

ABSTRACTS

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Poster Presentations

The influence of social behavior and stability on disease transmission in a songbird host

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Human wildlife provisioning has long been overlooked as a major ecological factor, but in the last ten years it has been shown to be an important factor on the social behavior and physiology of wildlife and, consequently, disease. A prime example is among house finches (*Haemorrhous mexicanus*) who, since the mid-1990s, have been subject to infection with a highly contagious bacterium, *Mycoplasma gallisepticum*, which causes debilitating conjunctival pathology. House finches congregate at bird feeders in social flocks, where most transmission takes place, making it an ideal system for testing hypotheses regarding how human provisioning influences social behavior, physiology, and disease transmission. To test the impact of bird feeders, I altered feeder density across several sites on the Virginia Tech campus while using radio-frequency identification to track social networks and individual behavior. By altering the density of feeders, my results show the effects of human feeding via bird feeders on this disease system by seeing changes in the social networks of house finches, individual behavior and physiology, and the prevalence of disease.

Assessing local adaptation and physiological plasticity of a montane lizard in a warming climate

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Determining how organisms will be impacted by a warming world is one of the most pressing scientific imperatives of the 21st century. Habitat tracking – species' range shifts to more suitable habitat – is perhaps the most commonly observed response to rising temperatures. Terrestrial species are clearly moving upward in elevation and poleward in latitude. Nonetheless, there is a key asymmetry in habitat tracking, with species' shifts to higher elevations occurring much more slowly than shifts to higher latitude. The mechanism for this asymmetry, however, remains predominantly unexplored. We do know that species-specific physiological thresholds, relating to climate, set species' distributions. For example, tracking suitable temperatures at higher elevations comes with the additional physiological challenge of contending with progressively limited oxygen concentrations. The goal of this project is to empirically test how oxygen availability across elevation may be limiting upslope migrations in a widespread terrestrial vertebrate the Common Wall Lizard (*Podarcis muralis*). I hypothesize that local temperature regimes and oxygen availability will interact to shape physiological traits, and the plasticity of these traits, in lizard populations from different thermal regimes and levels of oxygen availability. By elucidating these interwoven factors, we can gain a more holistic understanding of the constraints organisms will encounter as they are faced with environmental warming.

***Ailanthus* Biocontrol**

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Ailanthus altissima (tree-of-heaven) is an invasive Chinese tree that has taken over portions of the Virginia landscape. Current control tactics are limited to expensive chemical and mechanical methods, and are impractical over large areas. Recently, two species of *Verticillium* fungi have been found naturally killing *Ailanthus* in Virginia. A statewide field inoculation study is underway to determine (1) if either of these isolates can be used as an effective biological control agent in the state, and (2) if any climate or stand variables impact *Verticillium*'s effectiveness. Preliminary results from the first field season indicate that *V. nonalfalae*, alone or in combination with *V. dahliae*, cause significantly higher disease ratings

than just *V. dahliae* or a control treatment. Additionally, disease progression was significantly influenced by two stand and climate variables: maximum temperature and tree height.

Examining the role of dispersal pathways in structuring aquatic insect communities

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Aquatic insects use different pathways to disperse between communities. This heterogeneity in dispersal behavior may affect how communities of stream macroinvertebrates are structured and how variable insect assemblages are over time. For my dissertation, I will investigate what role different dispersal pathways play in the assembly of aquatic macroinvertebrate communities in a stream network and how this dispersal-driven assembly changes with position in the network. I will also investigate how this dispersal-driven community assembly affects the stability of stream macroinvertebrate communities, taking into account both the taxonomic and trait composition of stream macroinvertebrate communities. I predict that isolated headwater communities are structured more by aerial dispersal, while mainstem communities located at nodes in the network are structured more by drift dispersal. The influence of drift dispersal from the headwaters that structures mainstem communities will diminish with an increase in the stream order of the mainstem. I predict community stability will be lowest in headwater assemblages and highest in the mainstem sites. These studies will help elucidate how different dispersal routes structure communities and stabilize communities. Determining how dispersal drives community assembly may give us insight into how these communities respond to disturbance, habitat fragmentation, and biological invasion. Understanding the assembly of aquatic insect communities may also inform conservation and restoration strategies.

Base cations as drivers of bacterial water quality impairment

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Base cations (Ca, Mg, K, Na) are common constituents of both terrestrial and aquatic environments. However, human activities including agriculture, deicing, surface mining, and construction have resulted in increasing ion concentrations in North American surface waters. While it is well established that the total inorganic ion concentration, or salinity, significantly impacts aquatic bacteria, the effects of individual base cations on bacterial ecology are unknown. Further, most studies focus on broad salinity ranges from freshwater to marine, and fail to address small scale changes in ion concentrations. As freshwaters continue to become saltier from manageable anthropogenic activity, small increases in salts (<50 mg/L or 350 $\mu\text{S}/\text{cm}$), as well as the types of salts causing those increases, may become increasingly important drivers of ecosystem health. We have previously identified strong correlations between base cations and the fecal indicator bacterium *E. coli* in watersheds in Southwestern Virginia. However, mechanisms driving these correlations in the environment have yet to be experimentally tested and remain a substantive knowledge gap. Here, we test the effect of elevated concentrations of individual base cations on the survivability of *E. coli* in controlled mesocosm experiments. Results suggest that divalent base cations, Ca and Mg, significantly increase the survivability of *E. coli* relative to K treatments and controls with no salt additions. These results suggest that elevated concentrations of divalent base cations may increase bacterial impairments in surface waters.

Does the microbiome impact reintroduction success of captive species? A test with an endangered frog

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Beneficial skin bacteria can protect amphibians against *Batrachochytrium dendrobatidis* (Bd), a deadly pathogenic fungus that is one of the largest threats to amphibian survival worldwide. For many amphibian species, long-term captive breeding programs have prevented extinction; however, captive management is known to modify the amphibian skin microbiome. In Panamá, threatened amphibian species survive in captive breeding facilities, but have only recently been experimentally reintroduced into the wild. For tropical amphibians, it is unknown how skin bacterial community diversity and structure change once captive-bred individuals are re-exposed to natural habitats. Thus, to inform the development of beneficial bacteria-based treatments, and also future reintroduction efforts, we attempted to understand amphibian-Bd-skin bacterial community interactions in reintroduced captive-bred individuals. Specifically, we assessed the changes that occur in the bacterial communities of *Atelopus limosus*, a critically-

endangered species, following reintroduction to a site where the species historically occurred. We aimed to investigate how the initial skin bacterial community influences: 1) bacterial community structure and composition after release, 2) host condition and 3) *Bd* infection status. Relative abundance of bacterial OTUs (operational taxonomic units, ~bacterial species) based on 16S rRNA gene amplicon sequencing was used to assess skin bacterial community diversity. We found significant variation in bacterial community structure before and after release. In addition, we found variation in bacterial community structure through time once exposure to natural conditions occurred. Moreover, after only two weeks, reintroduced and wild individuals had more similar skin microbiomes. These preliminary findings suggest that skin-associated microbiomes can be restored once captive-bred individuals are re-exposed to natural habitats, but future research needs to address whether these changes in bacterial structure ultimately result in higher survival and *Bd* protection of captive-bred amphibians.

Connecting long-term data with fine-scale variation: using remote sensing to evaluate spatiotemporal dynamics of drylands ponds

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Hydroperiod is a major driver of aquatic communities in lentic systems and may be particularly relevant in areas where water availability is a major limiting factor. In the American Southwest, water availability is threatened by unsustainable water use and increased drought. There, manmade lentic habitats such as cattle ponds may provide critical habitat for aquatic organisms when natural systems are lost. However, spatial distribution and hydroperiod dynamics of manmade ponds in this region are poorly understood, representing a knowledge gap about spatiotemporal availability of lentic habitat. To address this, we asked: (1) How are manmade ponds spatially distributed in this region? (2) Which ponds are permanent, and which are intermittent? (3) What are the ponds' hydroperiods, and do they change over time? We will use graph theory and spectral mixture analysis to analyze 34 consecutive years (1983-2017) of satellite imagery in Coronado National Forest, Arizona, to characterize the spatial distribution of ponds on the landscape, estimate surface water, and classify hydroperiods across multiple time scales. As global change progresses, understanding regional water availability is increasingly important for contextualizing aquatic community stability and optimizing management to promote persistence of native aquatic organisms.

Evidence of an adaptive trade-off in a weedy, invasive grass grown near the edge of its distribution

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The rapid range expansion of some exotic invasive plants is thought to be facilitated by their ability to quickly adapt to the novel environmental conditions they experience in their new ranges. However, fitness trade-offs may constrain adaptation, especially at the geographic range periphery where genetic diversity may be low, thereby, restricting further range expansion. One important fitness trade-off is that of earlier flowering time. Flowering earlier has been found in plant populations growing near the periphery of their distributions. Life history theory predicts that plants that flower early will be smaller in size, which results in decreased reproductive output. We used the globally distributed, invasive plant Johnsongrass (*Sorghum halepense*) to determine whether populations originating from the range periphery (where Johnsongrass is rare) exhibit characteristics consistent with the adaptive trade-off between flowering time and reproductive output. We collected populations of Johnsongrass from the center, edge, and periphery of its distribution and grew them in a common garden experiment located near Blacksburg, VA. We found the periphery populations were half the size of the other populations and flowered 10 days earlier, but we did not find evidence of reduced reproductive output in the periphery populations. This suggests that there is a trade-off between flowering time and investment in growth, but this trade-off did not seem to affect the reproductive output of Johnsongrass. Further studies are needed to determine why Johnsongrass has not successfully colonized regions beyond the edge of its distribution.

Evolutionary mechanisms of toxin resistance in snakes and lizards

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Parallelism describes convergent evolution using a shared mechanism and can occur at multiple scales (i.e. at the molecular, phenotypic, and/or ecological levels). Convergent evolution of

toxin resistance in snake species is a well-characterized example of molecular parallelism. Tetrodotoxin (TTX), used as a chemical defense by some fish and amphibian species, causes paralysis by targeting vertebrate sodium channel proteins necessary for the propagation of action potentials in muscles. Nine types of sodium channel proteins are present in vertebrates, each with different kinetic properties and levels of tissue expression. Substitutions in a functionally conserved region of the sodium channel gene expressed in skeletal muscle (SCN4A) provide some snakes with resistance to high levels of TTX, and have evolved convergently in distantly related species that consume toxic amphibian prey. Resistance to TTX in SCN4A appears to have evolved over a relatively short timespan in snakes experiencing strong selective pressure from consuming toxic amphibians. In contrast, sodium channels expressed in heart muscle and sensory neurons acquired resistance before the split of the last common ancestor of snakes and lizards, and may be necessary to drive selection on skeletal muscle channels. Using the genome sequences of species representing major phylogenetic branches of the order *Squamata* (snakes and lizards) as well as the tuatara, we will gain insight into the evolutionary history of the entire voltage gated sodium channel gene family. This will shed light on the amount and scale of parallelism in this gene family and the mechanisms controlling convergent evolution under conflicting selective pressure.

Microbiome mediated plant-pollinator interactions

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Plants and their pollinators depend heavily on the synergy of one another. The majority of flowering plants require pollinators to ensure the spread of pollen and pollinators often depend on plants for pollen and nectar as a food source. In agriculture alone native pollinators contribute between \$4.1 to \$6.7 billion dollars annually. Woven into this relationship are microorganisms that form close relationships with their hosts forming the microbiome. The microbiome is intricately associated with the organismal health through processes such as nutrient acquisition and disease suppression. Recent studies have found that pollinators exchange microbes with the flowers they pollinate—leaving a microbial fingerprint. This suggests that flowers and their pollinators could have reciprocal influences on their associated microbes that have been shaped over evolutionary time. However, few studies have examined the impact of this reciprocal interaction on microbial community structure, eco-evolutionary dynamics, or plant health. This study aims to fill this gap through three specific objectives: 1) characterizing the floral and pollinator microbiome across several natural populations of *Solanum carolinense* and its pollinator *Bombus spp.*, 2) examining the same traits in

populations (paired with 1) of a congener *Solanum dulcamara* that was introduced less than 200 years ago, and 3) investigating the impact of the pollen microbiome on seed endophytic communities. By focusing on the microbial interactions between a native plant species *Solanum carolinense*, horsenettle, and an introduced species *Solanum dulcamara*, bitterweet nightshade and their pollinators, *Bombus* spp. in Virginia. This study will contribute to the body of knowledge on plant-pollinator interactions at the microbial level and help further determine how the microbiome is linked to plant and pollinator health.

Chemical defense gland evolution in a millipede Müllerian mimicry ring

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Apheloriine millipedes are common detritivores found in the undergrowth of Appalachian temperate forests. They exhibit an array of bold color patterns, which function as aposematic signals advertising their unpalatability to potential predators such as birds. The toxicity of these millipedes is due to their paired, bi-compartmental chemical defense glands, which produce a poisonous mix of hydrogen cyanide and benzaldehyde at levels sufficient to kill 18 pigeon-sized birds. Shared chemical defenses and color patterns have been noted in the group before, and a Müllerian mimicry ring among seven species in three different genera (*Apheloria*, *Appalachioria*, and *Brachoria*) has recently been documented in the Cumberland Mountain Thrust Block Region of Virginia, Tennessee, and Kentucky. In this mimicry ring, *Apheloria* was hypothesized to be the more toxic model, with *Appalachioria* and *Brachoria* mimicking *Apheloria* color patterns. However, the hypothesis of *Apheloria* as the model in this mimicry ring has not been directly tested. To investigate this question, we compared the size of the chemical defense glands in sympatric populations of the genera *Apheloria* and *Brachoria* as a proxy for toxicity. We found that the chemical defense glands of *Apheloria* were significantly larger than those in *Brachoria*, supporting the hypothesis that *Apheloria* acts as the more toxic model in the mimicry ring.

Sexually transmitted pathogenic bacteria as a cost of extra-pair activity to female birds

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Important questions in evolutionary and organismal biology often center around the trade-offs of different mating strategies. Up until the 1980s, most bird species were considered to be truly monogamous, or sexually faithful to a social partner. However, with recent molecular advances, the evidence suggests quite the opposite pattern: nearly 90% of bird species engage in fertile copulations outside of the social pair (i.e., extra-pair fertilizations). Sexually transmitted diseases have been suggested to be a cost of extra-pair fertilizations in birds for the past four decades, but has not yet been adequately tested. This research focuses on a local population of box-nesting tree swallows (*Tachycineta bicolor*), a species in which individuals have been shown to be socially monogamous, yet also engage in high rates of extra-pair fertilizations. We collected cloacal samples from adult male and female tree swallows during the 2016 breeding season, and subsequently extracted, amplified, and sequenced the bacterial DNA from those cloacal samples. Here, we present preliminary data that we used to answer the question: What is the relationship between the cloacal bacterial communities of males and females, in general, and of social pairs? With regard to cloacal bacterial communities, we found that 1) there is variation within sexes and 2) social pairs were not more similar compared to other sampled individuals in the same population. Our next step is to assess the relationship between cloacal bacterial communities and rates of extra-pair fertilizations. Ultimately, we hope to shed some light on the relationship between extra-pair fertilizations and the presence, prevalence, and potential pathogenicity of sexually transmitted microbes, with respect to fitness, in a wild avian population.

Implications of a changing climate on bird development

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Our changing climate may pose a threat to the early developmental environment of animals. The effect of climate change on developing reptiles is well-studied, and there is evidence that changes in incubation temperature can have substantial effects on offspring. In contrast, the effects of temperature changes on bird phenotypes have been historically overlooked because parents regulate incubation temperature. However, studies have shown that changes in the environment can affect avian parental incubation behavior, and that small changes in incubation temperature can affect avian offspring phenotypes. Yet, few studies have

investigated how environmental changes may directly and indirectly influence incubation temperature, and no studies have investigated how incubation temperature influences avian offspring behavior. We used wood ducks as a model system to address these questions. Our results show that wood duck nests with the largest clutch sizes and the lowest ambient temperatures led to the lowest incubation temperatures. We also found that ducklings incubated at 35 and 37°C exhibited bolder and more exploratory behaviors than those incubated at 35.8°C, while those incubated at 35°C were less successful at exiting the nest (a crucial behavior for wood duck ducklings) than those incubated at the other two temperatures. This research shows that environmental changes influence avian incubation temperature and thus, may influence offspring behaviors that are critical for survival. In this case, warming temperatures may be beneficial to developing birds, but future work should address how extreme weather events or changes in food availability due to climate change affect incubation temperature.

Mapping Climate Envelopes to Hypothesize Ecotypic Variation of an Invasive Plant

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Invasive plants cause an estimated 35 billion dollars in damage and control costs in the United States annually (Pimentel et al., 2005). Johnsongrass (*Sorghum halepense* Pers., Poaceae) is a global invasive species with a prominent range in the southern half of the continental United States. Over its 190-year invasion history in the U.S., it has shown a directional transition from agricultural to non-agricultural habitats (Sezen et al., 2016). Recently, agricultural and non-agricultural lineages were found to respond divergently to climate variables (Atwater et al., 2016). By studying human land uses as drivers of ecotypic divergence, we can begin to predict invader spread and physiology in the landscape with greater sensitivity.

In this project, U.S. Johnsongrass observations 1981-2018 from the Global Biodiversity Information Facility (GBIF) and the Early Detection and Distribution Mapping System (EDDMapS) were used to sample PRISM climate norm data for 1981-2010. The observations were then subset based on human land uses and the resulting climate envelopes were projected on the continental United States. This method found divergent climate envelopes based on temporal, (non)agricultural, land-use-change, and impervious surface subsetting. It also found three distinct cores within the range, which had previously been considered as largely an east-west dichotomy.

Geospatial evidence supports the connection between human land uses and Johnsongrass climate responses. These GIS analyses are a rationale for locating range cores with the highest likelihood of ecotypic variation for in-situ measurement of soil and plant community predictors of divergent adaptation.

Urbanization impacts nestling corticosterone but not offspring growth in song sparrows

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Urbanization represents a dramatic and relatively rapid change in environment, which animals may cope with through phenotypic plasticity. In previous studies, it has been shown that male song sparrows (*Melospiza melodia*) in urban habitats show higher levels of territorial aggression than their rural counterparts. Such differences in male behavior could have consequences for offspring, as territorial aggression can be traded off against paternal care. Therefore, we compared nestling growth, corticosterone (CORT) levels, and survival among three rural populations (N = 15 nests/30 nestlings) and two urban populations (N=19 nests/45 nestlings) of song sparrows near Blacksburg, VA. We found that nest predation was higher in rural habitats, based on evidence of disturbance at the nest site. Additionally, we found that nestling baseline CORT levels were significantly higher in rural habitats, though there were no differences in overall nestling growth rates. Finally, there was a non-significant trend towards increased nest parasitism by brown-headed cowbirds in urban habitats. These findings suggest that male territorial aggression does have consequences for offspring CORT levels. Additionally, these findings suggest that there are differences in relative risks of predation and nest parasitism across rural and urban habitats, which could potentially drive variation in male territorial aggression.

Whole-ecosystem experiments reveal differential responses of phytoplankton functional groups to epilimnetic mixing

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Phytoplankton blooms are increasing in lakes and reservoirs worldwide, causing detrimental effects on drinking water quality. One management strategy for controlling phytoplankton is epilimnetic mixing systems, intended to decrease surface scums by increasing water column turbulence. However, past work has demonstrated that the efficacy of epilimnetic mixing for decreasing phytoplankton biomass is equivocal. This may be because phytoplankton community responses to epilimnetic mixing are mediated by mixing effects on other ecosystem processes, such as nutrient dynamics and thermal stratification, and quick-sinking phytoplankton taxa may benefit from a well-mixed water column. To assess effects of epilimnetic mixing at the whole-ecosystem scale, we conducted two mixing experiments in a drinking water reservoir. We measured a suite of physical, chemical, and biological variables before, during, and after mixing and compared the results to a nearby, unmixed reference reservoir. We found that phytoplankton biomass, especially cyanobacteria, green algae, and cryptophytes, significantly increased after our first mixing event due to an increase of nutrients, likely from entrainment of sediments into the epilimnion. Total phytoplankton biomass did not significantly change after our second mixing event; however, phytoplankton community composition after the second mixing event exhibited a shift from taxa with filamentous morphology to smaller, rounder taxa. Our results suggest that phytoplankton responses to epilimnetic mixing are intertwined with turbidity and nutrient dynamics, and that these responses may vary depending on the timing of mixing and morphology of phytoplankton taxa. Whole-ecosystem dynamics and functional traits should be considered when managing phytoplankton biomass by epilimnetic mixing.

Disparate drinking water quality and compliance across urban and rural Virginia under the Safe Drinking Water Act

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Approximately 299 million Americans receive household drinking water from one of 51,350 community water systems (CWSs) under the Safe Drinking Water Act (SDWA). Despite a history of amendments and financial investment, repeated violations and noncompliance persists. This study hypothesizes that community exposures to drinking water contaminants are significantly different between rural and urban US communities. The goal was to analyze historic SDWA violations in Virginia to 1) understand the relationships between system size, rurality, and compliance and 2) evaluate the most prevalent drinking water contaminants.

Violation data from 1999-2016 for 1,135 Virginia CWSs were analyzed (n>9500 violations, source: Safe Drinking Water Information System). Systems were geocoded in ArcGIS, with the US Department of Agriculture's Rural-Urban Commuting Area (RUCA) codes defining rurality at the zip code level. As would be expected, small systems serving less than 3,300 people each had 64% of all health-based violations across the state while very large systems serving more than 100,000 people each had 0.07% of all health-based violations. Analyses of geocoded CWSs (n=671) indicated that rurality had a significant effect on total (Kruskal-Wallis, $\chi^2=22.39$, $p<0.01$) and monitoring and reporting violations ($\chi^2= 28.03$, $p<0.001$). Additionally, both health based and monitoring and reporting violations were significantly different between differently sized systems.

Confirmation that SDWA compliance differs by rurality suggests that rural communities may be more likely to be exposed to drinking water contaminants of health concern. Ongoing efforts will expand this analysis to include the influence of community demographics (e.g. race, % foreign born) on SDWA compliance.

Why do birds of different feathers flock together? A case study on a cooperatively breeding habitat specialist

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Birds are known to form flocks in numerous systems, many of which are mixed-species flocks. Individuals may choose to mixed-flock in order to increase foraging efficiency, limit intraspecific competition, or reduce predation. In the longleaf pine system, brown-headed nuthatch (*Sitta pusilla*) join mixed flocks during the nonbreeding season, but are subject to variable predator presence and food availability. I plan to record mixed-flocking rates of brown-headed nuthatch, as well as predator interactions at Marine Corps Base Camp Lejeune. Nuthatches will be color banded and surveyed using a combination of scan and focal sampling. Additionally, I will experimentally manipulate food availability by placing feeding stations in portions of the field site. I will then record station usage rates and flocking behavior surrounding these stations. I expect that tendency to join mixed flocks is inversely correlated to pine seed availability and individual territory quality. Alternatively, I expect mixed flocking to positively correlate with predator presence, particularly during the winter influx of migrant predators. Determining how these factors impact nonbreeding nuthatch behavior will inform population management strategies for improved winter survival.

Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

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For decades ecologists have contemplated the potential consequences of biodiversity loss, which has resulted in a rich literature searching for links between biodiversity and ecosystem function. Within this context, our research has aimed to understand the link between diversity and function by investigating the amphibian skin bacterial communities and their role in controlling the disease chytridiomycosis, caused by the fungus *Batrachochytrium dendrobatidis* (Bd). Chytridiomycosis is decimating many amphibian populations in the Neotropics. Thus, our work has focused on investigating the link between bacterial community structure and function in Panamanian amphibians. We conducted a field survey to examine six host species that vary in Bd susceptibility at a Bd naïve site, and a second survey to examine three non-susceptible host species across sites that varied in timing of Bd arrival. Bacterial community structure was assessed using 16S rRNA gene amplicon sequencing, and their potential function was assessed by using HPLC-MS to produce profiles of secondary metabolites. In addition, we also assessed inhibition of Bd growth by bacterial isolates cultured from these skin communities. Overall, we found host species-specific skin bacterial communities, and that these communities may vary among populations of the same species across sites. In addition, host species that are more susceptible to Bd differed in their skin bacterial communities from more resistant species. Moreover, the arrival of Bd at a site may result in shifts in bacterial community structure. However, metabolite profiles across species were not always distinct, suggesting that similar functions might result from different bacterial community structures.

Resource Use and Interspecific Interactions in a Namibian Cavity-nesting Community

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Cavity-nesting guilds are diverse communities of vertebrates and invertebrates found in forest ecosystems worldwide. Due to their dependence on tree holes for nesting, species in these communities are limited by an availability of suitable nest cavities. This dependence therefore leaves these species susceptible to forms of disturbance that diminish cavity availability, such as anthropogenic forest management, stochastic events, and climatic shifts. Namibia is the driest country in sub-Saharan Africa, with a landscape largely depauperate of large trees, the most common harborers of cavities. This community is threatened by numerous anthropogenic disturbances, including charcoal production, altered grazing and fire regimes, and increasingly frequent and severe droughts caused by climate change. To aid the conservation of this threatened community, we have embarked on a multi-year nest-web analysis to quantify community structure. Through this analysis, we will seek to describe the type and structure of available nest cavities, species-specific resource use preferences, and direct and indirect interactions between community members. By quantifying community structure, we will provide important information for land use managers to mitigate the impacts of anthropogenic disturbance on this community. We have also coupled our ecological research with a human dimensions study on wildlife perceptions of local communities. Using focus-group interviews, we are using emotional prompts as a way to identify a potential flagship species. By combining ecological and sociological research, we hope to generate both ecological management plans for conserving this community as well as sociological strategies to generate local support for a conservation campaign.

Time budgets of juvenile male Red-cockaded Woodpeckers before dispersal

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Natal dispersal is the movement of individual animals from a birth site to a breeding site. Often, before dispersal, juveniles explore outside their natal territory to gather information from the environment and conspecifics regarding habitats and conditions. Understanding the behavior of these individuals while they explore is key for understanding and predicting how a species interprets and interacts with the biotic and abiotic landscape, and is especially important for creating and implementing effective management strategies especially for endangered species, such as the Red-cockaded Woodpecker (RCW). The cooperatively breeding RCW is a federally listed endangered species endemic to open, southern pine savannah in the Atlantic and Gulf Coastal Plains of the United States. Male

RCWs have two dispersal syndromes: they can either delay dispersal and remain on their natal territory as non-breeding helpers, or disperse their first year in search of territories with open breeder positions. Dominance within broods plays an important role in determining which dispersal strategy a juvenile male will use. Dominant males almost always remain as helpers, while subordinates disperse their first year. Despite understanding dispersal outcomes of male and female RCWs, very little is known about the males behave during dispersal. Therefore, I followed dominant and subordinate juvenile males using radio-telemetry and made behavioral observations to determine the time budgets of these individuals. I found that subordinate and dominant juvenile males both foraged extensively. Juveniles spent most of their time foraging while foraging, especially in the morning, although dominant males tended to spend more time traveling than subordinate males. Also, subordinate juveniles spent time exploring cavities in other RCW territories, which dominant males did not.

Representing forest management in Earth System Models

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As the major terrestrial carbon sink forests are seen as a critical tool to help combat climate change. A quarter of the emissions reductions pledged in the Paris Climate Accords come from preservation and expansion of forests. Given the stakes it is critically important that we make wise choices in employing these mitigation approaches. In this context forest management techniques developed to increase timber production might be usefully repurposed to increase carbon sequestration. Forests both influence and are influenced by climate. Therefore, fully coupled Earth System Models (ESMs) must be used to fully understand the effects of the mitigation approaches that employ forests. Currently ESMs simulate forest management in a rudimentary manner. Some important management activities, like harvest rotation and fertilization, are not represented at all. We have completed the initial steps to incorporate these management activities into the Community Land Model, the terrestrial component of NCAR's CESM Earth System Model. We have altered the hierarchical representation of vegetation on the model's gridded land surface. This allows us to isolate portions of forest in a grid cell for management activities. In initial experiments, we have demonstrated the isolation of wood harvest onto a specified segment of forest, where previously it occurred everywhere. This lays the groundwork for increasingly relevant activities such as fertilization, fire exclusion, harvest rotations, as well as representing protected forest areas. We hope these improvements will increase the value of these models to decision makers in the climate policy arena.

Population trends in northern Madagascar's endangered and critically endangered lemurs: Should we be concerned?

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Habitat loss, hunting, and climate change continue to threaten Madagascar's lemurs. Despite the rapid creation of protected areas during the first part of the century, we still know precious little about lemur populations across the island. Three diurnal lemur species can be found across less than 440 km² of fragmented forests within the Loky-Manambato Protected Area. Critically endangered golden-crowned sifakas (*Propithecus tattersalli*) are endemic to the region and have been the focus of several studies across the protected area. Little is known about endangered crowned (*Eulemur coronatus*) and Sanford's brown (*E. sanfordi*) lemurs in the region. Standard line transects were used to survey these and other vertebrate species in a total of nine fragments from 2016-2017. Species densities and abundance were determined using the "Distance" package in Program R. Population estimates suggest a decline in sifaka populations since 2006/2008. However, local taboos seem to continue to protect this species from hunting. Here, we present the first estimates of crowned and Sanford's brown lemurs in the region. Evidence of continued forest loss, disturbance, and hunting of the two *Eulemur* species was found across all survey areas, even those that were conducted in strict conservation zones (*noyaux durs*). We suggest that increased patrols of conservation areas be conducted to prevent continued biodiversity loss in the protected area.

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Exploring group cohesion and social proximity in golden-crowned sifakas

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Traditionally, studies examining group cohesion in primates have taken a “boots and binoculars” approach. While observational data is effective in understanding primate social behavior, it is challenging and the data are limited by the amount of time the investigator can spend monitoring the troop. Commercially available tracking equipment is promising but their application limited due to high cost. To address this issue, we have designed a modular, open-source tracking collar, FitPET (“FITness, Proximity, Energetics, and Tracking”), that is capable of collecting data on primate cohesion and can provide truly innovative insights into how habitat structure and fragmentation influence group cohesion. To determine how primate social cohesion is impacted by landscape type and to ground-proof the use of our devices, we completed 7 full-day behavioral follows for eleven groups of golden-crowned sifakas (*Propithecus tattersalli*) in an array of rainforest and dry forest fragments surrounding Daraina, Madagascar (August-December 2017). Using scans at ten-minute intervals, we recorded activity, height, feeding information, nearest neighbor proximity, and group spread. Group spread was determined by measuring the distance between the farthest two individuals in each group. Overall, we observed a relationship between fragment type and group spread; with sifakas displaying decreased group cohesion in rainforest fragments. Now that we have an understanding of how *P. tattersalli* social cohesion differs between fragment types, we will be employing the use of our FitPET devices to automate our data collection and more effectively collect data on spatial dynamics and social interactions of sifaka groups.

Land use versus climate drivers of algal production in an oligotrophic lake: it depends on season

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Globally, lake water quality is decreasing as a result of global warming and excess nutrient loading from land use change (e.g. clearing of forests). Clear-water, or oligotrophic, lakes are particularly vulnerable to changes in water quality; they can “flip” to a low-water quality state

through the essentially irreversible process of eutrophication. To work toward maintaining oligotrophic lakes and the highly valuable ecosystem services they provide (e.g. drinking water and recreation), managers and scientists need to understand the relative contribution of land use and climate drivers to water quality change. Here, we address the question, how is land use and climate affecting water quality in an oligotrophic lake over 3 decades? Our study site is Lake Sunapee, which is the 3rd largest lake in New Hampshire. The lake experiences variable annual phosphorus loading, precipitation, and air temperature. Average annual air temperature is increasing at a rate of 0.04 °C per year (from 1979 to 2016; $r^2 = 0.36$). We calibrated and validated a 1-dimensional hydrodynamic model coupled with an aquatic ecosystem model to simulate lake dynamics over 3 decades. In analyzing each summer growing season, multiple linear regression analysis shows that summer (Jun-Jul-Aug) chlorophyll-a, a measure of algal production, is driven primarily by summer temperature (contributing to 91% of overall model fit), whereas fall (Sept) chlorophyll-a is driven primarily by spring (Mar-Apr-May) phosphorus loading (contributing to 83% of overall model fit). Unique drivers to algal production at different times of year have important implications for managing valuable oligotrophic lake ecosystems in the face of global warming and land use change.

Environmental dissemination of antibiotic resistance in dairy manure and compost-amended vegetable fields

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Increasing evidence links the widespread use of antibiotics in livestock production to the transfer of bacteria carrying antibiotic resistance genes (ARGs) to the broader environment. It is therefore critical to understand the persistence and mobility of both resistant microorganisms and associated genetic material in these systems in order to understand potential threats to consumers. We evaluated the effects of soil amendment type (inorganic fertilizer, raw dairy manure, composted dairy manure, or no amendment), vegetable type (lettuce, radish), and antibiotic use (pirlimycin and cephalosporin) of cattle manure-derived amendments on the incidence of culturable antibiotic-resistant fecal coliforms through a field-scale controlled plot experiment. Antibiotic-resistant culturable fecal coliforms were recoverable from soils across all treatments immediately following application, though persistence throughout the experiment varied by antibiotic class and time. Compost-amended soils had the highest levels of cephalosporin-resistant fecal coliforms, regardless of the antibiotic history of the cows

providing the manure. Significantly, higher levels of total, ceftazidime, and erythromycin-resistant fecal coliforms were recovered from compost-amended as compared to the raw manure-amended soils. Parallel quantification of resistance genes (*sul1*, *tet(W)*, *erm(B)*, *int11*) was used to confirm observed culturable trends. Soils amended with raw dairy manure yielded high relative *sul1* and *tet(W)* gene copies on Day 0, correlating with an observed spike in associated ARBs, and remained detectable for 113 and 39 days longer than resistant bacteria, respectively. Interestingly, *erm(B)* was not detected, despite detection of erythromycin-resistant bacteria in the soil and *erm(B)* in a parallel runoff study. This work is of particular interest given the relevance of fecal coliforms in tracking human pathogen risk in multiple environments (e.g., water, crops) throughout agricultural production.