University of Toronto, Toronto, Ontario, Canada

Integrative Chondrichthyan Paleobiology: The Present is the Key to the Past

The chondrichthyan fossil record is composed primarily of teeth, though occasionally other body parts are preserved. This often translates into using fossils for studying taxonomy, biostratigraphy, paleoecology, and evolutionary history. Studies that integrate across disciplines are few, and those that do tend to utilize extant taxa. We will discuss those studies that have used integrative techniques, focusing on the use of fossil teeth to understand chondrichthyan evolution in a broad sense. We then will examine trends in tooth morphology coincident with trends in prey availability across geological time. Finally, we will identify holes in our knowledge of chondrichthyan evolution and look forward to how integrative techniques can help us explore this topic.

0413 Herp Conservation I, Carson 1, Saturday 18 July 2015

Steven Whitfield¹, Gilbert Alvarado², Juan Abarca², Hector Zumbado², Adrian Pinto², Valerie McKenzie⁴, Jacob Kerby³

¹Gonzaga University, Spokane, WA, USA, ²Universidad de Costa Rica, San Pedro, Costa Rica, ³University of South Dakota, Vermillion, SD, USA, ⁴University of Colorado - Boulder, Boulder, CO, USA

Enigmatic Survival Follows Enigmatic Decline: Conservation Ecology of Presumed Extinct Amphibians in Costa Rica

Approximately 41% of the world's amphibian species are threatened with extinction, and species in tropical regions are disproportionately threatened with extinction. Anthropogenic factors associated with apparent extinctions and mass mortality events have been contentious for decades, and have largely diverged on interpretations of whether a single anthropogenic stressor (emergence of the amphibian chytrid fungus, *Batrachochytrium dendrobatidis* "Bd") or multiple anthropogenic stressors (interactions among Bd and climate, Bd and contaminants, Bd and other emerging infectious diseases) have driven population declines and/or extinctions. Here, we summarize evidence that amphibian species from Central America that are widely perceived to be globally extinct are instead persistent in small, fragile "relict populations" that comprise the last known living individuals of their species. We show that while the extinction of these species is presumably driven by the emergence Bd, all relict populations co-exist with Bd, and we evaluate evidence for the disparate adaptive strategies of tolerance or resistance to infection by Bd among species. We explore evidence that resistance or tolerance to Bd is driven by cutaneous microbial symbionts as a primary line of immune defense, and interpret these results in the context of potential probiotic supplementation programs for amphibian populations vulnerable to Bd emergence elsewhere. Finally, we demonstrate that while controversy lingers over a single-stressor versus multiple stressor causality of amphibian declines, we show that restoration of threatened amphibian will require a detailed understanding of the multiple stressor environment in which relict amphibian populations now survive.

0595 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Brigid Wieman¹, Peter Berendzen²

¹University of Arkansas, Fayetteville, AR, USA, ²University of Northern Iowa, Cedar Falls, IA, USA

Conservation Genetics and Habitat Associations of *Rhinichthys cataractae*: a Fish of Conservation Need in Iowa

A pressing issue in conservation is to assess demographic and population genetic patterns of species of conservation concern and elucidate the cause of these signatures. *Rhinichthys cataractae*, the longnose dace, is a fish species of greatest conservation need

listed in the Iowa Wildlife Action Plan. Within Iowa, the distribution of longnose dace is primarily isolated to four drainages in the northeastern portion of the state. This distribution largely coincides with the Paleozoic plateau landform region which was not glaciated during the last glacial maximum. The aim of this study was to use habitat, genetic and GIS data to elucidate the demographic patterns of this species and the environmental factors impacting its distribution and population structure in Iowa. Multiple sites within each of the four drainages were sampled for habitat and genetic data. Landscape level variables were obtained with GIS techniques and an ecological niche model (ENM) was constructed with these data to predict habitat and environmental variables influencing suitability of habitat for *R. cataractae*. The ENM indicated that geologic factors (e.g., geologic history, depth to bedrock) likely play a key role in determining the distribution and abundance of *R. cataractae* in Iowa. Population genetic analyses of 7 microsatellite loci revealed two distinct, but somewhat admixed genetic populations corresponding with a signature of isolation by distance (IBD) and possessing moderate to high levels of intra-group diversity. These results suggest that IBD, historical processes, and underlying geology are primarily responsible for the genetic and distributional patterns of *R. cataractae* in Iowa.

**0087 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD,
Carson 1, Friday 17 July 2015**

Kristoffer H. Wild, C.M. Gienger

Austin Peay State University, Clarksville, TN, USA

Fire-altered Landscapes Influence Locomotor Performance of Eastern Fence Lizards

Habitat disturbance through fire plays a key role in shaping the biodiversity of forest communities in the Southeastern US. Prescribed burns are an essential management technique used to help maintain the persistence of oak-hickory savanna, an early seral stage vegetative community. *Sceloporus undulatus* is a sexually dimorphic forest lizard that is relatively common throughout the eastern US, which makes it well-suited for studying the effects of fire-altered landscapes on lizard ecology. Our objective is to quantify the effect of fire-altered landscapes on *S. undulatus* locomotor performance. We compared performances of lizards from habitats with three different known fire histories; a control habitat, which had not experienced fire in more than 60 years, a recovering burn habitat that has not experienced fire in four years, and a recent burn habitat that was burned three months prior to the study. There were significant differences in locomotor performance among lizards from the different habitats, and lizards in the recent burn habitat had significantly faster maximum sprint speeds than lizards in recovering and control habitats. Understanding how performance of *S. undulatus* is influenced by fire-altered habitats is essential for assessing the effect of human activities (e.g. prescribed fire) on wildlife. Such data are crucial for implementing conservation and management strategies for similar organisms in fire managed landscapes.

0175 Donn Rosen and the Assumptions Symposium I, Crystal 3 & 4, Saturday 18 July 2015

E. O. Wiley

University of Kansas, Lawrence, KS, USA

Species Concepts

Macroevolution in the age of phylogenetic systematics is precisely the dynamics of speciation and extinction. What we recognize as the products of speciation depends on finding the best species concept that is consistent with what we understand to be the various ways species can form (that is, speciation) and how we understand the relationships among species as reflected in genealogical history (phylogeny). The evolutionary species concept, formulated by an opponent of phylogenetics, G. G. Simpson, turns out to be consistent with Hennig's understanding of the nature of species and with the nature of phylogenetic trees as we presently understand them. That is: species are lineages and individuals and the effect of speciation through time is a phylogenetic tree that may be at least partly discovered using phylogenetic techniques. All other species concepts are either synonyms of the evolutionary species concept or concepts about how one might discover a species. For example, Donn Rosen's concept that a species is a population or group of populations defined by one or more apomorphous feature is not a species concept per se but Donn's method of discovering species. He seemed to be pretty good at it and along the way exposed weaknesses in the biological species concept.

0282 Fish Ecology II, Carson 3, Sunday 19 July 2015

Jonathan P. Williams, Daniel J. Pondella II, Jeremy T. Claisse

Biology Department and Vantuna Research Group, Moore Laboratory of Zoology, Occidental College, Los Angeles, CA, USA

Kelp Forest Fish Communities at San Clemente Island, California

San Clemente Island, the southernmost of California's Channel Islands, is located approximately 85 km from the Ports of Los Angeles and Long Beach, and approximately 100 km from Mission Bay and San Diego Bay. The 150-km² island is owned, operated, and occupied entirely by the United States Navy and is an active naval warfare training and ship-to-shore live firing area. Due to the frequent use of nearshore waters for military training and live fire exercises, much of the kelp forest/rocky reef area surrounding the island is closed to commercial and recreational fishing on either a temporary or permanent basis. The distant location from urban areas, combined with entry restrictions for non-military vessels and personnel, creates a unique opportunity to examine reduced and relative levels of fishing pressure around the island where

restrictions are based solely on when any of the eight “Safety Zones” are in use by the Navy. This study looks at the community and size structure characteristics of kelp forest/rocky reef fishes at San Clemente Island using data from scuba surveys (to 30 m depth) at 17 sites from 2004-2013, and compares those results among Safety Zones as well as other island and mainland sites in the Southern California Bight.

0198 Fish Genetics, Carson 3, Saturday 18 July 2015

Stuart Willis, Christopher Hollenbeck, Jonathon Puritz, David Portnoy, John Gold

Marine Genomics Lab, Harte Research Institute, Dept. Life Sciences, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA

Identifying Recruitment Patterns Among Silk Snapper (*Lutjanus vivanus*) off the West Coast of Puerto Rico: Challenges and Solutions with Using ddRADseq-based Single Nucleotide Polymorphisms

Silk snapper (*Lutjanus vivanus*) represent a major fishery along the west coast of Puerto Rico that is overexploited and at risk of collapse. One of the major issues facing the fishery is whether recruitment patterns are predictable and whether some areas serve to supplement the fishery more than others. We are using a genetic approach to assess whether recruitment across the region is random across fishing sites or correlated with geographic proximity and mediated by current patterns. Settling larvae also may experience habitat-specific selective regimes that produce non-random, predictable patterns of recruitment. To address these questions, we tested stability (homogeneity) in genetic variance of recruits among sites, among years, and within years by using a ddRAD approach to generate single nucleotide polymorphisms (SNPs) among samples of age-0 and adult silk snapper from Puerto Rico. We identified a few small but significant genetic differences among fish sampled at different sites or in different years. We also found that at low levels of genetic divergence, library-generation artifacts potentially confound biological signal, particularly with reference SNP loci built *de novo* from the same short-read data. We discuss approaches for circumventing this bias. We also show that generating haplotypes in contiguous RAD sequences can avoid signal bias without loss of information content. Using haplotypes also enables filtering of paralogous loci and genotyping errors based on the expected number of haplotypes per individual.

0514 Herp Conservation I, Carson 1, Saturday 18 July 2015

John Willson¹, Jacquelyn Guzy¹, William Hopkins²

¹University of Arkansas, Fayetteville, AR, USA, ²Virginia Tech, Blacksburg, VA, USA

Influence of Landcover, Spatial Configuration, and Species Life-history on Amphibian Abundance and Productivity in Fragmented Landscapes

Although inter-wetland dispersal is thought to play an important role in regional persistence of pond-breeding amphibians, few studies have modeled the dynamics of amphibians inhabiting multi-wetland networks. Previously, we used a stochastic structured metapopulation model to demonstrate that spatial configuration of wetland networks within a homogeneous landscape was important in driving source-sink dynamics and landscape-scale productivity of pond-breeding anurans. Here, we extend this analysis to consider how loss of forested upland habitat interacts with spatial configuration of wetlands to influence amphibian population density and productivity. Specifically, we modified our model to incorporate reduced movement distance and behavioral avoidance of non-forested habitats by dispersing juveniles and loss of critical upland habitat for adults. We parametrized models to represent the contrasting life-histories of a terrestrial anuran (*Anaxyrus* sp.) and a pond-breeding salamander (*Ambystoma* sp.) and conducted simulations evaluating the effects of increasing inter-wetland distance and decreasing forest cover on adult population size and annual metamorph production. We found that decreasing the proportion of forested upland habitat decreased the inter-wetland distance at which maximal productivity was observed, but that this optimal distance varied strongly among species. *Anaxyrus*, which was characterized by high vagility and fecundity, benefitted from close spacing of wetlands and was relatively resilient to forest loss. *Ambystoma*, conversely, displayed a much narrower range of optimal distances and was strongly affected by forest loss. Our results have implications for understanding regional dynamics and productivity of pond-breeding amphibians and for maximizing the efficacy of restoration activities such as re-forestation and wetland creation.

0022 Chemical Ecology Symposium, Crystal 3 & 4, Sunday 19 July 2015

Natasha Wilson¹, Edmund Brodie, Jr², Craig Williams¹

¹University of South Australia, Adelaide, South Australia, Australia, ²Utah State University, Logan, UT, USA

The Role of Toxin Tolerance in Predator-prey Relationships Between Freshwater Crustaceans and Amphibians

Freshwater invertebrates reportedly consume toxic amphibians with little or no ill effects. In this research we aimed to identify common invertebrate predators of amphibians in Australia, to determine levels of toxin tolerance, and understand how this tolerance may have evolved. Field collections and laboratory experiments revealed that

freshwater crayfish are a major predator of native frog eggs and tadpoles. Literature analysis revealed that freshwater crayfish from both superfamilies are tolerant of a range of toxic amphibians, suggestive that toxin tolerance may be a primitive trait in these predators. To explore this, the ability of crayfish from both Australia and North America to consume toxic amphibians was assessed. Studies of Australian freshwater crayfish revealed that they were able to consume toxic cane toad (*Rhinella marina*) eggs and tadpoles. However, dose response experiments revealed that these animals lack cellular-level resistance to bufotoxins and bufadienolides. The capacity of North American crayfish to tolerate tetrodotoxin (TTX) was also investigated by studying predation of toxic newt *Taricha granulosa* eggs, and via intramuscular injection of toxin. Once again, whilst crayfish were capable consumers of highly toxic newt eggs they did not demonstrate cellular-level resistance to TTX. These findings suggest that crayfish have some functional (organismal-level) resistance that renders them capable of consuming toxic prey despite a lack of cellular resistance to these amphibian toxins. Demonstration of this functional resistance in crayfish on two continents is suggestive of it being a basal trait acquired early in crayfish diversification.

0599 Herp Ecology, Carson 4, Saturday 18 July 2015

Kevin Wiseman, Ronald Jackman, Joseph Drennan, Karla Marlow, Ian Chan
Garcia and Associates, San Francisco, CA, USA

Feeding Ecology of the Sierra Garter Snake (*Thamnophis couchii*) from the North Fork Feather River, California

We studied the feeding ecology of the Sierra garter snake (*Thamnophis couchii*) from three regulated reaches of the North Fork Feather River, California, during field surveys conducted annually from 2002-2014 focused on river-breeding foothill yellow-legged frogs (*Rana boylei*). Prey items were primarily obtained from palpation of live snakes in the field supplemented by the examination of museum specimens. A total of 739 snakes were observed during 4,359 person-hours surveying, including 262 snakes that were palpated, yielding 131 prey from 77 snakes. Sixty-six percent of prey were fish and 44% were amphibians in relative frequency, however amphibians, especially *Rana boylei*, were the most important prey taxa in terms of biomass. Relative prey mass values averaged 0.16 (range= 0.01-0.53; n=32) and larger snakes continued to eat relatively small prey items. The most frequent prey item taken in our study was the smallmouth bass, demonstrating the capability of a dietary shift to invasive prey as observed in other species of *Thamnophis*.

0442 Herp Systematics & Genetics, Carson 4, Saturday 18 July 2015

Guinevere Wogan

UC Berkeley, Berkeley, CA, USA

Model Selection, Partitioning Schemes, and Phylogenetic Informativeness: A Case Study from the Dicroglossidae (Amphibia:Anura)

Partitioning schemes and model selection can have dramatic impact on phylogenetic inference, with partitioning affecting tree topology, branch lengths, and support estimates. In this study I use a multi-locus dataset for the Old World frog family Dicroglossidae to first evaluate model adequacy using simulations and the multinomial likelihood statistic (Tx). I then assess the impact of model selection and partitioning schemes on phylogenetic informativeness (PI), tree topology, and a series of tree-based statistics (tree length, tree height, symmetry, and treeness). I found that for several loci, the selected models of nucleotide substitution were not adequately able to model the empirical data adequately. Phylogenetic informativeness was greatly impacted by partitioning scheme, with un-partitioned analyses possessing low values of PI, and Bayesian estimates possessing higher levels of PI relative to Maximum likelihood estimates. I also found that PI was highest for simpler models with gene rather than gene/codon codon partitioning. While tree topology remained statistically congruent across partitioning schemes, there was topological variation in accord with partitioning and model selection choices. The family Dicroglossidae was recovered as monophyletic in all analyses as were the two subfamilies Occidozyginae and Dicroglossinae. Within Dicroglossinae, multiple genera were recovered as paraphyletic, suggesting that additional work is needed to fully resolve the evolutionary history of the lineages within this group of frogs.

0124 ASIH STOYE AWARD CONSERVATION, Carson 4, Thursday 16 July 2015

Zachary Wolf, Rebecca Blanton

Austin Peay State University, Clarksville, TN, USA

Conservation Status and Phylogeography of the Tennessee-endemic Egg-mimic Darter (*Etheostoma pseudovulatum*)

Restricted to two counties in the Duck River system of Tennessee, *Etheostoma pseudovulatum* is state endangered and has been petitioned for federal listing. In addition to its small range, the mainstem Duck River may act as a barrier isolating smaller tributary populations. Despite this, little is known about the species and a recent status survey has not been conducted. Thus, objectives were to describe the current status, habitat use, and genetic diversity of *E. pseudovulatum*. To evaluate its current status, historical localities were sampled using standard seining techniques to assess presence and estimate abundance using the Petersen method. Microhabitat variables were

measured and analyzed for association with *E. pseudovulatum* presence, and range-wide genetic diversity was examined using the mitochondrial ND2 gene. *Etheostoma pseudovulatum* was present at all 25 historical localities sampled and abundance estimates ranged from 5 to 258 individuals per locality, comparable to those observed historically. The species was associated with pools and presence of root wads. Nine haplotypes were detected, including one haplotype shared across five of the six tributaries. One tributary, Beaverdam Creek, had a unique haplotype assemblage. Haplotypes were recovered in two clades: 1) Beaverdam Creek, and 2) the other five tributary populations. These results suggest recent gene flow among all tributaries except Beaverdam Creek, which has potentially been isolated. Overall, the species was locally abundant and appears stable, however future management efforts should monitor the species with special focus on smaller tributaries, which had the lowest abundances, and the genetically distinct Beaverdam Creek population.

0312 Lightning Talks, Crystal 1 & 2, Friday 17 July 2015

Calvin Won, Larry Allen

California State University, Northridge, Northridge, CA, USA

Spatial Characterization of Barred Sand Bass Spawning Aggregations Using Active Acoustic Technology

Spawning aggregations have long been essential to commercial and recreational fish harvest around the world. Predictability of aggregations in both time and space allows for plentiful yield with relatively low fishing effort. However, this places certain species at risk of overharvest. One such species, the Barred Sand Bass (*Paralabrax nebulifer*), has been shown to be exhibiting the characteristics of an aggregation-based fishery that is on the verge of collapse, as annual catch estimates have shown a greater than 90% decrease in the last decade. Population declines of aggregation-based fisheries have a tendency of going unnoticed, as fishery-dependent stock assessments do not generally account for spatio-temporal variability. This phenomenon is known as hyperstability. The present study aims to investigate the spatial and temporal dynamics of spawning in the Barred Sand Bass at Huntington Flats, California. Preliminary transect surveys were conducted using split-beam SONAR to examine spatial and temporal variability of spawning aggregations in relation to environmental factors (e.g., temperature, thermocline, lunar phase). The objective was to identify any environmental factors that would aid in the predictability of aggregating behaviors. However, spawning activity during the summer of 2014 appeared to be minimal and is mostly likely explained by environmental conditions associated with El Niño Southern Oscillation. Future plans will take an ethological approach to reproductive behaviors using videography on SCUBA.

0451 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Kirsten Work, Missy Gibbs, Vanessa Rubio, Cliff Bryan

Stetson University, DeLand, FL, USA

Abundant Feces from an Exotic Armored Catfish, *Pterygoplichthys disjunctivus*, Create Nutrient Hotspots in a Florida Spring

Over the past 15 years, *Pterygoplichthys disjunctivus* has colonized many Florida systems, including Volusia Blue Spring. Unlike any other species in the spring run, *Pterygoplichthys disjunctivus* grazing repackages periphyton with sand into a fecal structure that remains relatively intact in the spring. Not only does *P. disjunctivus* produce copious feces, but the fecal persistence allows the feces to contribute to nutrient loading when the fish are not present. What, then, is the effect of this nutrient loading on the spring ecosystem? We surveyed the spring run to assess fecal abundance, analyzed fecal samples from live fish and from the substrate for nutrient content, and conducted flume experiments to measure nutrient content of leachate. We found that feces were abundant in the spring and, although each sample leached minute quantities of nutrients (NO₃⁻, TKN, SRP), the total quantity of nutrients released from local accumulations of feces was substantial. Our results suggest that leachate from *P. disjunctivus* fecal deposition could create transient biogeochemical hotspots lasting longer than those described for excreta, and thus it is likely that it alters nutrient cycling in this spring system significantly.

0156 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Bryenna Workman¹, Callahan Clarke¹, Melissa Gall², Paul Hampton¹

¹Colorado Mesa University, Grand Junction, CO, USA, ²Carroll University, Waukesha, WI, USA

Single Large or Several Small: Prey Size Selection and Its Effect on Terrestrial Locomotion of Ribbon Snakes

It has been suggested that extra weight in the form of carrying offspring or ingested meals may reduce locomotor performance in snakes. In general, colubrids move by serpentine locomotion, creating lateral undulations and using push-points in their environment. Consequently, a rigid prey item may confound the adverse effects of a meal on locomotion by limiting the maneuverability. We hypothesized that consumption of several small fish will have less hindered movement of the spinal column compared to a single large fish. We chose western ribbon snakes (*Thamnophis proximus*) as our study species. This is a slender snake that depends upon speed to avoid predation. Ribbon snakes were fed meals approximately 20% of the snake's mass. The large meal treatment was a single fish that was approximately 20% of the snake's mass. For the several small treatment, snakes were offered four fish that were each approximately 5% of the snakes size, thus totaling an equivalent meal size. After

feeding, individuals were video-recorded while crawling through a track with push-points. Using Logger Pro, a motion-analysis program, we determined the maximum velocity and we used Image J to determine the amplitude and angle of spinal flexion from the fastest trial for each snake. Preliminary results suggest that meal type had no impact on maximum velocity, amplitude or spinal flexion.

0613 Plenary, Carson 1, 2 & 3, Thursday 16 July 2015

Jennifer Wyffels

South-East Zoo Alliance for Reproduction and Conservation, Yulee, FL, USA

The Changing Face of AES

There has been a steady demographic shift occurring in life sciences over the last 30 years, so maybe it's not so unexpected to see it in the field of elasmobranch science as well. While all fields of science have historically been largely male-dominated, there are now far more women training in biological fields than men; however, the proportion of women entering and remaining within professional careers is still proportionally behind that of males. This trend is particularly true for women and underrepresented groups in AES. Not unlike other fields in the life sciences, pioneers like Eugenie Clark, one of the first women to establish herself as force among elasmobranch scientists in the 1960s, led the way for the next generation of female scientists. Despite increasing numbers of female student members, the number of women remaining in the society as professional members has not increased proportionally. Male AES members have served as president for 26 out of the 30 year history of the society and only two women have been elected as President of AES, the first being Merry Camhi in 2002. There has been a growing number of women serving important leadership roles in AES, particularly over the last 10 years, which is needed to support the needs of our changing society. However, there is also a need to further enrich our ranks with greater diversity.

0461 ASIH STOYE AWARD ECOLOGY & ETHOLOGY I, Crystal 3 & 4, Thursday 16 July 2015

Katharine T. Yagi¹, David M. Green^{1,2}

¹McGill University, Montreal, Canada, ²Redpath Museum, Montreal, Canada

Strategies of Dispersal in Pond Breeding Amphibians

Dispersal is a necessary process for any species living in a fragmented landscape and therefore the dispersal strategies of endangered amphibians are important considerations for population recovery and effective management. Fowler's toads, *Anaxyrus fowleri*, exist in three remnant populations in Canada, one of which is at Long Point, Ontario. Although adult body size in this population negatively correlates with

density, it is unknown precisely how body size is related to dispersal. If dispersal is in some way size-dependent, then by manipulating larval density conditions to produce toads of varying sizes in the field, we should see a correlation between movement and body size among individuals. To address this, we reared Fowler's toad tadpoles in eight density treatments within four ponds located in the Long Point National Wildlife Area. A random sample of eighteen tadpoles at stage 40 were placed alone in a dish of water and filmed for one hour to assess activity level. A similar test was conducted on the same treatment groups as toadlets. Six individuals were filmed in a terrestrial enclosure for 6 hours and activity was scored based on whether the subject changed positions every 1 minute. We predicted tadpole activity level will correlate positively with density because crowded conditions can cause increased competitive behaviour, and we predicted a negative relationship for toadlets because high density toadlets emerge at small sizes suggesting smaller energy stores will be allocated towards movement. These results will be a component in predicting the effect of larval density on amphibian dispersal.

0050 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

Lei Yang, Richard Mayden

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Nuclear Gene Cloning, Polyploid Evolution and the Subdivision of the Subfamily Cyprininae

Cyprininae is the largest subfamily of Cyprinidae and contains more polyploid species than any other group of fishes. The large number of polyploid taxa poses significant challenges for phylogenetic studies of this subfamily. Our recent study with several of our collaborators explored the polyploid evolution and subdivision of the Cyprininae based on extensive taxon sampling and DNA sequence data from mitochondrial genes and the cloned nuclear RAG1 gene. In the present study, we cloned and sequenced RAG1 for 13 more species and two additional single-copy nuclear loci EGR2B and IRBP for 27 species to further investigate these interesting questions. Species of different ploidy levels (diploids, tetraploids, and hexaploids) were analyzed and all tribes are represented. Partitioned Maximum Likelihood searches and bootstrap analyses were performed separately on the RAG1 dataset (110 taxa, 1497 bp), EGR2B dataset (62 taxa, 801 bp), and IRBP dataset (62 taxa, 815 bp). Topologies of the resulting trees were compared with those of previously published mitochondrial trees and the nuclear RAG1 tree. New data provided in the present study provide further support for the subdivision of the subfamily Cyprininae into 11 tribes. This study also provided further corroboration for the phylogenetic placements of some important taxa and the hybrid origins of the tribes Torini, Cyprinini, Spinibarbini, and Barbini.

0159 Fish Systematics II, Carson 3, Sunday 19 July 2015

Lei Yang, Shannon Corrigan, Gavin Naylor

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Phylogenetic Relationships of Batoids Inferred from Gene Capture Data of 1076 Nuclear Loci and the Mitogenome

Batoids (skates and rays) are a large group of fishes that account for more than half of the species diversity of cartilaginous fishes. The present study is aimed at resolving the phylogenetic relationships among batoid fishes based on the largest taxon and genomic sampling to date. A preliminary Neighbor-Joining tree was estimated from mitochondrial ND2 sequences derived from more than 10,000 tissue samples collected as part of an NSF funded Tree of Life project. Representative samples of batoid lineages identified as distinct in the Neighbor-Joining analysis were subsequently subjected to cross-species single-copy nuclear gene capture and sequenced on an Illumina MiSeq. Counterpart complete mitogenomic sequences were also collected through next-generation sequencing. Partitioned Maximum Likelihood searches and bootstrap analyses were performed for 1076 single-copy nuclear exons and the complete mitogenome sequences obtained. Most nodes were resolved with high bootstrap support in both the nuclear tree and the mitochondrial tree. Topologies of the two trees were compared and relationships among major lineages were discussed. Monophyly of some currently recognized genera were evaluated and taxonomic revisions are planned.

0189 Fish Biology, Crystal 1 & 2, Saturday 18 July 2015

Hyo-Jae Yu, Jin-Koo Kim

Department of Marine Biology, Pukyong National University, Busan, Republic of Korea

Early Life History of *Sebastes koreanus* (Pisces, Scorpaenoidei) in the Yellow Sea

The early life history of *Sebastes koreanus*, an endemic marine fish species of the Yellow Sea, was investigated using wild-captured larvae [6.11-11.10 mm body length (BL)] and a juvenile (18.60 mm BL). The flexion of the notochord tip started at ca. 6.75 mm BL and was complete at ca. 8.84 mm BL. The caudal and pectoral fin rays first appeared at the preflexion stage (6.11 mm BL), the dorsal and anal fin rays appeared later, at the flexion stage (7.66 mm BL), and the pelvic fin rays appeared at the postflexion stage (8.84 mm BL). Head spines began to appear at the flexion stage (6.75 mm BL) and their appearance was complete at the postflexion stage (more than 8.84 mm BL). Among the cephalic bones, which are related to feeding, breathing, and swimming, the jaw bone, opercle, pectoral girdle, and hyoid arch were first observed at ca. 6.27 mm BL. The neurocranium began to ossify in the frontal, pterotic, and parietal regions at ca. 6.27 mm BL, and then in the parasphenoid and basioccipital regions at ca. 8.17 mm BL. The vertebrae began to ossify at ca. 7.17 mm BL and their ossification was almost complete at ca. 11.10 mm BL.

Melanophores were present on the head and abdominal region during the larval stage, and were often present behind the nape (which may be an intraspecies variation). Three transverse stripes were present in the juvenile stage, corresponding to the coloration observed in the adult.

0190 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

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Significantly Low Levels of Genetic Diversity in *Hyporhamphus sajori* (Pisces, Hemiramphidae) from Korea and Japan Inferred from Mitochondrial DNA Control Region Sequence Data

The genetic diversity, relationships, and population structure of *Hyporhamphus sajori* collected from Korea (five locations, n = 30) and Japan (three locations, n = 27) were analyzed using 484-base-pair sequences of the mitochondrial DNA control region. All *H. sajori* individuals were indistinguishable, on the basis of their location, as demonstrated with a neighbor-joining tree and minimum spanning network. All individuals collected from the eight locations comprised a single panmictic species. Analysis of molecular variance revealed a lack of significant differentiation among the eight locations. The prevalent lack of genetic differentiation is probably attributable to the reproductive behavior and spawning ecology of *H. sajori*. For example, the eggs of *H. sajori* are attached to drifting seaweed, and larvae are also dispersed with drifting seaweed. Therefore, we speculate that the eggs and larvae of *H. sajori* are highly dispersed, far from their natal grounds. Further research with more sensitive DNA, such as microsatellite DNA, is required to clarify more recent differentiation events.

0037 Herp Ecology, Carson 4, Saturday 18 July 2015

Peter A. Zani

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The Life and Demography of Side-blotched Lizards, *Uta stansburiana*, in Eastern Oregon: A Tribute to Don Tinkle

Five decades ago Don Tinkle published several classic studies of side-blotched lizards including comparative demography of northern (Colorado) and southern (Texas) populations. In the spirit of Tinkle's work, and in an attempt to understand how climate affects lizard life histories, I have conducted a long-term mark-recapture study of a population of *Uta stansburiana* in eastern Oregon. For 12 years (2004-15) I have marked

150-500 lizards annually. Timing of reproductive bouts has been estimated from abdominal palpations in the field and oviposition in the lab, which has also yielded data on clutch size. Results confirm Tinkle's finding that *Uta* experience reduced mortality at higher latitudes (annual adult mortality is only 65%), but also achieve fewer reproductive bouts. Field observations indicate that fluctuations in the onset of the growing season may constrain *Uta* to two clutches in some years, but enable three clutches in other years. Demographic analyses suggest that resulting population growth oscillates between negative and positive values depending on the number of reproductive bouts possible in a season. Thus, while Tinkle suggested that northern *Uta* are limited to as many as three clutches per year by the shorter growing season, my analyses indicate that side-blotched lizards actually require three clutches per year to avoid population decline.

0276 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Peter A. Zani, Bridget Walker, Elizabeth Wagner

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

Effects of Drought on Reproductive Life History of Side-blotched Lizards, *Uta stansburiana*

During 2013, drought conditions in central Nevada appeared to cause some populations of side-blotched lizards to terminate breeding earlier than usual in an apparent shift from reproduction to survival. This observation led us to investigate which aspects of drought are the causal agent of this shift in life history. To do so we kept adult wild-caught side-blotched lizards in identical lab conditions for six months (including a winter inactivity period) before assigning them to drought (no supplemental watering) or non-drought (supplemental watering) treatment groups. Animals were fed *ad libitum* to test the hypothesis that lack of water, but not lack of food, was sufficient to induce a reproductive response. Although body condition was not affected by drought during the lab breeding season, results indicate that as the drought progressed animals lacking water were negatively affected in terms of reproductive timing and success. These findings suggest that for desert-adapted reptiles drought conditions and the lack of drinking water alone may be enough to affect life history even if the food supply is not altered in nature.

0046 Fish Biogeography, Carson 3, Saturday 18 July 2015

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How Big is the Greater Caribbean Shore-fish Fauna, and How Long to Describe It?

To estimate the size of the shallow shore-fish fauna of the Greater Caribbean (GC), we examined the long-term dynamics of description of species in relation to their biological characteristics, using the 1,549 named species from that region that were described between 1758-2013. The rate of accumulation of species-descriptions for the entire fauna has remained unchanged for the past 100y, while that of non-endemic species has slightly declined, and that of regional endemics has increased. Species-accumulation curves of minor habitat groups of the fauna may be declining, but those of the largest subsets (soft-bottom and reef species, especially reef endemics), have generally accelerated. These curves indicate that there must be many undiscovered species in the GC fauna. Both body-size and latitudinal-range of newly described species have declined in recent years, while the upper limit of the depth range has deepened. Hence, many of the undiscovered species are small fishes living in deeper reef and soft-bottom habitats in the Caribbean heart of the GC. The exponential scaling relationship between the number of higher taxa and their rank predicts, with very low reliability, that there are more than twice as many species as currently named. Proportional increases in species richness across a range of genera due to recent descriptions of new species indicate that the fauna is ~45% larger than currently known. At the currently low species-description rate a full faunal inventory will take a very long time.

0081 Poster Session I, STORER ICHTHYOLOGY AWARD, Reno Ballroom & Tahoe Room, Friday 17 July 2015

Zachery D. Zbinden, William J. Matthews, Edie Marsh-Matthews

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A Contemporary Fish Survey of the Muddy Boggy River Drainage, Southeast Oklahoma, U.S.A.

Sixty-six fish-community collections were made between May and September 2014 at sites throughout the Muddy Boggy River basin, a major tributary of the Red River in southeastern Oklahoma. The primary objective was to document the distribution of fish species and community composition within the basin. Samples were taken by exhaustively seining approximately 100 m of stream reach (mean sampling duration 47 min.), and also measuring 22 environmental variables (e.g., substrate, habitat, water quality, land use, etc.) at each study site. Study sites were widely distributed from headwaters to lower mainstream to maximize coverage across the watershed, and the

survey resulted in 63 species found throughout the Muddy Boggy River system (mean per site= 11.2 species). The purpose of this study is to *i.*) Use environmental variables to determine which factors are correlated with variation we see in contemporary fish community structure throughout the watershed, *ii.*) Compare results of this survey to a past survey conducted by Mr. Jimmie Pigg in the same drainage which yielded 90 species (1974-1975, sites=277), and *iii.*) Draw conclusions about the factors likely responsible for changes seen in the fishes of this watershed over time. Special attention is given to anthropogenic disturbance within the Muddy Boggy drainage area, which has a long history of producing and exporting oil and natural gas, and has been experiencing an increase in production in recent years.

0355 Herp Conservation I, Carson 1, Saturday 18 July 2015

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Post-release Survival of Juvenile Captive-reared Chinese Giant Salamander (*Andrias davidianus*) Reintroduced to the Wild

Reintroduction of captive-reared Chinese giant salamanders may help to augment the declining wild populations and conserve this critically endangered species. We released 32 juvenile salamanders surgically implanted with radio transmitters at two sites in the Qinling Mountains of central China and monitored their survival from March 2013 to July 2014: 3 year-old head-started animals (n = 16) at the Heihe River, and captive-born 5 year-old animals (n =16) at the Donghe River. Two salamanders at Heihe River and 10 animals at Donghe River survived through the entirety of the project timeline. Ten salamanders were confirmed dead, two were possibly poached, while the status of the other eight animals was undetermined. The annual survival rate of salamanders at the Heihe River was 0.593 (95% CI: 0.387 - 0.907), which was lower than the rate of 0.800 (95% CI: 0.621 - 1.000) at the Donghe River ($\chi^2 = 3.6$, $P = 0.056$). All salamanders recaptured from the Donghe River site (n = 8) increased in mass (0.50 ± 0.13 kg) and length (5.5 ± 1.5 cm) after approximately 11 months in the wild. Their body condition indexes were smaller to wild conspecifics; however, this difference was reduced by the end of the project such that they were only 7% lighter than wild animals of the same length. No external parasites or diseases were discovered on recaptured giant salamanders. Our results indicate that captive-reared giant salamanders can survive in the wild, although adequate surgical recovery time is extremely important to post-release survival.

0333 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

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Sound Production in Marbled Rockfish, *Sebastes marmoratus*, and Implications for Fisheries

Recently, several rockfish species (genus *Sebastes*) have been reported to be soniferous. To determine whether an additional rockfish species produces sounds, passive acoustic recordings were analyzed from captive marbled rockfish (*Sebastes marmoratus* Cuvier, 1929) during the non-spawning season. Three distinct sounds were identified based on frequency features. The common characteristics among all sounds were low frequency (below 300 Hz) and rapidly dampened pulses consisting of 3-5 acoustic energy cycles. During free-swimming conditions in the canvas tank, the fish produced voluntary sounds with lower frequencies than the disturbance sounds produced by individuals during prodding. Two types of sounds were identified in the disturbance context: one type consists of single or double pulses with 2 peak frequencies, and another type consists of a series of pulses with a single peak frequency. These results suggest that specific-species and behavior-associated sounds are potentially useful in passive acoustical surveys to monitor rockfish populations and distributions remotely.

0045 Cypriniformes Inventory Symposium, Crystal 1 & 2, Sunday 19 July 2015

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Beauty Under Ground: Cavefishes in China

Cavefishes, or hypogean fishes, are a distinctive group of fishes restricted to subterranean environments for at least for part of their lives. Based on their troglomorphy, which includes morphological adaptations to the cave environment such as the reduction or loss of eyes and pigmentation, cavefishes can be divided to two types: troglobites (troglomorphic) and troglophiles (non-troglomorphic). China is home to the highest number of cavefish species in the world, with more than 60 troglobitic species out of about 120 cavefish species. As fieldwork continues, more species are being found and described. All of these cavefish species in China are endemic to China. With the exception of *Onychostoma macrolepis* in north China, all species are found in southwest China, mostly in the karst environment of the Yunnan-Guizhou Plateau. *Sinocyclocheilus*, the largest cavefish genus, has experienced rapid evolution and diversification. Species from this genus possess horns and humpbacks (i.e. horn-like structures and hyperdevelopment of a dorsal protuberance similar to a humpback), probably resulting from parallel evolution. Sympatric distribution of Chinese cavefishes is common, and sometimes several species are found in the same cave or subterranean

river. Caves and karsts are very fragile, balanced habitats, and cavefish species are extremely sensitive to environmental change. Threats from rapid economic growth have increased the need for conservation efforts for cave-dwelling communities in recent decades. Conservation of Chinese cavefishes is an urgent issue.

0236 Herp Morphology & Biogeography, Crystal 1 & 2, Friday 17 July 2015

Mingna Zhuang, Timothy E. Higham

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The Modulation of Foot Position and Adhesion During Arboreal Locomotion in Day Geckos (*Phelsuma*)

By using adhesion, geckos can navigate through challenging habitats. Behaviorally modulating how the adhesive system is applied can occur by altering the alignment of the foot relative to the long axis of the body and/or the angles between the digits (interdigital angle). Given the directionality of the adhesive system, we expect geckos to vary the application of the system via these mechanisms as they run. We quantified 3D movements (with high-speed video) of *Phelsuma madagascariensis* running on a range of ecologically relevant inclines (0°, 45°, 90 °) and perch diameters (1.5cm, 10cm and flat). We measured instantaneous interdigital angle and foot alignment relative to the body across each condition, as well as other kinematic variables. The geckos decreased speed with decreasing perch diameter, but increased speed at 45°. This suggests that *P. madagascariensis* may favor inclined perches. Additionally, proximal limb variables respond to substrate condition in a manner to increase stability and reduce toppling. Finally, foot alignment in the forelimb acts in opposition to that of the hindlimb, suggesting that *P. madagascariensis* is able to maintain multiple directions of adhesion at one time. The modulation of interdigital angle and foot alignment suggests that aspects other than the mechanism of adhesion are important for arboreal movement in geckos. Our study reveals patterns of foot usage in arboreal locomotion, which can lead to a better understanding of adhesive system constraints. This is essential for understanding how biomechanical traits respond to the evolution of novel adaptations and morphologies. Supported by NSF IOS-1147043.

0553 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

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Measuring Gene Flow Among Populations Within the Reef Fish Species, *Melichthys niger*

The black triggerfish, *Melichthys niger*, is one of just a few tropical reef fish thought to have a circumglobal distribution. Considering the rarity of circumglobal reef fishes, and the challenges reef fish larvae face crossing large stretches of open-ocean, the objective of this research is to determine whether *M. niger* is truly circumglobal or rather, if *M. niger* is really a complex of closely related, but evolutionarily isolated sub-species or species. Gene flow between collection sites in the Atlantic, Indian, and Pacific oceans is being investigated by examining sequence data from three genes: control region (D-Loop), cytochrome oxidase I (CO1), and the second intron of the large ribosomal subunit (S7-2). Preliminary analysis of mtDNA diversity (D-loop and CO1 genes) indicates extensive genetic connectivity with no evidence of cryptic evolutionary divergence. Investigations are ongoing and will include an analysis of the S7-2 nuclear marker as well as additional samples from sites in the Eastern Pacific and Western Atlantic, which have been geographically isolated from one another for more than 3 million years.

0137 HERPETOLOGISTS' LEAGUE GRADUATE RESEARCH AWARD, Carson 1, Thursday 16 July 2015

Julie Ziembra, Carl Anthony, Cari-Ann Hickerson

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Invasive Asian Earthworms (*Amyntas* spp.) Negatively Affect Juvenile Abundance, Alter Microhabitat Use, and Reduce Foraging Efficiency of Woodland Salamanders (*Plethodon cinereus*)

Asian earthworms (*Amyntas* spp.) are invading North American forests and consuming the vital detrital layer that forest-floor biota (including the Eastern Red-backed Salamander, *Plethodon cinereus*) rely on for protection, food, and habitat. Salamander population decline has been associated with European earthworm-mediated leaf litter loss, but there have been no studies on the interactions between *Amyntas* and *P. cinereus*. Since the large, active *Amyntas* earthworms spatially overlap with salamanders beneath natural cover objects and in detritus, they may compound the negative consequences of resource degradation by physically disturbing important salamander activities (foraging, mating, and egg brooding). I predicted that *Amyntas* would exclude salamanders from high quality microhabitat, reduce foraging efficiency, and negatively affect salamander fitness. In laboratory trials, salamanders used lower quality microhabitat and consumed fewer flies in the presence of earthworms than when alone. In a field experiment conducted on salamander populations from "non-invaded" and

“*Amyntas*-invaded” sites in Ohio, salamanders and earthworms shared cover objects ~60% less than expected. *Amyntas* density was negatively associated with juvenile density, but had no relationship with overall, male, or gravid female salamander density. Also, *Amyntas* invasion had no effect on salamander body condition. Juvenile salamanders do not hold stable territories, which results in reduced access to prey and a higher risk of desiccation. Thus, they may be more vulnerable to the negative effects of *Amyntas* invasion than adults. If habitat degradation and physical exclusion of salamanders from cover objects reduce juvenile salamander performance, then recruitment and ultimately salamander abundance may decline following *Amyntas* invasion.

0157 Poster Session II, Reno Ballroom & Tahoe Room, Saturday 18 July 2015

Menemsha Zotstein

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Geographic Variation in Agonistic Push-up Displays Across a Contact Zone in the Side-Blotched Lizard *Uta stansburiana*

This study examined the pattern of behavioral, genetic, and morphological variation occurring between phenotypically divergent populations of *Uta stansburiana* across a contact zone between the Mojave Desert and Colorado Desert ecosystems. I characterized the shift in agonistic display type across the zone to determine if individuals in the intergrade zone displayed intermediate phenotypes or enhanced variation in display. Individuals with diverse behavioral repertoires were found in all populations, but display type changed gradually and continuously along the transect of sampled populations, indicating a complex and possibly polygenic or multi-allelic mode of inheritance. Nuclear and mitochondrial markers indicate restricted gene flow though the discordance of the genetic data type suggest female-biased dispersal. Selection appears to be shaping the evolution of morphological traits such as size and limb length as these were significantly related to elevation differences along the transect.

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