

# ABSTRACTS

## IGC Symposium April 25, 2019

### Oral Presentations

#### ***Platform Session 1***

9:00 AM – 10:00 AM

Session Chair: Nicole Ward

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#### **Switchgrass as a Climate Change Mitigation Tool in Central Virginia**

**Authors:** Benjamin J. Ahlswede\* 1, Tom L. O'Halloran 2, R. Quinn Thomas 3

**Affiliations:** 1. Department of Biological Sciences, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 2. Department of Forestry and Environmental Conservation, Clemson University, Clemson, South Carolina 3. Department of Forest Resources and Environmental Conservation, Virginia Polytechnic Institute and State University, Blacksburg, Virginia

Switchgrass (*Panicum virgatum*) has emerged as an ideal bioenergy crop due to its ease of maintenance, high productivity, and potential for climate change mitigation. However, only a handful of studies have examined the year-round carbon dynamics of a switchgrass field, and these have typically been conducted with newly established fields, or on experimental plots with active management plans. Here we present intra- and inter-annual dynamics of carbon dioxide exchange from three growing seasons of eddy covariance observations above a mature and minimally managed switchgrass field in central Virginia. This field was a net-source of carbon to the atmosphere over the entire observation period. However, the field can switch from a sink to a source depending on weather conditions and harvest timing. This observation period includes the wettest year ever recorded for this region. This increase in precipitation enhanced respiration, but also reduced productivity leading to a marginally small source of carbon at the end of the observation year. Previous work has shown switchgrass to be a sink of carbon from the atmosphere. In order to evaluate the effectiveness of biofuel switchgrass as a climate change mitigation strategy, all potential conditions and management scenarios need to be considered.

**Analysis of antibiotic resistance genes and present microbial communities in agricultural soils amended with various manure-derived amendments**

**Authors:** Wind L.\* 1, Krometis L.-A. 1, Hession W.C. 1, Pruden A. 2

**Affiliations:** 1. Dept. of Biological Systems Engineering, Virginia Tech 2. Dept. of Civil and Environmental Engineering, Virginia Tech

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. The relative impacts of agricultural practices, climatological factors, and native soil microbiota on the local resistome is complex. The overall goal of the present study is to employ molecular “indicator”- and next-generation sequencing-based techniques to characterize the impacts of various manure-derived soil amendments on ARG profiles in agricultural soils. Observations of multiple resistance markers in tandem allows for a more holistic characterization of present soil microbial community composition and the potential impacts from common agricultural practices. In brief, fifteen 9-m<sup>2</sup> field plots were planted with lettuce and fertilized to test the effects of fertilizer type (inorganic, compost, raw manure) on the soil resistome. Soil samples were collected over 120 days, and quantitative polymerase chain reaction (qPCR), 16S rRNA gene amplicon sequencing, and shot-gun metagenomic sequencing were used to analyze the present soil microbial communities. ARGs (*sul1*, *tet(W)*, *erm(B)*) and the class 1 integrase gene (*intl1*) were monitored as “indicators” of anthropogenic sources of antibiotic resistance. Raw dairy manure amended soils yielded high relative *sul1* and *tet(W)* gene copies on Day 0, correlating with an observed spike in associated ARBs. Network analysis of the soil microbiome identified *rpoB2* as the most abundant plasmid-associated gene, which may prove to be useful targets for monitoring in agricultural scenarios. Analysis of the microbial community composition and broader metagenome is underway, with the goal of comprehensively comparing effects of the amendments on the soil taxonomic and functional profiles. These findings will provide insight on how ARGs potentially spread throughout agricultural soils by linking known microbial community presence and metagenomic profiles.

### **Forest disturbance alters soil microbial community structure and function in Appalachian ecosystems**

**Authors:** Ernest D Osburn\* 1, Jennifer D Knoepp 2, John E Barrett 1

**Affiliations:** 1. Dept. of Biological Sciences, Virginia Tech 2. USDA Forest Service, Coweeta Hydrologic Laboratory, Otto, NC

In Appalachian ecosystems, human disturbances such as forest clearcutting have been shown to alter rates of soil ecosystem processes such as carbon (C) and nitrogen (N) cycling. However,

effects of forest disturbance on soil microbial communities and relationships between altered microbial communities and ecosystem processes have not been examined. To address these questions, we selected four historically disturbed watersheds and four undisturbed reference watersheds at the Coweeta Hydrologic Lab in the mountains of North Carolina. In each watershed, we established six plots and sampled soils from each plot. We then determined concentrations of dissolved organic carbon (DOC), total dissolved nitrogen (TDN), ammonium (NH<sub>4</sub>), and nitrate (NO<sub>3</sub>) in all soil samples. We also determined rates of microbial C and N mineralization in laboratory incubation experiments. Finally, we isolated DNA from soil samples and assessed bacterial vs fungal dominance via qPCR and microbial community structure via sequencing of the 16s rRNA gene. Our results show reduced DOC concentrations and elevated inorganic N (NH<sub>4</sub>, NO<sub>3</sub>) concentrations in disturbed soils. Additionally, we found that microbial communities in disturbed soils displayed higher rates of C and N mineralization relative to reference soils. Finally, we found that disturbed soils had increased dominance of bacteria over fungi and that disturbed soil bacterial communities were distinct from reference soil bacterial communities. We suggest that higher rates of C and N cycling following forest disturbance may be attributed to increased abundance of copiotrophic microbial taxa (i.e. increased bacterial dominance) characterized by inefficient use of soil C and N resources.

## **Using Social Science to Understand the Relationship between Recreationists and State Wildlife Agencies**

**Authors:** Grooms, B. P.\* 1, Dayer, A. A. 1, and Peele, A. 2

**Affiliations:** 1. Dept. of Fish and Wildlife Conservation, Virginia Tech; 2 Conservation Management Institute, Blacksburg, VA

State wildlife agencies benefit from wildlife recreationists' financial contributions and support of agency conservation efforts. Yet, agencies currently face a changing stakeholder base, including declines in traditional sources of support (i.e., hunters and anglers), and increased interest for involvement from other stakeholders (i.e., birders and wildlife viewers). As such, research into recreationists' perceptions of agencies can help agencies better respond to them and engage them in conservation. For this reason, we investigated recreationists' trust and the perceptions of distributive justice of provided services of the Virginia Department of Game and Inland Fisheries (DGIF). We conducted two focus groups with each of four wildlife recreation groups (birders, wildlife viewers, hunters, and anglers), involving 83 recreationists. We found birders', wildlife viewers', and anglers' trust was rooted in positive, personal interactions with DGIF employees, and on positive perceptions of past effectiveness by the agency. Birders and wildlife viewers were generally less trusting of DGIF than hunters and anglers. Additionally, we found all recreation groups felt DGIF did not equally distribute services. These feelings were

more common in birders and wildlife viewers who felt their services were sometimes secondary to those for hunters and anglers. Results suggest DGIF focus on building trust with birders and viewers by forming positive, personal interactions. DGIF could also expand the availability of benefits to their broader stakeholder base to address concerns of equity. Doing so may help DGIF engage with new stakeholders, foster support in agency programs, and facilitate public participation in agency conservation efforts.

## Platform Session 2

10:30 AM – 11:45 AM

Session Chair: Brenen Wynd

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### **Ecological recovery following the end-Permian Mass Extinction recorded in Middle Triassic tooth assemblage**

**Authors:** Hoffman, D.K.\* 1, Edwards, H. 2, Barrett, P.M. 3, Nesbitt, S.J. 1

**Affiliations:** 1. Dept. of Geosciences, Virginia Tech, Blacksburg, VA 2. Dept. of Geology, University of Georgia, Athens, GA 3. Earth Sciences, Natural History Museum, London, UK

Mass extinctions provide a biological “reset” often linked to subsequent biological radiations, which are marked by species diversification and ecological specializations. However, the relative timing of species and ecological diversification is unclear. The radiation of archosauromorphs (birds, crocodylians, and their extinct relatives) following the end-Permian Mass Extinction provides a test for disentangling radiations. One measure of ecology in the fossil record is teeth through diet, although tooth assemblages immediately following the extinction are rare, limiting their utilization during this critical time. However, recent fieldwork in the Middle Triassic of Tanzania has revealed a tooth assemblage that partially fills this gap. To reconstruct the species composition of the assemblage we used in situ teeth of known taxonomic assignment and additional 31 isolated teeth of unknown species affiliation. Continuous measurements (observations = 71) produced a linear relationship of tooth height predicting tooth base ratio (=base length/base width). Using this relationship, we generated a morphospace in which the majority of isolated teeth fell within a zone of overlap shared by several species. The discrete method (observations = 67) of eleven binary characters removed the potential influence of size and reduces overlap among species. The majority of the isolated teeth fall within an overlap of two taxa morphospace. The significant overlap of tooth shape among species and overall similarities indicate that ecological diversification lagged behind species diversification in archosauromorphs. Though only a single locality, the methods used herein offer a promising lens to reconstructing ecological radiations and are readily transferable across Earth history.

## **Variation in seed germination traits of an invasive grass is explained by climate**

**Authors:** Rebecca Fletcher\* 1, Kayla Varnon 1, Jacob Barney 1

**Affiliations:** 1. School of Plant and Environmental Science, Virginia Tech

Seed germination is an essential life history event for most flowering plants, because it leads to subsequent generations and dispersal to new habitats. Because germination is one of the earliest phenotypes expressed by plants, the timing of seed germination in response to environmental cues can have important implications for seedling survival and lifetime fitness, as well as range dynamics. Variation in climate conditions throughout a species' range, especially invasive species which often span large geographic ranges, may promote adaptation of germination in response environmental cues such that germination timing is optimized in order to maximize fitness. We investigated germination in response to temperature using the invasive grass *Sorghum halepense* (Johnsongrass). Previous work with Johnsongrass has provided strong evidence of genetic and phenotypic differentiation associated with climate as populations have expanded increasingly northward. We collected seeds from 10 populations of Johnsongrass throughout its North American range and exposed them to temperatures ranging from 11°C to 48°C. We estimated the minimum ( $T_{min}$ ), maximum ( $T_{max}$ ), and optimum ( $T_{opt}$ ) temperature of germination. We found substantial differences between populations for all three temperature parameters. All three germination traits had a positive relationship with mean annual temperature suggesting that there has been divergence in germination response of Johnsongrass populations to local climate conditions. It is possible that adaptation of germination in response to environmental cues has been a contributing force in the range expansion of Johnsongrass.

## **Effects of freshwater salinization and associated base cations on fecal indicator persistence and bacterial community structure**

**Authors:** DeVilbiss, S.E.\* 1, Badgley, B.D. 1, Steele, M.K. 1

**Affiliations:** 1. School of Plant and Environmental Sciences; Virginia Tech

Anthropogenic activities including agriculture, urbanization, and surface mining have been increasing total salinity and associated base cations in surface waters worldwide. It is well documented that large increases in salinity (i.e. freshwater to marine) significantly decrease the

persistence of the fecal indicator *E. coli* and alter aquatic bacterial community structure. However, linkages between small increases in salt concentrations within the freshwater range ( $\leq 1,500 \mu\text{S/cm}$ ) and bacterial surface water quality have yet to be explored. Further, effects of different types of salts and their associated base cations (Ca, Mg, K) on aquatic bacterial ecology remain unknown. Through a series of controlled mesocosm studies, we demonstrate that freshwater salinization increases the persistence of *E. coli* at very low salt concentrations ( $<200 \mu\text{S/cm}$ ), which is opposite the trend observed over broad salinity gradients. Specific base cations also had a significant effect with Mg increasing *E. coli* persistence by up to 40%. Additionally, different base cations had significant, differential effects on freshwater bacterial community structure. These results indicate that low levels of freshwater salinization may exacerbate bacterial impairments and alter bacterially mediated ecosystem functions. Effects may be magnified in watersheds with high Mg concentrations. Implications include: 1) reducing salt loads to surface waters may reduce bacterial impairments and 2) a more nuanced approach to salinity research and management that considers salt sources and types rather than total salinity may be required to preserve surface water quality.

### **Forest Management in Space and Time, When it Matters and When it Doesn't**

**Authors:** Rady, J.M.\* 1, Ahlswede, B.J. 1, Thomas, R.Q. 1

**Affiliations:** 1. Forest Resources and Environmental Conservation, Virginia Tech

Managed forests differ from unmanaged “natural” forests in ways that are relevant to climate. By manipulating forests to maximize timber production land surface properties and carbon fluxes are altered in time and space. Despite the potential implications for climate, the Earth System Models (ESMs) used to examine the climate influences of forests and land-use/land-management at global scales capture few aspects of forest management. To explore the potential importance of forest management to climate we conducted experiments using the Community Land Model (CLM) Version 5.0 within the Community Earth System Model. We changed the CLM’s assumptions about how wood is harvested in order to simulate protected areas (e.g. national parks, conservation lands) and clear-cut harvest rotations and examined the impact on forest carbon stocks, structure, and surface energy fluxes. We found that removing wood from a reduced area of forest caused limited changes to model output. On the other hand, we found that harvesting wood in clear-cut rotations caused notable changes in carbon stocks and surface energy fluxes. This suggests that the uniform approach to wood harvest in the CLM may lead to overestimation of forest biomass and carbon sequestration. Furthermore forests with rotational harvest show a different response to changing climate in the twenty first century. This work is a step towards better understanding how human manipulation of forests

influences climate and allows the further exploration of how altering these practices might be used to mitigate climate change.

### **Amphibian translocations: skin microbiome, body condition and disease status**

**Authors:** Angie Estrada\* 1, Daniel Medina 1, Brian Gratwicke 2, Roberto Ibáñez 3, Lisa K. Belden 1

**Affiliations:** 1. Department of Biological Sciences, Virginia Tech 2. Smithsonian's National Zoo & Conservation Biology Institute 3. Smithsonian Tropical Research Institute, Panama

Beneficial skin bacteria can protect amphibians against *Batrachochytrium dendrobatidis* (Bd), a deadly pathogenic fungus that is one of the largest threats to amphibians worldwide. For many 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 it is unknown how skin microbiome change once captive-bred individuals are re-exposed to natural habitats. Thus, to inform the development of beneficial bacteria-based treatments and future captive-to-wild translocation efforts, we aimed to assess the changes that occur in the bacterial communities of *Atelopus limosus*, a critically-endangered species, following soft-release to a site where the species historically thrived. 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. Frogs were housed in mesocosms to be monitored and sampled through time and next-generation sequencing technology was used to identify bacterial taxa. We found significant variation in skin microbiome once exposure to natural conditions occurred. Moreover, after only two weeks, reintroduced and wild individuals had more similar skin microbiomes. Body condition decreased and a small proportion of frogs got infected with Bd but mortalities were not associated with weight loss nor disease status. These preliminary findings suggest that skin-associated microbiomes of captive-bred amphibians can be restored, but future research needs to address whether these changes in bacterial structure ultimately result in higher survival and Bd protection of captive-bred amphibians.

## **Platform Session 3**

1:00 PM – 1:45 PM

Session Chair: Sydney Hope

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## **Ecological recovery following the end-Permian Mass Extinction recorded in Middle Triassic tooth assemblage**

**Authors:** Zach Martin\* 1, and Paul Angermeier 1,2

**Affiliations:** 1. Department of Fish and Wildlife Conservation, Virginia Tech 2. U.S. Geological Survey, Virginia Cooperative Fish and Wildlife Research Unit, Virginia Polytechnic Institute and State University, Blacksburg, Virginia

Spawning behaviors represent an understudied bottleneck to fitness in stream fishes and play a mechanistic role in how substrate embeddedness leads to local extirpations. For example, embeddedness may limit reproductive success of cavity-nesters by reducing optimal nesting space underneath rocks. We designed two laboratory experiments, using cavity-nesting fantail darters, to test effects of embeddedness on oviposition. We placed spawning pairs in Living Stream tanks for five-day trials with sand as a bottom substrate and 6-in x 6-in ceramic tiles as potential nest substrates. We presented fish with four “embeddedness” treatments vary in degree of tile burial and availability of a benthic cavity. One experiment presented spawning pairs (n=120; 30 per treatment) with one tile and one treatment; oviposition (0/1) and clutch size were responses. The second experiment (n=90) presented spawners with four tiles (one per treatment); nest-rock choice, oviposition, and clutch size were responses. Spawners from both experiments oviposited on tiles of all but the most embedded treatment, and most commonly on tiles lying flat on sand with a cavity provided. Four spawning pairs excavated cavities and oviposited on moderately embedded tiles. Spawners also oviposited on tank walls; in experiment one, these instances coincided with the two most embedded treatments. Our observations suggest this tolerant darter has limited ability to spawn in habitats smothered by fine sediments. The nonlinear, negative relationship between embeddedness and reproductive success we found conflicts with traditional assumptions made by researchers, and ultimately managers, about the role of sediment pollution in reproductive failure and extirpations.

## **Can agricultural practices mitigate climate change? The impact of ‘no-till’ practices on soil carbon using an Earth system model**

**Authors:** Michael W. Graham\* 1, R. Quinn Thomas 2, Danica L. Lombardozzi 3, Megan E. O’Rourke 4

**Affiliations:** 1. Geospatial and Environmental Analysis Program, Virginia Tech 2. Dept. of Forest Resources and Environmental Conservation, Virginia Tech 3. National Center for Atmospheric Research, Boulder, CO 4. School of Plant and Environmental Sciences, Virginia Tech



Soil tillage is a ubiquitous management practice on croplands globally, and is thought to have historical impacts on climate through accelerated decomposition of soil C and increased CO<sub>2</sub> emissions on agricultural land. Conservation tillage (e.g. 'no-till') has been proposed as a mechanism for mitigating climate change through increased soil C storage on croplands. The magnitude of these effects remains unknown and likely varies through space and time. Earth system models (ESMs) are useful tools to understand the spatial and temporal impacts of tillage, though few studies have examined different soil tillage practices in ESMs. ESMs tend to underestimate historical C fluxes and aggregate biogeochemical impacts of land management practices on climate relative to empirical records. Here we use the Community Land Model (CLM), the land component of the Community Earth System Model, to assess 1) biogeochemical effects of soil tillage by testing the global sensitivity of soil C stocks in CLM to intensive conventional tillage practices of different intensities over the historical time period (1850-2014), and 2) climate change mitigation potential of conservation tillage practices by evaluating the sensitivity of CLM soil C stocks to lower levels of tillage intensity associated with conservation tillage practices for a future climate scenario (2014-2100). Results indicate that increasing tillage intensity increases soil C decomposition rates; total losses in soil C due to intensive tillage practices are 17 Pg C for the historical time period, or 11% of estimated historical C emissions from land use change. Larger differences in tillage intensity and lower decomposition rates for conservation tillage relative to intensive tillage results in greater soil C storage over the future climate scenario. Historical losses are tightly coupled temporally and spatially with land use change to crops and losses due to tillage increase over time with cropland expansion. These results show that carbon impacts of tillage depend on parameters governing the decomposition rates when tillage is applied, as lower tillage intensities have smaller soil carbon impacts.

### **Relative importance of top-down versus bottom-up control of phytoplankton vertical distribution in north temperate lakes**

**Authors:** Mary E. Lofton\* 1, Taylor H. Leach 3, Beatrix E. Beisner 2, and Cayelan C. Carey 1

**Affiliations:** 1. Department of Biological Sciences, Virginia Tech, Blacksburg, VA, USA 2. Department of Biological Sciences, Rensselaer Polytechnic Institute, Troy, NY, USA 3. Department of Biological Sciences, University of Québec at Montréal, Montréal, QC, Canada

Many freshwater and marine ecosystems exhibit deep chlorophyll maxima, in which phytoplankton biomass is most concentrated below the water surface. In lakes, these deep layers of biomass are hypothesized to be either controlled by nutrient and light concentrations or zooplankton grazing pressure in surface waters. However, few studies have explicitly compared the importance of both bottom-up and top-down forces on vertical distributions of

different phytoplankton groups. We collected fluorescence-based depth profiles of four phytoplankton spectral groups and a suite of environmental data (zooplankton, total phosphorus, temperature, and water color) from 56 dimictic lakes in Québec, Canada at the height of summer stratification in 2004 and 2005. We calculated several phytoplankton vertical distribution metrics for each spectral group and used regression trees to assess the most important driver of phytoplankton vertical distributions at each time point. We found that while bottom-up drivers control most characteristics of phytoplankton vertical distributions, zooplankton abundance is the most important driver of the depth of chlorophyll maximum. Furthermore, vertical distributions of various phytoplankton spectral groups respond to different drivers, which may be related to the life history of these taxa. For example, zooplankton emerged as the most important driver for two of three vertical distribution metrics for brown algae, a spectral group containing taxa that are known to be particularly nutritious and therefore a preferred food source for zooplankton. Our results provide empirical evidence to support both top-down and bottom-up control of deep chlorophyll maxima in lakes during the stratified period.