

ABSTRACTS

IGC Symposium April 19, 2018

Oral Presentations

Platform Session 1

10:00 am – 11:00 AM

Session Chair: Angie Estrada

Causes and consequences of the cooperative display behavior of wire-tailed manakins

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Manakins of the family Pipridae are a fascinating family of birds known for their bright plumage and complex courtship displays. Among male manakins, variance in reproductive success has been found to be dependent on a male's display performance, and in the case of species that exhibit male-male coordinated courtship displays, their ability to form and maintain social bonds with display partners. Accordingly, elucidating the proximate causes and consequences of individual variation in reproductive and cooperative courtship behavior can broaden our understanding of the evolution of cooperative behavior. Here, we quantified social and hormonal correlates of individual variation in display behavior of territory-holding wire-tailed manakins by using video recordings of and blood samples collected from territory-holding males. Our results show that males with a higher proportion of cooperative displays performed longer display bouts and also spent a higher proportion of time displaying. However, males with high circulating testosterone levels engaged in fewer cooperative display bouts suggesting that high levels of testosterone may interfere with effective cooperative behavior. Our results suggest that individual differences in circulating testosterone levels likely play an important role in mediating a male's ability to form and maintain social partnerships and, thus, indirectly mediates individual variation in male reproductive behavior. This research ultimately adds to our knowledge about the evolution of cooperative courtship behavior and the proximate mechanisms that mediate individual variation in both reproductive and cooperative behavior.

Hypolimnetic oxygenation increases methane bubble fluxes in a eutrophic drinking water reservoir

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Freshwater reservoirs contribute a considerable source of methane (CH₄) to the atmosphere via bubble fluxes from the sediments (ebullition). Despite their importance, the controls of CH₄ ebullition patterns remain poorly understood, especially in reservoirs managed for drinking water. Throughout the stratified period of 2017, we measured ebullition rates at 20 sites in Falling Creek Reservoir, a small eutrophic drinking water reservoir in Virginia, USA that is managed with a hypolimnetic oxygenation system (HOx) to improve water quality. Ebullition rates across the reservoir experienced predicted seasonal trends that increased with elevated sediment temperatures until fall turnover. However, contrary to previous studies that observed the highest ebullition rates occurring in the shallowest sites of waterbodies with elevated sediment temperatures, we also observed elevated ebullition rates in the deepest site of the reservoir, likely a result of HOx operation. Activation of the HOx system mixed the sediments at the deep hole, generating enough mixing near the sediments to release ebullition bubbles stored in the anoxic sediments that were able to rise to the surface. Thus, while oxygenation systems are generally thought to decrease net CH₄ emissions by promoting CH₄ oxidation, our results suggest that in some reservoirs, oxygenation may actually *stimulate* ebullition. As reservoir construction and management increases globally, it is imperative to understand how their drinking water management may affect CH₄ emissions in the future.

A mathematical modeling approach to the Cort-Fitness Hypothesis

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The Cort-Fitness Hypothesis continues to be challenged by experimental studies. The inconsistency of the relationship between cort levels and the relative fitness of individuals and populations often results in the failure of the hypothesis. Meanwhile, other studies provide support for the hypothesis, hence a deeper understanding of the mechanisms underlying the hypothesis is needed. Motivated by reviews on studies testing the Cort-Fitness Hypothesis, we propose a mathematical model representing the link between, cort levels, environmental challenges, and fitness. Our model explores how variation in the predictability and intensity of

environmental challenges, reproduction strategies, and fitness metrics all contribute to the cort-fitness relationship. We provide qualitative results showing the cort-fitness relationship for different environmental scenarios as well as how the model can be used to inform cort-fitness future experiments.

Livestock antibiotics alter soil microbial communities and ecosystem function

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The health crisis resulting from the declining effectiveness of antibiotics has called all antibiotic usage into question, including their use in livestock production – accounting for 80% of domestic use. Between 40-95% of antibiotics administered to livestock enter the environment via manure at a rate of up to 14-million kg-yr⁻¹. Previous work has shown that additions of manure from antibiotic-treated cattle can affect microbial communities compositionally, genetically, and physiologically. Most importantly, changes in antibiotic resistance gene (ARG) abundance were found to be associated with microbial stress, resulting in altered ecosystem functioning. To better understand the relative contribution of manure and antibiotics, an experiment was established where plots were amended with manure from cattle treated with one of two types of antibiotics, or untreated cattle at a rate of 650-g m⁻² month⁻¹ for three years. Each spring, plots were pulse-labeled using ¹³C and ¹⁵N. Plots were harvested in successive days to determine how these treatments affect the microbial community and elemental cycling. Initial findings suggest that antibiotic-laden manure impacts a number of important soil microbial parameters. Manure from cattle treated with pirlimycin elicited an ~6,000 kg ha⁻¹y⁻¹ increase in respired carbon compared to cephalosporin-laden manure. Analysis of the ¹³C and ¹⁵N pulsed into the system also revealed that the antibiotic treatments do alter elemental cycling in soils. Although analysis is ongoing, initial results from this study show that antibiotics can impact microbial communities and soil functioning, however effects are not uniform, instead depending on the antibiotic in question.

Platform Session 2

11:30 AM – 12:30 PM

Session Chair: Jon Doubek

How can the cavity nest-web inform conservation of the endangered Bahama Swallow (*Tachycineta cyaneoviridis*)?

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The Bahama Swallow (*Tachycineta cyaneoviridis*) only breeds in the northern Bahamas, and is considered endangered due to decline in its population. However, causes of population decline are unknown. As an obligate secondary cavity nester, the swallow requires other species or processes to create cavities in which to nest. We constructed a cavity nest-web to investigate whether nest site availability and interactions between swallows and other cavity-nesting species could provide insight into causes of decline and the design of conservation strategies. We conducted surveys to assess the availability of cavity-nesting resources in Caribbean Pine (*Pinus caribaea*) forest and other habitats. We also examined potential competition by locating nests of all other cavity-nesting species. We measured reproductive success by monitoring swallow nests in different cavity types. Swallows built nests in several cavity types, primarily those excavated by Hairy Woodpeckers (*Picoides villosus*) and West Indian Woodpeckers (*Melanerpes superciliaris*). La Sagra's Flycatchers (*Myiarchus sagrae*) were the only other secondary cavity nesters that utilized the sparsely distributed pine snag cavities, which are excavated by Hairy Woodpeckers. Other cavity types were in anthropogenic structures and were concentrated in developed areas, where swallows face potential competition with American Kestrels (*Falco sparverius*), and non-native House Sparrows (*Passer domesticus*) and European Starlings (*Sturnus vulgaris*). Reproductive success was high during all nest stages in pine snags, while success in other cavity types appeared to vary. These findings indicate that managing for pine snags and the presence of Hairy Woodpeckers in the pine forest may be crucial to Bahama Swallow conservation.

Varying Temperature Effects on the Growth of the Amphibian Chytrid Fungus

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Temperature is an important factor in many disease systems by influence traits like, growth rate or reproductive rate. However, the role of temperature in these systems is often studied in an artificial way, not allowing the temperature to change. Relating this data back to a more natural temperature scenario is difficult and relies on inaccurate methods. Temperature is especially important in the amphibian chytrid fungus system (*Batrachochytrium dendrobatidis*), where cooler temperatures lead to higher infection rates. With temperature being a main factor in many disease systems, it is important to develop accurate methods to relate constant temperature experiments to a varying temperature environment.

One of the most common methods used to take constant temperature experiments to predict traits in a varying temperature regime is rate summation. This method has not been widely tested to see when and where this technique works. To test this method in the amphibian chytrid fungus system we fit a logistic growth model to optical density data. The logistic growth rate of the growth model was plotted against temperature and used to fit a Briere curve. Using the Briere curve, we can use rate summation to make predictions about Bd growth in the varying temperature conditions. When comparing the prediction against varying temperature growth data we found that rate summation over predicted the growth of Bd using constant temperature.

Diversity of Chondrichthyes through the uppermost Cretaceous Hell Creek Formation of Garfield County, Montana, with implications for the Cretaceous-Paleogene mass extinction in freshwater environments

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The Cretaceous-Paleogene (K-Pg) mass extinction is a well-studied mass extinction event, but there remain two main competing hypotheses that explain the diversity changes observed in

the fossil record: (1) a sudden and rapid loss of many species at the K-Pg boundary (ca. 66 Ma) caused by a Bolide impact (Chicxulub); and (2) vertebrate biodiversity declines prior to and at the K-Pg boundary due to multiple factors (e.g., changing sea levels, volcanism, bolide impact). To examine these two hypotheses, we examined the diversity changes of Chondrichthyes (sharks and relatives) from freshwater deposits of the Hell Creek Formation (HC), leading up to the end of the Cretaceous. We analyzed diversity dynamics using 1065 fossil teeth stored at the University of Washington, Burke Museum of Natural History and Culture and the University of California Museum of Paleontology from eight vertebrate microfossil localities stratigraphically distributed throughout the HC. Our samples include the occurrences of three new shark species based on morphologically distinct teeth, as well as a novel batoid (i.e., rays). We also report on the first sand tiger shark from the HC, as well as a tentative carchariniform tooth, indicating a freshwater incursion by these, otherwise, marine taxon. Using raw taxonomic, standing, subsampled analytic rarefied, and shareholder quorum subsampling (SQS) richnesses, our study shows richness increases to seven species between 30.5 and 35 m above the Hell Creek/Fox Hills contact (HFC). Heterogeneity indices surrounding this interval indicate a faunal restructuring in which relative abundance of the guitarfish *Myledaphus pustulosus* starkly declines throughout the remainder of the HC section resulting in more species-even localities. Species diversity decreases between 35 and 83.2 m above the HFC and rise to a peak of nine species at 84.3 m above the HFC (4.2 m below the Hell Creek/Tulloch contact). Nine of the ten HC chondrichthyans extend into the last 10 m of the HC, showing a very rapid, abrupt extinction in HC chondrichthyans. These changes in diversity resemble the abrupt extinction patterns shown for mammals (terrestrial) rather than the stepwise extinction patterns shown for amphibians (aquatic) although the later shared the same environments. Changes in chondrichthyan community structure and diversity in relation to other HC taxa indicate a unique and complex pattern of extinction, one suggesting that HC chondrichthyans were acted upon by a variety of selection pressures, supporting a multi-cause extinction hypothesis.

Physiological and life-history trait variation in an invasive lizard, *Anolis sagrei*

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During biological invasions, non-native invaders often experience environments that differ substantially from those found in their native range; these novel conditions can impose strong directional selection and lead to rapid phenotypic divergence between native and invasive populations. The brown anole (*Anolis sagrei*) is a small lizard native to Cuba and the Bahamas

that has invaded the southeastern United States over the past century. Native and invasive populations experience different climatic variables with more northern invasive populations experiencing lower mean annual temperatures and greater seasonal variation than more southern native populations. We hypothesized that invasive populations would subsequently display phenotypic differentiation in physiological and life-history traits in order to conform to the newly encountered environment, and further that these trait changes would result from genetic adaptation. We collected brown anoles from native populations in the Bahamas and invasive populations in the southeastern United States ranging from southern Florida to Georgia. We then measured a suite of physiological and life-history traits in both the wild-caught adults and their lab-reared offspring. We found that physiological and life history traits do differ across native and invasive populations, but that genetic adaptation does not underlie all trait changes equally. Our results indicate that the divergence of physiological and life-history traits may have facilitated the successful establishment and expansion of the brown anole.

Platform Session 3

1:30 PM – 2:45 PM

Session Chair: Derek Hennen

Soil tillage, carbon, and global change

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Soil tillage is a ubiquitous agricultural management practice on croplands globally. Tillage impacts climate via biogeochemical processes by accelerating decomposition of soil carbon (C) and releasing of CO₂. Conservation tillage practices (NT), which reduce soil C decomposition and leave more crop residue on the soil surface compared to more intensive, conventional tillage practices (CT), have potential to serve as a climate change mitigation measure through increased soil C storage on agricultural land. But, much is unknown regarding the direction and magnitude of tillage effects on climate, and effects of NT on C storage may be quite variable. Earth system models (ESM) are fully-coupled models of the entire Earth system capable of comprehensively representing all physical processes affecting climate and interactions thereof. ESMs can represent the terrestrial carbon cycle and carbon-climate feedbacks, and ESM

outputs form the basis of international agreements and reports on climate change. Few studies have conducted ESM simulations to comprehensively assess the effects of different tillage practices on global climate. This research will elucidate the effects of different tillage practices on soil C and emissions by simulating soil tillage in a major ESM, the Community Terrestrial Systems Model (CTSM). Effects of intensive CT practices on soil C cycling will be evaluated by enhancing soil decomposition rates over the historical time period (1850-2014). The mitigation potential of changing from CT to NT practices will be assessed by reducing decomposition rates relative to those under CT for a future climate change scenario (2014-2100).

The human dimensions of wildlife recreationists: understanding the role of wildlife recreation in conservation and management

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Wildlife recreationists are important constituents of state wildlife agencies. Participation in wildlife recreation has been linked to pro-environmental behaviors and can facilitate positive collaborations between recreationists and state wildlife agencies. As such, state wildlife agencies are interested in engaging wildlife recreationists to aid in conservation and management. However, the ability of state wildlife agencies to engage wildlife recreationists depends on their understanding of the needs, attitudes, and behaviors of wildlife recreationists. Social factors, such as motivations, trust, and preferences, can influence wildlife recreationists' willingness to engage in conservation behaviors and support state wildlife agency actions. Further, these social factors may differ among and within wildlife recreation groups.

We have begun using a mixed methods approach to study wildlife recreationists in Virginia. Data collection is occurring in two phases, beginning with a series of 8 focus groups targeting 4 recreation strata: wildlife viewers, birdwatchers, hunters, and anglers. Focus groups (i.e., group interviews) are informing questions on a statewide online survey that will be implemented in a second phase of the research. Findings will inform the development of a recreation management plan to aid the Virginia Department of Game and Inland Fisheries in better engaging and serving the diversity of wildlife recreationists in conservation and management.

The effect of aquaculture on the genetic purity of natural populations of Nile tilapia *Oreochromis niloticus* in Ghana

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Aquaculture has the potential to provide food on a sustainable basis for sub-Saharan Africa. However, the rapid expansion of aquaculture in the region could threaten the local adaptation and genetic diversity within wild populations if farmers import and grow alien strains deemed to have growth advantage over native strains. We investigated the genetic background of aquaculture strains of Nile tilapia *Oreochromis niloticus* in Ghana and assessed the genetic impact of aquaculture on wild populations using samples from selected farms on the Volta Lake and wild populations from the Volta River. We analyzed mitochondrial DNA sequences from the *D-loop region* and the *ND1 gene* among populations and compared them with GenBank sequences of the Genetically Improved Farmed Tilapia (GIFT) strain of *O. niloticus* and its derivatives, and USA grocery tilapia samples with labels from China and Ecuador. We also screened the populations at ten nuclear microsatellite loci. Our preliminary analysis revealed a "Ghana cluster" comprising both farmed and wild samples, which were genetically distinct from the GIFT and related strains. We also found that at least one farm had samples that clustered with the GIFT and related strains. Furthermore, some wild samples clustered with the GIFT and related strains, suggesting that the GIFT strains being farmed in Ghana have already escaped into the wild. Ongoing analysis of the nuclear microsatellite data should provide insight into the degree of genetic mixing of the GIFT strains and natural populations of *O. niloticus* in Ghana and help prioritize populations for conservation actions.

Soil microbial response to *Rhododendron maximum* removal in Appalachian forests

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Rhododendron maximumis a native evergreen shrub that has expanded in Appalachian forests following declines of American Chestnut and Eastern Hemlock. *Rhododendronis* of concern to forest managers because it slows forest succession by limiting light and soil nutrient availability needed for tree seedling recruitment. We are testing *Rhododendron* canopy removal with and without organic soil (O-horizon) removal as a management strategy to promote forest recovery. We hypothesized that *Rhododendron* canopy removal in combination with O-horizon removal would increase soil nitrogen (N) availability, resulting in a shift towards a bacterially-dominated microbial community and increased microbial demand for carbon (C), leading to higher activities of microbial enzymes associated with C acquisition. Two years following canopy removal and one year following O-horizon removal, we sampled soils and found that dissolved organic carbon (DOC), microbial biomass, and soil N all increased with *Rhododendron* canopy + O-horizon removal. Additionally, we observed increases in C-acquisition enzymes involved in degrading cellulose (β -glucosidase) and hemicellulose (β -xylosidase) in soils with canopy and O-horizon removed. Contrary to our predictions, we did not see treatment effects on bacterial dominance, though microbial communities from all treatments shifted towards fungal dominance from spring to summer. Our results show that *Rhododendron*+ O-horizon removal stimulates microbial activity by increasing soil C and N availability and suggest that *Rhododendron* canopy combined with O-horizon removal will alter soil C cycling by increasing microbial demand for soil C resources.

A modeling-monitoring approach to relate sediment loads to stream habitat quality and agricultural best management practices in Copper Creek (Clinch River)

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Sediment pollution is a common driver of stream impairment and aquatic species imperilment. Although sediment dynamics and their connections to shifts in species distribution and habitat quality are poorly understood, stakeholders invest heavily in best management practices (BMPs) presumed to reduce sediment loading, improve water and habitat quality, and benefit aquatic biota. Copper Creek watershed (CCW) in the upper Tennessee River basin of Virginia illustrates the complexities of this issue in Central Appalachia. The stream hosts 12 imperiled aquatic species that rely on high-quality benthic habitats while the upland areas support a local economy dominated by agriculture. We address two main questions about CCW: (1) How does upland sediment load relate to benthic habitat conditions? and (2) Are agricultural BMP investments positively related to benthic habitat conditions? Ultimately, we will link a)

sediment load estimates from a CCW model, b) our field data on physical habitat throughout CCW, and c) public data on BMP implementation in CCW to create stream network models of benthic habitat conditions. To date, we have generated sediment load estimates and collected habitat data from 78 study reaches, covering >11 fluvial km. Preliminary analyses suggest several benthic habitat metrics (e.g. D50, D35, % substrate as silt/clay, % embeddedness) are responsive to subwatershed-scale sediment loads and BMP metrics. However, some correlations suggest counter-intuitive relationships (e.g. poor habitat in subwatersheds with high BMP investment) and much variance in habitat quality is not explained by BMP metrics. Overall, our analysis suggests several tactics that may improve BMP cost-effectiveness.