



Colorado State University



Ecology of  
**SOIL  
HEALTH**  
SUMMIT



**SOIL  
ECOLOGY  
SOCIETY**

2017 Summit + SES Meeting

June 5th - 9th

@ Colorado State University

Fort Collins, Colorado



Ecology of  
**SOIL  
HEALTH**  
SUMMIT



**SOIL  
ECOLOGY  
SOCIETY**

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**W**elcome to the Ecology of Soil Health Summit and the biennial meeting of the Soil Ecology Society. This meeting comes at a time when interest in soil health—a concept that embraces not only the importance of soil organic matter content and physical structure, but also the key role of soil biology for productive and efficient agroecosystems—is rapidly growing. In parallel, our scientific understanding of the ecology of the soil system has advanced tremendously in recent years, in many cases challenging longstanding paradigms. This international summit provides a unique opportunity to advance the development and implementation of science-based programs that enhance Soil Health.

I hope that all meeting participants come away with a broader perspective, new ideas and new collaborators. It has been my pleasure to help organize this meeting, and I thank you for joining us.

A handwritten signature in blue ink that reads "Matt Wall" with a long, sweeping underline.

Matthew Wallenstein, PhD  
President, Soil Ecology Society  
Director, Innovation Center for Sustainable Agriculture



**Colorado State University**

# Acknowledgements

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Chairman Matthew Wallenstein

Program Assistant Laurie Richards

Soil Ecology Society Conference Committee Loren Byrne

Samantha Chapman

Jen Krumins

Michael Weintraub

Ecology of Soil Health Summit Committee Nicholas Goeser

Mary Beth Miranda

Whendee Silver

Allison Thomson

Local Conference Committee Charlotte Alster

Courtland Kelly

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Summit Supporters

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The Soil Ecology Society (SES) is an international professional organization dedicated to furthering the science, education and awareness of soil ecology and the importance of soils for human and environmental well-being.

## *Commitment to Diversity*

Just as healthy soils rely on interactive networks of incredibly diverse organisms, SES depends on all dimensions of human diversity. SES actively promotes participation and inclusion of all individuals regardless of age, gender, gender identity, race, cultural background, religion, physical ability, sexual orientation, professional status, geographic location, and all other characteristics that make our members unique. We strive to cultivate a scientific society of excellence built on mentorship, encouragement, tolerance, and mutual respect. SES is committed to proactively rejecting and denouncing prejudice and stereotyping whenever it is encountered in the Society or the profession.

### Soil Ecology Society Awards 2017 (sub-committee chair, Becky Ball)

Career Achievement Award- Mary Firestone,

Service Award- Deborah Neher

Early Career Research Award- Thomas Crowther

### Parkinson Travel Awards (sub-committee chair, Sam Chapman)

Lea Carlesso, Roberto Carrera-Martinez,

Martha Mary Gebhardt, Brittany

McAdams, Daniel Kane, Matthew Reid

### Board of Directors 2015-2017

Matthew Wallenstein (President)

Stuart Grandy (Past-President)

Michael Weintraub (President Elect)

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Jennifer Krumins (At-Large)

Loren Byrne (Communications)

Amanda Daly (Student Member)



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To feed increasing global populations, global crop production will need to double in the coming decades while minimizing environmental impacts. New innovations are needed to meet emerging sustainability metrics related to nutrient use efficiency, greenhouse gas emissions, soil carbon sequestration without sacrificing yield and farmer profit. To advance truly sustainable agriculture, new technologies and practices must be not only developed, but also broadly adopted.

Healthy soils are critical to sustainable farming systems, yet 40% of our agricultural soils are degraded. Agronomic practices and technologies that rebuild our soils can enable enhanced productivity with decreased inputs. Healthy soils are teeming with microbes that enhance nutrient use efficiency and improve plant health—harnessing this natural plant-microbe interaction can hold the key to enhanced farm productivity and sustainability. ICSA's objective is to catalyze innovations that advance sustainable agriculture and soil health through partnerships with industries, governments, grower organizations, and other academic institutions.

The hallmark of our unique approach is an integrated systems view of agricultural technology development, adoption and implementation. We combine cutting-edge scientific expertise in soil science, plant biotechnology, the microbiome, and big-data analytics with rigorous socioeconomic analyses. Examples of our current initiatives:

- Integration of cutting-edge crop and economic models to optimize production systems
- Application of biogeochemical models to optimize nutrient use efficiency and minimize greenhouse gas emissions

- An integrated economic and biophysical assessment of organic waste products for soil quality;

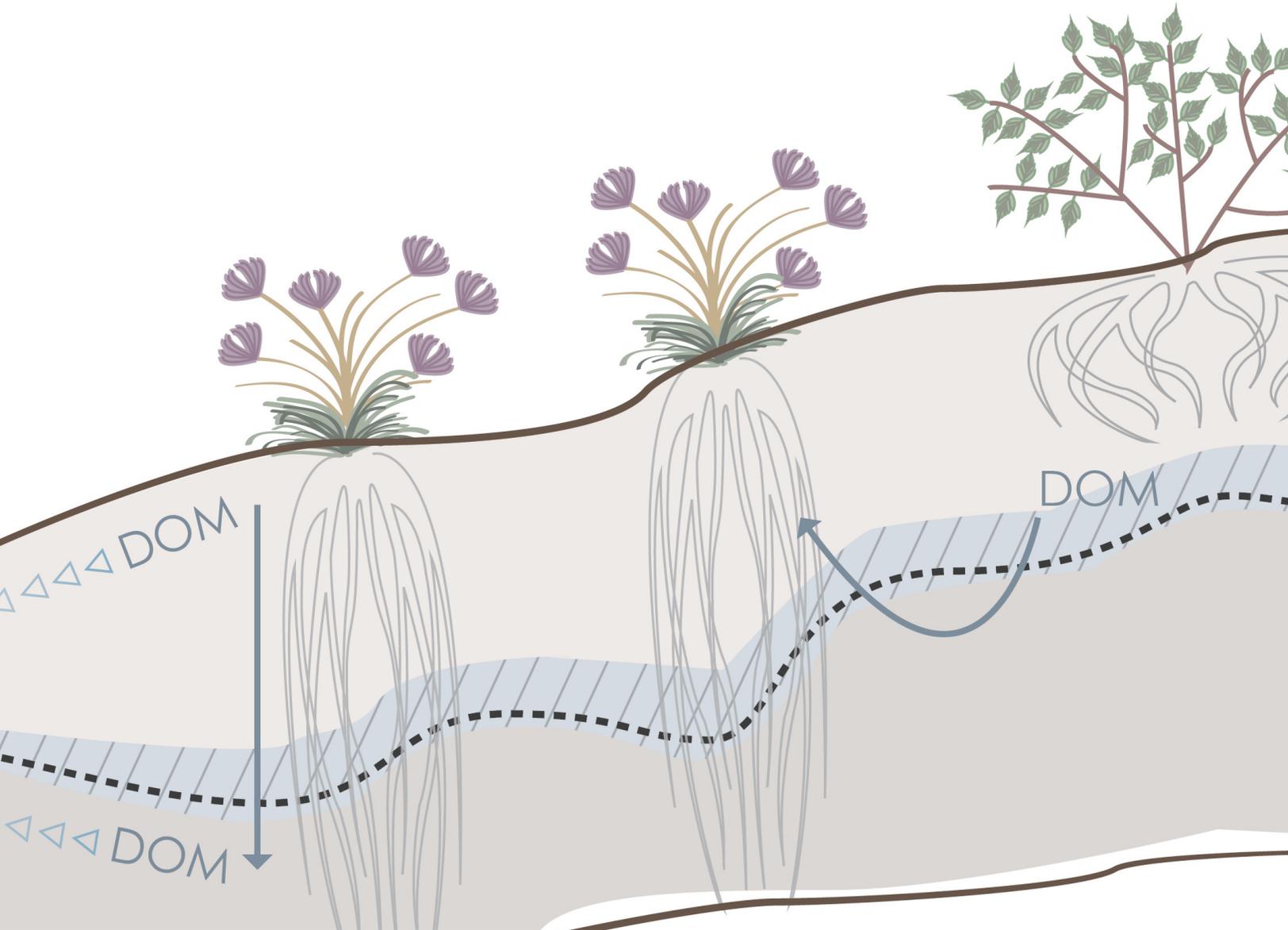
- Development of training programs for the next generation of agricultural innovation scientists;

- Development of below-ground sensor technologies to improve understanding of plant-soil-microbe interactions.

We seek to expand and strengthen our partnerships with corporations and NGO's in order to incorporate the scientific best practices into sustainability incentive programs, to provide training, and to commercialize new innovations. ICSA aims to be the premier global center for practical innovations in sustainable crop production.



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## Event Agenda

June 5th - 7th

@ Colorado State University  
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# Monday June 5th

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*Lory Student Center, Ballroom 350 C & D, Colorado State University*

**2:00** Welcome: Matthew Wallenstein, Director, Innovation Center for Sustainable Agriculture;  
President, Soil Ecology Society; Associate Professor, Colorado State University

Plenary session: Overview of Soil Health Science & Challenges

**2:30** Michael Doane, The Nature Conservancy

**3:00** Wim van der Putten, Head, Depart of Terrestrial Ecology, Netherlands Institute of Ecology  
Soil health: from ecological concepts to the Holy Grail of sustainability

**3:30** Esther Ngumbi, Auburn University  
Harnessing science-based soil solutions to revolutionize African Agriculture: Challenges and opportunities.

**4:00** Moderated Panel Discussion: What is soil health? How do we manage it?

Miles O'Brien, Moderator

*Keynote panel discussion moderated by Miles O'Brien, Emmy-award winning veteran independent journalist who focuses on science, technology and aerospace. He is the science correspondent for the PBS NewsHour, a producer and director for the PBS science documentary series NOVA, and a correspondent for the PBS documentary series FRONTLINE and the National Science Foundation Science Nation series*



# Monday June 5th (Continued)

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*Lory Student Center, Ballroom 350 C & D, Colorado State University*

## **4:30** IGNITE Session 1: The Science of Soil Health

*5 minute lightning talks; selected from submitted abstracts from The Soil Ecology Society*

*Jessica Gutknecht*

*Is your farm ready for the next storm? Soil health as a win-win for sustainability and resiliency to climate change*

*Stephen Wood*

*Can different types of organic matter can have contrasting effects on soil health?*

*Matt Ruark*

*Why isn't soil ecology considered when developing nitrogen fertilizer recommendations?*

*Loren Byrne*

*Soil health fosters student engagement and deepens environmental literacy in soil ecology education*

## **5:00** Poster Session and reception (appetizers and open bar)



# POSTER SESSION I

Ballroom B, Lory Student Center

5:00 – 7:00 PM

S1.1 Kerri Steenwerth, Rachel Greenhut, \*Francisco Calderon

Fine soil organic matter fractions in wine grape vineyards (Napa, CA) reflect distinctions in soil microbial community composition

S1.2 Lisa Windom, Maria Dragila, Noam Weisbrod

Carbon dioxide sequestration in karst micro-fissures: the solution of a droplet

S1.3 Catherine Stewart, Damaris Roosendaal, Karolien Deneff, Louise Comas, Gautam Sarath, Virginia L. Jin, Marty Schmer

Seasonal switchgrass ecotype contributions to soil organic carbon, deep soil microbial community composition and rhizodeposit uptake during an extreme drought

S1.4 Adi Oren

Examination of residual chloroform interference in the measurement of microbial biomass C by fumigation-extraction

S1.5 Michael Allen, Michael Taggart, George Rothbart, Thomas Harmon, Rebecca Hernandez, Philip Rundel

Peering into the Soil Black Box: A soil ecosystem observatory by rhizosystems, LLC.

S1.6 Emily Webster, Amélie Gaudin, Mirjam Pulleman, Pablo Siles, \*Steven Fonte

Establishment of improved pastures supports early indicators of soil restoration in low-input agroecosystems of Nicaragua

S1.7 Adam Cobb, Gail Wilson

The influence of agricultural practices on the abundance of arbuscular mycorrhizal fungi in rural eastern Zambia

S1.8 Terry Woodford-thomas, \*Sandra Arango-Caro

MO DIRT - Missourians Doing Impact Research Together - A citizen science project to monitor soil health in the state of Missouri

S1.9 Cam Gudmundson, Louise Egerton Warburton

Soil aggregation and organic matter stabilization in green roof systems and implications for C sequestration

S1.10 Daniel Kane

Estimating soil carbon with open-source VNIR spectroscopy

S1.11 Edward Ayres, Natchaya Durden, David Durden, Monique Leclerc, Josh Roberti  
Mitigating the impact of slow sensor response times on calculating soil CO<sub>2</sub> fluxes from NEON's soil CO<sub>2</sub> measurements

S1.12 Adam von Haden, Christopher Kucharik, Randall Jackson, Erika Marín-Spiotta  
Changes in physical protection of soil organic matter following five years of biofuel cropping system cultivation: soil texture matters

S1.13 Phil Murray, Jennifer Dungait, Umran Akkan, Stuart Norris  
Long-term land use change and impacts on soil faunal diversity

S1.14 Sudan Kariuki, Mitch McClaran, Rachel Gallery  
How does recreational camping affect cover mediated soil microbial activity?

S1.15 Daniel Almeida Melman, Courtland Kelly, Joel Schneekloth, Francisco Calderon, Steven Fonte  
Conservation agriculture enhances soil quality and function in an irrigated cropping system of Eastern Colorado

S1.16 Courtland Kelly, Meagan Schipanski, Wilma Trujillo, Daniel Melman, Angie Moore, Steven Fonte  
Soil health implications of grazed vs. ungrazed cover crops in the U.S. high plains

S1.17 Tucker Andrews, \*Deborah Neher, Thomas Weicht  
Microbial ecology of composting bedded pack

S1.18 Emmanuel Deleon, Troy Bauder, Steven Fonte, Erik Wardle  
Conservation tillage impacts on soil quality parameters under furrow irrigation

S1.19 Diana Vargas-Gutierrez, John Zak, Veronica Acosta-Martinez, Bobbie McMichael  
Reduction in daily soil temperature range increase microbial community dynamics in a dryland cotton production system in west Texas

S1.20 Lea Carlesso, Graham Hartwell, Karl Ritz, Phil Murray  
Responses to soil mesofauna to agricultural practices and arable field-margin management

S1.21 Lea Carlesso, Andrew Beadle, Graham Hartwell, Debbie Sparkes, Karl Ritz, Lianhai Wu, Phil Murray  
Impact of compaction on decomposition in an arable field and possible improvement by managing the headland.

S1.22 Sarah Evans  
Empirical evidence that passive microbial dispersal maintains soil community and ecosystem function

S1.23 Pablo Tovar, Veronica Acosta-Martinez, John Zak  
Soil microbial dynamics in a long-term sustainable cotton for semi-arid West Texas

S1.24 Gordon Custer, William Stump, Linda van Diepen

Rhizosphere and bulk soil microbial dynamics in Engelmann Spruce stands in response to Spruce beetle attack

S1.25 Kholoud Ghanem

How bed design in a dryland cotton system can influence subsequent microbial dynamic

S1.26 Bethany Avera, Charles Rhoades, Francesca Cotrufo

Investigating changes in soil organic matter pools following bark-beetle outbreak and salvage logging: Implications for soil organic matter formation

S1.27 Brittany McAdams, Sylvie Quideau, Mathew Swallow, Lisa Lumley

The influence of invasive earthworms on oribatid mite assemblages in a boreal aspen stand

S1.28 Luci Wilson, Gail Wilson, Karen Hickman

Consequences of invasion by *Bothriochloa bladhii* and implications for tallgrass prairie restoration

S1.29 Joanna Carey, Jianwu Tang, Kevin Kroeger, Pamela Templer

Uniform response of soil respiration to experimental temperature manipulation

S1.30 Noelle Espinosa, \*Rachel Gallery

Stability of microbial activity in an experimentally warmed dryland

S1.31 Paul Brewer, Francisco Calderon, Merle Vigil, Joseph von Fischer,

Impacts of moisture, soil respiration, and agricultural practices on gross CH<sub>4</sub> production in upland soils measured by stable isotope pool dilution

S1.32 Lisa Tiemann, Nzube Egboluche

Long- and short-term nitrogen additions increase decomposition of cover crop residues in agricultural soils

S1.33 Emily Kyker-Snowman, Will Wieder, Stuart Grandy

The Microbial-MIneral Carbon Stabilization model with coupled N cycling (MIMICS-CN) simulates litter decomposition and soil organic matter dynamics at landscape scales

S1.34 Daniel Revillini, Bo Stevens, Kara Gibson, Aradhana Roberts, Peter Motyka, Nancy C. Johnson

Committee for Evidence-Based Action: Educating the public and policy-makers for a scientifically sound future

S1.35 Martha Gebhardt, Elizabeth Sparks, Rachel Gallery

Inquiry-based STEM education for high school students: strengths, possibilities, and opportunities to get involved

S1.36 Martha Gebhardt, Rachel Gallery

Woody shrub encroachment alters ecosystem processes: Linking imaging spectroscopy and microbial biogeochemistry

S1.37 Caley Gasch

Earthworm distribution and demographics along a naturally occurring salinity gradient

S1.38 Ryan Lancione

Understanding interactions between nitrogen-fixing bacteria and switchgrass for sustainable biofuel production

S1.39 Zander Venter, Samantha Luise Scott, Johann Strauss, Karin Jacobs, \*Heidi Hawkins

Increasing crop diversity increased soil microbial activity, N-sourcing and crop N, but not soil microbial diversity

S1.40 William Salas, Stephen Hagen, Ian Cooke

Operational tillage information system: Tracking conservation practices at field to watershed scales

S1.41 Rachel Bechtold, Anuradha Ghosh

Bacterial Diversity of an Abandoned Coal Mine Soil in Southeast Kansas

S1.42 Na Yin, Roger Koide

Mechanism of non-additive heterogeneous litter decomposition

S1.43 Antreas Pogiatis, John Klironomos, Pat Bowen, Miranda Hart, Taylor Holland

Comparative response of six grapevine rootstocks to inoculation with arbuscular mycorrhizal fungi

S1.44 Adam Langley, Brendan Kelly, Samantha Chapman

Realistically simulating the effects of oxidation on soil decomposition

S1.45 Megan Foley, Adam Langley

Does microbial community composition influence decomposition in wetland ecosystems?

## Tuesday June 6th

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*Lory Student Center, Ballroom 350 C & D, Colorado State University*

- 8:30 Steven Tucker, AgriForce Seed
- 9:00 Ami Gunasekara, Manager, Office of Environmental Farming and Innovation  
California Department of Food and Agriculture
- 9:20 Matt Carstens, Senior VP, SUSTAIN at Land O' Lakes
- 9:40 Nick Goeser, Director of Soil Health and Sustainability, National Corn Growers Association
- 10:00 Break
- 10:30 Jennifer Moore-Kucera, USDA NRCS
- 10:50 Allison Thomson, Science & Research Director, Field to Market
- 11:20 Moderated Panel Discussion: What can we do now to enhance soil health?  
Moderator: Luke Runyon, Harvest Public Media
- 12:00 Lunch
- 1:30 Wayne Honeycutt, CEO, Soil Health Institute
- 1:50 LaKisha Odom, Director, Foundation for Food and Agriculture Research
- 2:10 Jacob Parnell, NovoZymes
- 2:30 Break



## Tuesday June 6th (Continued)

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*Lory Student Center, Ballroom 350 C & D, Colorado State University*

- 3:00** Innovations in Soil Health:  
Dan Morash, CEO, California Safe Soil  
Colin Bell, Co-Founder & Chief Growth Officer, Growcentia, Inc.  
Brian Buege, Head of Technology, CoolPlanet, Inc  
Virginia Ursin, Indigo Ag  
Diane Wu, Co-Founder, Trace Genomics
- 4:00** Panel Discussion: What is the role of startups in enhancing soil health?  
Moderator: Greg Graff, Associate Professor of Agricultural Economics, CSU
- 4:30** IGNITE Session 2: The Science of Soil Health  
5 minute lightning talks; selected from submitted abstracts from The Soil Ecology Society
- Joseph Blankinship, Corey Lawrence  
Nurturing a mechanistic view of soil health
- Aradhana Roberts, Michelle Mack, Nancy C. Johnson  
Eighteen years of mob-grazing increases soil carbon in a semi-arid grassland
- Steven Fonte  
Soil macrofauna as drivers of soil and ecosystem function Ignite Sessions
- Felicity Crotty, Chris Stoate  
Understanding how to harness the power of underground livestock Ignite Sessions
- Rachel Rubin, Kees Jan Van Groenigen, Bruce Hungate  
Plant growth promoting rhizobacteria are more effective under drought: a meta-analysis



## Tuesday June 6th (Continued)

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*Lory Student Center, Ballroom 350 C & D, Colorado State University*

**5:00** Poster Session II and Mixer

**7-10** Ecology of Soil Health Summit Banquet  
Ballroom 350 CD

# POSTER SESSION II

Ballroom B, Lory Student Center

5:00 – 7:00 PM

- SII.1 Thomas Forge, Tristan Watson, Paige Munro, Denise Neilsen, Gerald Neilsen, Louise Nelson  
Soil management practices to enhance soil health and early growth of sweet cherry planted into old orchard land
- SII.2 Maxwell Helmberger, Kyle Wickings  
Microarthropod response to foot traffic in sports turf
- SII.3 Pingting Guan, André L.C. Franco, Osvaldo Sala, Diana Wall  
Community composition of free-living soil nematodes under anomalous precipitation across sites
- SII.4 Kevin Butt, \*Mac Callaham  
Earthworms from soils developed below long term experimental plantations at Holt Down, Southern England
- SII.5 Mac Callaham, Sophia Bonjour, Brent Brock, Clinton Meyer, Bruce Snyder, Matt Whiles  
Periodical cicada expansion lags, but matches, woody plant encroachment in tallgrass prairie landscapes
- SII.6 Daniel Revillini, Peter B. Reich, Nancy C. Johnson  
Elucidating the importance of bacterial network connectivity from a long-term environmental change experiment
- SII.7 Newton Lupwayi, Derrick Kanashiro, Andrea Eastman, Xiyang Hao  
Manure but not N fertilizer improved biological soil health after 38 annual applications
- SII.8 Ryan Byrnes, Leslie Roche, Kenneth Tate  
Do livestock grazing regimes influence soil biogeochemical processes and function? A global analysis of grazing effects on soil nitrogen and carbon dynamics.
- SII.9 Cynthia Kallenbach, Fnu Junaidi, Steven Fonte, Patrick Byrne, Mathew Wallenstein  
Wheat genotypic and phenotypic effects on microbial-mediated nitrogen cycling
- SII.10 Kurt Reinhart, Lance Vermeire  
Power and limitation of soil properties as predictors of rangeland health and ecosystem functioning in a Northern mixed-grass prairie
- SII.11 Kalyn Diederich, Kavya Krishnan, Erin Silva, Matt Ruark  
Increasing labile carbon and nitrogen pools in agricultural soils requires a change in system, rather than practice

- SII.12 Grace Crain, Eva Dettweiler-Robinson, Anthony Darrouzet-Nardi, Jennifer Rudgers, Robert Sinsabaugh  
Mixed evidence for carbon transfer between biocrust cyanobacteria and plants in multiple dryland ecosystems using natural abundance  $\delta^{13}\text{C}$
- SII.13 Rachel Brockamp, \*Sharon Weyers, Margaret Kuchenreuther, John Zaharick, Alan Wilts  
Influence of fertilization on mycorrhizal dynamics in a perennial biomass production system
- SII.14 Chelsea Carey, Rachel Sullivan, Doug Millar, Mel Preston, Nathaniel Seavy, Thomas Gardali  
Monitoring biotic and abiotic soil parameters to inform regenerative grazing practices across California's coastal range
- SII.15 Natalie Bray, Grant Thompson, Jenny Kao-Kniffin, Kyle Wickings  
Soil macrofauna modify soil microbial community composition and function and alter belowground carbon inputs
- SII.16 Colin Tucker, Sasha Reed, Anita Antoninka, Matthew Bowker  
Restoration of biological soil crust on the Colorado Plateau in a warming climate.
- SII.17 Tahir Zaman, Timothy Fegel, Paula Fornwalt, Charles Rhoades  
Are soil changes responsible for persistent, non-forested burn scars in Colorado forests?
- SII.18 Landon Gibbs, Mark Coyne  
Cover crop mixes differentially stratify mineralizing microbes and residual nitrogen.
- SII.19 Tyler Poppenwimer, Louis Gross, Joseph Bailey, Megan Rúa  
Modelling the root age structure of perennial woody plants
- SII.20 Meghan Midgley  
The Tollway Trees Initiative: From right tree, right site to right soil, right tree
- SII.21 Thomas Ducey, Phil Bauer  
Effect of tillage and cover crops on the cotton rhizosphere
- SII.22 Emm Fulk, Jonathan J. Silberg, Caroline Masiello  
Microbial genetic memory to study heterogeneous soil processes
- SII.23 Carl Wepking, Brian Badgley, John Barrett, Matthew Hedin, Katharine Knowlton, Kevan Minick, Partha Ray  
Ecological effects of livestock antibiotics on agricultural soils
- SII.24 Deirdre Griffin, Daoyuan Wang, Sanjai Parikh, Kate Scow  
Effects of walnut shell biochar on soil microbial communities in a long-term field experiment.
- SII.25 Paulina Beatriz Ramírez, Sebastián Fuentes, Beatriz Díez, Carlos A. Bonilla  
Bacterial composition patterns distinguish two contrasting soils in organic carbon content: andisols and inceptisols

SII.26 Di Liang, G. Philip Robertson

Management intensities and seasons affect the relative contribution of ammonia oxidizing bacteria (AOB) and ammonia oxidizing archaea (AOA) to nitrification across a Midwest management gradient

SII.27 Tye Morgan, Matthew O'neill, Robert Blank, Edith Allen, Michael Allen

Why is *Taeniatherum caput-medusae* (medusahead) Invasive in North America and not in its Native Eurasia?

SII.28 Jessica Susser, Shannon L. Pelini, Michael Weintraub

Can we reduce phosphorus runoff potential by stimulating decomposers with carbon and sodium?

SII.29 Jayprakash Singh, Nina Goodey, Jennifer Krumins

Variation in microbial community composition may explain soil functioning in an urban brownfield

SII.30 Michala Phillips, Andrew Krohn, Edith Allen

Invasion shifts soil fungal community composition in California chaparral

SII.31 Jennifer Schmidt, Clare Casteel, Rachel Vannette, Christian Nansen, Scott Park, Kate Scow, Amélie Gaudin

Soil health mediates tomato resistance to insect vectors and viral pathogens

SII.32 Amisha Poret-Peterson, Natalia Ott, Greg Browne

Bacterial communities associated with *Prunus* replant disease

SII.33 Kaiyue Zhou, Louise Egerton Warburton

Plant species and functional group effects on soil properties in a green roof community

SII.34 Megan Rúa

Disturbance history and environmental characteristics shape the ectomycorrhizal fungal community of two varieties of *Pinus clausa*

SII.35 Eric Vukicevich, José Ramon Úrbez-torres, Pat Bowen, D. Thomas Lowery, Miranda Hart

The effect of ground cover management on vine performance and fungal root endopyte communities

SII.36 Chen Ning, Gregory Mueller, Louise Egerton Warburton

Profiling ectomycorrhizal fungal diversity and function in seedlings of south China native masson pine and introduced slash pine

SII.37 Ilene Del Valle, Tara M. Webster, Caroline Masiello, Jonathan J. Silberg, Johannes Lehmann

Environmental multi-input circuit to understand plant-microbe communication

SII.38 Akihiro Koyama, Teresa Dias, Angela Dukes, Pedro Antunes

Soil microbial feedback in agricultural crop rotation

SII.39 Natalia Ott, Amisha Poret-Peterson, Hossein Gouran, Greg Browne  
Oomycete and fungal root communities associated with Prunus replant disease and its control in conventionally fumigated or anaerobically disinfested soil

SII.40 Ma. Lourdes Edano, Gail Wilson, Karen Hickman, James Bever  
Will the use of nurse plants inoculated with native AM fungi help restore the native plant community after eradication of invasive grasses?

SII.41 Franz Lichtner, Kirk Broders  
Ecology of temperate belowground fungi through ITS sequence analysis over four years in mixed successional perennial systems

SII.42 John Dighton  
Comparisons of mycorrhizae and plant growth between the NJ pine barrens and serpentine barrens

SII.43 Tom Bolger, Tara Dirilgen, Edite Jucevica, Pascal Querner, Viesturs Melecis  
Analysis of spatial patterns informs community assembly and sampling requirements for Collembola in forest soils

\*Denotes presenting author if other than first author

Wednesday June 7th

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*Lory Student Center, Ballroom 350 C & D, Colorado State University*

- 8:30** Kate Scow, Professor of Soil Science and Soil Microbial Ecology, University of California, Davis
- 8:50** Stuart Grandy, Associate Professor of Sustainable Agriculture and Food Systems, University of New Hampshire  
Revising Paradigms of Nitrogen Mineralization and Availability in Agroecosystems
- 9:10** Lynne Macdonald, CSIRO
- 9:30** Panel Discussion: What are the most important research needs to advance soil health?
- 10:00** Break
- 10:30** IGNITE Session 3: The Science of Soil Health  
Emily Oldfield, Mark Bradford, Stephen Wood  
Increasing soil organic matter can reduce global yield gaps
- Kelly Gravuer, Kate Scow  
Can “macrobial” diversity and invasion theories explain microbial outcomes of compost addition to agricultural soils?
- Brendan O’Neill, Christine Sprunger, John Kerr, G. Philip Robertson  
Aligning Soil Health Testing and Farmer Knowledge for Improved On-farm Soil Management
- Michael Lehman, Shannon Osborne  
Measuring and Managing Soil Health – Multidimensional Solutions



## Wednesday June 7th(Continued)

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*Lory Student Center, Ballroom 350 C & D, Colorado State University*

Phillip Taylor  
The Jury is Out on Carbon Farming

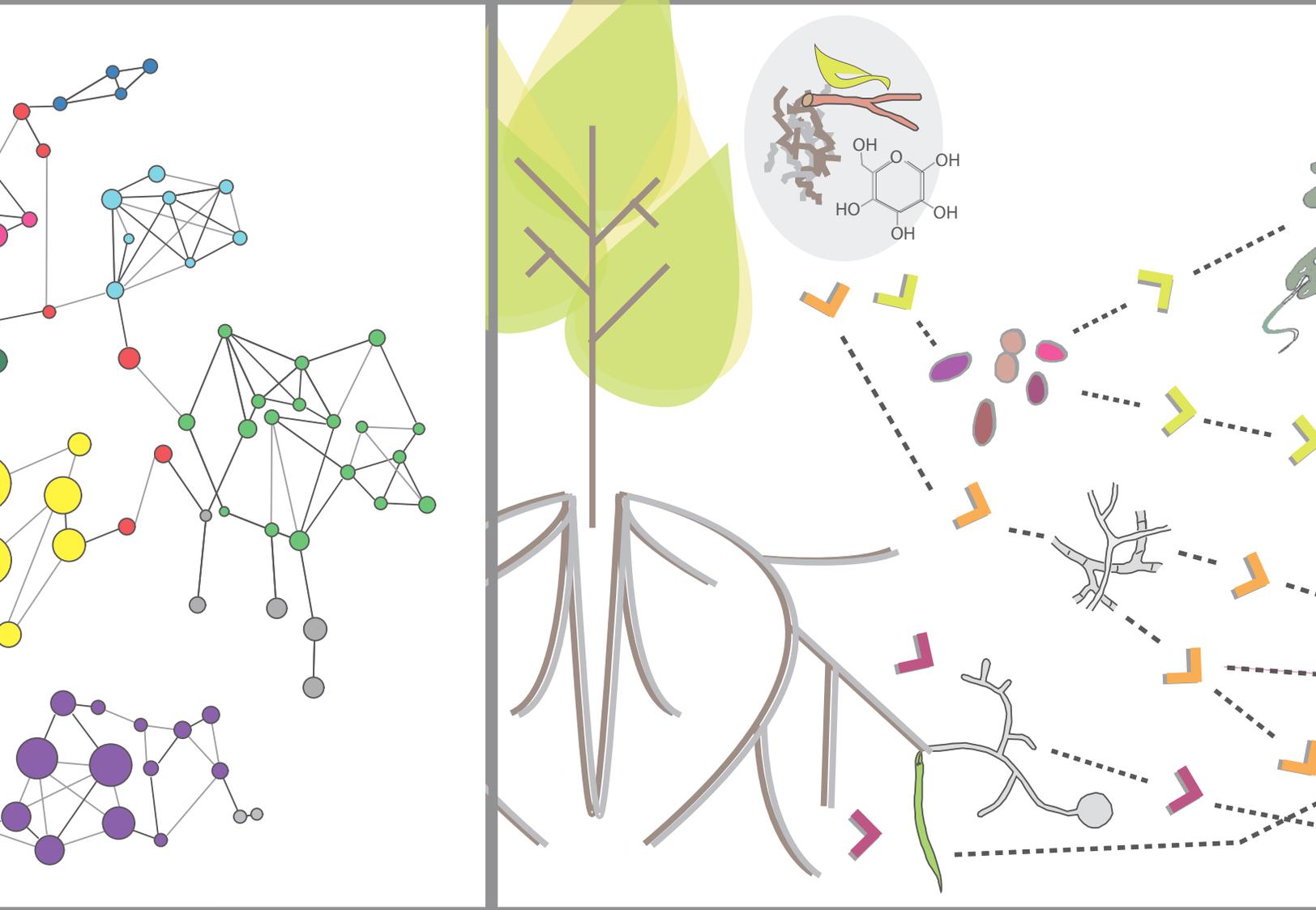
**11:00** Moving forward: Building Bridges Between Industry, Scientists, and Practitioners  
Bill Buckner, President, Noble Foundation  
LaKisha Odom, Scientific Program Director, Foundation for Food and Agricultural Research  
Keith Paustian, Professor, Dept of Soil and Crop Sciences, Colorado State University

**12:00** Wrap-Up Lunch: Box lunches served – please select your box lunch and enjoy it outside or in another area of the Lory Student Center to allow for reconfiguration of ballroom for afternoon SES meeting





Colorado State University



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## Event Agenda

June 7th - 9th

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PARALLEL ORAL SESSION A  
BALLROOM C

- 2:00** Michael Allen, Amanda Swanson, Emma Aronson, Thomas Harmon, Robert Johnson, Diego Dierick, Zhan Chen, Steve Oberbauer, Adrian Pinto, Tamara Zelikova, Luitgard Schwendenmann, Philip Rundel, Angel Fernandez  
Soil Net Primary Production and Carbon Emissions in a Tropical Rainforest: Effects of Leaf Cutter Ants through an ENSO cycle
- 2:15** Racheal Upton, Kirsten Hofmockel  
Soil fungi response to seasonal and annual variance in three agroecosystems
- 2:30** Michael Remke, Matthew Bowker, Nancy C. Johnson, Matthew Williamson, Karen Haubensak  
Mycorrhizal allocation determines their function across varying environmental contexts
- 2:45** Eldor Paul  
Quantifying the controls on SOM characteristics by MAT, disturbance, vegetation, depth and the soil matrix: An Opus approach
- 3:00** Steven Rosenzweig, Meagan Schipanski, Steven Fonte, Mary Stromberger  
Crop rotation impacts on AMF, P acquisition and C sequestration in semi-arid agroecosystems.
- 3:15** Noah Sokol, Mark Bradford  
Is root carbon better stabilized than shoot carbon? Testing features of the above- versus below-ground pathway



# SES Meeting: Session A (continued)

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## PARALLEL ORAL SESSION A BALLROOM C

- 3:30** Elizabeth Porzig, Chelsea Carey, Nathaniel Seavy  
Plant community composition and variation in soil organic carbon in California rangelands
- 3:45** Sarah Castle, Zewei Song, Stuart Grandy, Linda Kinkel  
Does climate warming alter plant diversity-soil carbon relationships and associated soil microbial communities?
- 4:00** Daniel Maynard, Thomas Crowther, \*Mark Bradford  
Competition reduces microbial carbon use efficiency
- 4:15** Cameron McMillan, \*Michael Weintraub  
How do plant seasonal dynamics drive root carbon inputs to the soil and their distribution?



PARALLEL ORAL SESSION B  
BALLROOM D

- 2:00** Steven Fonte, Steven Vanek, Katherin Meza, Anne De Valenca, Raul Carlos Ccanto Retamozo, Edgar Olivera, Maria Scurrah  
Land-use impacts on soil biodiversity and ecosystem services in an Andean farming community
- 2:15** Yamina Pressler, John Moore, Francesca Cotrufo  
Fire reduces soil biota biomass and diversity: a cross-biome meta-analysis
- 2:30** Emma Aronson, Denise Jackson  
Soil Microbial dispersal by way of terrestrial slugs
- 2:45** Charlotte Alster, Joseph von Fischer  
Characterizing Temperature Sensitivity as a Microbial Trait: A Meta-Analysis Using Macromolecular Rate Theory
- 2:45** Eric Duell, Anna O'Hare, Gail Wilson  
Improving grassland restoration efforts: the power of soil amendments
- 3:00** Maria Soledad Benitez, Shannon L. Osborne, Michael Lehman  
Rotation history effects on soybean plants and rhizosphere microbiome
- 3:30** Parker Coppick, Gail Wilson  
Soil biotic and abiotic properties following *Bothriochloa ischaemum* invasion into native tallgrass prairie
- 3:45** Matthew Reid, Sarah Emery  
*Leymus arenarius* invasion alters belowground interactions with mycorrhizae and nematodes without altering nematode community structure



# SES Meeting: Session B (Continued)

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## PARALLEL ORAL SESSION B BALLROOM D

- 4:00** Gail Wilson, Tim Todd  
Tallgrass prairie restoration: Does functional group matter?
- 4:15** Kyle Wickings, Huijie Gan  
Soil ecological responses to pest management practices in turfgrass vary with pesticide use intensity, identity, and application program
- 5:30** David Knaebel, USDA ARS - USDA only meeting, Room 390, Lory Student Center



# SES Meeting Session C

## Thursday June 8th

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**8-8:45** Soil Ecology Society Business Meeting BALLROOM D  
Full Breakfast Served

### PARALLEL ORAL SESSION C BALLROOM C

- 9:00** Tamara Zelikova, Diego Dierick, Luitgard Schwendenmann, Thomas Harmon, Nicole Trahan, Michael Allen  
Industrious leaf cutter ants and their big footprints in tropical soils
- 9:15** Roberto Carrera-Martínez, Mitchell J Greer, Bruce A Snyder  
Invasive Yellow Bluestem and European earthworms: Conspiracy for ecosystem domination?
- 9:30** Jessica Gutknecht, Cameron Blake  
Microbial C use in peat depth profiles under warming, as revealed with isotopic profiling
- 9:45** Felicity Crotty, Chris Stoate  
Untangling the effects of individual cover crop species compared to mixes on soil ecology
- 10:00** Samantha Weintraub, Lee Stanish  
Using NEON data to explore continental-scale patterns in soil communities and processes
- 10:15** Stuart Grandy, Andrea Jilling  
From where and how do plants and microbes get their nitrogen?
- 10:30** Break



# SES Meeting: Session C (Continued)

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## PARALLEL ORAL SESSION C BALLROOM C

- 11:00 Phillip Taylor, Pete Newton, Alan Townsend  
The Future of Protein
- 11:15 Erika Foster, Matthew Wallenstein, Francesca Cotrufo  
Biocarbon as an effective microbial inoculum carrier in an agricultural maize field trial
- 11:30 Kelly Ramirez, Wim Van Der Putten, Basten Snoek  
The role of the belowground plant microbiome in climate change induced range shifts
- 11:45 François-Xavier Joly, Sylvain Coq, Mathieu Coulis, Stephan Hättenschwiler, Johanne Nahmani  
The transformation of leaf litter into feces by millipedes reshuffles the control of litter traits on decomposition



# SES Meeting Session D

## Thursday June 8th

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### PARALLEL ORAL SESSION D

#### BALLROOM D

- 9:00** Megan Machmuller, Carsten Mueller, Jennifer Soong, Carmen Hoeschen, Claudia Boot, Francesca Cotrufo  
Advancing the understanding of organo-mineral interactions: Insights from nano-scale Secondary Ion Mass Spectrometry
- 9:15** Samantha Chapman, Chelsea Barreto, Ember Morrissey  
Wetland plant range shifts may alter soil microbial communities and carbon storage
- 9:30** Kara Gibson, Channing Laturno, Andrea Raya, Anita Antoninka, Nancy C. Johnson  
Effect of restoration treatments and forest type on soil mesofauna, fungi, and physicochemistry in Valles Caldera National Preserve
- 9:45** Matthew Hedin, John Barrett  
Effects of antibiotic residues on extracellular enzyme activity in soils
- 10:00** Caroline Masiello, Jonathan J. Silberg, Hsiao-Ying Cheng, Ilene Del Valle, Emm Fulk, George Bennett  
Spies and Bloggers: New Synthetic Biology Tools to Understand Soil Microbial Processes
- 10:15** Amanda Daly, Andreas Richter, Stuart Grandy  
Influence of wet-dry cycles and organic management on gross nitrogen depolymerization in agricultural soils
- 10:30** Break



# SES Meeting: Session D (Continued)

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## PARALLEL ORAL SESSION D BALLROOM D

- 11:00 A. Peyton Smith, Malak Tfaily, Kent Rod, Vanessa Bailey, Ryan Renslow  
Temperature, moisture and mineral interactions alter the vulnerability of organic matter turnover
- 11:15 Colin Averill, Bonie Waring  
Nitrogen limitation of decomposition and decay: how can it occur?
- 11:30 Becky Ball, Suzanne Dietrich, Don Goelman  
An interactive learning module for teaching ecology students (and professors) about databases for managing and querying large datasets
- 11:45 Loren Byrne  
Integrating soil biodiversity and soil ecology into non-soil-focused undergraduate courses
- 12-1:30 LUNCH



# SES Meeting Session E

## Thursday June 8th

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### PARALLEL ORAL SESSION E BALLROOM C

- 1:30** SES Early Career Research Awardee: Tom Crowther  
Quantifying global soil carbon losses in response to warming
- 1:45** Drew A. Scott, Sara G. Baer  
Partial support for the 'environmental heterogeneity hypothesis' in tallgrass prairie restorations
- 2:00** Mark Anthony, Serita Frey, Kristina Stinson  
Fungal Responses to an Invasive Plant in a Warmer, Fertilized Forest
- 2:15** Nora Flynn, Louise Comas, Catherine Stewart, Steven Fonte  
Investigating deficit irrigation impacts on belowground processes and climate change mitigation potential
- 2:30** Joseph Blankinship, Kenneth Marchus, Joshua Schimel  
Using extracellular polymeric substances (EPS) from bacteria to make soils more drought-adapted
- 2:45** Tyler Rippel, Pasquale Succi, Samantha Chapman  
The influence of Japanese stiltgrass on soil microbes, edaphic properties, and tree regeneration in a nitrogen saturated environment
- 3-3:30** BREAK
- 3:30** Kate Glanville, G. Philip Robertson  
Consequences of Changing Rainfall Patterns on Nitrous Oxide Fluxes in Cropping Systems



# SES Meeting: Session E (Continued)

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## PARALLEL ORAL SESSION E BALLROOM C

- 3:45** Meghan Midgley, Quinn Taylor  
Prescription side effects: Controlled burning alters resource stoichiometry in a Midwestern forest soil
- 4:00** Brendan O'Neill, Thomas Schmidt, G. Philip Robertson, Sasha Kravchenko, Stuart Grandy  
Linking soil C and N cycling and trace gas fluxes with soil bacterial communities along a gradient of simple to complex crop rotations
- 4:15** Joni Baumgarten, John Dighton  
Edaphic manipulation of the soil community of biofuel switchgrass (*Panicum virgatum*) in three soils
- 4:30** Darian Smercina, Lisa Tiemann, Sarah Evans, Maren Friesen  
Environmental Controls on Free-living Nitrogen Fixation and Nitrogen Mineralization
- 4:45** **SES Service Awardee: Deborah Neher**  
Soil health – what progress have we made in the past 25 years?



PARALLEL ORAL SESSION F  
BALLROOM D

- 1:30** Becky Ball, Kyle Wickings, Lynn Christenson  
Pathways and patterns of plant litter chemistry throughout decomposition
- 1:45** Monica Farfan, David Wise  
Augmentation of basal resources in a soil food web changes patterns of intraguild predation and decomposition rate
- 2:00** Michael LeDuc, Tucker Andrews, Thomas Weicht, \*Deborah Neher  
Microarthropods in Bedded Pack: A Source for Biocontrol of Biting Fly Pests on Dairy Farms?
- 2:15** Rachel Hestrin, Maria Harrison, Johannes Lehmann  
Soil Microbial Communities and Gas Dynamics Contribute to Arbuscular Mycorrhizal Nitrogen Uptake and Transfer to Plants
- 2:30** Huijie Gan, Chao Liang, Kyle Wickings  
Invasive root herbivores accelerate soil carbon inputs and soil organic matter decomposition
- 2:45** Brittany McAdams, Sylvie Quideau, Mathew Swallow, Lisa Lumley  
Oribatid mites as a tool to assess soil recovery after oil sands mining
- 3-3:30** Break



# SES Meeting: Session F (Continued)

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## PARALLEL ORAL SESSION F BALLROOM D

- 3:30** Anthony Darrouzet-Nardi, Michael Weintraub, Jane Martinez, Daniela Aguirre  
Is soil pore water an exchange depot for nutrients in Arctic tussock tundra soils?
- 3:45** Bo Stevens, Jeffrey Propster, Gail Wilson, Andrew Abraham, Chase Ridenour, Chris Doughty, Nancy Johnson  
A Serengeti Without Arbuscular Mycorrhizas: Quantifying Interactions Between Migratory Mammals and Fungal Symbionts
- 4:00** François-Xavier Joly, Heather Throop  
Pulse size, frequency and soil-litter mixing alter the control of cumulative precipitation over litter decomposition in drylands
- 4:15** Ashley Keiser, Montana Smith, Sheryl Bell, Kirsten Hofmockel  
Peatland microbial community response to altered climate tempered by plant – soil interactions
- 4:30** Anna Cates, Thea Whitman, Randall Jackson  
The effect of C decomposition environment on plant detritus C in soil organic matter
- 4:45** Kirsten Hofmockel, Alison King  
Organic N cycling in agroecosystems

*\*Designates Presenting Author*

- 7-10** Soil Ecology Society Banquet Award Dinner  
Agave Room, 149 W Mountain Avenue, Fort Collins, CO 80524



# SES Meeting Session F

## Friday June 9th

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**8:30** Field Trip: Rocky Mountain National Park  
Meeting place TBA  
Box lunch provided



## Appendix I

# *ECOLOGY OF SOIL HEALTH SUMMIT POSTER SESSION ABSTRACTS*

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Monday June 5th

POSTER SESSION 1

5:00 – 7:00 PM

Ballroom B, Lory Student Center

## #SI.1

### **Fine soil organic matter fractions in wine grape vineyards (Napa, CA) reflect distinctions in soil microbial community composition**

Kerri Steenwerth<sup>1</sup>, Rachel Greenhut<sup>1</sup>, \*Francisco Calderon<sup>2</sup>

<sup>1</sup>USDA-ARS Crops Pathology and Genetics Research Unit, United States

<sup>2</sup>USDA - Agricultural Research Service, United States

Recently, Burns et al. (2015) demonstrated that soil-borne microbial communities differentiate themselves with respect to American Vineyard Areas, defined for their distinguishing features of climate, geology, soils, physical features (topography and water), and elevation. Of these features, location (latitude, elevation, topography, precipitation) and edaphic variables were the strongest drivers of beta-diversity of microbial communities at the landscape scale, especially total soil carbon and nitrogen contents in the <53  $\mu\text{m}$  and 53-250  $\mu\text{m}$  particulate organic matter (POM) fractions. Given that soil microbial communities mineralize, contribute to and preserve these soil organic carbon pools, we hypothesized that the chemical composition of the SOC pools would reflect that of microbial communities. Twenty four vineyards were sampled from 0-5 and 5-10 cm for physical and chemical attributes, C and N resources and land use history. The fine soil OM that is thought to reflect residues that have been highly decomposed by soil microorganisms (i.e. < 53  $\mu\text{m}$  organomineral fraction) was analyzed by diffuse reflectance Fourier transformed mid-infrared spectroscopy (DRIFTS). Canonical correspondence analyses of the FTIR output demonstrated that POM chemical fingerprints did *not* structure themselves with respect to compost addition, tillage, soil depth, and farming system (conventional vs. organic vs. biodynamic). Similar to drivers of microbial community structure, location attributes, soil type, cover crop type strongly differentiated clusters of FTIR fine soil OM fingerprints among samples. The correspondence between the microbial community structure and the POM chemical fingerprints will be discussed further in this presentation.

**#SI.2**

**Carbon dioxide sequestration in karst micro-fissures: The solution of a droplet**

Lisa Windom<sup>1</sup>, Maria Dragila<sup>1</sup>, Noam Weisbrod<sup>2</sup>

<sup>1</sup>Oregon State University, United States

<sup>2</sup>Ben-Gurion University of the Negev, Israel

The concern for increased atmospheric carbon dioxide concentration calls for improved understanding of natural sequestration processes. Increased carbon dioxide storage in soil shows promise because the net storage is compromised by loss to the atmosphere but aided by downward drainage. We ask how the mechanism of infiltration into karst aquifer micro-fissures below the soil can additionally sequester carbon dioxide. Karst aquifers occupy conduits and caverns carved into limestone (calcium carbonate). These caverns form by prolonged erosion of micro-fissures in the epikarst, soil solution percolates down micro-fissures (< 2 mm thick) in the form of thin films (~200 microns). There are three gas-liquid fluid modes that can be sustained in microfractures and that allow for a three-phase interaction of carbon dioxide in the gas phase, water, and calcium carbonate in the solid phase. Limestone erosion, commonly approached through calcium dissolution, is limited by the presence of dissolved carbon dioxide but accelerated by advective carbon dioxide gas assimilation into solution. The process fixes carbon by exchanging for calcium within the limestone matrix; the kinetics of calcium dissolution is well-defined but how it is impacted by different flow modes remains to be studied. By understanding the advective potential of naturally developing modes of flow, we can more accurately understand the storage of carbon dioxide gas into subsurface limestone.

### #SI.3

#### **Seasonal switchgrass ecotype contributions to soil organic carbon, deep soil microbial community composition and rhizodeposit uptake during an extreme drought**

Catherine Stewart<sup>1</sup>, Damaris Roosendaal<sup>2</sup>, Karolien Deneff<sup>3</sup>, Louise Comas<sup>1</sup>, Gautam Sarath<sup>4</sup>, Virginia L. Jin<sup>5</sup>, Marty Schmer<sup>5</sup>

<sup>1</sup>USDA - Agricultural Research Service, United States

<sup>2</sup>USDA-ARS Soil Management and Sugarbeet Research, United States

<sup>3</sup>Colorado State University-Central Instrument Facility, United States

<sup>4</sup>USDA - Agricultural Research Service Grain, Forage, and Bioenergy Research, United States

<sup>5</sup>USDA ARS Agroecosystems Management Research, United States

The importance of rhizodeposit C and associated microbial communities in deep soil C stabilization is relatively unknown. Phenotypic variability in plant root biomass could impact C cycling through belowground plant allocation, rooting architecture, and microbial community abundance and composition. We used a pulse-chase <sup>13</sup>C labeling experiment with compound-specific stable-isotope probing to investigate the importance of rhizodeposit C to deep soil microbial biomass under two switchgrass ecotypes (*Panicum virgatum* L., Kanlow and Summer) with contrasting root morphology. We quantified root phenology, soil microbial biomass (phospholipid fatty acids, PLFA), and microbial rhizodeposit uptake (<sup>13</sup>C-PLFAs) to 150 cm over one year during a severe drought. The lowland ecotype, Kanlow, had two times more root biomass with a coarser root system compared to the upland ecotype, Summer. Over the drought, Kanlow lost 78% of its root biomass, while Summer lost only 60%. Rhizodeposit uptake under Kanlow had a higher relative abundance of gram-negative bacteria (44.1%), and Summer rhizodeposit uptake was primarily in saprotrophic fungi (48.5%). Both microbial community composition and rhizodeposit uptake shifted over the drought into gram-positive communities. Rhizosphere soil C was greater one year later under Kanlow due to turnover of unlabeled structural root C. Rhizosphere  $\delta^{13}\text{C}$  was not significantly different between the two ecotypes, suggesting greater microbial C input under the finer rooted species, Summer, whose microbial associations were predominately saprotrophic fungi. Root-derived C inputs drive soil C processes and these data suggest that individual plant interactions with the microbial community and extreme drought events affect soil C sequestration.

**#SI.4**

**Examination of residual chloroform interference in the measurement of microbial biomass C by fumigation-extraction**

Adi Oren

Institute of Soil, Water and Environmental Sciences, Volcani Center, Agricultural Research Organization (ARO), Israel

Chloroform fumigation-extraction (CFE) is by far the most widely used method for determining microbial biomass in soils. Using the CFE method, a presumption is followed, i.e., that chloroform becomes fully evacuated from the fumigated soil before extraction. Otherwise, the C-containing fumigant may comprise an unknown part of the extractable C flush, resulting in certain overestimation of soil microbial biomass. A quantitative assessment of extractable residual chloroform levels in fumigated soils was performed, testing soils varying in clay and organic matter contents. The tests were performed over a broad range of soil moisture conditions as to facilitate a mechanistic interpretation of possible chloroform interactions in the studied soils (i.e., dissolution, sorption). The results support the validity of the CFE method's application in agricultural soils, demonstrating the insignificance of biomass overestimation arising from residual chloroform. However, attention must be given to potential biomass overestimation in low-biomass samples (e.g., subsoil) where extractable-C flushes are characteristically low, sorption of chloroform may be relatively high, and thus extractable chloroform-C contribution to the extractable-C flush can be significant.

#SI.5

**Peering into the soil black box: A soil ecosystem observatory by rhizosystems, LLC**

Michael Allen<sup>1</sup>, Michael Taggart<sup>2</sup>, George Rothbart<sup>2</sup>, Thomas Harmon<sup>3</sup>, Rebecca Hernandez<sup>4</sup>, Philip Rundel<sup>5</sup>

<sup>1</sup>University of California, Riverside, United States

<sup>2</sup>Rhizosystems, LLC, United States

<sup>3</sup>University of California, Merced, United States

<sup>4</sup>University of California, Davis, United States

<sup>5</sup>University of California, Los Angeles, United States

Understanding soil dynamics is a critical step in managing ecosystem processes. However, tools that facilitate temporal and spatial observations are constrained in that observations must occur belowground, and must occur at high frequencies to delineate rapid change associated with events. Coring disrupts soil structure, and changes through time can be either variation in time, or variation in space. These cannot be differentiated. A critical value, often missing, is lifespan. Yet lifespan is critical to calculating turnover, and turnover is just as important as production to estimating net primary production. We designed an integrated network of sensors, CO<sub>2</sub>, O<sub>2</sub>, H<sub>2</sub>O, and temperature, placed in a depth profile. From these, concentrations can be measured and fluxes calculated using Fick's Law. Embedded within the sensor network are automated minirhizotrons that image roots, fungal hyphae, soil animals, soil structure up to four-times daily, and manual minirhizotrons that can be used at intervals as determined by the user. Automated minirhizotrons allow for continuous observation increasing understanding of temporal variation. Manual minirhizotrons can provide for evaluating spatial variation across a site. Here we will show examples of the units, and test systems from a tropical rainforest to a hot desert, to a subalpine coniferous forest. Observations include under snow dynamics, carbonate crystallization along hyphae, root grazing, mycorrhizal development, root and hyphal regrowth into abandoned ant nests, and integration into a carbon flux model.

## #SI.6

### **Establishment of improved pastures supports early indicators of soil restoration in low-input agroecosystems of Nicaragua**

Emily Webster<sup>1</sup>, Amélie Gaudin<sup>1</sup>, Mirjam Pulleman<sup>2</sup>, Pablo Siles<sup>3</sup>, \*Steven Fonte<sup>4</sup>

<sup>1</sup>University of California - Davis, United States

<sup>2</sup>International Center for Tropical Agriculture, Colombia

<sup>3</sup>International Center for Tropical Agriculture, Nicaragua

<sup>4</sup>Colorado State University, United States

Pasture degradation hinders livestock production and ecosystem services that support rural smallholder communities. Silvopastoral systems, featuring improved pasture grass species, are promising restoration strategies. However, studies evaluating the impact of such systems, in conjunction with common management practices, on indicators of soil health are lacking. We sought to evaluate the impact of low-input, improved pasture establishment on soil health indicators, in actively grazed silvopastoral systems. In August 2013, paired pasture management treatments (improved vs. degraded) were established on nine farms with similar management histories and edaphic characteristics in the Matagalpa department of Nicaragua. On each farm, one treatment was left as degraded pasture with naturalized grass species *Hyparrhenia rufa* while the adjacent area was sown with the improved *Brachiaria brizantha* cv. *Marandu* species without fertilizer. We measured a suite of soil chemical, biological, and physical variables as well as standing biomass in August 2015, 2 years after establishment of the trial. The improved (*B. brizantha*) pastures were found to produce more standing grass biomass and support higher levels of earthworm populations and permanganate oxidizable carbon (POXC) compared to the degraded control. Correlation analysis revealed that earthworms and POXC were associated with incipient improvements to soil structure and water holding dynamics. We report measurable improvements to soil health within just two years following the establishment of improved silvopastoral systems under common smallholder management practices and suggest that promotion of these systems, even with minimal fertility inputs, has the potential to enhance sustainability in this region.

#SI.7

## **The influence of agricultural practices on the abundance of arbuscular mycorrhizal fungi in rural eastern Zambia**

Adam Cobb, Gail Wilson

Oklahoma State University, United States

Zambia and many developing countries are struggling to protect natural resources, such as productive soils. Fortunately, symbiotic partnerships between agronomic crops and arbuscular mycorrhizal (AM) fungi can help make agricultural systems more sustainable and improve soil quality. While the effects of industrial agriculture on AM fungi have been studied in the US, much less is known about consequences of farm methods in African soils. We compared soils from four farms in Zambia with soil from nearby grassland (control) to assess microbial abundances, including AM fungi, using phospholipid and neutral lipid fatty acid (PLFA/NLFA) analyses. We also measured soil pH, soil organic matter, and nutrients, and categorized farms to link microbial abundances with agricultural practices including: low and high input cultivation; conservation farming; and agroforestry. Soil organic matter was significantly greater in grassland, compared to farms. The concentrations of N, P, and K were greater in farm soils compared to grassland soil, but Fe and Zn were significantly diminished on all farms. AM fungal abundance (PLFA) was significantly greater in grassland compared to the farms, and grassland contained more than double the total microbial biomass compared to any farm. Abundance of AM fungal storage biomass (NLFA; e.g. spores) did not differ between grassland soil and the conservation farm; however, all other farm practices reduced abundance of AM storage biomass. Our results indicate agricultural practices in eastern Zambia are negatively affecting AM fungi as well as other soil microbes. However, conservation farming shows promise in facilitating AM fungal recovery.

#SI.8

**MO DIRT - Missourians doing impact research together - A citizen science project to monitor soil health in the state of Missouri**

Terry Woodford-thomas, \*Sandra Arango-Caro

Donald Danforth Plant Science Center, United States

MO DIRT – Missourians Doing Impact Research Together, an NSF-supported citizen science initiative, educates individuals on soil science and soil-climate interactions. One component of MO DIRT is monthly soil health surveys (February-November) conducted by volunteers at test sites. A cohort of 170 citizens has been trained, of which 61 have received soil survey kits. Currently, 45 sites representing forest (13), woodland (4), prairie (8), grassland (11), pasture (4) and cropland (5) habitats are actively monitored. The data collected is stored in an on-line data portal that will soon be open-access ([modirt.missouriepescor.org](http://modirt.missouriepescor.org)). Participants are exposed to the scientific process by collecting and managing soil health data while developing a sense of stewardship for Missouri soils. Citizen-collected data on the temporal relationship between soil respiration (SR) and soil temperature (ST) are presented. SR, an indicator of soil microbial activity, is expressed as lb/acre/day of CO<sub>2</sub>-C and measured using the Solvita method. In 2016, SR increased in all habitats studied from February to a peak in July and declined until November indicating a response to seasonal changes. This was supported by a positive relationship between SR and ST in all habitats. Grasslands showed the highest levels of SR, followed by forests and prairies. Site-specificity influenced these results as sites of the same habitat differed in history of management, natural disturbances, soil types, etc. The inclusion of additional survey sites and analytical results will improve our understanding of SR and its interplay with changes in weather patterns and climate.

#SI.9

## Soil aggregation and organic matter stabilization in green roof systems and implications for C sequestration

Cam Gudmundson<sup>1</sup>, Louise Egerton Warburton<sup>2</sup>

<sup>1</sup>Lake Forest College, United States

<sup>2</sup>Chicago Botanic Garden, United States

Green roof systems are purported to offset urban CO<sub>2</sub> emissions by sequestering C in soil substrates. However, few studies have examined C sequestration in green roof systems, meaning that it is equally plausible that roof substrates could act as sinks or sources of CO<sub>2</sub>. In natural soils, physical protection of soil organic carbon (SOC) within aggregates is considered to be one of the major C stabilization mechanisms. In this study, we quantified SOC in soil aggregate fractions in green roofs to determine if: a) physical stabilization of SOC in soil aggregates occurred, and b) stabilization resulted in similar SOC levels to natural soils. Soils were collected under native tallgrass species and *Sedum* in a seven year-old green roof and in natural soils, wet-sieved, and each aggregate size fraction analyzed for C by combustion. We found that water-stable aggregates were formed in green roofs as well as natural soils, and that microaggregates were more abundant than macroaggregates. However, the abundances of both aggregate size classes were lower in green roof than natural soils. Microaggregates were also relatively enriched in total SOC compared to the macroaggregates but again, aggregate SOC and particulate organic C were significantly lower in green roof than natural soils. Taken together, these results indicate a reduced capacity for SOC stabilization in green roofs in comparison to natural soils. Possibly, C mineralization exceeds new C inputs, or there is reduced binding of mineral and organic particles to form stable aggregates in green roofs.

**#SI.10**

**Estimating soil carbon with open-source VNIR spectroscopy**

Daniel Kane

Yale School of Forestry & Environmental Studies, United States

Studies have found that visible/near-infrared (VNIR) spectroscopy can be successfully used to estimate soil carbon concentrations instead of more expensive GCMS analyses. But standard benchtop and spectrometers are still expensive and require expertise to operate. We have recently developed a protocol that makes use of low-cost field spectrometers built on the PhotosynQ open-source hardware/software platform to estimate soil carbon content. First, we sample soil throughout a given site to capture a range of soil carbon contents using traditional, highly accurate lab-based techniques. Those data are then used to build statistical models relating lab-measured soil carbon levels to the spectral data collected with the field spectrometer. These models are further improved by integrating different data types that may be predictive of soil carbon levels from spatially explicit datasets, such as soil type or net primary productivity. After the initial site-specific calibration, carbon content can be determined in the field using only the spectrometer and the site model, dramatically reducing sample collection time and cost and allowing managers to sample more frequently in the future and over broader areas. Furthermore, the device integrates with a simple to use app that allows several users to coordinate a data collection effort at the same time, creating the opportunity for participatory, citizen science projects. With these reductions in cost and streamlining of sample efforts, managers can work with researchers to quantify soil carbon at landscape scales and at more frequent intervals, allowing them to inexpensively monitor soil carbon responses as new management practices are adopted.

#SI.11

## Mitigating the impact of slow sensor response times on calculating soil CO<sub>2</sub> fluxes from NEON's soil CO<sub>2</sub> measurements

Edward Ayres<sup>1</sup>, Natchaya Durden<sup>1</sup>, David Durden<sup>1</sup>, Monique Leclerc<sup>2</sup>, Josh Roberti<sup>1</sup>

<sup>1</sup>NEON, United States

<sup>2</sup>The University of Georgia, United States

The National Ecological Observatory Network (NEON) is measuring vertical profiles of soil CO<sub>2</sub> concentration at 47 sites to allow calculation of soil CO<sub>2</sub> fluxes using the gradient method. NEON designed a soil CO<sub>2</sub> assembly to protect the sensors from the soil, while ensuring they are removable for calibration without disturbing the surrounding soil. However, the assembly's relatively large volume slows the sensor's response time. In this study, we quantify the response time of CO<sub>2</sub> sensors installed in these assemblies, as well as the response time's impact on soil CO<sub>2</sub> flux calculations. We used a controlled environmental chamber to determine the response time of sensors in assemblies following a rapid increase in CO<sub>2</sub> concentration. We then combined the response time derived from the chamber data with a 10-day time series of CO<sub>2</sub> concentrations made by sensors installed directly in the soil to approximate the impact of NEON's assembly, and calculated the CO<sub>2</sub> flux for both time series. Initial response time tests indicated 95% of the sensor response occurred within  $2.5 \pm 0.3$  hours. Mean CO<sub>2</sub> fluxes over the time series were similar for sensors outside and inside the assembly ( $2.30 \pm 0.36$  and  $2.30 \pm 0.33$   $\mu\text{mol m}^{-2}\text{s}^{-1}$ , respectively), but the measurement range was smaller for sensors in the assembly (0.98-3.06 versus 0.59-3.15  $\mu\text{mol m}^{-2}\text{s}^{-1}$ ). The temporal pattern of fluxes outside and inside the assembly were similar, but the assembly caused a ~30 minute lag. Accounting for the lag improved the Pearson correlation between the time series from 0.95 to 0.98.

**#SI.12**

**Changes in physical protection of soil organic matter following five years of biofuel cropping system cultivation: soil texture matters**

Adam von Haden, Christopher Kucharik, Randall Jackson, Erika Marín-Spiotta

University of Wisconsin-Madison, United States

Physical protection of soil organic matter (SOM) within aggregates is regarded as an important mechanism of SOM accrual, but the efficacy of SOM protection is thought to vary by soil texture. While the conversion of annual row crops to perennial systems has been shown to build SOM, it is not clear whether soil texture modifies short-term SOM storage potential through its effect on soil aggregation. We examined changes in the unprotected free light fraction (FLF) and the aggregate-protected occluded light fraction (OLF) after five years of biofuel crop cultivation on two soils with contrasting textures. The cropping systems were established at the Arlington Agricultural Research Station in Wisconsin and the Kellogg Biological Station in Michigan and included no-till maize, switchgrass, poplar, and prairie. Preliminary results indicate that the initial sizes of the FLF and OLF were similar between soil textures. However, after five years of cultivation, the OLF tended to remain similar or increase in the fine-textured soil but decreased dramatically in the coarse-textured soil in all treatments except poplar. At both sites the perennial cropping systems tended to have greater OLF and less FLF than the annual corn system. Notably, the poplar system contained the largest OLF and smallest FLF, suggesting rapid comminution and incorporation of plant litter into aggregates. Overall our preliminary results indicate that perennial systems are more likely to store aggregate-protected SOM than annual row crop systems in the short-term, but initial losses of aggregate SOM might be expected in coarse-textured soils.

## #SI.13

### Long-term land use change and impacts on soil faunal diversity

Phil Murray<sup>1</sup>, Jennifer Dungait<sup>1</sup>, Umran Akkan<sup>2</sup>, Stuart Norris<sup>1</sup>

<sup>1</sup>Rothamsted Research, United Kingdom

<sup>2</sup>Directorate of Plant Protection Research Institute Bornova-İzmir, Turkey

Here we focus on the effect of historical management changes in a very well documented managed areas covering a small geographical distance to control for confounding factors such as differing soil type and climate. This approach allowed us to decouple the impacts of climate and other environmental factors from managed, vegetation-imposed effects. Ultimately this will tell us whether there are contextual relationships, or whether we can make general rules on how soil biota respond to longer term anthropogenic change and the relative resilience of these systems to change. This investigation assessed the diversity and abundance of arthropods along a chronosequence of land use types. The habitats compared and the approximate ages since anthropogenic disturbance were; ancient woodland (>200y), old woodland (<200y), unimproved semi-natural grassland (>50y), willow/poplar coppice (>30y), unimproved permanent pasture (<20y), improved permanent pasture (<10y) and recently grazed and reseeded grassland (>2y), all habitats were on the same soil type and within a 5km radius. Land use type and age since anthropogenic disturbance significantly influenced ( $p < 0.05$ ) the community composition of soil fauna. Woodlands generally correlated with lower pH and were richer in arthropods compared with recently managed grassland. This study has confirmed a significant effect of land use types and age since disturbance, clarifying how underlying abiotic factors alter abundance, richness and diversity of soil arthropods.

## **#SI.14**

### **How does recreational camping affect cover mediated soil microbial activity?**

Sudan Kariuki, Mitch Mcclaran, Rachel Gallery

University of Arizona School of Natural Resources and the Environment, United States

Recreation management of popular outdoor activities such as camping is becoming increasingly important in natural areas of the United States. Likewise, recreation ecologists are tasked with investigating how these activities affect ecological processes. This case study uses the Santa Rita Experimental Range (SRER) in Southern Arizona to investigate how recreational camping influences the relationship between soil microbial activity and local plant composition in a desert grassland. In 2013, fences were installed to limit the spread of frequently used campsites. Therefore, these campsites each provide a direct comparison of recently disturbed, formerly disturbed, and undisturbed areas within a 10 meter radius. Previous research shows that soil beneath trees exhibits greater microbial activity than soil in bare areas. Stratified ground cover, microbial biomass assay, and enzyme assay data will be collected in these respective areas in order to study the effects of camping-related disturbances on plant-soil interactions. Expected results include corresponding low herbaceous and litter ground cover, enzyme activity, and microbial biomass in currently disturbed areas relative to undisturbed areas, and high enzyme activity in both undisturbed shaded areas and disturbed shaded areas. Trampling reduces cover and limits plant litter available for microbial decomposition. However, campers are likely to deposit nutrient-rich waste in the shade of trees, which may stimulate microbial activity. Camping introduces complex changes to ongoing ecological processes, but does not necessarily eliminate potential for healthy active soils and revegetation.

**#SI.15**

**Conservation agriculture enhances soil quality and function in an irrigated cropping system of Eastern Colorado**

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Tillage and stover harvest are common management practices in corn-based cropping systems around the globe. However, given that frequent soil disturbance and biomass export are likely to have negative long-term impacts on soil fertility, soil structure and belowground biological activity, there is great concern surrounding the sustainability of these practices. To address this issue, experimental plots were established in April 2014 in Akron, Colorado to understand the impacts of conservation agriculture practices, no-tillage and residue retention, in a full factorial design with the following treatments: no-till + residue retention (NT/R); no-till + residue removal (NT/NR); conventional tillage + residue retention (T/R); and conventional tillage + residue removal (T/NR). In year three of the experiment soil health parameters were assessed including: soil macrofauna communities, enzyme activity, aggregate stability, infiltration, and chemical fertility measures. The combined practice of residue retention with no-tillage (NT/R) greatly enhanced macrofauna communities, but this was especially apparent with a five-fold increase in earthworm abundance and biomass. Greater earthworm populations were also strongly related to an increase in aggregate stability under NT/R and a trend for greater water infiltration. Enzyme and soil chemical parameters indicated relatively less dramatic differences between treatments. Our findings suggest that no-till and residue retention practices offer great promise for improving soil structure and hydrologic function, and that these effects are largely mediated by greater earthworm abundance when these two practices are combined.

## #SI.16

### **Soil health implications of grazed vs. un-grazed cover crops in the U.S. high plains**

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Cover cropping is an important agroecological management option for improving soil health, but adoption in the High Plains region has been slow due to water/economic concerns. Our study investigates the impacts of grazed vs. un-grazed cover crops on a range of soil quality parameters in dryland wheat-based rotations. On-farm trials were established at five sites across eastern Colorado, Western Kansas and Western Nebraska by planting a seed mixture (eight species of warm and cool season grasses, legume and broadleaf species) in the Spring of 2016. The planted fields (> 20 ha) were divided into four blocks and grazing exclosures were established together with fallow plots (maintained with minimal vegetation) to create three treatments per replicate block. Soil was sampled in Summer 2016 at cover crop termination (by herbicide) for evaluation of soil compaction, aggregate stability, nutrient availability, and water storage in the soil profile. Preliminary results suggest greater soil moisture down to a depth of 100 cm in the fallow vs. cover crop treatments at the time of cover crop termination, but moisture at shallower depths (0-60 cm) in the cover-cropped treatments recovered to fallow levels by wheat planting in Fall 2016. Preliminary results suggest that impacts on aggregate stability, bulk density, and nutrient availability appear to be less dramatic. These results indicate that grazing does not significantly affect soil structure or other aspects of soil health, but that soil water use may be a critical driver of adoption.

#SI.17

### **Microbial ecology of composting bedded pack**

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Bedded pack dairy systems use carbon rich substrate such as straw or wood chips to bed cows throughout the cold Vermont winter. Rather than remove the bedding and manure, it is simply re-bedded with more substrate and left to accumulate for up to 8 months. Decomposition warms the lower levels of the bedded pack as the cows happily congregate on the freshly bedded surface. When spring weather allows cows to return to pasture, barns are scraped clean, and the bedding is spread in the field. As these systems gain popularity with dairies throughout Vermont, our group noted the important potential of biological interaction between the bedded pack and other parts of the agro-ecosystem such as bovine mastitis and biting fly pests. We use a microbiome approach to study the disease cycle of mastitis of dairy cows by exploring 16S/ITS DNA sequencing of the microbiome of cows, flies and bedded pack. Highly abundant fungal taxa include *Aspergillus*, *Candida* and *Thermomyces*. Highly abundant bacterial taxa include families Moraxellaceae, Pseudomonadaceae and Sphingobacteriaceae. Bedded pack microbial taxa observed to have two-fold shift in relative abundance in the presence of clinical mastitis include Comamonadaceae, Flavobacteriaceae, Moraxellaceae, Sphingomonadaceae, and Ruminococcaceae. Fungal taxa in greater than 1% abundance in bedded pack that were also greater in mastitic milk included *Debaryomyces*. Sampling at five farms revealed that management practices and choice of bedding material influence the microbial community of bedded pack.

**#SI.18**

**Conservation tillage impacts on soil quality parameters under furrow irrigation**

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Furrow irrigation is widely practiced in Colorado and it's expected to continue across much of the State. Under furrow-irrigated systems, conventional tillage practices are common, but such practices can have adverse environmental impact and degrade soil quality. The project sought to examine the effects of conservation tillage on soil health at a production scale, understand relationships between soil parameters, and to evaluate the economic feasibility of conservation practices. Soil biological, physical, and chemical parameters were evaluated during the fifth and sixth years (2015 and 2016) of a study comparing two different management systems, minimum till (MT), and strip-till (ST), vs. a conventional tillage (CT) control. Measurement included active carbon, macrofauna communities, aggregate stability, infiltration, and total suspended solids (TSS), and residue cover. Active carbon was significantly higher for minimal tillage when compared to conventional and strip till. Results from both years suggest that conservation treatments increased macrofauna abundance, especially earthworms, and diversity (richness) relative to the control. Aggregate stability was significantly higher in the conservation treatments for 2015, but not in 2016. Infiltration rates were slightly higher under strip-till, while TSS in runoff water were significantly reduced in both conservation treatments. Residue cover was strongly correlated with macrofauna and earthworm abundance and TSS loss. When comparing economic cost, and returns among systems, strip till had a 16% greater return when compared to conventional tillage plots. These preliminary results show potential for conservation tillage under furrow-irrigation to improve soil quality parameters as well as increasing net income.

#SI.19

## **Reduction in daily soil temperature range increase microbial community dynamics in a dryland cotton production system in West Texas**

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Sustainability of agriculture in the Southern High Plains of West Texas faces challenges due to the climate change variability is imposing on soil health, microbial dynamics, water use and plant productivity. Soil temperature is crucial for plant growth, and the ability of microorganism to carry out fundamental process. Variation in Daily Temperature Range ( $DTR_{soil}$ ) has a large impact on microbial activity in arid and semi-arid environments. Thus, it is imperative to understand how temperature variability at the daily scale influences microbial communities and their roles in nutrient cycling, and carbon storage. We evaluated the impacts of modifying  $DTR_{soil}$  on microbial responses. For 2014-2015 growing season, 3 treatments were established: Control, Reduced  $DTR_{soil}$  using erosion blankets (shade), and Reduced  $DTR_{soil}$  using sorghum residue (stubble) to modify  $DTR_{soil}$ , with six plots (4 x 3 m) in each treatment. Soil samples were collected monthly to evaluate edaphic parameters, extractable  $NH_4^+-N$  and  $NO_3^- -N$ , and microbial parameters. The stubble and shade reduced the  $DTR_{soil}$  by 6 °C on average at the soil surface and 2 °C at 15 cm during the hottest months. Microbial biomass carbon increased in stubble by 43 % on average irrespective of any changes to soil moisture while extractable nitrogen levels were higher under control plots in comparison with reduced  $DTR_{soil}$  plots. The reduction in  $DTR_{soil}$  in these semi-arid systems positively affected microbial dynamics and their contributions to soil productivity, this will help cotton producers mitigate climate variability impacts and improve soil health leading to sustainable cotton production in West Texas.

**#SI.20**

**Responses to soil mesofauna to agricultural practices and arable field-margin management**

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Soil health is a key factor controlling crop quality and yield in which soil fauna underpin soil processes in relation to organic matter decomposition and nutrient cycling. A better understanding of abundance and composition of soil faunal populations is therefore essential in determining agricultural ecosystem health and preserving soils and their functions. Over two seasons, we studied soil invertebrate populations in an arable field and its associated grass margin. The aim of the study was to understand whether field margins affect population structure, and if such effects extended into the field. Results showed that distribution of soil fauna varied depending on both environmental and seasonal factors. In comparison to the crop, margin did not strongly modify populations of soil invertebrates. However, these populations were reduced in the fallow area between field and margin, and in the tramlines further into the field. Some soil properties and faunal distributions showed a spatially diagonal orientation to the margin. Agricultural activities, such as trafficking, could be the origin of non-conducive conditions for soil fauna but none of the current field activities explain the diagonal pattern and at the present time, only assumptions can be made about it. Digging in the landscape history of Rawcliffe Bridge suggested that far older agricultural managements may still affect soil properties. The study showed that field activities may mask inherently effects of landscape diversity. It also raises possible issues about the 'agricultural footprint' on soils and the necessity to care about the potential long-term legacy of management practices.

#SI.21

**Impact of compaction on decomposition in an arable field and possible improvement by managing the headland**

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Soil compaction is a major threat on agricultural soil and heavy machineries are responsible for damaging soil chemical, physical and biological properties. Among these, soil decomposition is the necessary process to nutrient cycling that transformed organic matter into mineral nutrients. Because nutrient turnover is essential to crop production, understanding what factors impact soil biota, and affect its functionality, is a first step to better agricultural practices.

In a previous study, we assessed whether margins affect soil biota in fields close by. Results showed that soil fauna was highly reduced within the first meters of field, where tramlines and wheeling were situated. To understand in which extent compaction affects soil ecology, we assessed decomposition in three distinct field areas: the margin, the tramlines and the crop. Three types of litter in two different mesh sizes litter bags were buried for 1, 2, 4 and 6 months. Soil physical properties were measured, and as expected bulk density was lower in the compacted tramline. It also confirmed that the grass margin improved soil structure compared to the field. Results showed the highest mass loss occurred in the grass, and the lowest in the tramline and differences between treatments increased with burial time. No significant difference of mass loss between the two mesh sizes was detected before the fourth month, implying that microbial decomposition was the main process involved at the beginning. Decomposition in the tramline was clearly affected by the structure degradation and limitation of water and nutrient supplies due to heavy compaction.

#SI.22

**Empirical evidence that passive microbial dispersal maintains soil community and ecosystem function**

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Dispersal rate is increasingly recognized as an important determinant of microbial community composition and function. The mechanisms that underlie the effect of dispersal on function are also relevant to efforts to optimize soil function by application of biological inocula (or colonists). However, knowledge of the ecological role of microbial dispersal *in situ* is limited. Rain hosts a diverse community of microorganisms, making it a proportionally small but consistent source of microorganisms to soil. To assess the ecological impact of passive dispersal on soil processes, we established mesocosms of intact soil cores at Kellogg Biological Station. After rain, cores received either filter-sterilized rain (no dispersal) or ambient rain (dispersal). We also overlaid a drought treatment on these cores to test whether zero dispersal constrained community and functional resilience under stress. We found that excluding rain immigrants significantly altered microbial community composition and substrate utilization, as well as soil properties. Soils experiencing dispersal limitation had lower water holding capacity and higher nitrate export. Although microbial biomass was similar among dispersal levels, we found that functional diversity was reduced under dispersal limitation. Drought treatments also had reduced functional capacity and diversity, but were unaffected by dispersal treatment. Overall, we observed an interaction between drought and dispersal, but saw no evidence of dispersal rescuing function. Our data demonstrate that rain-dispersed microbes maintain soil microbial function, but the disturbance state of soils modulates the effect of dispersal. Ultimately our understanding of dispersal and colonization can inform strategies for managing microbiomes for ecosystem function.

**#SI.23**

**Soil microbial dynamics in a long-term sustainable cotton for semi-arid West Texas**

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Sustainable agriculture practices can improve microbial capabilities to carry out fundamental soil processes. Understanding microbial dynamics in soils within long-term sustainable practices is critical for addressing impacts of increasing climate variability within a semiarid system. This study describes microbial dynamics from a 10-year-old sustainable cotton production system on the Southern High Plains of West Texas (no-till and stubble application). In 2016, 8 replicate plots were randomly selected from a full section center pivot irrigated cotton field. A layer of corn stubble from the previous growing season along with terminated winter wheat covered the soil. Soil samples were collected and analyzed monthly to evaluate edaphic parameters, nutrient levels, and microbial community structure. In addition, each plot had a data logger to record hourly data on temperature and volumetric water content (VWC) through the growing season. Soil microbial biomass decreased over the growing season irrespective of soil moisture levels. However, using FAME analyses, relative abundances of saprophytic fungi and arbuscular mycorrhizae were dominant (27.4% and 30.9%) with Gram positive, Gram negative and Actinomycetes, relative abundance was between 26.4% and 27.6% across the growing season with little seasonal changes. Between 0.8% and 1.7% of the FAME signatures were assigned to protozoans. Lastly, 40.9% to 45.1% the total FAME relative abundances were assigned as unidentified. Nutrient analyses showed a general decrease across time. Nonmetric multidimensional scaling analysis indicated that daily temperature range (daily  $T_{\max}$  – daily  $T_{\min}$ ) and VWC were the two most important abiotic variables shaping microbial community structure.

**#SI.24**

**Rhizosphere and bulk soil microbial dynamics in Engelmann Spruce stands in response to Spruce beetle attack**

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The current outbreak of spruce beetle in the Colorado and Wyoming mountain forests is causing widespread tree death. As trees die, the associated microbial community is likely to change. With new advances in genomic technologies, scientists are beginning to understand the intricacies of these plant-microbe interactions. The phytobiome includes the microbes that are on or in close proximity to the plant and are responsible for many beneficial plant and ecosystem functions. One of the most studied phytobiome components, the rhizosphere, is likely most important due to the advantages a healthy functioning rhizosphere conveys. To understand how the rhizosphere of Engelmann spruce, as well as the surrounding bulk soil, changes in response to beetle attack and colonization of blue stain fungi, a chronosequence of beetle infestation was utilized. The rhizosphere and bulk soil of three phases; healthy, infested and dead tree clusters were sampled. Significant differences in soil gravimetric water content were observed between all three phases, as well as an increased soil pH and EC in the dead and infested phase compared to the healthy phase. These physical and chemical changes, based on previous studies, are predicted to have direct impacts on the microbial community structure. Using high-throughput sequencing of the fungal and bacterial communities in the rhizosphere and bulk soil associated with each of the three phases we will analyze the impacts of beetle infestation. We expect to find distinct microbial communities at each phase, with more saprotrophs in the dead phase and more pathogens in the diseased phase.

**#SI.25**

**How bed design in a dryland cotton system can influence subsequent microbial dynamic**

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Soil temperature in dry-land cotton production systems can influence soil microflora activity and nutrient availability, and plant production. Field maintenance practices and soil temperature needs at planting could result in altered microbial dynamics as the season progresses. For conventional tilled cotton system on the Southern High Plains pitched beds are used to reduce erosion and increase temperatures at planting. However, bed design could influence soil heat dynamics, by increasing the Daily Temperature Range (DTR) of the soil. The goals of this project were to investigate the impacts of bed design (pitched vs flat) on  $DTR_{soil}$  dynamics and microbial responses, six 4 meter plots with five rows per plot were established in 2014 and 2015 at the TTU farm in Lubbock, TX. Soil samples to 15 cm depth were collected starting in May and followed monthly through November. Microbial biomass carbon, enzymatic activities, FAME, and carbon usage by bacteria and fungi along with nutrient dynamics and soil moisture were evaluated. Bed design did impact soil temperature dynamics and moisture status, especially during the hottest and driest portions of the growing season. Pitched beds were warmer than flat beds at both depths, and experienced a higher  $DTR_{soil}$  through the growing season. Subsequently flat beds contained 26% more microbial biomass carbon than the pitched across the growing season. Bed design is one management tool that could be employed in cotton production systems across the SHP to ameliorate soil temperature variability and the high  $DTR_{soil}$  that occurs in the region.

#SI.26

## **Investigating changes in soil organic matter pools following bark-beetle outbreak and salvage logging: Implications for soil organic matter formation**

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Continent-scale forest disturbance caused by recent bark beetle outbreaks renewed concern about the implications of forest management on soil organic matter (SOM) formation and persistence. Decomposition of plant residue creates a range of physically-distinct SOM pools with unique contributions to SOM dynamics. To investigate the connection between management of disturbed forest ecosystems and distribution SOM pools, we fractionated mineral soils (0-10 cm) from 12 sites in Colorado, subject to three management treatments: (1) uncut bark beetle-infested forest and, (2) adjacent salvage-logged stands with either logging residue retention or (3) removal. Mineral soils were fractionated into three SOM pools: light ( $<1.85 \text{ g/cm}^3$ ), sand-sized ( $> 53 \mu\text{m}$ ) and mineral-associated organic matter (MAOM,  $< 53 \mu\text{m}$ ). Logging with residue retention increased the mass of the surface, Oi, organic horizon ( $P<0.05$ ); however, increased Oi did not result in increased carbon (C) in the deeper, more decomposed organic horizons (Oe and Oa) or the mineral soil. In contrast to expectations, logging followed by residue removal increased mineral soil C compared to uncut stands ( $P<0.10$ ). No detected changes in the MAOM mean there are no changes to the persistent soil C pool with the logging residue treatments. Therefore, the light and sand-sized fractions, particularly the sand-sized ( $p<0.05$ ), largely drove the change in whole soil C. Further analysis of changes in the MAOM fraction, as well as of the composition and recalcitrance of the light and sand-sized fractions may help elucidate which mechanisms link OM inputs following logging and SOM formation and persistence in coarse-textured forest soils.

#SI.27

## **The influence of invasive earthworms on oribatid mite assemblages in a boreal aspen stand**

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Non-native earthworm species, specifically Lumbricidae, are invading areas of the boreal forest in Alberta, Canada. Lumbricidae species are ecosystem engineers, and when introduced into a new environment may strongly alter soil biogeochemical cycling. Earthworm invasion has been studied in Southwestern Alberta with only a small series of studies conducted in Northern Alberta. Northern Alberta soils have a thick forest floor that stores ~24% ecosystem carbon and houses the majority of soil biological interactions. Oribatid mites are key detritivores in these soils as they initiate litter decomposition and maintain forest floor structure. Earthworms also function as detritivores, and when introduced into non-endemic environments, can have adverse effects on oribatid mite composition. However, there is a dearth of field studies in the Northern Alberta regarding invasive earthworm disturbance on oribatid mite assemblages. The objectives of this study were to (1) characterize earthworm and oribatid mite assemblages present in a boreal aspen stand and (2) assess how oribatid mite assemblages respond to changes in soil biogeochemical properties as a result of earthworm disturbance. The case study was conducted in a boreal aspen stand near Wolf Lake, Alberta. Four plots were established in areas of both high and low earthworm density and sampled for earthworms and oribatid mites, which were identified to species when possible. Earthworm invaded plots had significantly lower forest floor carbon, thinner forest floor, and lower oribatid mite abundance. Further work will use a multivariate approach to analyze oribatid mite species composition as a function of earthworm density and environmental characteristics.

**#SI.28**

**Consequences of invasion by *Bothriochloa bladhii* and implications for tallgrass prairie restoration**

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Grasslands cover 35% of earth's land surface, provide many essential ecosystem services, and play an important role in driving global biogeochemical cycles. One of the greatest current threats to these ecosystems is invasion by non-native plant species. While the underlying biological mechanisms facilitating non-native species invasion are still unknown, there is growing recognition that alterations in belowground processes may play fundamental roles in their success. Our study was conducted at Konza Prairie Biological Station, Manhattan, KS, USA. The objectives of our study are two fold; 1) assess above- and belowground consequences of invasion by a non-native warm-season grass, *Bothriochloa bladhii*, and 2) eradicate the invasive and assess potential restoration management practices. Replicate plots were established in invaded and adjacent non-invaded native grassland. Above- and belowground biomass, plant species composition, and soil biotic (relative abundance of soil microbial functional groups and intra-radical mycorrhizal hyphal abundance), and abiotic parameters (plant-available N/P, soil aggregate distribution) were assessed. Aboveground biomass of the invasive grass was significantly greater than that of the native prairie, while root biomass and soil organic matter was reduced. Eradication of *B. bladhii* using solarization was initiated spring 2016. Tarps were removed at the end of the growing season with successful eradication of *B. bladhii*. This upcoming field season, we will establish restoration treatments to assess if inoculation with native AM fungi improves the establishment of native plant species while simultaneously suppressing re-establishment of the invasive grass.

**#SI.29**

**Uniform response of soil respiration to experimental temperature manipulation**

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The respiratory release of carbon dioxide (CO<sub>2</sub>) from soil is one of the primary determinants of atmospheric CO<sub>2</sub> concentrations<sup>1</sup>. Climatic warming is hypothesized to increase soil respiration, potentially fueling further increases in global temperatures<sup>2</sup>. However, despite considerable scientific attention in recent decades, the response of soil respiration to anticipated climatic warming remains unclear<sup>3</sup>. Here we synthesize >3800 observations from 27 temperature manipulation studies spanning nine biomes to reveal shared responses of soil respiration to experimental warming. Contrary to the results from numerous single-site studies<sup>4-6</sup>, we find no differences in the temperature response of soil respiration between control and warmed plots in several biomes; temperature sensitivity between control and warmed plots was only significantly different in deserts and boreal forests. Thus, our data provides limited evidence of acclimation of soil respiration to warming. Across all non-desert biomes, respiration rates increased exponentially with soil temperature up to a threshold of ~25°C, above which, the relationship between respiration and temperature became neutral or negative. This consistent decline in the temperature sensitivity at higher temperatures could not be attributed to changes in soil moisture availability at elevated temperatures. Our analysis highlights that rising global temperatures will result in regionally variable responses in soil respiration, with colder climates being considerably more responsive to increased ambient temperatures compared to warmer regions.

**#SI.30**

**Stability of microbial activity in an experimentally warmed dryland**

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Dryland ecosystems cover about 40% of the global land surface and play a significant role in global water and biogeochemical cycles. Encroachment of woody shrubs into dryland grasslands is a global phenomenon that alters the ecohydrology, plant biodiversity, fire regimes, and productivity of these systems. The projected warmer and drier conditions in these regions may further alter the function and stability of these ecosystems through direct effects on soil microbiota and plant-microbe interactions. In drylands, microbial activities are regulated by nutrients and pervasive, seasonal water limitation. In mesic ecosystems, warming results in increased extracellular enzyme pools, but these results might not apply to drylands. We used a long-term passive warming experiment to explore the effects of warming and nutrient supply on extracellular enzymes after summer and winter monsoons. We monitored plant biomass, soil respiration, and enzyme activity over two years in soils common to the Arizona Sonoran desert. Soils were amended with biochar and woodchips to mimic woody shrub encroachment. We hypothesized that warming would increase carbon acquisition extracellular enzyme pools and create a positive feedback on carbon mineralization following bi-annual monsoons. Soil respiration responded positively to warming for certain carbon additions and seasons. For seven hydrolytic enzymes, there was no significant response to warming regardless of soil moisture and temperature. These results are consistent with other dryland warming experiments and suggest complex responses of dryland soil microbial activity to climate warming. Analysis of the microbial community composition is underway and will provide further understanding of soil microbial community stability.

#SI.31

**Impacts of moisture, soil respiration, and agricultural practices on gross CH<sub>4</sub> production in upland soils measured by stable isotope pool dilution**

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Methanogenesis that occurs in upland, unsaturated soils indicates the likely presence of anoxic microsites hosting other anaerobic activities. These activities affect processes that are critical for agricultural production and natural ecosystems such as nutrient cycling and greenhouse gas fluxes, however, little is known about the controls of anoxic microsite formation, persistence, and biogeochemical impact. Agricultural practices may alter anoxic microsites and related processes through changes to soil properties. We hypothesized that methanogenesis, as an indicator of anaerobic activity in microsites, is primarily affected by soil moisture and respiration. To test this, we examined relationships between soil properties, methanogenic microsite dynamics, and biogeochemical responses in a full factorial laboratory experiment over soil source (semi-arid and mesic ecosystems), agricultural practice (conventional, no-till, and organic), and moisture (10 to 95% water-filled porespace, WFPS) in a five month intact core incubation. We found that organically-managed soils had higher rates of methanogenesis than conventionally tilled soils, and soils with more than 60% WFPS were three times as likely to host methanogenesis as drier soils. Rates of methanogenesis varied temporally, with early methanogenesis (6<sup>th</sup> week) correlated with higher soil respiration and WFPS while later methanogenesis (21<sup>st</sup> week) was only predicted by WFPS. The importance of soil respiration and WFPS in our soils is similar to findings in better studied wetland systems, suggesting that upland anaerobicity can also arise from increased O<sub>2</sub> demand or decreased O<sub>2</sub> diffusion. Higher rates of methanogenesis were associated with higher soil NH<sub>4</sub><sup>+</sup>, less NO<sub>3</sub><sup>-</sup>, and greater N<sub>2</sub>O emissions.

**#SI.32**

**Long- and short-term nitrogen additions increase decomposition of cover crop residues in agricultural soils**

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Recent studies have shown increases in microbial biomass and activity nitrogen (N) amendments in annual cropping systems. Here we explore the effects of short- and long-term fertilizer N additions on the decomposition cover crop residues in soils from a corn-soy-wheat cropping system. Our study site at the Kellogg Biological Station in Michigan is an experiment started in 2000 that includes a gradient of N fertilizer. We sampled soils in November 2015 with N additions of 134 and 291 kg ha<sup>-1</sup> N during years in corn. Duplicate sets of soils were amended with 5 mg g<sup>-1</sup> soil residue from four different cover crops: millet, rye, hairy vetch and field pea. One set was also amended with urea equivalent to 134 kg ha<sup>-1</sup>. Soils and residues were incubated for 360 days, and sub-sampled four times to measure extracellular enzyme activities, inorganic N and microbial biomass and net N mineralization and nitrification rates. The short-term (lab) N additions had a greater impact on N transformations than long-term (field) N additions. N mineralization and nitrification processes were both increased by short-term N addition, but only in soils that also received long-term N. This was true regardless of the different cover crop residues. Long-term N addition affected the timing of net positive mineralization and nitrification and therefore plant N availability. These data provide evidence for interactions between long- and short-term N additions to soils that have implications for microbial activities related to residue decomposition and the timing and magnitude of plant available N pools.

**#SI.33**

**The Microbial-Mineral Carbon Stabilization model with coupled N cycling (MIMICS-CN) simulates litter decomposition and soil organic matter dynamics at landscape scales**

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Microbes are increasingly recognized as critical mediators of climate change effects on soil carbon (C) and nitrogen (N) transformations, both in field studies and theoretical models. The Microbial-Mineral Carbon Stabilization model with coupled nitrogen cycling (MIMICS-CN) uses explicit microbial dynamics and microbe-mineral interactions to simulate measured patterns of C and N cycling at landscape scales. The model simulates C and N losses from litterbags in the LIDET study (6 litter types, 10 years of observations, 14 sites across North America) with reasonable accuracy (C:  $R^2=0.59$ ; N:  $R^2=0.33$ ). MIMICS-CN simulations of litterbag N dynamics are better than Community Land Model (CLM-cn) simulations of the same data and as good or better than DAYCENT simulations. Across the 14 simulated LIDET sites, MIMICS-CN produces reasonable equilibrium values for total soil C and N, microbial biomass C and N, respiration, inorganic N, and N mineralization rate. Parameter sensitivity analysis indicates that carbon use efficiency and microbial turnover are critical controls over model behavior that are poorly constrained by experimental data. We also simulated a theoretical double litter addition experiment at one of the LIDET sites (Kellogg Biological Station) to explore transient model behavior across microbial and mineral pools. Unlike first-order models where added litter can only result in increases in soil organic matter (SOM) pools, MIMICS-CN allows fresh litter additions to stimulate microbe-mediated C losses and N release from SOM pools.

**#SI.34**

**Committee for evidence-based action: Educating the public and policy-makers for a scientifically sound future**

**Daniel Revillini, Bo Stevens, Kara Gibson, Aradhana Roberts, Peter Motyka, Nancy C. Johnson**

Northern Arizona University, United States

The role of critical, scientific thinking in the future of American society is uncertain, and the disregard of evidence is detrimental at multiple levels of society. The Committee for Evidence-Based Action is a new graduate student group at Northern Arizona University with the goal of introducing evidence-based decision making as a platform to be adopted at the individual, local, state, and federal levels. Our mission is to (1) advocate the use of evidence-based decision making to the public and policy-makers, (2) open direct lines of communication between scientists and the public through open-access forums and community events, and (3) promote open, public discourse and implement coordinated actions that disseminate committee ideals. We have initiated community forums to provide the public with direct access to scientists, and also to learn how scientific thinking helps us develop our stance on issues. We have presented issue-focused seminars on campus across multiple departments, and disseminated educational materials to help scientists develop their writing and speaking skills for broad audiences. We've also developed online training and discussion workshops to help increase scientific outreach to the public, policy-makers, and the media. Our goal is not only to influence policy, but the collective conscious of the public to bring the role of science and evidence-based thinking to the forefront of our daily lives. Only then can we, as a nation, influence the decisions made by legislators to protect human-health, education, and the environment in a scientifically sound manner.

**#SI.35**

**Inquiry-based STEM education for high school students: strengths, possibilities, and opportunities to get involved**

Martha Gebhardt, Elizabeth Sparks, Rachel Gallery

University of Arizona, United States

Although many high school science teachers incorporate climate science into their courses, their effectiveness of teaching these topics may be hindered by lack of training and confidence in their own understanding of these concepts. Educators with a greater appreciation and knowledge of science literacy will be more successful at encouraging students to enjoy science and motivating them to pursue science careers. Inquiry-based science learning engages students in hands-on activities and cooperative learning strategies, which have been proven to increase their knowledge and interest of scientific concepts. To help overcome obstacles teachers encounter with science education, and engage and excite students in STEM, I worked with high school teachers and scientific experts in school districts in Southeastern Arizona to develop a series of inquiry-based lessons and videos focused on climate and human impacts on vegetation abundance and diversity across spatial and temporal scales. Students use the scientific method to examine vegetation at their own school, compare these trends to patterns of vegetation across space and time at the Santa Rita Experimental Range, and relate these patterns to climate and cattle grazing data to study their potential impact on vegetation. All materials developed, which are publicly available online, align with educational standards and provide the tools and resources needed to make any educator feel confident they can incorporate them into their classroom. Here I outline the successes and challenges faced in implementing this project. As lesson development continues, I hope to expand scientific concepts and both researcher and educator participation.

**#SI.36**

**Woody shrub encroachment alters ecosystem processes: Linking imaging spectroscopy and microbial biogeochemistry**

Martha Gebhardt, Rachel Gallery

University of Arizona School of Natural Resources and the Environment, United States

Arid and semi-arid grasslands are undergoing prolific changes in vegetation due to woody shrub encroachment that causes large-scale shifts in biogeochemistry. Nitrogen-fixing mesquites, a common shrub to invade these areas, fundamentally alters ecosystem processes by changing plant community diversity, net primary productivity, and soil functioning. Although the proliferation of these shrubs is well documented, uncertainties related to landscape-scale biogeochemical consequences and spatial patterns associated with shrub invasion remain. This information is needed to quantify the effects of vegetation changes on ecosystem processes and services. This study combines hyperspectral foliar chemistry data with soil biogeochemical and microbial parameters to quantify the impacts of shrub encroachment on nutrient dynamics at The Santa Rita Experimental Range (SRER) in southeastern Arizona. We propose that hyperspectral data can be used to quantify changes in ecosystem services due to differences in vegetation chemistry and associated belowground processes across a landscape. These data are used to investigate the link between soil nutrients, topography and the abundance of shrubs and grasses; the potential effects of shrub encroachment on landscape-scale nutrient dynamics; and the utility of imaging spectroscopy to inform management practices through remote monitoring. SRER is an ideal location to investigate these questions because long-term data on vegetation dynamics across SRER is publicly available and the proposed National Ecological Observatory Network (NEON) airborne observation platform offers a unique opportunity to map patterns of plant species, litter inputs and microbial-mediated biogeochemical cycling across the landscape.

#SI.37

## **Earthworm distribution and demographics along a naturally occurring salinity gradient**

Caley Gasch

North Dakota State University, United States

Over 90% of crop producers in North Dakota are affected by naturally occurring soluble salts (primarily sodium, calcium, and magnesium sulfates), which originate in the parent material and migrate to the soil surface. Salinity levels can be high enough to limit crop production and influence soil management decisions. Our objective was to examine the distribution and demographics of earthworms in an annual cropping field that is affected by surface salinity, and that is currently undergoing management to limit salt migration and improve soil health. We established a transect to capture increasing levels of soil electrical conductivity (EC), and collected intact soil cores for worm counts and soil samples for chemical analyses. With increasing salinity levels, we observed a decrease in soil organic matter content and total worm counts for all worm age classes. Worm cocoon counts were not different across salinity levels. Juvenile worms were the most abundant age class in non-saline soils, but was the group most reduced by increasing salinity levels. Consistent cocoon counts and decreasing juveniles across the salinity gradient indicate that adult worms migrate into saline areas, but are not able to establish a viable population. Earthworm species present in the study were predominately *Aporrectodea trapezoides* and *Aporrectodea tuberculata* with *Octolasion tyrtaeum* present. Worm occurrence and age classifications may be an easy indicator for producers to monitor salinity levels and soil health.

#SI.38

**Understanding interactions between nitrogen-fixing bacteria and switchgrass for sustainable biofuel production**

Ryan Lancione

Northern Arizona University, United States

Switchgrass (*Panicum virgatum*) has been recognized to have great potential as a biofuel feedstock. Switchgrass can function as an agricultural cash crop on marginal farmlands, a soil restoration tool, and a sustainable, renewable energy source. Bacteria that live on or around switchgrass roots have been shown to fix nitrogen (N) and improve the nutritional status of switchgrass. The nif genes code for enzymes involved in atmospheric N fixation. We used quantitative polymerase chain reaction (qPCR) to determine the absolute abundance of the nifH gene found in the rhizosphere of switchgrass from a long-term experimental research site at Argonne National Laboratory. This site tests the differences between three switchgrass cultivars and the effect of N fertilization on biomass production. We identified trends where the nifH gene was lower in N-fertilized plots, but contrary to our hypothesis we found no variation in nifH gene abundance between the three cultivars. If the beneficial relationship between switchgrass and N-fixers can be optimized to minimize fertilizer use and sustain or promote plant biomass production, it could lower the cost of switchgrass production substantially and increase the sustainability of national renewable energy production.

**#SI.39**

**Increasing crop diversity increased soil microbial activity, N-sourcing and crop N, but not soil microbial diversity**

Zander Venter<sup>1</sup>, Samantha Luise Scott<sup>2</sup>, Johann Strauss<sup>3</sup>, Karin Jacobs<sup>4</sup>, \*Heidi Hawkins<sup>2</sup>

<sup>1</sup>University of Cape Town / University of Stellenbosch, South Africa

<sup>2</sup>University of Cape Town, South Africa

<sup>3</sup>Western Cape Department of Agriculture, South Africa

<sup>4</sup>University of Stellenbosch, South Africa

The relationships between crop diversity, soil microbial diversity, and agro-ecosystem functioning (N-sourcing) were compared in wheat monoculture versus two wheat-legume rotations within a 19-year old trial in South Africa. The relative increase in historical wheat yields (28%) and foliar [N] (106%) of wheat-legume rotations compared to wheat monoculture was related to increased microbial activity but not genetic diversity as measured by Community Level Physiological Profiling and automated rRNA intergenic spacer analysis, respectively. Soil microbial diversity was rather related to known abiotic drivers. A <sup>15</sup>N-<sup>13</sup>C dual isotope mixing model supported the idea that enhanced N cycling and yield in crop-legume rotations was not a result of microbial diversity per se, but rather increased microbial activity when keystone legume species and their associated N<sub>2</sub>-fixing symbionts were present.

#SI.40

**Operational Tillage Information System: Tracking conservation practices at field to watershed scales**

William Salas, Stephen Hagen, Ian Cooke

Applied GeoSolutions, LLC, United States

Applied GeoSolutions (AGS) has developed and deployed a system for operational mapping of tillage practices and cover crops over wide areas. The system, known as the **Operational Tillage Information System** or OpTIS, produces spatially comprehensive maps of crop residue cover and cover crops using information integrated from multiple earth-observing satellites. These detailed, retrospective (1984 to present) and on-going, large area maps of conservation agriculture practices are produced at the farm-field level, but are often used to produce summaries at aggregated political or natural scales. These data are used to drive DNDC, a soil biogeochemical model that simulates crop growth, nutrient cycling, GHG emissions, and soil carbon dynamics, for field to watershed modeling on impact of conservation agriculture on soil health. The integration of these technologies facilitates the estimation of ecosystem services associated with the adoption of conservation agriculture management practices. We propose to present a poster on the OpTIS Remote Sensing – DNDC modeling platform for mapping and monitoring adoption and performance of conservation practices at field and watershed scales.

**#SI.41**

**Bacterial Diversity of an Abandoned Coal Mine Soil in Southeast Kansas**

Rachel Bechtold, Anuradha Ghosh

Pittsburg State University, United States

Acid mine drainage (AMD) occurs near abandoned coal mines in southeast Kansas, the waste product decreasing pH. Soil bacteria are useful indicators of ecosystem health in these perturbed areas. The goal of the study was to assess microbial diversity of an AMD site. In fall (2015) and summer (2016), soil samples were aseptically collected from five topographically diverse sites and physico-chemical characteristics were evaluated. A total of 58 morphologically different colonies were typified using physiological and biochemical tests and were identified at the species level through 16S rRNA gene sequencing. Additionally, acidophilic bacterial strains were screened using selective media. Soil pH ranged from 2.5-6.8 and varied concentrations of arsenic, manganese, and iron were detected. Biochemical tests revealed a diverse metabolic potential of the bacterial population. The majority of bacterial species belonged to common soil inhabitant phyla *Firmicutes* and *Actinobacteria*. A total of 17 acidophilic bacterial isolates were identified and would be subjected to small-scale bioremediation process using lyophilization complemented with other physico-chemical techniques. A baseline measurement of bacterial diversity and soil chemistry of AMD sites in this region is novel in its kind. The findings have potential use in AMD remediation and restoration of natural habitat for plants and animals.

**#SI.42**

**Mechanism of non-additive heterogeneous litter decomposition**

Na Yin, Roger Koide

Brigham Young University, United States

Litter decomposition is a fundamental ecosystem process that stimulates energy flow and drives nutrient cycling. The factors that control the decomposition of homogeneous litter have been well researched. In nature, however, litter is usually heterogeneous, consisting of either material from the same species in varying decomposition states, or material from multiple species. Heterogeneous litter may not decompose the way homogeneous litter does, which makes the fluxes associated with decomposition impossible to predict. For example, heterogeneous litter decomposition may be non-additive. We focus on investigating the effect of litter mixing (oat straw/clover system) on oat straw decomposition. None of the frequently-evoked mechanisms (nutrient transfer, increased water content) explain non-additive decomposition of oat straw when associated with clover. Preliminary studies suggest that clover increases the rate of oat straw decomposition by stimulating the activity of cellulase enzymes produced by decomposer microorganisms, and that the mechanism for this stimulation involves the availability of labile C from clover litter.

**#SI.43**

**Comparative response of six grapevine rootstocks to inoculation with arbuscular mycorrhizal fungi**

Antreas Pogiatzis<sup>1</sup>, John Klironomos<sup>1</sup>, Pat Bowen<sup>2</sup>, Miranda Hart<sup>1</sup>, Taylor Holland<sup>1</sup>

<sup>1</sup>University of British Columbia-Okanagan, Canada

<sup>2</sup>Agriculture & Agri-Food Canada, Summerland Research & Development Centre, Canada

Arbuscular mycorrhizal fungi are soil fungi that form a symbiotic association with plant roots. The symbiosis is largely nutritional. The fungi depend on the plants for carbon resources, and the plants benefit from increased access to soil nutrients. The magnitude of plant benefit, however, can vary significantly. It has been suggested that root architecture is a key factor that determines plant responsiveness to arbuscular mycorrhizal fungi, and some studies have been conducted and support this notion. However, a major limitation in such studies is the lack of control for phylogenetic constraints among tested plants, making it difficult to control for confounding variables that are not associated with root architecture. I explored the variation in plant responsiveness among closely related species (grapevines) and investigated the potential relationship between root architecture and responsiveness to arbuscular mycorrhizal fungi. I found that root colonization by arbuscular mycorrhizal fungi can improve grapevine growth, although the degree of benefit differed among grapevine rootstocks. The magnitude of the benefit can be partially explained by the pre-colonization root architecture, and in particular, by root branching, which is associated with plant nutrient foraging ability. In addition, root colonization by arbuscular mycorrhizal fungi can influence the expression of root traits, by increasing plant biomass per unit of root length and root branching.

**#SI.44**

**Realistically simulating the effects of oxidation on soil decomposition**

**Adam Langley, Brendan Kelly, Samantha Chapman**

Villanova University, United States

Soil oxygen availability strongly regulates microbial function and varies along sharp gradients through space and time. Moreover, soil oxygen status is changing in many ecosystems as climate, hydrology and plant communities change, yet we lack a basic understanding of the consequences for processes like decomposition. The factor by which fully oxygenating previously anoxic soils accelerates decomposition (O:A ratio) varies widely across studies, ranging from 1.3 to 22 even within highly controlled lab-based studies. Our goals were to determine the O:A ratio of peat from a brackish marsh and explore what factors may explain disparities in estimates across studies. We used three methods to experimentally oxygenate and deoxygenate soils for two months: (1) incubations with intact soil cores, (2) incubations with soil slurries and (3) flow-through mesocosms. Over two months, the three methods yielded O:A ratios of 2.2, 1.8 and 4.2, respectively. O:A ratios were stable through time. We found that even on small monoliths (roughly 1 cm cubes) of intact soil, headspace O<sub>2</sub> treatments failed to fully oxygenate soils, likely leading to an underestimate of the O:A ratio. Slurrying and shaking soil allows for precise and homogenous treatment application but dramatically accelerates decomposition rates compared to static soil, again likely biasing the O:A ratio downward. The flow-through mesocosms maintained soil structure and successfully oxygenated the entire soil profile. We may be underestimating the effects of soil oxygenation on soil decomposition rates, which could have dramatic consequences for predicting future carbon fluxes, particularly from wetlands.

**#SI.45**

**Does microbial community composition influence decomposition in wetland ecosystems?**

Megan Foley, Adam Langley

Villanova University, United States

Microbial communities are generally regarded to be functionally redundant for general ecosystem processes, such as decomposition. However, microbial community composition varies dramatically with depth, particularly in wetland soils, where anoxic conditions dominate in deep soils. We performed a laboratory incubation experiment to test the functional redundancy of very distinct microbial communities from surface (0-10 cm) and deep (50-60 cm) soils in two wetland ecosystems. Surface and deep soil microbial communities were used to inoculate sterilized soils taken from two depths (0-10 cm, 50-60 cm) in two tidal marshes in Barnegat Bay, NJ. We factorially manipulated oxygen availability to represent realistic “surface” and “deep” marsh environments. We estimated substrate-induced respiration to evaluate the potential activity of initial microbial communities, and there were no differences between surface and deep microbial communities. We performed the incubation experiment in two phases, and measured C<sub>2</sub> production weekly for four weeks in each phase. Mean microbial respiration did not differ between surface and deep soil microbial inocula under any condition. These results suggest even very distinct soil microbial communities can adapt rapidly to new conditions and may exhibit redundancy in function across a wide range of environments.

## Appendix I

# *ECOLOGY OF SOIL HEALTH SUMMIT POSTER SESSION ABSTRACTS*

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Tuesday June 6th

POSTER SESSION 2

5:00 – 7:00 PM

Ballroom B, Lory Student Center

## #SII.1

### **Soil management practices to enhance soil health and early growth of sweet cherry planted into old orchard land**

Thomas Forge<sup>1</sup>, Tristan Watson<sup>2</sup>, Paige Munro<sup>2</sup>, Denise Neilsen<sup>1</sup>, Gerald Neilsen<sup>1</sup>, Louise Nelson<sup>2</sup>

<sup>1</sup>Agriculture & Agri-Food Canada, Summerland Research & Development Centre, Canada

<sup>2</sup>Biology Department, University of British Columbia-Okanagan, Canada

An assemblage of soil-borne plant pests including root-lesion nematodes (*Pratylenchus penetrans*) builds up in orchard soils, causing poor growth of juvenile trees when orchards are replanted. In two field experiments we assessed the efficacy, relative to fumigation, of using organic matter inputs to enhance overall soil health and thereby improve early growth of cherry trees replanted into old orchard soil. Specifically, we studied the effects of pre-plant incorporation of compost (50 Mg ha<sup>-1</sup>) and bark mulch on populations of plant-parasitic nematodes and key rhizosphere microbial populations, in relation to soil health indicators and tree growth during the first three years after replanting. The compost amendment enhanced total and labile fractions of soil organic carbon and nitrogen through at least three growing seasons in both field experiments. The compost treatment, particularly when combined with bark mulch, suppressed root-lesion nematode populations while enhancing gross populations of fungi and bacteria, *Pseudomonas*, and the abundance of bacterial strains producing antibiotics pyrrolnitrin and 2,4-diacetylphloroglucinol in the rhizosphere. Laboratory assays of biologically-mediated nematode suppression potential paralleled results from the field, with greater suppressive potential in amended soil than in fumigated or untreated soil. In one field experiment tree growth was greatest in fumigated plots at the end of the first growing season but by the end of the third growing season the largest trees were in the combined compost and bark mulch treatment, demonstrating that soil management practices that enhance overall soil health can have greater cumulative benefits to orchard establishment than fumigation.

## **#SII.2**

### **Microarthropod response to foot traffic in sports turf**

Maxwell Helmberger, Kyle Wickings

Cornell University, United States

Urban soil communities are important drivers of key ecosystem functions and services, yet must contend with numerous anthropogenic disturbances, including vehicle and foot traffic. We investigated the effects of foot traffic on a unique urban soil ecosystem, the sports field. We sampled microarthropod communities and measured soil compaction in the high-traffic and low-traffic areas of two central New York turfgrass soccer fields differing in soil type and management practices during fall of 2016. We found significant differences between fields and traffic areas in the abundance of several common microarthropod taxa. Collembolan abundance differed between fields and was lower in high-traffic areas. Oribatid mite abundance differed between fields but not between traffic areas, and mesostigmatid mite abundance varied by traffic, but not between fields. Astigmatid mites were much more abundant in high-traffic areas. The observed differences in the high-traffic areas could be due to soil compaction or to differing temperature and moisture conditions at the soil surface caused by degradation of the turf. Future surveys in the spring, late summer, and fall of 2017 will produce a more complete picture, as they will allow us to determine the extent of the high-traffic areas' recovery as fields sit inactive and the exact magnitude of any shifts in community composition upon initiation of play.

### #SII.3

#### **Community composition of free-living soil nematodes under anomalous precipitation across sites**

Pingting Guan<sup>1</sup>, André L.C. Franco<sup>2</sup>, Osvaldo Sala<sup>3</sup>, Diana Wall<sup>1</sup>

<sup>1</sup>Institute of Applied Ecology, Chinese Academy of Sciences, China

<sup>2</sup>Colorado State University, United States

<sup>3</sup>Arizona State University, United States

Climate change will increase the occurrence of extreme wet and dry events especially in dryland ecosystems. Free-living soil nematodes are important players in decomposition and nutrient cycling processes. We compared the genus composition of free-living nematode communities between an arid and a semi-arid grassland, and studied the effects of changes in water precipitation at each site on nematode community structure. We manipulated incoming precipitation (PPT), from extreme and intermediate reduction levels to intermediate and extreme addition levels, in the arid desert grassland (Jornada Long Term Experimental Range, New Mexico) and semi-arid (Semiarid Grassland Research Center, Colorado) grassland sites, and analyzed the diversity and community composition of soil free-living nematodes. Abundance, genus diversity and maturity index were significantly higher in the semi-arid than in the arid site (Shannon's index of  $2.03 \pm 0.03$  and  $2.18 \pm 0.03$  and maturity index of  $2.47 \pm 0.02$  and  $2.70 \pm 0.05$  for the arid and semi-arid sites, respectively). There were distinctive communities at sites, with the most relative abundant bacterial feeders were *Cephalobus* at the semi-arid site, and *Acrobeles* at the arid site. The dominant omnivore genera were, *Thonus* at the arid site and *Mesodorylaimus* at the semi-arid site. Abundance, diversity, and community composition of free-living nematodes, although differing between sites, did not respond at either site to precipitation manipulation. We conclude that free-living nematodes are more abundant and diverse in semi-arid than arid grasslands, with communities in both sites not responding to changes in water availability.

## #SII.4

### Earthworms from soils developed below long term experimental plantations at Holt Down, Southern England

Kevin Butt<sup>1</sup>, \*Mac Callahan<sup>2</sup>

<sup>1</sup>University of Central Lancashire, United Kingdom

<sup>2</sup>USDA Forest Service, Southern Research Station, United States

Seminal research from the 1980s undertaken at Holt Down, Hampshire, showed that the species of trees planted influenced subsequent soil development and understory vegetation. The work monitored plantations of beech (*Fagus sylvatica*) and small-leaved lime (*Tilia cordata*) planted on identical soils that had been used for sheep grazing for centuries prior. After a period of >50 years, a brown podzolic soil (pH <4) and a brown forest soil (pH > 5) had developed under beech and lime, respectively. In the latter, evidence of earthworm presence was reported but no detail provided. On a return to this site in 2013, we examined soils of these and an adjacent spruce (*Picea abies*) plantation, specifically sampling for earthworms. Soil and litter measurements were made, and earthworms collected by hand-sorting soil in replicated 0.1 m<sup>2</sup> plots (20 cm depth), followed by application of a mustard vermifuge. Scant leaf litter was present below lime, but large amounts were present below beech and spruce. Significantly more earthworms were present below lime, with mean ( $\pm$ SE) density of 29.2 m<sup>-2</sup>( $\pm$ 0.9), when compared with 1.7 m<sup>-2</sup> ( $\pm$ 0.1) for beech, and 10.8 m<sup>-2</sup> ( $\pm$ 0.5) for spruce, with corresponding differences in biomass. Six species were collected. *Dendrobaena octaedra* were collected exclusively beneath spruce trees. Anecic *Aporrectodea longa* and *Lumbricus terrestris* were found below lime along with endogeic *A. caliginosa* and *Octolasion cyaneum*. Additional targeted sampling of *L. terrestris* middens also revealed *A. rosea* and *S. mammalis* in the lime plantation, where earthworm species richness was greater compared to beech and spruce.

## #SII.5

### **Periodical cicada expansion lags, but matches, woody plant encroachment in tallgrass prairie landscapes**

Mac Callahan<sup>1</sup>, Sophia Bonjour<sup>2</sup>, Brent Brock<sup>3</sup>, Clinton Meyer<sup>4</sup>, Bruce Snyder<sup>5</sup>, Matt Whiles<sup>2</sup>

<sup>1</sup>USDA Forest Service, Southern Research Station, United States

<sup>2</sup>Southern Illinois University, United States

<sup>3</sup>Holoscene Wild, Inc.

<sup>4</sup>Simpson College

<sup>5</sup>Georgia College and State University, United States

Periodical cicadas are long-lived soil invertebrates, and their spectacular emergences represent significant fluxes of nutrients and energy from belowground to aboveground pools. Because they feed exclusively on tree-roots, they allow examination of long-term dynamics of woody vegetation within the grass-dominated prairie landscape. We used emergence data from the 1998 periodical cicada emergence at Konza Prairie Biological Station (KPBS), and collected emergence data from the 2015 emergence to evaluate patterns of emergence (and associated nutrient/energy fluxes) with respect to woody vegetation expansion at KPBS. Results indicated that ~35.2 million cicadas emerged from riparian forests at KPBS in 2015. This number represents an increase over the 1998 emergence by a factor of 1.8. Forest cover in the watershed increased by a factor of 1.6 over the same period. These figures correspond to total emergence biomass estimates of 59 kg C ha<sup>-1</sup>, and 7 kg N ha<sup>-1</sup> within the forested area at KPBS. Differences between emergence estimates of 1998 and 2015 suggested that dispersal distances in 1998 were potentially quite long and that areas with highest density in 1998 were considerably reduced in 2015. Conversely, some areas that had zero emergence in 1998 had densities of 90-100 individuals m<sup>-2</sup> in 2015. Our results show that periodical cicadas emerged from virtually every area that had forest cover in the year of emergence (when oviposition occurred), and suggest that continued expansion of forests in the region will likely result in more cicada biomass that will be redistributed in periodic resource pulses of energy and nutrients.

## #SII.6

### **Elucidating the importance of bacterial network connectivity from a long-term environmental change experiment**

Daniel Revillini<sup>1</sup>, Peter B. Reich<sup>2</sup>, Nancy C. Johnson<sup>1</sup>

<sup>1</sup>Northern Arizona University, United States

<sup>2</sup>University of Minnesota, United States

Environmental changes including elevated atmospheric CO<sub>2</sub> and increasing nitrogen deposition are predicted to influence the structure and function of soil microbial communities by altering the availability of belowground carbon (C) and nitrogen (N), respectively. Bacteria are notably C-limited microbes, and have the potential to play a vital role in N-cycling via N-fixation or ammonia oxidation. The connectivity among bacterial communities can reveal the potential for niche-sharing (modularity) and may provide insight into keystone bacterial interactions. Using random matrix theory, we performed bacterial network analyses to identify the effects of elevated CO<sub>2</sub> (eCO<sub>2</sub>) and N fertilization on bacterial community co-occurrence patterns and modularity from the rhizosphere of 'diverse' prairie plots from the BioCON experiment. eCO<sub>2</sub> increased network complexity, but had no effect on modularity of the rhizobacterial communities. N fertilization had strong positive effects on both network complexity and modularity, indicating that the interactions as a result of fertilization at this N-poor site were likely driven by increased competitive or niche-sharing interactions among bacterial taxa. We found an inverse relationship where diversity decreased as network connectivity increased when comparing beta-diversity to connectivity of the bacterial communities in N fertilized plots. These results are consistent with recent network studies indicating increased development of niches populated by dominant taxa. Our study indicates the need to understand both the connectivity of soil bacterial communities as well as the more commonly studied alpha- and beta-diversity metrics to determine the multifunctional responses of entire bacterial communities.

## #SII.7

### **Manure, but not N fertilizer, improved biological soil health after 38 annual applications**

Newton Lupwayi<sup>1</sup>, Derrick Kanashiro<sup>1</sup>, Andrea Eastman<sup>2</sup>, Xiying Hao<sup>1</sup>

<sup>1</sup>Agriculture & Agri-Food Canada, Lethbridge Research & Development Centre, Canada

<sup>2</sup>Agriculture & Agri-Food Canada, Beaverlodge Research Farm, Canada

Adding cattle manure to the soil improves its quality by building soil organic C, but manure effects on the vertical distribution of soil microbial properties are rarely evaluated. Soil phospholipid fatty acid (PLFA) biomarkers and  $\beta$ -glucosidase activity were measured down to 120 cm depth in an irrigated field trial that had received 38 (1973-2010) annual manure or 21 (1990-2010) annual N fertilizer applications. The manure application rates were 0, 60, 120 and 180 Mg ha<sup>-1</sup>. The effect of N fertilizer (ammonium nitrate) applied at 100 kg N ha<sup>-1</sup> was compared with that of manure applied at 60 Mg ha<sup>-1</sup>. Total PLFAs, fungal PLFAs, bacterial PLFAs and  $\beta$ -glucosidase activity in manured treatments were about 3-4x the amounts in the control treatment, but fertilizer N had no effects on these soil microbial properties. These manure effects occurred mainly in the 0-15 cm soil depth which contained 75% of the total PLFAs and 79% of the enzyme activity, with smaller effects in the 15-30 cm soil depth which had 20% of the total PLFAs and 18% of the enzyme activity. There were no manure effects in the 30-60 cm and 60-120 cm soil depths. Increasing manure rates from 0 to 180 Mg ha<sup>-1</sup> increased total PLFAs and bacterial PLFAs linearly, but quadratic increases were observed for fungal PLFAs and  $\beta$ -glucosidase activity. Therefore, manure improved biological soil health by increasing soil microbial biomass and activity in the top 30 cm of soil, but N fertilizer had no effects.

## #SII.8

### **Do livestock grazing regimes influence soil biogeochemical processes and function? A global analysis of grazing effects on soil nitrogen and carbon dynamics**

Ryan Byrnes, Leslie Roche, Kenneth Tate

University of California - Davis, United States

Globally, grazed ecosystems comprise approximately 40% of terrestrial land. These lands support numerous environmental and economic services. Given the prolific nature of these lands they also have the potential to improve or degrade their grazed environment based on livestock management. Grazed lands, while diverse, are commonly less productive than their highly managed and high input field and horticultural crop counterparts. As a result, these lands have the potential to become quickly degraded and may harm the broader environment they are in if they are not managed properly. Soils in grazed lands serve as the backbone of stability and resilience in these heterogenous systems and provide numerous ecosystem services such as the provision of food and fiber, filtering of pollutants through the soil profile and the cycling of nutrients. Our objective is to conduct a global analysis on the response of grazing management and intensity on numerous soil biochemical processes. The results of this analysis will be used to determine global trends in the response of soil to grazing management regimes and ultimately, understand which environments may respond more favorably to certain regimes. Our results will help inform the global discussion surrounding the importance of soil health, as well, our results will inform the grazing and policy stakeholder communities as to how grazed lands, which have a massive global footprint can continue to be productive landscapes as well as supportive in providing positive environmental health outcomes.

**#SII.9**

**Wheat genotypic and phenotypic effects on microbial-mediated nitrogen cycling**

**Cynthia Kallenbach, Fnu Junaidi, Steven Fonte, Patrick Byrne, Mathew Wallenstein**

Colorado State University, United States

Modern agriculture and breeding under high mineral nitrogen (N) fertilization may have disrupted plant-microbe coevolutionary relationships through alterations to belowground carbon inputs and associated impacts on the soil microbiome. Consequently, modern crop cultivars may be constrained by crop roots' ability to effectively support microbial-mediated N mineralization. We investigated how differences in root traits across a historical gradient of wheat genotypes influence the rhizosphere microbial community and the effects on soil N. Five genotypes, representing wild (Wild), pre-Green Revolution (Old), and modern (Modern) wheat were grown under greenhouse conditions. Wheat was grown in soils with and without compost to also compare how these genotypes respond to inherent difference in native soil microbiomes and organic resource availability. We analyzed rhizosphere soils at three wheat growth stages for soil enzyme activities, inorganic N, and microbial biomass. Wheat yield, N uptake, and root traits were measured at wheat harvest. Root length and fine root density were 6 times higher in Wild wheat compared to Old and Modern genotypes. Genotypic differences in enzyme activities and soil inorganic N only emerged with compost amendments, where older genotypes had relatively greater soil nitrate and N-cycling enzyme activities compared to Modern. We also observed that Wild and Old wheat had the most positive N-cycling responses to compost amendments, indicating a strong genotype X environment interaction influencing organic N turnover. Thus, genotype selections that enhance beneficial interactions between roots and their rhizosphere microbiome should be considered to optimize crop N availability from organic sources.

## **#SII.10**

### **Power and limitation of soil properties as predictors of rangeland health and ecosystem functioning in a Northern mixed-grass prairie**

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Soil properties are thought to affect rangeland ecosystem functioning (e.g., primary productivity, hydrology), and thus soil variables that are consistently correlated with key ecosystem functions may be general indicators of rangeland health. We summarize results from several studies in mixed-grass prairie of the Northern Great Plains. We tested many would-be predictor variables of local variation in peak aboveground biomass and water infiltration. Individual properties explained a moderate amount of variation in plant biomass ( $\leq 18\%$ ) and infiltration ( $\leq 15\%$ ). For example, plant biomass was positively correlated with field-saturated infiltration, subsurface microbial biomass, and some plant available nutrients (boron, manganese, and phosphorus). Plant biomass was negatively associated with two soil properties, subsurface soil carbonate concentration and the stability of soil macroaggregates near the soil surface. Many popular indicators of soil and rangeland health, such as soil organic carbon, organic matter, and water-stable aggregates, were found to be poor predictors. For example, water infiltration was unrelated to aggregate stability but was related to plant biomass. We hypothesize that other plant and soil properties (i.e., litter and bare ground cover) explain greater amounts of variation in infiltration. While protection of soil is critical to overall rangeland ecosystem functioning, our findings suggest that the relationship between soil properties and plant biomass (or infiltration) in natural grasslands is complex. A major challenge is to uncover indicator variables that consistently explain appreciable variation in peak grassland biomass, especially variation within an ecosystem independent of precipitation.

## #SII.11

### **Increasing labile carbon and nitrogen pools in agricultural soils requires a change in system, rather than practice**

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Labile soil carbon (C) and nitrogen (N) dynamics are key variables in soil health assessments and are critical for soil ecosystem services. Understanding these dynamics will provide insight into how seasonality and farm management practices within forage and dairy cropping systems influence soil C and N. The objective of this research is to study the effects of six different long-term cropping systems on potentially mineralizable nitrogen (PMN), permanganate oxidizable carbon (POxC), and potentially mineralizable carbon (PMC); indicators of labile C and N pools. These labile pools were evaluated using incubation and chemical extraction methods at two soil depths and five times during the growing season at the Wisconsin Integrated Cropping Systems Trial. Preliminary results indicate POxC and PMN were greater in the forage-based systems (FBS) compared to the grain-based systems (GBS), and that FBS had mineralizable N pools steadily replenished throughout the growing season until September. GBS experienced a significant decrease in PMN mid-season (a key point in plant growth), and had significantly lower POxC values in the beginning of the growing season. PMC analysis is currently underway. The significant differences in these biological indicators of soil health metrics between GBS and FBS are likely due to reduced soil disturbance, frequent manure additions, and the incorporation of a perennial legume phase in the FBS. Since management practice shifts within a cropping system (GBS/FBS) in the context of this study were not enough to affect labile pools, system changes such as complete tillage reduction combined with annual cover cropping is required.

## #SII.12

### **Mixed evidence for carbon transfer between biocrust cyanobacteria and plants in multiple dryland ecosystems using natural abundance $\delta^{13}\text{C}$**

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In drylands, plant-biocrust mutualisms are important drivers of nutrient cycling. Recent data has shown that biocrust cyanobacteria are able to incorporate plant-derived carbon into their structures. Specifically, biocrusts have been found to show  $\delta^{13}\text{C}$  signatures of respective nearby  $\text{C}_3$  and  $\text{C}_4$  plants. Using the natural difference in  $\delta^{13}\text{C}$  signature between photosynthetic pathways ( $\text{C}_3$  average -28‰ and  $\text{C}_4$  average -14‰), we hypothesized that if biocrusts incorporate plant-derived carbon, the cyanobacterial filaments would reflect the signature of the nearby plant. We investigated this pattern by collecting paired leaf and biocrust samples from under the plant (0cm) to the interspace (25cm) near  $\text{C}_3$  and  $\text{C}_4$  individuals found in the Chihuahuan Desert and Colorado Plateau.  $\delta^{13}\text{C}$  of cyanobacterial filaments near  $\text{C}_3$  plant species were depleted by ~2‰ per mil under the plant in comparison to the interspace.  $\delta^{13}\text{C}$  of filaments near two  $\text{C}_4$  plant species did not differ between distances. However, filaments near one  $\text{C}_4$  grass showed a depletion of ~3‰ per mil between distances. This result was unexpected as we hypothesized that all  $\text{C}_4$  plants would not differ. While  $\delta^{13}\text{C}$  signatures of cyanobacterial filaments near  $\text{C}_3$  plants is consistent with interactions between biocrust communities and plants, we are careful to note that translocation is not the proven mechanism. The unexpected results in the  $\text{C}_4$  grass suggests that these patterns may not hold true for all plant species. If the mechanisms can be shown using more detailed isotopic tracer studies, natural abundance data could provide a means for quick assessment.

## #SII.13

### **Influence of fertilization on mycorrhizal dynamics in a perennial biomass production system**

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Interest among landowners in diversified production systems is growing in the Upper Midwest. Diversification in the form of perennial biomass production systems from converted cropland is supported by developments in livestock integration as well as cellulosic and gasification energy platforms. Management strategies are needed that balance productivity with the ecosystem services perennial systems often offer. Within a low-diversity, native perennial production system, we established a randomized block experiment to evaluate the impact of four whole plot fertilizer treatments (zero, composted cattle manure, half rate (30-10-30 NPK) and full rate (60-20-60 NPK)) and two split-plot harvest rates (annual fall harvest versus no-harvest) on biomass production dynamics, soil health, and associated ecosystem services. Mycorrhizal inoculum potential (MIP) was evaluated as an indicator of soil health benefits. Big bluestem (*Andropogon gerardii*) seed was used to bioassay the MIP of soil collected within the four different fertilizer treatments under annual fall harvest. To support bioassay results field collected roots were also assessed for mycorrhizal colonization. The MIP, measured as fraction of infection in the bioassay roots, was significantly lower in treatments that had received fertilizer at the recommended rate than treatments receiving no fertilizer or composted cattle manure. In field collected big bluestem roots, mycorrhizal colonization was not significantly different among fertilizer treatments, but did reflect a trend similar to the bioassay. Despite colonization of field-grown hosts, the bioassay results in conjunction with established reduction in plant diversity, suggest that recommended fertilizer management may have unforeseen consequences for mycorrhizal diversity and abundance.

## #SII.14

### **Monitoring biotic and abiotic soil parameters to inform regenerative grazing practices across California's coastal range**

Chelsea Carey<sup>1</sup>, Rachel Sullivan<sup>2</sup>, Doug Millar<sup>3</sup>, Mel Preston<sup>1</sup>, Nathaniel Seavy<sup>1</sup>, Thomas Gardali<sup>1</sup>

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Regenerative agriculture aims to restore healthy, robust, and resilient agro-ecosystems. Soils – which provide nutrients to plants, harbor diverse macro and microbiota, and mediate critical biogeochemical cycles – play a central role in regenerative agriculture. Thus, soils must be monitored concurrently with more traditional metrics like plant community composition in order to ensure that practices are truly regenerative. In 2016 we sampled surface soil (0-10 cm) from two ranches (Paicines, n = 12; TomKat, n = 8) practicing regenerative agriculture along California's central coast with the goal of providing baseline data from which future changes could be benchmarked. The soil was analyzed for phospholipid fatty acid analysis, cations, total C and N, inorganic N, P, pH, and soil organic matter (SOM). Soil abiotic parameters (e.g., pH, organic C), total microbial biomass, and microbial composition differed significantly between ranches – and compost application at one site altered microbial composition dramatically. Despite these differences, fungi to bacteria ratios remained consistent across sampling points at both ranches, highlighting the importance of carefully identifying dynamic indices of soil health at regional or local scales. In addition, distance-based redundancy analysis showed that soil pH, SOM, K, Ca, and inorganic P best explained the variation in soil microbial community composition across all sampling locations. These preliminary findings suggest that regenerative agricultural practices may be able to modify microbial dynamics by influencing targeted soil parameters such as organic matter content and pH.

## #SII.15

### **Soil macrofauna modify soil microbial community composition and function and alter belowground carbon inputs**

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Soil animals can have impacts on microbial processes by fragmenting organic matter and grazing on microbial communities; however, the importance of soil animals in shaping soil microbial function is not fully understood. Our experiment aims to assess soil animal community impacts on soil microbial community composition and function and determine if their effects influence the fate of carbon in soil. In order to modify soil animal communities *in situ*, we used mesocosms constructed from different mesh sizes to include or exclude macrofauna. We measured soil animal community composition and soil microbial biomass and quantified shifts in soil carbon pools both within and outside the mesocosms. Fine mesh mesocosms successfully excluded soil macrofauna and differed from the macro-mesh mesocosms in microarthropod composition. Mesocosms where macrofauna were excluded also had lower microbial biomass nitrogen than in mesocosms where macrofauna were present. Soil carbon fractions such as macroaggregates, microaggregates and particulate organic matter will also be evaluated across treatments. Changes to the microbial community will be further investigated through Illumina sequencing for bacteria and fungi. Our results indicate that alterations to soil animal communities, particularly the exclusion of macrofauna, can have effects on belowground communities and processes.

## #SII.16

### **Restoration of biological soil crust on the Colorado Plateau in a warming climate**

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Biological soil crusts (biocrusts) are soil surface communities of bryophytes, lichen, cyanobacteria, algae and associated heterotrophs, which cover a large fraction of many dryland ecosystems. Biocrusts contribute many ecosystem functions including soil stabilization, water regulation, carbon and nitrogen cycling, and may be important for co-occurring vegetation communities. Yet across drylands globally, and in particular in the southwest US, biocrusts have been severely impacted by anthropogenic disturbances, including livestock grazing and associated trampling, off-road vehicle use, industrial development. Because biocrusts are composed of slow growing organisms, with limited dispersal distances, one perspective has been that degraded biocrust will only recover on long timescales (i.e., decades to centuries), and thus that minimizing disturbance is the primary method for preserving biocrusts. Yet, because of the scale of biocrust degradation across the southwest US, and the criticality of the ecosystem functions biocrusts provide, increasing interest and effort has been placed on methods of biocrust restoration. In general, restoration practices revolve around protecting an area from repeated disturbance and inoculating the soil surface with target organisms or communities. One potential problem with this approach is that recent climate manipulation experiments (warming and altered precipitation) indicate extreme negative impacts of warming and subtle precipitation shifts on key late-successional elements of biocrust communities. In this study we evaluate the use of biocrust communities from warmer regions to promote ecosystem function of a degraded rangeland site on the Colorado Plateau near Moab, UT, specifically considering the response to a warmer climate as an experimental treatment.

## #SII.17

### **Are soil changes responsible for persistent, non-forested burn scars in Colorado forests?**

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Pile burning is the most common method of disposing logging residue in Rocky Mountain forests yet the practice is known to alter and potentially degrade soil properties. Though extreme heating has short-term effects on soils beneath burn piles, it is uncertain if the practice has long-term, ecologically-relevant consequences. In Colorado, lodgepole pine ecosystems we have established a 50-year time series of pile burn scars located within pine stands regenerating after clear cut harvesting. The burn scars support herbaceous vegetation but have resisted tree colonization. We hypothesize that lasting changes in 1) soil resources (i.e., nutrients, water relations or plant symbionts), 2) tree seed availability, 3) herbaceous plant competition, or 4) herbivory may explain the scarcity of pine recruitment within pile burn scars. To evaluate these factors we combine soil nutrient and ectomycorrhizal analysis, greenhouse bioassays, and *in situ* plant establishment trials to evaluate the probable causes. Here we present preliminary soil-related findings. Pile burning increased mineral soil pH (upper 10 cm depth) and a 0.8 pH unit difference persisted throughout the 50 year chronosequence. Total soil carbon and nitrogen in burn scars was twice as high on average as the surrounding forest. Our preliminary analyses do not support the existence of a soil nutrient or chemical barrier to forest recovery and suggest that some above- or belowground biotic factor may be responsible for preventing trees from recolonizing burn scars.

**#SII.18**

**Cover crop mixes differentially stratify mineralizing microbes and residual nitrogen**

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There have been very few studies on the benefits of various legume species mixtures with rye concerning the stratification and composition of microbial communities and soil nutrients. As industrial hemp grows as a Kentucky agricultural commodity, there have been no studies concerning cover crop addition in hemp production. The objectives of this study are: (1) demonstrate the extent that differing cover crops and cover crop mixes containing grasses and legumes stratify nitrogen, carbon, and phosphorus to a depth of 45 centimeters; (2) determine the change of microbial communities in soils planted with these specific cover crops and cover crop mixes; (3) show that cover crop use with oil seed hemp production enhances yield and quality; (4) determine the change (if any) that hemp has on microbial communities and nutrient stratification following cover crops. Baseline samples were collected at depths of 0-15 centimeters and 15-30 centimeters following a seasonal fallow and then following a summer annual maize crop. Initial data of yield, chlorophyll content, nutrient analysis, and labile carbon show no significant differences following mixes. The plots have been replanted to collect data immediately following cover crop presence because initial cover crops were planted two years prior to analyses. We predict that rye treatments will stratify carbon deeper into the soil profile than legumes, but total residual nitrogen will be stratified deeper in mixes. These mixes will more profoundly diversify microbial community structure by improving soil nitrogen mineralization. Oil yield in summer hemp crops will benefit.

## #SII.19

### **Modelling the root age structure of perennial woody plants**

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Root age and nutrient uptake efficiency are typically inverse. It has been suggested overall growth is enhanced by maintaining a large population of younger roots while minimizing biomass allocation to older roots which have low efficiency. However, there are trade-offs in senescing scheduling for new roots and a root age distribution could be skewed towards older roots. Root turnover and root production have been proposed as two methods by which plants control the age distribution of roots. Unfortunately, direct examination of these hypotheses is not experimentally tractable as measuring root age can be difficult. However, an age based theoretical model with varying cost-benefit ratios for roots of different ages could be used to examine the impact on overall uptake of alternative root age distributions. The ability of this model to analyze how root age distribution affects growth may enhance our capability to project whole-plant growth. To our knowledge, no such model has been constructed. We apply an integral equation approach, similar to many structure population models, using varying death, survivorship, and cost-benefit curves to analyze the age distribution of the roots. To simulate growth and aging, we include feedbacks between roots and shoots to incorporate the additional influx of nutrients from roots and carbon from shoots as the plant ages. An objective is to observe the impacts on plant growth of changing root age structure throughout the life cycle and determine conditions for which age distribution dynamics tends towards a steady state, a cycle, or if the age distribution fluctuates.

## #SII.20

### **The Tollway Trees Initiative: From right tree, right site to right soil, right tree**

Meghan Midgley

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The Illinois Tollway is undertaking a three-year initiative to plant 58,000 trees along their 292 mile right-of-way to increase the regional forest canopy in the Chicagoland area. Soils in the sites available for this project are likely of poor quality: compacted, nutrient-poor, and saline due to topsoil removal, grading, and compaction that occurred during Tollway construction and pollution by de-icing salts. Two broad strategies are commonly used to maximize tree survival and health in such an extreme environment: 1) extensive soil preparation to mimic natural forest soil – that is, with horizons, higher porosity and aggregation, and increased organic matter, and 2) choosing the “right tree” for the “right site” – that is, selecting tree species that are salt-, pollution-, and drought-tolerant. However, the Tollway seeks to not only increase the number of trees, but also the diversity of trees in the region. Furthermore, there is not one “forest soil,” but rather many types of forest soils that vary with tree community composition. Here, I propose a new paradigm and research project to evaluate the extent to which organic matter amendments that best match the chemical properties of a tree species’ natural environment maximize tree growth and survival as well as soil ecosystem functioning. In other words, can we enhance the diversity of tree species that can persist in a roadside environment by moving from “right tree, right site” to “right amendment, right tree”?

**#SII.21**

**Effect of tillage and cover crops on the cotton rhizosphere**

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Cover crops and tillage (conservation vs. conventional) management practices are frequently utilized to increase soil fertility, both in terms of plant productivity and building soil carbon. These management practices can also have significant impacts on soil microbial communities. Since these microbial communities (both bacterial and fungal) can both directly and indirectly provide plants with nutrients and water, understanding their response to agricultural manipulations may help us optimize management practices such that they spur microbial activity beneficial to cotton production. We will report the response of the cotton rhizosphere to both tillage managements with or without winter cover crop additions. Soil enzymatic assays demonstrate an influence on microbial populations by both tillage and cover crop.

## #SII.22

### **Microbial genetic memory to study heterogeneous soil processes**

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Microbes can be engineered to sense environmental conditions and produce a detectable output. These microbial biosensors have traditionally used visual outputs that are difficult to detect in soil. However, recently developed gas-producing biosensors can be used to noninvasively monitor complex soil processes such as horizontal gene transfer or cell-cell signaling. While these biosensors are suitable for reporting on what fraction of a microbial population is exposed to a process or chemical signal at the time of measurement, they do not record a “memory” of past exposure. Synthetic biologists have recently developed a suite of genetically encoded memory circuits capable of reporting on historical exposure to the signal rather than just the current state. We will provide an overview of the microbial memory systems that may prove useful to the soil ecology community, including both “software” memory that can be re-written and “hardware” memory that is permanently encoded into the microbial DNA. Simple memory circuits can give a yes/no report of any past exposure to the signal (for example anaerobic conditions, osmotic stress, or high nitrate concentrations). More complicated systems can report on the order of exposure of a population to multiple signals or the experiences of spatially distinct populations, such as those in root vs. bulk soil. We will report on proof-of-concept experiments showing the function of a simple permanent memory system in soil-cultured microbes, and we will highlight additional applications. Finally, we will discuss challenges still to be addressed in applying these memory circuits for ecological studies.

## #SII.23

### Ecological effects of livestock antibiotics on agricultural soils

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Antibiotic use is under increased scrutiny due to their declining effectiveness; this includes the use of antibiotics in livestock production, which accounts for 80% of national antibiotic use. Much of this 80% passes through livestock via manure, with high estimates at approximately 14-million kg-yr<sup>-1</sup>. Studies have shown that additions of manure from cattle treated with antibiotics can have effects on soil microbial community composition, antibiotic resistance gene abundance, and ecosystem functioning. However, studies have also shown that additions of manure from cows receiving no antibiotics can also cause increases in antibiotic resistance genes. To better understand the relative contribution of manure and antibiotics, a common garden experiment was established where plots were amended with manure from cattle either treated with one of two types of antibiotics, or untreated cattle. Manure was added monthly for three years. Each spring, plots were pulse-labeled using <sup>13</sup>C and <sup>15</sup>N. Soils and plant biomass from these plots were collected and analyzed using a range of assays to better understanding how soil microbial communities are impacted by manure as well as antibiotics. We have found that manure type does have an impact on a number of important microbial parameters. For instance, manure from cattle treated with the antibiotic pirlimycin elicited an ~6,000 kg ha<sup>-1</sup> y<sup>-1</sup> increase in respired carbon compared to manure from cattle treated with cephalosporin. Although further analysis needs to be completed, the results from this field study highlight the potential influence antibiotics and the type of antibiotics have on soil and ecosystem processes.

## #SII.24

### **Effects of walnut shell biochar on soil microbial communities in a long-term field experiment**

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Significant biochar research has elucidated that biochar amendment to soils can influence microbially mediated nutrient cycling. Increases in microbial abundance and plant-available nutrients have been reported after biochar application, particularly in more nutrient-poor, acidic soils. However, less is known about how biochar affects microbial and nutrient dynamics in fertile soils of temperate agroecosystems, such as those in California. Additionally, the majority of studies have taken place in lab incubations over a short-term timeframe; more long-term field studies are needed to examine the relationships between biochar and microbial ecology in soils on the farm-scale. We investigated the lasting effects of walnut shell (WS) biochar on microbial communities and microbially mediated nutrient cycling over four years in a field experiment. Long-term plots of a tomato-corn rotation were established in a 2x2 factorial design of treatments i) with or without WS biochar amendment (10 t ha<sup>-1</sup>) and ii) fertilized with mineral fertilizer or composted poultry manure. Soil samples were collected throughout each growing season, and phospholipid fatty acid analysis (PLFA) was used to evaluate changes to soil microbial community composition as a result of WS biochar application. In addition, quantitative PCR (qPCR) was used to analyze how WS biochar affected the abundance of bacterial and archaeal 16s rRNA genes and nitrogen (N) cycling genes *amoA*. Both PLFA and qPCR analyses showed that microbial communities were much more affected by the fertilizer type used than the presence of biochar. Similarly, nitrogen transformations were affected by fertilizer but not by biochar application.

## #SII.25

### **Bacterial composition patterns distinguish two contrasting soils in organic carbon content: andisols and inceptisols**

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Pontificia Universidad Católica de Chile, Chile

The soil organic carbon (SOC) is crucial to maintain and improve many ecosystem services provided by soils. Chilean soils derived from volcanic material (Andisols) have a high SOC content, reaching values up to 12%. These soils enclose important agroecosystems as a result of their high natural fertility and physical properties (low bulk density, high available water and aggregate stability). The goal of this study was to determine the bacterial structure and composition in soils with high organic carbon (8-11%) Andisols compared with lower organic carbon (1-3%) Inceptisols. We characterized the bacterial communities by 16S rRNA gene sequencing (Illumina) in native and cropped land use under the same climate conditions at 10 cm depth. Our results showed no variation in soil bacterial richness or diversity as SOC increased. However, differences were observed in bacterial composition between the types soils studied. The common core of operational taxonomic units (OTUs) was represented by less than 0.5% over the total OTUs. Regarding common core taxonomy, phyla *Acidobacteria* (28%), *Proteobacteria* (26%) and *Actinobacteria* (14%) were dominant. Interestingly, major differences between soils were found within the most abundant OTUs (>1%) that represent 10% approximately of the total bacterial community. Among dominant OTUs, phyla *WD272*, *Firmicutes* and *Planctomycetes* were only observed in Inceptisols. Minority and rare OTUs (90% of the total community) showed less differences at taxonomic level. Our results provide additional insights into how soil bacterial communities may relate to SOC content, becoming potential indicators of soil quality for improving carbon restoration and conservation practices.

## #SII.26

### **Management intensities and seasons affect the relative contribution of ammonia oxidizing bacteria (AOB) and ammonia oxidizing archaea (AOA) to nitrification across a Midwest management gradient**

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Soil ammonia oxidizing bacteria (AOB) and ammonia oxidizing archaea (AOA) are the two main taxa involved in nitrification, which converts ammonia to nitrate with nitrous oxide (N<sub>2</sub>O) released as a byproduct. Previous studies have shown that AOB thrive in high ammonium conditions while AOA are more adapted to acidic soil environments. Little is known about how AOA and AOB respond to management intensities and seasons. In this study, we explored the seasonal contributions of AOA and AOB to nitrate accumulation and nitrification-derived N<sub>2</sub>O emission from seven ecosystems along a management intensity gradient: two annual crop ecosystems, one perennial crop ecosystem and four native successional ecosystems including a late successional forest. Our results showed that AOB were the major contributor to both nitrate and N<sub>2</sub>O production across management intensities and seasons. AOA and AOB did not respond differently to changing seasons in conventional and biologically fertilized wheat ecosystems. However, for native successional ecosystems, nitrification contributed by AOB in winter was twice as high as in summer, while AOA demonstrated no seasonal response. In poplar and deciduous forest ecosystems, both AOA and AOB exhibited higher nitrification rates in winter than summer. Our research suggests distinct dynamics of soil nitrifier communities affected by different management intensities and seasons.

## #SII.27

### **Why is *Taeniatherum caput-medusae* (medusahead) invasive in North America and not in its native Eurasia?**

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*Taeniatherum caput-medusae* (medusahead grass) is an exotic annual grass introduced to North America (NA) that has invaded ~ 4 million ha of western rangelands. In contrast, in native ranges of Eurasia (EA), medusahead is not considered to be invasive. Why is medusahead invasive in NA, but not in its native lands in EA? We considered two prominent hypotheses: enemy release and soil resource availability. We hypothesized: 1) Medusahead-invaded soils of NA are more fertile than native soils in EA and thus support invasion; 2) Invaded soils of NA have a lower rate of infection of pathogenic organisms, which in native environments reduce the growth and invasiveness of medusahead. We designed a project to test the effects of soil, seed source, inoculum treatments on biomass, arbuscular mycorrhizae, and pathogen root counts of medusahead. In general, NA soils had higher levels of nutrients than the EA soils. The NA populations, regardless of soil origin, generally had higher biomass responsiveness to both filtrate and whole soil inoculum. EA populations tended to have higher or equal biomass in sterile soils than inoculated or filtrate soils. For both NA and EA populations, biomass in sterile soils was related to soil nutrients rather than continent of origin. Microscopic observations showed higher pathogen counts in EA populations. Microbial communities from filtrate and whole soil treatments in NA soils enhanced plant growth, while microbial communities in EA soils had reduced or neutral growth. Results conclude that both resource availability and enemy release hypotheses support medusahead invasions in NA.

## #SII.28

### **Can we reduce phosphorus runoff potential by stimulating decomposers with carbon and sodium?**

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Loss of phosphorus (P) from agricultural fields into water bodies represents an inefficiency in the cycling of fertilizer P from soils to plants. Stimulation of biological microbial and faunal decomposers may help to maintain P availability while decreasing P application rates, thereby increasing P application efficiency while reducing runoff potential. Although soil microbes (e.g. bacteria and fungi) and fauna (e.g. beetles and millipedes) accelerate P cycling in natural systems, their combined effects on P availability in agricultural ecosystems are largely unknown. We tested the hypothesis that stimulating soil fauna with sodium (Na) and microbes with carbon (C) will increase soil P availability to plants. We added corn stover and Na solution to plots in conventionally-managed corn fields in Northwest Ohio. Stover treatments increased microbial biomass and activity but Na treatments had little effect on microbes and soil fauna. The fields tested had relatively low levels of decomposer activity – likely partially due to their low biomass in these systems and exacerbated by drought conditions in 2016. In this depurate soil, decomposer activity was not correlated with P availability. Therefore, in fields with low levels of decomposer activity, organisms may play a limited role in soil P cycling. In these types of ecosystems, treatments to stimulate decomposers already in those systems may be ineffective in reducing P runoff potential, at least in the short term.

**#SII.29**

**Variation in microbial community composition may explain soil functioning in an urban brownfield**

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Phosphatase activity (PA) is sometimes used as a proxy for soil function, especially in metal contaminated soils where PA can be depressed. We measured PA to investigate soil function in Liberty State Park (LSP), an urban brownfield in northern New Jersey, using PA as a proxy for soil health. We measured PA from four different sites at LSP of known heavy metal contamination, two of them represented high heavy metal load (LSP 146 and 25R) and the other two displayed relatively lower heavy metal loads (25F and 43). We compared the PA of sites at LSP with an uncontaminated site of the similar successional state that is exposed to similar climatic conditions, Hutcheson Memorial Forest (HMF). As expected based on prior experiments, we found almost no PA at 25R. However, we found relatively high levels of PA at LSP 146 and 25F. This led us to hypothesize that microbial community composition might be driving the notably high PA at LSP 146 and 25F. We therefore sequenced the 16s rRNA and ITS genes from whole community DNA and found that the bacterial community is distinctly different at 25R. In contrast to the bacterial community, the fungal community at HMF seemed to be distinctly different from the LSP sites. Further, CCA analysis showed that PA and moisture accounted for the variation associated with the microbial community at LSP 146, and pH at 25R. Results from the study suggest its potential implication in improving soil function via microbial transplantation in soil.

## #SII.30

### Invasion shifts soil fungal community composition in California chaparral

Michala Phillips<sup>1</sup>, Andrew Krohn<sup>2</sup>, Edith Allen<sup>1</sup>

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<sup>2</sup>Northern Arizona University, United States

Invasion persistence is likely driven by multiple interacting mechanisms, such as the *a priori* presence of both mutualistic and parasitic soil organisms or alteration of the belowground community by the invasive species. Invasive neighbors may alter the community composition of arbuscular mycorrhizal fungi (AMF) found colonizing native roots. We hypothesized that (1) invasive annuals will associate with an 'early successional' AMF community; and (2) invasive grasses will have a relatively lower pathogen abundance. We collected roots and soils in March 2016 from two sites underneath individuals of a native shrub (*Adenostoma fasciculatum*) and invasive grasses (*Bromus diandrus* and *Avena fatua*). We extracted DNA from roots and soils, amplified ITS2 and SSU rDNA using primers specific to all fungi (ITS2) or to AMF (SSU), sequenced amplicons on an Illumina MiSeq, and processed reads through QIIME. ITS2 sequences were aggregated to functional guilds using FUNguild. Host-plant identity drove differences in fungal community composition. NMDS ordination shows grouping of total fungal and AMF communities by host-plant identity. Invasion increased abundance of Acaulosporaceae, in support of the first hypothesis. In contrast to the second hypothesis, invasives had a greater relative abundance of pathotrophic OTUs, whereas natives had a greater relative abundance of symbiotrophic OTUs. Invasion resulted in an increase of 'early successional' AMF that primarily have intra-radicle colonization, which may decrease the presence of extra-radicle foraging hyphae in the soil. These natives depend on associations with foraging hyphae to increase access to resources; a loss of this inoculum may reduce success of re-establishment.

## #SII.31

### Soil health mediates tomato resistance to insect vectors and viral pathogens

Jennifer Schmidt<sup>1</sup>, Clare Casteel<sup>1</sup>, Rachel Vannette<sup>1</sup>, Christian Nansen<sup>1</sup>, Scott Park<sup>2</sup>, Kate Scow<sup>1</sup>, Amélie Gaudin<sup>1</sup>

<sup>1</sup>University of California - Davis, United States

<sup>2</sup>Park Farming Organics

Exploiting multitrophic interactions between soil microbial communities, crops, insect pests, and pathogens has the potential to increase soil and plant health and build broad resilience to multiple environmental stresses. However, the underlying mechanisms are unclear and the potential of soil health-building management practices to increase pest and virus resistance remains to be quantified in economically relevant crops. Processing tomato (*Solanum lycopersicum*) is a major crop in California, where production is limited by insect-vectored viruses such as Beet Curly Top Virus (BCTV), transmitted by the beet leafhopper (*Circulifer tenellus*), and Potato Virus Y (PVY), transmitted by aphid (*Myzus persicae*). Two greenhouse experiments using field soil representing a soil health gradient from farmer fields and the Century Experiment at Russell Ranch investigated the effect of soil health and microbial community composition on plant growth, attractiveness to insect vectors, induction of defense compounds, and resistance to viral pathogens. Results support a key role of the microbial community in plant nutrition and attractiveness to vectors: plants grown in organically managed soils responded differently to soil sterilization and were less attractive to leafhoppers than plants grown in soils from conventional or integrated management. Microbes from organically managed soil also conferred increased resistance to aphid vectors and induced higher levels of the defense hormone salicylic acid (SA), suggesting possible mechanisms. As tomato production expands into marginal soils, a better understanding of the role of soil health in multitrophic interactions affecting plant health can inform management decisions to improve pathogen resistance and productivity over the long term.

## #SII.32

### **Bacterial communities associated with *Prunus* replant disease**

Amisha Poret-Peterson, Natalia Ott, Greg Browne

US Department of Agriculture, Agricultural Research Service

*Prunus* replant disease (PRD) is a soil-borne complex that suppresses productivity of replanted stone fruit and nut orchards. Symptoms of the disease include reduction of fine root growth and aboveground biomass. PRD is likely microbially-mediated, as pre-plant soil fumigation or pasteurization prevents symptom expression. Previous studies implicated fungi and oomycetes as potential contributors to PRD. Here, we characterize bacterial communities from roots of peach seedlings exhibiting various levels of PRD severity in soils from California's Central Valley. The soils were left untreated or subjected to chemical fumigation or pasteurization before planting with seedlings. After 2 months, we measured seedling biomass and sequenced 16S rRNA gene amplicons from combined root and rhizosphere DNA extracts. Seedlings accumulated much less biomass in untreated PRD-conducive soils than in non-conducive or treated soils. In all treatments, the bacterial communities consisted mostly of Proteobacteria, Actinobacteria, and Bacteroidetes. NMDS analysis showed that the communities from roots in PRD-conducive and non-conducive soils differed compositionally from each other and from those of the cognate fumigated and pasteurized soils. We applied the Dirichlet Multinomial Mixture model to cluster OTUs into meta-communities, assign samples to particular meta-communities, and identify potential contributors to PRD. This analysis revealed four meta-communities within the dataset consisting of (1) fumigated and pasteurized soils (regardless of PRD potential), (2) fumigated soils from the most severe PRD-conducive sites, (3) mostly non-PRD-conducive soils, and (4) mostly PRD-conducive soils. OTUs classified as Streptomycetaceae and *Steroidobacter* were diagnostic of this last meta-community, suggesting a potential role of these bacteria in PRD.

#SII.33

## Plant species and functional group effects on soil properties in a green roof community

Kaiyue Zhou<sup>1</sup>, Louise Egerton Warburton<sup>2</sup>

<sup>1</sup>Northwestern University, United States

<sup>2</sup>Chicago Botanic Garden, United States

Green roofs are increasingly used to compensate for the loss of green space and biodiversity in many cities. The ecosystem services and aboveground plant performance on green roof have been extensively studied. However, there is surprisingly little information on the belowground habitat, even though the growing media makes a large and indispensable proportion of green roof system. In this study, we asked: what is the effect of individual plant species or functional groups on soil abiotic and biotic properties in green roof versus natural soils? We indexed the abiotic (nutrients; organic matter; pH) and biotic properties (enzymes linked to C, N, P cycling; microbial substrate-induced respiration) of rhizosphere soils in 12 native prairie plants (forbs, legumes, grasses) and *Sedum* (generic roof plant) in a green roof and a restored prairie in natural soil. Plant species and functional groups differentially partitioned abiotic properties in both natural ( $\text{NO}_3$ , P) and green roof ( $\text{NH}_4$ ,  $\text{NO}_3$ ) soils. Plant identity also played a key role in shaping the biotic properties in natural soils. Microbial respiration and enzyme activity differed markedly among plant functional groups, especially between forbs and grasses, and native plants and *Sedum*. Conversely, microbial respiration and enzyme activity were similar between plant species or functional groups in green roof soils, meaning that rhizosphere microbial activity and nutrient levels were not closely coupled, or that abiotic factors (e.g., N) overruled microbial functioning in green roof communities. Understanding these responses and their underlying mechanisms will be important for the sustained health of roof soil communities.

#SII.34

**Disturbance history and environmental characteristics shape the ectomycorrhizal fungal community of two varieties of *Pinus clausa***

Megan Rúa

Wright State University, United States

The soil biota is diverse, yet the ecological and evolutionary processes that regulate species diversity and abundance of soil microorganisms across space and time remains elusive. In forest ecosystems, periodic disturbances which operate at different time scales represent one possible avenue by which diversity in the soil biota may be maintained due to their effect on genetic and phenotypic characteristics of the host and associated environment. To investigate the degree to which host variety and environmental characteristics shape the belowground ectomycorrhizal (ECM) fungal community, we sampled ten populations of a single pine species that has diverged into two genetically distinct varieties as a result of disturbance history (*Pinus clausa* var. *immuginata* and var. *clausa*) and used multivariate analysis to relate the community matrices of ECM fungi to host and environmental characteristics. Host variety was an important determinant of ECM fungal community structure and diversity at both the species level and when fungi were grouped into categories based on their substrate exploration and nutrient acquisition strategies independent of environmental characteristics. Overall, our results suggest that periodic disturbances which shape the host populations are also important for structuring the ECM fungal community independent of environmental effects.

#SII.35

**The effect of ground cover management on vine performance and fungal root endopyte communities**

Eric Vukicevich<sup>1</sup>, José Ramon úRbez-torres<sup>2</sup>, Pat Bowen<sup>2</sup>, D. Thomas Lowery<sup>2</sup>, Miranda Hart<sup>1</sup>

<sup>1</sup>University of British Columbia, Okanagan, Canada

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The purpose of this study was to determine if different ground cover management strategies could influence vine disease resistance via changes in soil fungal communities. We used whole soil inoculum collected from a field trial of groundcover management schemes in a greenhouse experiment planted to grapevine rootstock *Vitis riparia* x *rupestris* 101-14. We introduced *Ilyonectria liriodendri*, a causal agent of black foot disease of grape, to observe the protective effect of each microbial community. After eight months, vine performance differed based on ground cover treatment and was correlated with differences in fungal communities isolated from vine roots. There were also community differences between healthy and necrotic roots. Total colonization by arbuscular mycorrhizal fungi did not differ among groundcover treatments. However, differences were seen in the proportion of different fungal structures (hyphae, arbuscules, vesicles) among some treatments and between healthy and necrotic roots. Our results indicate that in the early stages of pathogen infection vine performance may depend on ground cover management and involve interactions between the soil community trained by the ground cover and endophytic fungi present in vine roots.

#SII.36

**Profiling ectomycorrhizal fungal diversity and function in seedlings of south China native masson pine and introduced slash pine**

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<sup>1</sup>Northwestern University, United States

<sup>2</sup>Chicago Botanic Garden, United States

It has been proposed that non-indigenous pine trees can overcome symbiont limitation and thus adapt in a new ecosystem. However, the process that exotic plants choose their obligate soil microbial communities and the associated function remains poorly understood. We took advantage of a large forest site in Guizhou, China that includes both conserved native pine (*Pinus massoniana*) forests and introduced pine (*Pinus elliottii*) plantations. Pine seedling bioassays were employed to examine ectomycorrhizal (ECM) fungal root tip communities using both high-throughput sequencing of pooled roots and single root tip enzyme assays. Field-collected soil cores were treated one of three ways, kept intact (undisturbed), homogenized, or autoclaved. We found that the pattern of recovery of ECM fungal communities differed from the original soil spore bank: a) pioneer colonizers such as *Rhizopogon* and *Tomentella* dominated the bioassay communities in all treatments; b) intact soil treatment increased the survivorship for short distance exploration type ECM fungal species such as *Russula*; c) ECM fungal community of the introduced pine was comprised of fewer fungal partners than the native pine. Enzyme activity of the two most abundant pioneer *Rhizopogon* species did not significantly differ across host associations or soil treatment. Thus, our results show that even after soil disturbance, the low-richness ECM fungal community of alien pines retains adequate enzyme function, suggesting that functional redundancy exists for exotic pines during the early establishment process.

#SII.37

### **Environmental multi-input circuit to understand plant-microbe communication**

Ilenne Del Valle<sup>1</sup>, Tara M. Webster<sup>2</sup>, Caroline Masiello<sup>1</sup>, Jonathan J. Silberg<sup>1</sup>, Johannes Lehmann<sup>2</sup>

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<sup>2</sup>Cornell University, United States

Many interactions between plants and microorganisms depend on communication through extracellular signaling molecules, whose bioavailable concentrations and half-lives can vary with soil conditions. Microbes synthesize chemical signals that diffuse across cell membranes to sense population density (quorum sensing). The accumulation of these molecules activates the expression of genes that regulate key biogeochemical processes such as nitrogen fixation. Microbes can also sense different plant produced signals found in root exudates to coordinate plant microbe communication. Flavonoids are one type of plant produced signal necessary for the symbiosis between legumes and nitrogen fixing bacteria. Flavonoids and quorum sensing molecules have structures with a range of electrostatic interaction potential and hydrophobic characteristics. Our understanding how dynamic signaling contributes to symbioses development in different types of soils is not yet complete. The objective of this study is to understand how the soil mineral and organic matter matrix interacts with the multiple signaling molecules that play a key role in plant microbe symbiosis formation. One flavonoid based sensor linked to green fluorescence protein (GFP) and an acylhomoserine lactone (AHL) biosensor linked to a red fluorescence protein (RFP) were chromosomally integrated into *E. coli*. The effect of different soil amendments including plant materials, pyrolyzed organic matter, clays and compost were analyzed using this biosensor. Results have shown that different soil amendments can have opposite effects on these two chemical signals. pH appears to play a more important role on AHL bioavailability, while naringenin bioavailability can be reduced through complexation with tannins present in plant biomass.

## #SII.38

### Soil microbial feedback in agricultural crop rotation

Akihiro Koyama<sup>1</sup>, Teresa Dias<sup>2</sup>, Angela Dukes<sup>1</sup>, Pedro Antunes<sup>1</sup>

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Plant-soil feedback can be a major driver to determine plant community dynamics. Although feedback with pests has been applied as a basis for crop rotation since the Roman Times, plant-soil feedback has rarely been considered. Potential benefits of crop rotation via plant-soil feedback include nutrient use optimization and pathogen reduction, but contributions of the two mechanisms have not been well understood. We investigated these mechanisms in a greenhouse pot experiment, using five crops commonly cultivated in Ontario, Canada (alfalfa, canola, maize, soybean and wheat). We trained soil by each of the five crops in the first phase, and reciprocally planted the five crops in the trained soils in the second phase. To tease out nutrient vs. soil microbial feedback, we established three treatments; soil biota (autoclaved soils + microbial inoculation from the first phase), nutrient (autoclaved soil in the both phases), and control (field soil without autoclave in the both phases). We measured total biomass of each crop at the end of the second phase, and calculated feedback by comparing total biomass of each crop grown in soils trained by the four other crops against biomass in self-trained soil. The two legume crops tended to reduce the biomass of subsequent crops due to soil microbial feedback, whereas microbial feedback of canola and wheat was mostly neutral. The three non-legume crops mostly benefited subsequent crops via nutrient feedback. Our results demonstrate different roles of nutrients and microbes in plant-soil feedback, which can be used to improve sequence in crop rotations.

## #SII.39

### **Oomycete and fungal root communities associated with *Prunus* replant disease and its control in conventionally fumigated or anaerobically disinfested soil**

Natalia Ott<sup>1</sup>, Amisha Poret-Peterson<sup>1</sup>, Hossein Gouran<sup>2</sup>, Greg Browne<sup>1</sup>

<sup>1</sup>US Department of Agriculture, Agricultural Research Service, United States

<sup>2</sup>Joint Genome Institute, United States

Every year, California growers replace thousands of hectares of old stone fruit and nut orchards to renew productivity. However, the renewals can be compromised, initially by *Prunus* replant disease (PRD) and later by phytopathogenic nematodes. Our focus was on PRD, a *Prunus*-specific growth suppression apparently mediated by an ill-defined soilborne microbial complex. PRD often occurs in absence of phytopathogenic nematodes. Conventional soil fumigation (CSF) with chloropicrin-containing fumigants effectively manages PRD, yet due to environmental concerns development of non-fumigant approaches is needed. In two field trials, both anaerobic soil disinfestation (ASD; driven by available carbon, moisture, and heat under tarp) and CSF prevented PRD, greatly and equally stimulating tree growth. Here, we report on oomycete and fungal root community shifts associated with the trial treatments. Oomycete and fungal ITS amplicon sequencing was completed for the control, SF, and ASD treatments using total DNA sampled from fine roots and rhizospheres twice per year per experiment. Among OTUs generated with oomycete primers, PERMANOVA and NMDS revealed significant community shifts in all treatments of both trials, and CCA constrained 42% to 58% of the variation to soil treatment, sampling month, and tree growth. OTUs consistently associated with reduced tree growth in the control treatment included *Pythium ultimum*, *Phytophthium vexans*, *Ceratobasidium* sp., and an unknown ascomycete. Less-consistent shifts occurred among OTUs generated with fungal primers. Both CSF and ASD can effectively prevent PRD and reduce incidence of certain PRD-associated species, yet each treatment generates different root communities that may be worthy of further study.

## #SII.40

### **Will the use of nurse plants inoculated with native AM fungi help restore the native plant community after eradication of invasive grasses?**

Ma. Lourdes Edano<sup>1</sup>, Gail Wilson<sup>1</sup>, Karen Hickman<sup>1</sup>, James Bever<sup>2</sup>

<sup>1</sup>Oklahoma State University, United States

<sup>2</sup>Kansas University, United States

Invasion by non-native plants can alter soil microbial communities, further promoting invasion and reducing mutualistic soil microorganisms such as arbuscular mycorrhizal fungi (AMF). We assessed restoration success following establishment of nurse plants inoculated with AMF, compared to nurse plants without inoculation. Our study was initiated in 2013 at Fort Riley Army Base in KS, USA. Large areas of the base are invaded by *Bothriochloa bladhii*, a non-native warm-season grass. We eradicated the invasive grasses in 4 m x 4 m experimental plots with seven replicates. Nurse plants *Andropogon gerardii*, *Amorpha canescens*, *Allium canadense*, *Echinacea augustifolia* were inoculated with whole soil from nearby native sites, AM fungal spores, or not inoculated, and transplanted along the center of each plot. One month after transplanting, all plots were sown with a diverse prairie seed mix. Plant species composition was assessed in late summer of 2014 and 2015 at distances of 0.5, 1.0, and 1.5 m from nurse plants. Percent cover by the invasive grass was almost twice as high in plots with non-inoculated nurse plants, compared to plots receiving AM-inoculated plants. However, native species such as *Bouteloua curtipendula* and *Schizachyrium scoparium* increased in relative abundance in plots with AM-inoculated nurse plants, compared to plots with non-inoculated nurse plants. In addition, nurse plants inoculated with native AM fungi increased in survival and growth, compared to non-inoculated plants. Our results indicate that AM-inoculated nurse plants and native seeding in post-invaded soil may suppress the reinvasion of *B. bladhii* and encourage the reestablishment of native grasses.

**#SII.41**

**Ecology of temperate belowground fungi through ITS sequence analysis over four years in mixed successional perennial systems**

Franz Lichtner, Kirk Broders

Colorado State University, United States

Fungal species diversity changes over time depending on both biotic and abiotic influences. This study measured the fungal ITS sequence diversity at two sites, Pennsylvania and New Hampshire, where the above ground plant diversity was manipulated through perennial rye grass cultivar mixtures. Over the course of the four years, cultivars and cultivar mixtures led to increased or decreased measures of specific fungal operational taxonomic units (OTUs). Specifically, members of the Glomeromycota responded uniquely to location, existing in significantly higher numbers and diversity of OTUs depending on location. Glomeromycetes increased in an exponential fashion in Pennsylvania while in New Hampshire the abundance and diversity oscillated year to year. Shannon and Simpson diversity showed specific cultivar mixture treatments correlated with greater fungal diversity than others. Phylogenetic analyses showed that there was specificity of composition within communities in association with cultivar mixtures. This analysis utilized the modern 'dada2' bioinformatics package in R which reaches single nucleotide resolution through unique error inference methods. This method allows for accurate amplicon analysis with fewer false positives than other commonly utilized amplicon analyses pipelines. This work utilizes current computational advances to interpret belowground ecological fungal succession at a high degree of precision and fine resolution, allowing for a more accurate view of belowground plant fungal interactions in a unique chronosequence. Understanding below ground community dynamics related to above ground genotypic variance is crucial to ensuring sustainable cropping systems and resilience across broad temperate gradients.

**#SII.42**

**Comparisons of mycorrhizae and plant growth between the NJ pine barrens and serpentine barrens**

John Dighton

Rutgers University, United States

In a comparison of the growth of the two grass species *Schizachyrium scoparium* and *Panicum virgatum* growing on pine barrens and serpentine barrens soils, the colonization of roots by both arbuscular mycorrhizae and dark septate hyphae was significantly higher in serpentine soil. In a reciprocal transplant experiment to assess site specific adaptations by these plants, survival of little bluestem declined significantly when planted into soil not of its origin, however this only occurs in switchgrass when serpentine seed source was planted into pine barrens soil. Overall plant biomass was greater in serpentine soil for both plant species, along with greater mycorrhizal and DSE colonization. Preliminary data suggests there are significant differences in the ectomycorrhizal community of pitch pine between the two soil types. Our data suggests some evolved adaptation of both plant species to its local edaphic environment.

**#SII.43**

**Analysis of spatial patterns informs community assembly and sampling requirements for Collembola in forest soils**

Tom Bolger<sup>1</sup>, Tara Dirilgen<sup>1</sup>, Edite Jucevica<sup>2</sup>, Pascal Querner<sup>3</sup>, Viesturs Melecis<sup>2</sup>

<sup>1</sup>University College Dublin, Ireland

<sup>2</sup>University of Latvia, Latvia

<sup>3</sup>Institute of Zoology, Vienna, Austria

The relative importance of niche separation, non-equilibrial and neutral models of community assembly has been a theme in community ecology for many decades with none appearing to be applicable under all circumstances. In this study Collembola assemblages were recorded over eleven consecutive years in a spatially explicit grid and used to examine (i) whether observed beta diversity differed from that expected under conditions of neutrality, (ii) whether sampling points differed in their relative contributions to overall beta diversity, and (iii) the number of samples required to estimate the species richness in the forest sites. This study examines data over several years and is therefore not merely a snapshot in time as is the case in many studies of spatial patterns. Neutrality could not be rejected on most occasions and the data suggest that stochasticity cannot be ruled out. Not alone is beta diversity consistent with those predicted under assumptions of neutrality but the lack of difference in individual- and sample-based rarefaction curves also suggests randomness in the system at this particular scale of investigation. At the scale investigated it would appear that Collembola are not spatially aggregated and community assembly is driven primarily by neutral processes. Whether this finding is due to small sample size or disturbance or both cannot be determined. Variability between dates and sites illustrates the potential of drawing incorrect conclusions if only a single site at a single point in time was used, i.e. if temporal and spatial heterogeneity is not accounted for.

## Appendix II

# SOIL ECOLOGY SOCIETY BIENNIAL ORAL PRESENTATION ABSTRACTS

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Wednesday June 7th

PARALLEL ORAL SESSION A  
Ballroom C

## **Soil net primary production and carbon emissions in a tropical rainforest: Effects of leaf cutter ants through an ENSO cycle**

\*Michael Allen<sup>1</sup>, Amanda Swanson<sup>1</sup>, Emma Aronson<sup>1</sup>, Thomas Harmon<sup>2</sup>, Robert Johnson<sup>1</sup>, Diego Dierick,<sup>3</sup> Zhan Chen<sup>4</sup>

<sup>1</sup>University of California Riverside, United States

<sup>2</sup>University of California Merced, United States

<sup>3</sup>Florida International University, United States

<sup>4</sup>Chinese Academy of Forestry, China

Tropical Rainforests are portrayed as the lungs of the earth because of the CO<sub>2</sub> absorbed and O<sub>2</sub> released. But soil CO<sub>2</sub> fluxes remain poorly understood. We studied soil net primary production and carbon emissions of a mature tropical rainforest at the La Selva Biological Station in Costa Rica through an ENSO climate cycle. We used a Soil Ecosystem Observatory with sensors for CO<sub>2</sub>, O<sub>2</sub>, H<sub>2</sub>O, and Temperature. Fluxes were modeled. Automated minirhizotrons took daily images. Monthly measurements of CO<sub>2</sub> and CH<sub>4</sub> were taken using chambers.

Standing crop of roots was 120g/m<sup>2</sup>. Root lifespan averaged 60 days (6 generations per year) for a fine root NPP of 720g/m<sup>2</sup>/y, equal to leaf NPP of 750g/m<sup>2</sup>/y. Fungal hyphal standing crop averaged 3.5g/m<sup>2</sup>, lifespan averaged 24.9 days (14.7 generations/y) for a fungal NPP of 52.9g/m<sup>2</sup>/y.

Respiration was 1720g/m<sup>2</sup>/y versus 1831g/m<sup>2</sup>/y in the canopy. During La Niña (wet) phase of ENSO) soils emitted up to 0.3mg/m<sup>2</sup>/day of CH<sub>4</sub>-C, but during the El Niño dry phase, soils consumed up to 1.3mg/m<sup>2</sup>/day. Ants rolled soil into balls reducing tortuosity and increasing air-filled porosity increasing gas diffusion. With standing water, CO<sub>2</sub> flux blocked, and CH<sub>4</sub> is emitted from control soils. A CO<sub>2</sub> diffusion gradient from soil-to-nest-to-vent-to-atmosphere develops. O<sub>2</sub> flows in the opposite direction. Leaf Cutter Ant nests form a chimney of CO<sub>2</sub> from soil through the forest canopy. We are currently estimating the strength of these chimneys.

## **Soil fungi response to seasonal and annual variance in three agroecosystems**

\*Rachael Upton<sup>1</sup>, Kirsten Hofmockel<sup>2</sup>

<sup>1</sup>Iowa State University, United States

<sup>2</sup>Pacific Northwest National Laboratory, Department of Energy, United States

The Comparison of Biofuel Systems (COBS) field-site is comprised of traditional corn agroecosystem and two restored prairie, fertilized and unfertilized, which diversify biofuel sources and promote soil organic matter (SOM) retention. During prairie restoration, plant communities vary over growing seasons and across years. Fungi play a key role in determining the fate of carbon in soil and are influenced by plant communities. Utilizing the COBS field-site, we wanted to determine the response of the fungal community to shifts in the cropping systems across years to determine potential changes in their role in carbon cycling. We hypothesized that although plant communities' shift in the prairies across years in response to seasonal variation and fertilization, a microbial "seedbank" for soil fungi exists due to the abundance of dormant fungal species. We also hypothesized that active, more selective fungal community responds to seasonal fluctuations in the plant community across the two prairies.

Using an amplicon sequencing approach (ITS) we elucidated the fungal community structure response due to seasonal changes and shifting plant communities across years. Our results showed that the two prairie fungal communities were significantly different from the continuous corn community. Additionally, we did not see a significant change in the fungal community across years in each agroecosystem. We did see a significant seasonal impact on a more select and dynamic group of fungi across agroecosystems. Our results show an early response of the fungal community to the prairie restoration and the lasting impact on the soil community for years to follow.

## **Mycorrhizal allocation determines their function across varying environmental contexts**

\*Michael Remke<sup>1</sup>, Matthew Bowker<sup>3</sup>, Nancy C. Johnson<sup>4</sup>, Matthew Williamson<sup>2</sup>, Karen Haubensak<sup>1</sup>

<sup>1</sup>Northern Arizona University, United States

<sup>2</sup>University California Davis, United States

Arbuscular mycorrhizal (AM) fungi are obligate symbionts to plants. Resource limitation may favor stronger mutualisms, where resource abundance may result in diminished mutualism or even parasitism. Co-adapted plants and mycorrhizal fungi have been documented to have greater mutualistic function. The mechanisms for these differences are not well understood, though it has been proposed that fungal allocation to different structures may have a role. Within plant roots, these fungi establish sites for nutrient exchange (arbuscules) and storage (vesicles). It is likely that greater investment in storage reduces their ability to gather and/or exchange nutrients and thus makes them less mutualistic and vice versa. We conducted a greenhouse study with *Boteloua gracilis* to test mycorrhizal allocation and how it varies based on environmental context. We manipulated both plant and AM fungi origin as well as created two levels of simulated drought. We also conducted a field transplant experiment to test our findings in more dynamic environments.

In the greenhouse, we found that plants consistently grew larger and survived drought longer when they were paired with sympatric AM fungi. Additionally, after 2 years in the field, sympatric plant-AM fungi pairings yield the greatest plant growth regardless of environment. In sympatric pairings, there was also more external AM fungal hyphae and a greater percentage of plant roots were colonized by hyphae and arbuscules. In allopatric pairings, plant roots were more heavily colonized by vesicles. These findings demonstrate potential mechanisms for how AM fungi can behave as either mutualists or parasites depending on environmental context.

## **Quantifying the controls on SOM characteristics by MAT, disturbance, vegetation, depth and the soil matrix: An Opus approach**

Eldor Paul

Colorado State University, United States

Analysis by NMR, molecular-biological markers, MiDIR, py-MBMS, py GCMS, physical and chemical fractionation, long-term incubation and  $^{13}\text{C}$   $^{14}\text{C}$  showed similarities over many soils. Sites included a MAT gradient from Alaska to Brazil, cultivated-virgin, US, mid-continent soils and afforested soils from Ontario to Mississippi. The tundra site had limited pedogenesis with good correlation between MiDIR and py MBMS. Long chain lipids increased with increasing MAT. Cultivation decreased SOC, labile C, cutin-derived C and C:N ratios but increased the proportion of microbial and suberin-derived C, and mean residence times (MRTs). It decreased carbohydrates, amine and cyclic N and lignin-phenol, derivatives. Lipids, sterols and high, molecular weight, unknown pyrolysis derivatives were increased. A subtropical, allophane soil with 20 % SOC of which only 4% was labile consisted primarily of matrix-protected, microbial-derived carbohydrates and N compounds. A sandy soil, with negligible matrix protection, showed some chemical recalcitrance with 84% protection of native grassland SOC under cedar with endomycorrhiza and Ca translocation. Pines on the native prairie had decreased SOC at depth with MiDIR spectra and biomarker analysis showing higher acid to aldehyde ratios indicating more advanced stages of lignin decomposition. Depth, with similar qualitative but much greater quantitative compound changes than cultivation, increased MRTs by thousands of years with decreased C:N ratios but often similar, labile SOC indicating spatial controls. Fractionations such as LF, POM-sand, microbial biomass, silt and clay produced significantly different pool sizes-turnover times. Chemical fractionations, while delineating turnover times, were not especially effective in determining pool sizes.

## **Crop rotation impacts on AMF, P acquisition and C sequestration in semi-arid agroecosystems**

\*Steven Rosenzweig, Meagan Schipanski, Steven Fonte, Mary Stromberger

Colorado State University, United States

Arbuscular mycorrhizal fungi (AMF) have the potential to increase plant nutrient acquisition and enhance soil aggregation, both key processes influencing the sustainability of dryland agroecosystems. In conjunction with no-till, cropping system intensification (reducing the frequency of fallow in crop rotations) may enhance native populations of AMF and other soil fungi through greater belowground inputs of C. We assessed soil organic carbon (SOC), water-stable aggregation, and microbial phospholipid fatty acid (PLFA) abundance on 72 dryland no-till fields. Three levels of cropping system intensity from wheat-fallow to continuous rotations were represented along a potential evapotranspiration (PET) gradient that increases from northwestern Nebraska to southeastern Colorado. On a subset of 53 fields, we assessed AMF colonization of winter wheat roots and whole-plant P concentrations at wheat heading. Intensified cropping systems were associated with increased SOC ( $p=0.03$ ), AMF colonization of wheat roots ( $<0.01$ ), fungal PLFA abundance ( $<0.01$ ), and aggregate mean weight diameter (MWD) ( $p=0.02$ ) compared to wheat-fallow systems when clay content, PET, and number of years in no-till were included as covariates. Plant P concentrations increased with % AMF colonization of wheat roots ( $p=0.01$ ) when PET and applied P fertilizer were included as covariates. Additionally, aggregate MWD significantly increased with total fungal PLFA abundance ( $<0.001$ ), independent of climate, soil type, or management. These results suggest that robust and positive effects of crop rotation on SOC and P availability are mediated by enhanced AMF symbioses and fungal abundance. Overall, in semi-arid environments, cropping system intensification fosters growth of native fungal communities that enhance soil function.

## **Is root carbon better stabilized than shoot carbon? Testing features of the above- versus below-ground pathway**

\*Noah Sokol, Mark Bradford

Yale School of Forestry & Environmental Studies, United States

Considerable debate exists around the relative roles of aboveground versus belowground plant inputs in supplying carbon to the stable soil organic carbon (SOC) pool. Yet, few empirical studies have tested actual mechanistic differences underpinning these two pathways, independent of the quantity and quality of C flowing through them. We examined three hypothesized features that may affect the proportion of above- vs. below-ground plant C inputs stabilized in the mineral horizon: 1) physical distance travelled, 2) proximity to the dense rhizosphere microbial community, 3) delivery to the soil as pulsed versus continuous inputs. We inserted a fixed quantity of the common plant compound *glucose* (99 atom%  $^{13}\text{C}$  labelled) into soil microcosms, through aboveground and belowground entry points, proximately and distally from an artificial root, and as pulsed versus continuous input.

We recovered 62.1% more C stabilized in microcosms where C was entering belowground versus aboveground, largely due to the physical barrier of the organic horizon. We found 52.5% more C stabilized from high-volume pulses (indicative of leaf litter leachate) than from low-volume continuous inputs (simulating root exudates), due to greater overall spread/coverage of the input. We recovered 57.6% more total stable SOC in inputs that entered distally from the root (i.e. 'bulk soil inputs) than proximately to the root ('rhizosphere inputs'), though a much higher concentration of SOC and of microbial biomass C in rhizosphere soil. Overall, these results help define specific attributes that may permit the above- or below-ground pathway to dominate C supply to the soil within different contexts.

## **Plant community composition and variation in soil organic carbon in California rangelands**

\*Elizabeth Porzig, Chelsea Carey, Nathaniel Seavy

Point Blue Conservation Science, United States

Rangeland managers are increasingly prioritizing ecological functions of soil. Soil organic carbon is central to these efforts because it plays a fundamental role in soil fertility, soil stabilization, and water holding capacity. On grazing lands, influencing soil organic carbon via vegetation management is one strategy through which managers may be able to affect change. For example, promoting deep-rooted perennial grasses is hypothesized to increase soil carbon. However, dynamics between soil organic carbon and the vegetation community are complex, and there is a need to understand broad patterns in soil organic carbon concentrations in relation to plant community composition. In 2016, we surveyed the herbaceous plant community and soil organic carbon (0-10 cm) at 220 locations in 15 counties in California. Using multiple regression on distance matrices, we found a significant relationship between vegetation community composition and percent soil organic carbon while controlling for geographic location, average annual precipitation, and soil texture. Using indicator species analysis, we found that plant species associated with high soil carbon included several functional groups, including perennial grasses, and plant species associated with low soil carbon were primarily annual forbs. This survey of plant community composition and soil organic carbon provides context for setting management objectives and generating mechanistic hypotheses about plant-soil interactions.

## **Does climate warming alter plant diversity-soil carbon relationships and associated soil microbial communities?**

\*Sarah Castle<sup>1</sup>, Zewei Song<sup>3</sup>, Stuart Grandy<sup>2</sup>, Linda Kinkel<sup>1</sup>

<sup>1</sup>University of Minnesota, United States

<sup>2</sup>University of New Hampshire, United States

Plant community richness can significantly influence the quantity, molecular diversity, and chemical identity of soil C and associated soil microbial communities and may have significant implications for how soils respond to elevated temperatures under global warming. Here we hypothesized that: i) soil carbon attributes vary with plant diversity; ii) differences in soil carbon profiles will be greater with varying plant diversity in warmed vs. non-warmed plant communities; and iii) microbial community diversity will be positively correlated with soil carbon diversity. We sampled soils from a plant biodiversity climate experiment established in 2008 at the Cedar Creek LTER, Minnesota, USA. Soils were collected from within the rhizosphere of *Andropogon gerardii* and *Lespedeza capitata* growing in monoculture or in 16-species polycultures, under ambient or warmed (~3-5 °C) conditions. We used amplicon sequencing of bacterial 16S and fungal ITS2 and pyrolysis-GCMS analyses of molecular soil C chemistry to test our hypotheses. Molecular soil C diversity was significantly greater in polyculture than monoculture plant communities ( $P < 0.0001$ ). Lignin and phenolic compounds, major C classes in soil from polycultures, were present in low abundances or were absent from soils of monocultures. Finally, fungal and bacterial community assemblages varied between mono- and polyculture plant communities. Our results suggest that plant diversity controls soil C pool size and molecular chemistry as well as the associated soil microbial community. We anticipate that plant diversity will moderate warming effects on microbial composition, which will be reflected in differences of metabolic potential among microbial communities.

## **Competition reduces microbial carbon use efficiency**

Daniel Maynard, Thomas Crowther, \*Mark Bradford

Yale School of Forestry & Environmental Studies, United States

The efficiency by which microbes decompose organic matter governs the amount of carbon that is retained in microbial biomass versus lost to the atmosphere as respiration. This carbon use efficiency (CUE) is affected by various abiotic conditions, such as temperature and nutrient availability. Theoretically, the physiological costs of competition should likewise alter CUE, yet the direction and magnitude of these costs are untested. Here we conduct a microcosm experiment to quantify how competitive interactions among saprotrophic fungi alter growth, respiration, and CUE. By comparing individual performance to community-level outcomes, we show that species interactions induce consistent declines in CUE, regardless of abiotic conditions. Competition lowers CUE by as much as 25%, with the magnitude of these costs equal to or greater than the observed variation across abiotic conditions. Our results suggest that the extent to which microbial-mediated carbon fluxes respond to environmental change may be influenced strongly by competitive interactions.

## **How do plant seasonal dynamics drive root carbon inputs to the soil and their distribution?**

Cameron McMillan, Michael Weintraub

University of Toledo Dept. of Environmental Sciences, United States

A primary constituent of stabilized soil organic carbon (C) is microbial necromass, much of which is derived from plant inputs of labile soluble C, such as saccharide rich root exudates, which stimulate microbial production. The question this study addresses is: how do the seasonality and distribution of soil saccharides vary in association with plants with different phenology?

We hypothesized that variations in plants' leaf expansion/senescence times are reflected in patterns of root exudation, based on the timing of C fixation. We conducted an observational field study of soil saccharide dynamics in a temperate deciduous forest sandy clay loam soil associated with *Acer rubrum* (red maple) and *Lonicera maackii* (honeysuckle), chosen because of their contrasting phenology, in Northwest Ohio, USA, from April-December 2015. Reducing sugars and nutrients were measured in soil solution, and water and K<sub>2</sub> SO<sub>4</sub> extracts, along with microbial biomass, respiration, and extracellular enzyme activities. Contrary to our predictions, reducing sugar concentrations and accessibility, and microbial biomass were not significantly different in the soils of these two plants. This suggests that soil saccharide concentrations may not be as tightly correlated with leaf presence as had been believed. We also found that the adsorbed saccharide pool was below detection, and estimate that 10 times more saccharides are spatially inaccessible than accessible in the soil solution. Thus, we conclude that a spatially inaccessible C pool should be added to our conceptual model of the soil C cycle.

## Appendix II

# SOIL ECOLOGY SOCIETY BIENNIAL ORAL PRESENTATION ABSTRACTS

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Wednesday June 7th

PARALLEL ORAL SESSION B  
Ballroom D

## **Land-use impacts on soil biodiversity and ecosystem services in an Andean farming community**

\*Steven Fonte<sup>1</sup>, Steven Vanek<sup>1</sup>, Katherin Meza<sup>2</sup>, Anne De Valenca<sup>3</sup>, Raul Carlos Ccanto Retamozo<sup>2</sup>, Edgar Olivera,<sup>2</sup> Maria Scurrah<sup>2</sup>

<sup>1</sup>Colorado State University, United States

<sup>2</sup>Grupo Yanapai, Peru

<sup>3</sup>Wageningen University, Netherlands

Growing food demand, agricultural modernization, and climate change in the Andean highlands have led to intensification of agriculture, with important implications for ecosystem services (ES) and biodiversity. Based on this challenge, we sought to understand the impact of current land-use and future trends on a suite of soil-based ES in an agricultural landscape of central Peru, so as to inform community-based land-use planning. Sampling points were stratified across ten dominant land-uses (production fields, forests, pastures and degraded lands) and each was evaluated using composite indicators of soil fertility/nutrient provision, erosion control, C storage, economic production and soil biodiversity (ground vegetation and macrofauna). Overall, land-uses differed substantially in the ES and biodiversity supported. At lower elevations, forests (especially alder and mixed forest) supported the highest C storage, soil fertility, and macrofauna abundance and diversity. Higher elevation (>3800 m) land-uses also supported high levels of soil fertility, C storage, and diversity of ground vegetation. Erosion control (assessed via infiltration, soil cover and bulk density) was lowest in degraded lands and highest in forests and high elevation pasture. Economic productivity was relatively high in the low-mid elevation cropping systems and eucalyptus forests, and especially in irrigated crop-forage rotations. While their economic productivity was low, alder forests supported high levels of soil biodiversity and ES, and show potential to restore degraded lands. Our landscape assessment identified important tradeoffs and synergies in ES and soil biodiversity across the landscape that will inform future community landscape planning and conservation efforts throughout the region.

## **Fire reduces soil biota biomass and diversity: A cross-biome meta-analysis**

\*Yamina Pressler, John Moore, Francesca Cotrufo

Colorado State University, United States

Soil biota play a critical role in carbon (C) cycling. Fire impacts soil biota directly through inducing mortality and indirectly by changing above- and belowground environments, with consequences for ecosystem C cycling. Given expected shifts in fire regimes with climate change, we conducted a global meta-analysis of studies to investigate patterns in how fires affect soil biota. We systematically reviewed relevant literature from Web of Science (1988-2016) and used ImageJ to extract data directly from figures and tables. We calculated standardized mean differences of soil biota biomass, abundance, richness, evenness, and diversity indices between burned and unburned sites. We compared mean differences between soil biota taxa, across biomes, along a time since fire gradient, between wildfire and prescribed burns, and across laboratory methods. Overall, fire negatively impacted belowground communities. Fungal biomass is more susceptible to fire than bacterial biomass. Fungal, bacterial, arthropod and nematode abundance all decreased significantly after fire. Fire significantly decreased fungal and arthropod richness, evenness, and diversity. Responses varied considerably by biome, fire type, and time since fire. Evaluating the effect of fire on diversity of bacteria, nematodes, and protozoa was not possible due to lack of studies. We integrate our findings into a conceptual framework that highlights important controls and knowledge gaps of the response of belowground community biomass, abundance and diversity to fire. Understanding the response of soil biota to fire may help predict how soil communities and the processes they regulate will function in fire regimes of the future.

## **Soil microbial dispersal by way of terrestrial slugs**

\*Emma Aronson, Denise Jackson

University of California Riverside, United States

Soil microbial communities are highly variable and can change over time and with shifting conditions. Newly transported bacteria may be able to invade existing bacterial communities, which can alter community structure and ecosystem functioning in terrestrial environments. However, there are limitations on the ability of these often-non-motile organisms to disperse on their own. One possible mechanism for bacterial dispersal is co-invasion with above-ground consumers that feed upon bacteria that have key ecological roles. One such consumer is the terrestrial slug. There are thousands of species of terrestrial slugs living in a variety of habitats from temperate to tropical regions. Slugs have the ability to thrive in a range of conditions and their success is attributed to mucus production that deters predators, high reproduction rates and having an adaptable appetite. Slugs frequently ingest soil and plant bacteria from dead and living plant material, while also picking up bacteria on their bodies and in their mucus; these bacteria can then be dispersed as they travel. Introduction of invasive species, such as slugs and their associated bacteria, into new regions endangers regional and native biodiversity worldwide and is one of the leading causes of global ecological change. We propose a range of experiments to evaluate the potential for terrestrial slugs to transport soil bacteria within and across ecosystems.

## **Characterizing temperature sensitivity as a microbial trait: A meta-analysis using macromolecular rate theory**

\*Charlotte Alster, Joseph von Fischer

Colorado State University, United States

Reaction rates in biological systems are strongly controlled by temperature, yet the degree to which temperature sensitivity varies for different enzymes and microorganisms is being largely reformulated. The Arrhenius equation is the most commonly used model over the last century that predicts reaction rate response with temperature. However, the Arrhenius equation does not account for large heat capacities associated with enzymes in biological reactions, thus creating significant deviations from predicted reaction rates. A relatively new model, Macromolecular Rate Theory (MMRT), modifies the Arrhenius equation by accounting for the temperature dependence of these large heat capacities found in biological reactions. Using the MMRT model we developed a novel framework (Alster et al., 2016) to assess temperature sensitivity as a biological trait in soils through a series of experiments, providing evidence that microbes and enzymes can have distinct temperature sensitivities independent of their external environment. Here, we performed a meta-analysis on 102 studies to analyze the distribution of these temperature sensitivity traits across a variety of biological systems (e.g., soils, the food industry, wastewater treatment) in order to identify commonalities in temperature responses across these diverse organisms and reaction rates. Our results reveal significant differences between many temperature sensitivity traits based on categories such as the diversity of the microbes measured and the source of the microbial community. These results have important implications for basic understanding of the temperature sensitivity of biological reactions and for ecological understanding of species' trait distributions, as well as for improved parameterization of temperature sensitivity in models.

## Improving grassland restoration efforts: the power of soil amendments

\*Eric Duell, Anna O'Hare, Gail Wilson

Oklahoma State University, United States

Restoration of native biodiversity has been met with little success following eradication of non-native plants. While much attention has been placed on aboveground processes, considerably less research has focused on assessing the role of belowground microbial processes in restoration success. Our research was conducted at Konza Prairie Biological Station in Manhattan, KS, USA, where several areas have become highly invaded by a non-native C<sub>4</sub> grass (*Bothriochloa bladhii*). These areas received regular applications of glyphosate for eight years. However, revegetation with native species has been unsuccessful. To assess mechanisms that prevent survival of native species and to improve native species establishment, we established six replicate plots of each of the following four treatments: (a) freshly collected prairie soil (intact native microbial communities) with native prairie seeds; (b) autoclaved prairie soil (absence of native microbial communities) with native prairie seeds; (c) non-inoculated (no soil amendments) with native prairie seeds; and (d) non-inoculated/non-seeded control. Although inoculation with native or sterile soil did not influence percent germination, the presence of soil microbes significantly improved native species seedling survival (41%), compared to sterile soil or no soil amendments (10-12%). At the end of the growing season plots receiving native soil had significantly lower re-invasion by the invasive grass (33% cover by *B. bladhii*), compared to 52% cover following inoculation with sterile soil, and 70% cover in plots receiving no soil inoculum. Our study indicates restoration success of degraded grasslands can be improved by additions of native plant seeds in combination with native soil microbial communities.

## **Rotation history effects on soybean plants and rhizosphere microbiome**

\*Maria Soledad Benitez, Shannon L. Osborne, Michael Lehman

USDA-ARS North Central Agricultural Research Laboratory, United States

Benefits of diversified cropping systems stem from the interactions between soil characteristics, crop growth patterns and physiology, and other organisms. In order to assist in the understanding and implementation of diversified rotation sequences, a long-term experiment was established to evaluate the effects of 4-year rotation sequences containing soybean compared to a 2-year corn and soybean rotation. Within this experiment, soybean plant establishment and vigor was measured at the seedling and flowering stage, after four 4-year rotation cycles. Whole plants were sampled in the field for shoot biomass and nutrient content measurements, and rhizosphere microbiome characterization at both time points. Rotation sequence significantly affected establishment, rate of development and shoot biomass, where rotations with corn preceding soybean exhibited on average 25% lower vigor, regardless of length of rotation (2-year vs. 4-year). Rotations incorporating pea resulted in up to 28% greater biomass when compared with counterpart rotations differing in only one crop in the sequence (e.g. corn, pea, winter wheat, soybean vs. corn, oat, winter wheat, soybean). Community-level analysis of rhizosphere-associated bacteria did not reveal differentiation in response to rotation or crop sequence. Rhizosphere-associated fungal communities, however, responded to previous crop at the seedling stage, where rotation sequences with winter wheat preceding soybean differentiated from rotation sequences with corn preceding soybean. Further analysis will focus on the interactions between rotation sequence length, crop species and order within each rotation sequence, and specific responses of rhizosphere communities. These data provide insight on the mechanisms promoting soybean establishment and vigor in diversified cropping systems.

## **Soil biotic and abiotic properties following *Bothriochloa ischaemum* invasion into native tallgrass prairie**

\*Parker Coppick, Gail Wilson

Oklahoma State University, United States

*Bothriochloa ischaemum* is a non-native, perennial, C<sub>4</sub> grass that has been seeded throughout the US Southern Great Plains for erosion control and increased forage production. This plant species frequently invades beyond planted areas, dominating native prairies as a monoculture. The invasion into native prairies may be facilitated by positive plant-soil feedbacks, where *B. ischaemum* alters soil biotic and abiotic properties to benefit itself, with negative effects on native plant species. Our research, conducted in Oklahoma and Kansas, USA, assesses plant community composition and soil biotic (e.g. soil microbial communities) and abiotic (e.g. soil aggregate stability, soil moisture) properties in sites invaded by *B. ischaemum*, and in adjacent non-invaded prairie sites. Our results indicate significantly lower plant species richness in *B. ischaemum* invaded sites compared to the non-invaded prairie at both OK and KS locations. Both OK and KS invaded sites were characterized by lower soil moisture and lower overall soil microbial biomass, compared to non-invaded sites. Significantly more macro-aggregates (>2mm) were present in soils from the OK invaded site, compared to adjacent non-invaded soils. However, this was not consistent between locations, as relative abundance of soil macro-aggregates of the invaded site in KS was lower than adjacent non-invaded soil. Our results indicate *B. ischaemum* may facilitate loss of soil water availability and reduce soil microbial biomass. At both KS and OK sites, *B. ischaemum* invasion resulted in negative above- and belowground effects, potentially leading to losses in other ecosystem services.

## **Leymus arenarius invasion alters belowground interactions with mycorrhizae and nematodes without altering nematode community structure**

\*Matthew Reid, Sarah Emery

University of Louisville, United States

Belowground interactions can be important drivers of plant community succession. Plant-parasitic nematodes (PPN) and arbuscular mycorrhizal fungi (AMF) play particularly important roles in regulating primary succession in sand dunes. PPN contribute to the dieback of early colonizing native grasses, allowing later-successional species to establish, while AMF facilitate plant establishment in low-nutrient soils, as well as contribute to soil formation. Invasive plants may cause shifts in these belowground communities, potentially altering successional trajectories. In Great Lakes sand dunes, the dominant native dune-building grass is *Ammophila breviligulata*. *Leymus arenarius*, a dune-building grass native to Europe, has recently invaded this system. In a field survey, we assessed nematode community composition and AMF root colonization associated with each plant species. We found no differences between *Ammophila* and *Leymus* in AMF root colonization, while nematode community composition varied only minimally. However, *Ammophila* and *Leymus* differed in their dependence on and susceptibility to these soil organisms in a companion greenhouse experiment. AMF provided more protection against nematode damage for *Leymus* compared to *Ammophila*, indicating that negative soil feedbacks due to buildups of PPN in *Ammophila* dominated systems may not apply when *Leymus* invades. These results provide evidence that changes to belowground community interactions may facilitate *Leymus* invasion, with potential consequences for successional dynamics.

## Tallgrass prairie restoration: Does functional group matter?

\*Gail Wilson<sup>1</sup>, Tim Todd<sup>2</sup>

<sup>1</sup>Oklahoma State University, United States

<sup>2</sup>Kansas State University, United States

While the overall goal of restoration ecology focuses on assisting the recovery of ecosystems that have been degraded, damaged, or destroyed, the most successful path to recovery is uncertain. Conversion of tallgrass prairie to row-crop agriculture can result in state changes and biotic or abiotic ecological legacies that inhibit return to grassland state and require human intervention (restoration). Our study assessed ecosystem processes, such as soil aggregate stability, soil organic carbon, relative abundance of soil microbial functional groups, and nematode community structure following seeding of an agricultural field with diverse mixtures of either native cool-season (CSG) or warm-season grasses (WSG). These replicate restoration plots were compared with adjacent undisturbed prairie. Eight years following seeding, arbuscular mycorrhizal fungal (AMF) biomass associated with WSG was greater than CSG, yet remained significantly lower than undisturbed prairie soils. Soil aggregate stability and SOC were also greater in WSG soils compared to CSG, but likewise continued to reflect degradation relative to undisturbed prairie soil. No divergences in nematode community structure, including trophic composition and maturity index, were observed between CSG and WSG mixes. Communities under both mixes, however, remained fundamentally different from that associated with undisturbed prairie, with restored prairie exhibiting lower relative abundances of herbivores and greater relative abundances of bacterivores. Our research indicates ecosystem processes are highly complex and may require extensive time for recovery. Nonetheless, restoration practices that include native warm-season grasses differentially promote AMF biomass, which has well-documented downstream influences on soil structure, SOC, and soil food webs.

## **Soil ecological responses to pest management practices in turfgrass vary with pesticide use intensity, identity, and application program**

\*Kyle Wickings, Huijie Gan

Cornell University, United States

Pesticides play an important role in maintaining plant health in agricultural and horticultural ecosystems. However, improper use of pesticides can lead to negative impacts on non-target beneficial organisms and ultimately the erosion of ecological services. There is increasing interest in understanding the effects of pesticides on soil biota in agricultural systems, however their impacts on soil food webs in urban ecosystems remain poorly characterized. We carried out two field experiments in golf turf ecosystems to investigate the impacts of pesticide use practices on the composition and functioning of soil biological communities. Specifically, we quantified the effects of pesticide input intensity, identity, application rate, and frequency on soil microarthropod communities, root symbiont colonization, belowground biological control, and extracellular enzyme activities in golf course soils. Our results indicate that increasing pesticide input intensity leads to reductions in decomposer arthropod densities, mycorrhizal colonization, and the activities of some hydrolytic enzymes, but has little effect on biological control and predatory arthropods. Our work also reveals that belowground communities are sensitive to differences in pesticide identity, application rate, and frequency. Overall, our findings identify pesticide use practices that are likely to compromise soil ecological function, but also highlight unique opportunities for achieving plant health standards without compromising belowground ecological services.

## Appendix II

# SOIL ECOLOGY SOCIETY BIENNIAL ORAL PRESENTATION ABSTRACTS

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Thursday June 8th

PARALLEL ORAL SESSION C  
Ballroom C

## **Industrious leaf cutter ants and their big footprints in tropical soils**

\*Tamara Zelikova<sup>1</sup>, Diego Dierick<sup>2</sup>, Luitgard Schwendenmann<sup>3</sup>, Thomas Harmon<sup>4</sup>, Nicole Trahan<sup>1</sup>, Michael Allen<sup>5</sup>

<sup>1</sup>University of Wyoming, United States

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<sup>3</sup>University of Auckland, New Zealand

<sup>4</sup>University of California Merced, United States

<sup>5</sup>University of California Riverside, United States

Leaf cutter ants are the most important herbivore in lowland tropical forest systems. They cut fresh leaves and bring large amounts of plant biomass into their nests to grow their fungus gardens. The excavation and continual maintenance of their large nests modifies soil characteristics and biogeochemistry with direct and indirect impacts on soil carbon dynamics. But a big question is how to quantify the ecosystem footprint of *Atta cephalotes* ants. We set up and instrumented a soil observatory and over 3 years, measured soil carbon dynamics. Because half of the nests we instrumented were abandoned during the course of our study, we were able to measure the legacy effects of nests. And because our study fell during an El Nino year, we were also able to measure the impacts of extreme climate variation. This project has been a lesson in perseverance but our results show that heterogeneity reigns supreme and that the impacts of leaf cutter ants are first and foremost structural. They truly engineer their nests, with large impacts for carbon dynamics in nest soils.

## **Invasive Yellow Bluestem and European earthworms: Conspiracy for ecosystem domination?**

\*Roberto Carrera-Martínez<sup>1</sup>, Mitchell J Greer<sup>2</sup>, Bruce A Snyder<sup>3</sup>

<sup>1</sup>Department of Biology, University of Puerto Rico, Mayagüez Campus, Mayagüez, PR; Warnell School of Forestry, The University of Georgia, Athens, GA, United States

<sup>2</sup>Department of Biological Sciences, Fort Hays State University, Hays, KS, United States

<sup>3</sup>Division of Biology, Kansas State University, Manhattan, KS; Department of Biological and Environmental Sciences, Georgia College & State University, Milledgeville, GA, United States

Invasional meltdown has been suggested between invasive plants and exotic earthworms, but mostly based on indirect observations. Invasive earthworms and the invasive grass Yellow Bluestem (YB) have both the potential to shift ecosystem function and structure. This research aimed to determine if there is an invasional meltdown between European earthworms and YB. A mesocosm experiment was designed to observe the earthworm effects on the germination of YB. A second mesocosm experiment aimed to observe the effect of native and invasive earthworms on the development of the seedlings of YB and the native grass Little Bluestem (LB). *Octolasion tyrtaeum* was used as the invasive earthworm, *Diplocardia smithii* as native, and no earthworm as controls. A field survey was performed to observe the distribution of invasive earthworms with relation to YB and native grasses. Germination rates of YB did not differ between treatments. Nonetheless, *O. tyrtaeum* gained a higher proportion of mass than *D. smithii*, suggesting a positive effect on the invasive earthworm that could be the result of seed predation. LB seedling mortality was higher when *O. tyrtaeum* was present than when LB was alone, and died substantially faster than YB seedlings in all treatments, which suggests an indirect positive feedback of *O. tyrtaeum* on YB rather than a direct interaction. In the field survey, only the invasive *Aporrectodea* was collected and exclusively in YB plots. This suggested another indirect positive effect on the invasive earthworms and reveals that this system is more complex than initially thought.

## **Microbial C use in peat depth profiles under warming, as revealed with isotopic profiling**

\*Jessica Gutknecht, Cameron Blake

University of Minnesota, Twin Cities, United States

Many of the world's peatlands are located in northern ecosystems where the climate is changing at a rapid pace, creating concern over the fate of these carbon rich ecosystems. The microbial community is a crucial aspect of biogeochemical functioning of these peatland ecosystems. <sup>13</sup>CPLFA analysis was used to characterize the microbial community and provide isotopic information about microbial carbon use through peat depth profiles taken from the Spruce and Peatland Responses Under Climatic and Environmental Change (SPRUCE) Project; an extensive study of the response of peatlands to climatic manipulation in northern Minnesota. SPRUCE warming treatments range from 5 temperatures from 0 to +9° C. Samples for this analysis were taken just before, and during direct peat warming down to 2 m depth on June 2014, September 2015, and June 2015, respectively. We found both strong vertical stratification and variation over time, both in bioindicator abundance and in isotopic carbon use profiles. In addition, the microbial community in the surface of the peat profile is more responsive to external conditions than deeper peat. Deep peat warming enhanced the existing sensitivity of surface peat communities. Warming was related to increased fungal relative abundance, and decreased anaerobic bacterial and actinobacterial relative abundance. Fungi also used newer carbon under warming. In summary, fungal communities could be the main drivers of change in peatlands under warming, and their use of new carbon either suggests that peat profiles may remain undecomposed under warming, or that fungal communities will eventually prime decomposition of older peat.

## **Untangling the effects of individual cover crop species compared to mixes on soil ecology**

Felicity Crotty, Chris Stoate

Allerton Project - Game and Wildlife Conservation Trust, United Kingdom

All plant species create legacy effects within the soil to some extent; changing the environment either physically or through the remaining plant residues. Crop choice, rotation, and management, as well as establishment practice and maintenance can all greatly affect soil organisms' diversity and abundance. Cover crops can be grown over the autumn and winter ensuring green cover throughout the year. They have been described as improving soil structure, reducing soil erosion and even a form of weed control. These crops retain nutrients within the plant, potentially making them available for future crops, as well as increasing organic matter in the soil profile. Different plant species can be used as cover crops, including oil and tillage radish, oats, phacelia, buckwheat, vetch, crimson and berseem clover, as well as mustard, rye and lupins. Each plant species grows at different rates, cycling nutrients in different ways; understanding which crop is doing what individually and in a mixture, is still poorly understood. Focusing on two years of cover crop experiments, we show the effect of cover crops as mixtures and their effects on earthworm abundance, soil structure and weed suppression as well as following crop yields. We also consider the impact of individual cover crop species on soil biology (nematodes, mesofauna and earthworms), decomposition, soil structure, soil chemistry and weed suppression. Overall, results are beginning to show the effect of agricultural practices and their consequences on biodiversity dynamics and function which could have an important impact on future arable production.

## **Using NEON data to explore continental-scale patterns in soil communities and processes**

\*Samantha Weintraub, Lee Stanish

National Ecological Observatory Network, United States

The National Ecological Observatory Network (NEON) is measuring surface soil biogeochemical pools and fluxes along with diversity, abundance, and functional potential of soil microbiota at 47 sites distributed across the United States. This includes co-located measurements of soil carbon and nitrogen concentrations and stable isotopes, net nitrogen mineralization and nitrification rates, soil moisture and pH, microbial biomass, and community composition via 16S and ITS rRNA sequencing and shotgun metagenomic analyses. Taken together, this suite of soil data have the potential to reveal new insights into the structure and function of soil microbial communities and how this may vary over time, across biomes, and with changes in climate and land use. Here, we describe the spatial and temporal components of the NEON soil sampling design, as well as the workflow for discovering and accessing NEON soil biogeochemical and microbial data. We will also present preliminary findings highlighting the types of ecological questions that can be addressed using NEON's soil data products. For example, early NEON data demonstrate edaphic controls on microbial community structure, gradients in soil stable isotopes within and across biomes, and relationships between community functional potential, soil organic matter, and climate.

## **From where and how do plants and microbes get their nitrogen?**

\*Stuart Grandy, Andrea Jilling

University of New Hampshire, United States

N transformations and bioavailability limit productivity and also regulate environmental N losses in most soils. However, in mineral soils, the pools and processes that produce bioavailable N remain contentious, leading to inaccurate predictions of key ecosystem processes and services. Here we argue that to better understand N availability we need to reconsider two basic assumptions: first that N mineralization is a coupled, predictable process that can be predicted without understanding microbial community dynamics; second, that N mineralization, per se, regulates N availability rather than mineral-N interactions. First, N mineralization is regulated by microbial processes that are inherently uncoupled. Decomposer community enzyme induction drives proteolysis, the extracellular first step in N mineralization. Yet, cellular carbon use efficiency and stoichiometry are internal processes driving ammonification. Second, while soil amino acids and inorganic N originate from litter and soil organic matter mineralization, we argue that in rhizospheres mineral-associated organic matter (MAOM) is the largest proximal source of N for plants and microbes. Several biochemical strategies enable plants and microbes to compete with mineral-organic interactions and effectively access MAOM. We show that the competitive balance between the potential fates of N monomers—bound to mineral surfaces or dissolved and available for assimilation—depends on the specific interaction between clay mineral properties, soil solution, mineral-bound organic matter, and microbial community. The strategies to mobilize and acquire MAOM N create unique plant and microbial community dynamics that promote niche differentiation and species coexistence in plant and microbial communities.

## **The future of protein**

\*Phillip Taylor<sup>1</sup>, Pete Newton<sup>2</sup>, Alan Townsend<sup>2</sup>

<sup>1</sup>Mad Agriculture, United States

<sup>2</sup>University of Colorado, United States

The global rise in meat consumption is a megatrend of modern civilization, and is projected to increase from 200 to 450 million tons by 2050. Livestock production has increased the allocation of land and resources to produce animals, which has driven climate change, deforestation, biodiversity loss and damages to global ecosystems. Sustainable animal feed is urgently needed, but few options exist. What is the future of animal feed, and particularly protein? We discover a rapid emergence of novel, sustainable proteins in research, development and market sectors. New proteins include algae, fungi, bacteria and insects. Nearly all these innovations include major co-benefits of economic competitiveness and solving agricultural sustainability challenges. These trends are paralleling with increasing cost of fishmeal, which is fueling investments in cost-competitive alternatives. The growth in novel, sustainable proteins is also driven by shifts in consumer consciousness and growing concerns over the impacts of the modern food system. Sustainable animal feed is already a \$4 billion market in the US, and demand has grown 400% over the past decade. We also find a rising proportion of consumers are willing to pay more for sustainable livestock; the growth in grass-fed beef and free-range chickens markets are telltale trends. There are number of barriers slowing the commercialization of novel proteins (e.g. feed regulations). Finally, we examine policy mechanisms that could accelerate the development and use of sustainable proteins, which is urgently needed to avoid further deterioration of global ecosystems used to procure animal feed.

## **Biocarbon as an effective microbial inoculum carrier in an agricultural maize field trial**

\*Erika Foster, Matthew Wallenstein, Francesca Cotrufo

Colorado State University, United States

As technologies develop in sustainable agriculture, we must ensure maximization of treatment effects. Research indicates that reduced irrigation and fertilizer inputs are possible with proper soil management. Two innovative strategies include use of microbial inoculum to promote plant nutrient availability and use of biochar-charcoal amendments to improve soil structure and add organic carbon. Since only low application rates of biochar are economically feasible, we tested rates of 0.78 Mg h<sup>-1</sup> and 0.39 Mg ha<sup>-1</sup> of Cool Terra® biocarbon (treated biochar) in a fully factorial maize field trial. We banded the biocarbon next to the seed to maximize effects. In combination with this treatment, we inoculated the biocarbon with phosphorus-cycling plant growth promoting microbes from Growcentia® (MAMMOTH P) and tested this versus the recommended three-time surface application. We used these treatments under two reduced input strategies: a 20% temporal reduction in irrigation and a 20% reduction in fertilizer application. We hypothesized that the combination treatment of biocarbon and microbial inoculum would maintain the highest maize yield under reduced irrigation and fertilizer. After one year, the low and high biocarbon application rates increased yield by 8.9% and 11.1%, respectively. The yield from plots with the microbial inoculum applied with a biocarbon carrier was equal to the repeated surface application of the inoculum alone. This may suggest that the biocarbon carrier increased the effect of the inoculum. Further microbial DNA analysis is in progress to analyze if the crop response correlates with changes in the soil microbial community structure.

## **The role of the belowground plant microbiome in climate change induced range shifts**

\*Kelly Ramirez, Wim Van Der Putten, Basten Snoek

Netherlands Institute of Ecology, Netherlands

With climate change, plants have been able to shift their ranges into novel environments where conditions have been made suitable due to warming temperature and changes in precipitation. Much belowground range expansion research has focused on either positive plant-soil interactions, such as AMF symbiosis, or on negative plant-soil interactions, such as pathogens. Less focus has been given to the core microbiome of plant hosts.

Using high-throughput Illumina sequencing we assessed soil and root microbial communities under native and range expanding plant species spanning a north-south latitudinal transect in central Europe. As expected, the soil and root microbiomes are both strongly influenced by the plant species under which they grow. Specifically, about 10% of the microbiome could be related to the host plant species. Interestingly, we found that microbiomes associated with range shifting species are less variable than those associated with native species. Further, the enrichment of microbes in roots (from the soil) is stronger with range expanding species than with native plant species. Our research indicates that the soil and root microbiomes can provide insight into plant range shifts and may be important for plant establishment.

## **The transformation of leaf litter into feces by millipedes reshuffles the control of litter traits on decomposition**

\*François-Xavier Joly<sup>1</sup>, Sylvain Coq<sup>2</sup>, Mathieu Coulis<sup>3</sup>, Stephan Hättenschwiler<sup>2</sup>, Johanne Nahmani<sup>2</sup>

<sup>1</sup>School of Earth and Space Exploration - Arizona State University, United States

<sup>2</sup>Center of Evolutionary and Functional Ecology, CNRS, France

<sup>3</sup>CIRAD, UPR GECO, France

Compared to the role of microorganisms, the role of soil fauna on litter decomposition remains poorly understood. Litter-transformers for instance are thought to fasten decomposition by reducing litter particle size and increasing its moisture. However, the few studies that compared decomposition of feces with that of litter reported contrasting results, ranging from negative to positive effects. We hypothesized that these discrepancies result from the use of different litter species with distinct quality. To test this hypothesis, we fed leaf litter from ten different European tree species to a common detritivore species, *Glomeris marginata*, and compared (i) the physical and chemical quality and (ii) decomposition rates of feces to that of the corresponding litter. We found that litter transformation into feces decreased the C/N ratio and the particle size for all litter species, and increased the water-holding capacity for eight out of ten litter species. Additionally, decomposition rates increased in feces for eight of out ten litter species, with relative differences ranging from 0% to + 150%. Differences in leaf litter decomposition rates were mostly related to differences in litter C/N ratio and water-holding capacity, while feces decomposition rates were largely related to differences in feces particle size. As hypothesized, our results indicate that this effect clearly depended on the type of litter ingested by the litter-transformers. Collectively, our results support the common view that litter-transformers enhance decomposition, and suggest that this effect is related to a reduction in particle size which likely increases the surface area available for microorganisms.

## Appendix II

# SOIL ECOLOGY SOCIETY BIENNIAL ORAL PRESENTATION ABSTRACTS

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Thursday June 8th

PARALLEL ORAL SESSION D

Ballroom D

## **Advancing the understanding of organo-mineral interactions: Insights from nano-scale secondary ion mass spectrometry**

\*Megan Machmuller<sup>1</sup>, Carsten Mueller<sup>2</sup>, Jennifer Soong<sup>3</sup>, Carmen Hoeschen<sup>2</sup>, Claudia Boot<sup>1</sup>, Francesca Cotrufo<sup>1</sup>

<sup>1</sup>Colorado State University, United States

<sup>2</sup>TU Munich, Germany

<sup>3</sup>University of Antwerp, Belgium

Traditional analyses limit our understanding of submicron scale interactions that control the persistence of organic matter (OM). By combining nano-scale secondary ion mass spectroscopy and isotopic tracing, we followed the decomposition of plant litter and its association with clay sized mineral particle surfaces over three years in a grassland soil. We found greatest spatial correlation of litter C and N at intermediate (18 months) stages of decomposition, where 70% of mineral associated OM had both <sup>13</sup>C and <sup>15</sup>N enrichment. C and N associations were spatially decoupled at early (7 months) and late (36 months) stages. 7 months following litter incubation, 72% of mineral associated OM originated from litter C and 14% from litter N, and 10% of C and N were co-located. Early-stage, high efficiency C sorption corresponded to the loss of non-structural compounds from litter and high microbial C incorporation. As decomposition proceeded, litter biochemical properties became more important than microbial pathways to the persistence of OM. This late stage of decomposition had mineral associated OM with the lowest (62%) amount of litter derived C and the highest amount of litter derived N (84%), and 54% of the C and N were co-located. As litter N moved into the clay fraction, it attached to existing organo-mineral surfaces and eventually sorbed without the presence of litter derived C. Through the use of nanoSIMS, we revealed new insights into the spatial heterogeneity of organo-mineral interactions, and demonstrate how this varies throughout decomposition as biological and biochemical mechanisms control OM persistence.

## Wetland plant range shifts may alter soil microbial communities and carbon storage

\*Samantha Chapman<sup>1</sup>, Chelsea Barreto<sup>2</sup>, Ember Morrissey<sup>2</sup>

<sup>1</sup>Villanova University, United States

<sup>2</sup>University of West Virginia, United States

Coastal ecosystems such as mangrove forests and salt marshes store large amounts of carbon due to high rates of plant productivity and low soil organic matter decomposition rates in anoxic soils. As woody mangroves continue to encroach into herbaceous salt marshes around the world, it is important to understand how this range shift will alter soil microbial communities and carbon processing. Mangroves have larger, more aerenchymous roots than salt marsh roots and these roots could create a different environment for soil microbes that process soil organic matter and thus, alter carbon cycling. In an ecotonal ecosystem in Florida, we compared wetland soil bacterial community composition and function in mangrove-dominated vs. salt marsh-dominated plots. Bacterial community structure and soil microbial function differed between mangrove-dominant and marsh-dominant plots. Specifically, we saw higher abundances of putatively aerobic bacteria in mangrove-dominant (e.g. *Acidobacteria*) than in marsh-dominant soils and conversely, more putatively anaerobic bacteria (*Chloroflexi*) in marsh-dominant soils. Further, mangrove-dominant soil organisms were more efficient at utilizing a labile C substrate than marsh-dominant soil organisms. In order to investigate how root changes in rhizosphere oxygen availability may change soil organic matter processing, we manipulated headspace oxygen availability in lab-based soil incubations. We found that carbon dioxide respiration was 40-50% higher in oxic conditions. Our results suggest that wetland plants strongly influence sediment microbial communities and that mangrove encroachment into salt marshes may have implications for wetland soil carbon storage.

## **Effect of restoration treatments and forest type on soil mesofauna, fungi, and physicochemistry in Valles Caldera National Preserve**

\*Kara Gibson<sup>1</sup>, Channing Laturno<sup>1</sup>, Andrea Raya<sup>2</sup>, Anita Antoninka<sup>1</sup>, Nancy C. Johnson<sup>1</sup>

<sup>1</sup>Northern Arizona University, United States

<sup>2</sup>Universidad Nacional Autónoma de México, Mexico

The structure of southwest forests has been dramatically altered over the past 140 years due to land use change and fire exclusion. Land managers are increasingly implementing restoration treatments (thinning, prescribed fire) to improve forest health and fire-resilience. The effects of these treatments aboveground have been studied extensively, but less is known about their influence on soil communities and ecological function. We are studying the responses of communities of soil mesofauna, fungi, and bacteria, as well as soil physicochemical properties to restoration treatments at Valles Caldera National Preserve to compare the resilience of soil communities in different forest types. We chose microarthropods and nematodes as our focal fauna since these taxa are functionally important and have demonstrated utility as indicators of soil food web status. We collected soil samples from four forest types (xeric mixed conifer, mesic mixed conifer, old-growth ponderosa, overgrown ponderosa) and three ponderosa pine restoration treatment sites (thin only, thin/burn, control). Litter depth, canopy cover, and ground cover were also measured. We will be reporting on differences in densities of microarthropods, nematodes, and fungal hyphae between ponderosa restoration treatments and among forest types, while observing patterns related to soil abiotic and aboveground variables. Our preliminary results show that microarthropod densities vary among forest types, but are similar among restoration treatments. Also, microarthropod abundance is positively related to canopy cover and total organic carbon, but negatively related to bulk density. Alteration of the abundance and composition of soil mesofauna can have important implications for decomposition and nutrient cycling.

## **Effects of antibiotic residues on extracellular enzyme activity in soils**

\*Matthew Hedin, John Barrett

Virginia Tech, United States

Antibiotic use in agricultural ecosystems has the potential to increase resistance in soil microbial communities since 40-95% of an antibiotic dose administered to livestock is excreted intact or as metabolites into soil. Exposure to antibiotics is also known to alter microbial community composition, biomass, and physiology. These changes in microbial communities have potential consequences on elemental cycling in agricultural ecosystems.

We examined the effect of dairy cattle manure on soil microbial communities by measuring their extracellular enzyme activity (4 carbon and 2 nutrient acquisition enzymes) along with several microbial and environmental variables including antibiotic resistance gene (ARG) abundance. Samples were collected from dairy farms in a nationwide study, and included sites with high and low levels of manure input and antibiotic exposure associated with stocking rates. Responses varied among individual enzymes, but we found an overall significant increase in total hydrolytic enzyme activity in high input sites indicating a change in the functioning of the microbial community. Principle components analysis suggest that while some of the variation in enzyme activities are associated with ARG abundance, soil organic matter was the most significant variable accounting for differences in enzyme activities. This reflects an inherent challenge in field studies of antibiotic exposure: the difficulty of distinguishing direct effects of antibiotic residues from the organic matter and nutrient subsidy associated with manure applications. In ongoing work we are experimentally manipulating soils to isolate the influences of antibiotics, manure resource subsidies, and bovine microbiome inoculants into soils.

## **Spies and Bloggers: New synthetic biology tools to understand soil microbial processes**

\*Caroline Masiello, Jonathan J. Silberg, Hsiao-Ying Cheng, Ilene Del Valle, Emm Fulk, George Bennett

Rice University, United States

Soil microbes can be programmed via synthetic biology to report on their behavior, informing researchers when they have participated in key biogeochemical processes (e.g. denitrification) or when their immediate environment has passed a particular physical threshold (e.g. a microbial-scale change in soil water conditions). This use of synthetic biology has the potential to significantly improve our understanding of microbes' roles in N, C, and water cycling; however, synthetic microbes have not yet seen wide laboratory use in soils because synthetic organisms typically report by fluorescing, making their signals difficult to detect outside the petri dish. We are developing a new suite of biosensors that report instead by releasing easily-detected gases, allowing the real-time, noninvasive monitoring of microbial behavior in soils. Biosensors can, in theory, be programmed to detect processes such as biofilm production, various steps in the N cycle, methanogenesis, and coordinated secretion of some forms of extracellular enzymes. Steps in the S cycle may also be detectable.

We will provide an overview of the potential uses of gas-reporting biosensors in soil ecology and will report the development of the systematics of these sensors. Successful development of gas biosensors for soil applications will require addressing issues including: engineering the intensity of microbial gas production to maximize the signal-to-noise using the tools of synthetic biology; normalizing the gas reporter signal to cell population size, managing gas diffusion effects on detected signal response; and developing multiple gases that can be used in parallel.

## **Influence of wet-dry cycles and organic management on gross nitrogen depolymerization in agricultural soils**

\*Amanda Daly<sup>1</sup>, Andreas Richter<sup>2</sup>, Stuart Grandy<sup>1</sup>

<sup>1</sup>University of New Hampshire, United States

<sup>2</sup>University of Vienna, Austria

In the water-insecure future predicted for many agricultural regions, crop producers will need to adopt practices that maintain both yields and soil quality despite dry conditions. These yields will depend on sufficient soil nitrogen (N) provisioning, a process that more frequent drying and rewetting cycles will likely disrupt. Water limitation could alter the rate at which soil microbes depolymerize organic N into plant-accessible mineral forms, but perhaps agricultural management regimes could establish favorable soil conditions that attenuate any negative effects of drought on N depolymerization and mineralization. To test these ideas, we exposed soils from paired organic and conventional plots at the Beltsville and KBS long-term agricultural experiment sites to either mesic conditions or four dry-rewet cycles during an eight-week laboratory incubation.

Wet-dry cycles increased DOC and amino acid pools, and decreased MBC and N-acquiring enzyme activities. We found site-specific and management-specific effects within site: At KBS, wet-dry cycles decreased LAP activity and increased ammonium pools more in organic soils compared to conventional soils. At Beltsville, wet-dry cycles increased ammonium and dissolved N pools in both management treatments and, in conventional soils, also increased amino acid pools. The influence of wet-dry cycles and agricultural management on gross N depolymerization and mineralization rates measured using <sup>15</sup>N isotope pool dilution will also be presented. Drying-rewetting cycles appear to reduce microbial biomass and activity but also release potentially plant-available N and improve microbes' N status; these effects appear to be amplified at some—but not all—sites in soils under organic management.

## **Temperature, moisture and mineral interactions alter the vulnerability of organic matter turnover**

\*A. Peyton Smith<sup>1</sup>, Malak Tfaily<sup>2</sup>, Kent Rod<sup>1</sup>, Vanessa Bailey<sup>1</sup>, Ryan Renslow<sup>1</sup>

<sup>1</sup>Pacific Northwest National Laboratory, Department of Energy, United States

<sup>2</sup>EMSL, Pacific Northwest National Laboratory, United States

Sorption of organic matter (OM) to mineral surfaces is a primary process governing its persistence. How climate change-induced shifts in temperature and moisture influence the bioavailability of previously-bound OM remains highly uncertain. We coupled Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR-MS) with CO<sub>2</sub> respiration rates and 16s sequencing in a short-term laboratory incubation to test the combined effects of temperature (4° vs 20°C) and moisture (50 vs 100% water-filled pore space, WFPS) on OM chemistry, microbial respiration and community composition in capillary fringe-sediments maintained under different mineralogical conditions (illite amended vs non-amended). We hypothesized that OM in illite-amended sediments would be less vulnerable to changes in moisture and temperature than OM in non-amended, natural sediments. We also hypothesized that increased temperature would alter mineral-OM interactions with more transformations of OM at 20°C than at 4°C. Our results show that transformations of OM primarily occurred in illite-amended sediments maintained at 50% WFPS at 20°C compared to all samples. However, more cumulative CO<sub>2</sub>-C was respired in non-amended sediments at 20°C. The nominal oxidation state of C and the aromaticity index of the OM were positively correlated with cumulative CO<sub>2</sub>-C respired, suggesting that complex forms of OM are thermodynamically available for microbial degradation. Using ordination analysis, moisture at illite-amendments altered bacterial community structure at 20°C. Bacterial diversity decreased in illite-amended sediments. Our results, contrary to our hypotheses, show that OM transformations were most vulnerable in illite-amended compared to non-amended, natural sediments and that moisture content interacted with temperature to alter OM turnover.

## **Nitrogen limitation of decomposition and decay: How can it occur?**

\*Colin Averill<sup>1</sup>, Bonie Waring<sup>2</sup>

<sup>1</sup>Boston University, United States

<sup>2</sup>Utah State University, United States

Nitrogen (N) limitation of terrestrial productivity is common, and soil N availability is assumed to control terrestrial productivity in many theories of ecosystem ecology. Yet there are conflicting conceptual models to explain how N availability influences decomposition of organic matter by soil microbial communities. Experiments find N can both stimulate and inhibit decomposition. Initial litter N content is strongly related to the rate of litter decay. Ectomycorrhizal fungi can exacerbate N-limitation of microbial decomposers and increase soil carbon (C) storage. In direct contrast to these findings, experimental additions of inorganic N to soils broadly show a suppression of microbial activity, inconsistent with N-limitation of decomposition. Additionally, N-rich substrates may increase carbon use efficiency (CUE) of microbial growth, thereby increasing retention of C in the microbial biomass and ultimately, enhancing soil C storage by increasing the mineral sorption rate.

We use a mathematical model to resolve contrasting interpretations of the role of N in decomposition and soil C storage. We believe some discrepancy between patterns observed across gradients of organic matter stoichiometry vs. N fertilization experiments may be linked to fertilized induced osmotic stress and acidification, rather than nutrient effects per se. Second, N-limitation of decomposition can increase C stored in particulate organic matter, but may decrease transfer rates of C to mineral surfaces due to a negative effect on microbial CUE. Hence, N availability may always limit the rate of decomposition, but the ultimate effect on soil C storage will depend on interactions between physiology, mineralogy.

## **An interactive learning module for teaching ecology students (and professors) about databases for managing and querying large datasets**

\*Becky Ball<sup>1</sup>, Suzanne Dietrich<sup>1</sup>, Don Goelman<sup>2</sup>

<sup>1</sup>Arizona State University, United States

<sup>2</sup>Villanova University, United States

Data and databases are ubiquitous: they are relevant across all disciplines to solve real-world problems. In the modern era of “big data” ecology, future generations of ecology students need to be problem solvers who can appropriately handle large amounts of data using applied computing approaches, despite majoring in STEM fields that are typically light in applied mathematical and computing coursework. Through an interdisciplinary collaboration with applied computing faculty, we have developed an ecology-specific interactive visualization module that teaches students the basic principles of databases. The goal of the module is to provide a foundation for students to understand how databases can be used as an effective tool in their future field of study. The learning module uses a specific ecological example examining data from a collection of hypothetical studies simulating multiple factors of climate change across multiple sites in the Long-Term Ecological Research Network (LTER). In the interactive visualization, students learn: (1) conceptually, what is a database and how does it differ from a spreadsheet? (2) How to query databases to answer their research questions. The module is available open-access online, utilizing not only the ecological customization described above, but also examples in GIS and other fields of study potentially relevant to ecology.

## **Integrating soil biodiversity and soil ecology into non-soil-focused undergraduate courses**

Loren Byrne

Roger Williams University, United States

Because soils underpin human well-being, societies need citizens who are environmentally soil literate—that is, who understand basic characteristics of soil ecosystems, and use knowledge about sustainable soil management to inform decisions. Cultivating such literacy depends on robust soil ecology education efforts that should be led by soil ecologists. At the undergraduate level, offering specialized soil ecology courses is a key strategy, though it has limitations. An alternative approach that will reach more students, and may be more practical in many contexts, is to integrate soil biodiversity and ecology into non-soil-focused courses, including introductory biology for majors and non-majors, and sustainability studies courses. The objective of this talk is to share reflections about and strategies for how to achieve this goal based on the author's teaching experiences at a small undergraduate university. For example, as part of revisions in an introductory biology laboratory, two sessions about phylogenetics and ecological interactions were developed using soil organisms. In other courses, soil ecosystem processes have been used to frame discussions about ecosystem services and sustainability. These brief introductions have been observed to increase students' appreciation for soil biodiversity and ecosystems. Thus, soil ecologists should identify and embrace more opportunities to use soil biodiversity in support of more general teaching aims (e.g., evolution education). In addition, soil ecologists should help non-soil scientist colleagues do the same by formally developing and sharing relevant teaching materials. Having more soil ecologists engaged in such efforts is essential for helping society's future leaders develop their environmental soil literacy.

## Appendix II

# SOIL ECOLOGY SOCIETY BIENNIAL ORAL PRESENTATION ABSTRACTS

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Thursday June 8th

PARALLEL ORAL SESSION E  
Ballroom C

## **SES Early Career Research Awardee Presentation – Tom Crowther**

### **Quantifying global soil carbon losses in response to warming**

Marie Curie Fellow at the Netherlands Institute for Ecology

The majority of the Earth's terrestrial carbon is stored in the soil. Predicting the balance of carbon between the soil and the atmosphere is critical if we are going to understand climate change. If anthropogenic warming stimulates the loss of this carbon to the atmosphere, it could accelerate planetary warming. Despite evidence that warming enhances carbon fluxes to and from the soil, the net global balance between these responses has remained uncertain. I present a comprehensive analysis of warming-induced changes in soil carbon stocks by assembling data from 49 field experiments located across North America, Europe and Asia. I show that the effects of warming are contingent on the size of the initial soil carbon stock, with considerable losses occurring in high-latitude areas. By extrapolating this empirical relationship to the global scale, we provide estimates of soil carbon sensitivity to warming that may help to constrain Earth system model projections. Under the conservative assumption that the response of soil carbon to warming occurs within a year, I show how a business-as-usual climate scenario would drive the net loss of ~1.5 Pg C from the soil each year. This value is approximately 12–17 per cent of the expected anthropogenic emissions over this time. This provides strong empirical support for the idea that rising temperatures will stimulate the net loss of soil carbon to the atmosphere, driving a positive land carbon–climate feedback that could accelerate climate change.

## **Partial support for the 'environmental heterogeneity hypothesis' in tallgrass prairie restorations**

\*Drew A. Scott, Sara G. Baer

Southern Illinois University, United States

The 'environmental heterogeneity hypothesis' proposed a mechanism to allow resource partitioning and species coexistence. In accordance with this hypothesis, plant diversity is predicted to increase with variability in resources, but there has been weak support from experimental studies. The objective of this research was to characterize the amount and heterogeneity (coefficient of variation) of soil nitrate and proportion of photosynthetically active radiation reaching soil surface as related to plant community structure during plant community development. This was accomplished using a geostatistically-informed sampling design and co-located plant, soil, and light measurements across a chronosequence of restored prairies. Mean nitrate decreased exponentially with restoration age ( $P < 0.001$ ), but there was no directional pattern in nitrate heterogeneity. Mean amount and heterogeneity of light availability decreased exponentially with restoration age ( $P < 0.001$ ). Light availability heterogeneity ( $P = 0.005$ ), mean soil nitrate ( $P = 0.001$ ), and mean light availability ( $P = 0.002$ ) were correlated with plant composition (Bray-Curtis dissimilarities). Mean nitrate was inversely related to Shannon's diversity ( $P = 0.002$ ) and richness ( $P < 0.001$ ). This study indicates that amount of nitrate is more strongly related to plant diversity than heterogeneity in measured resources. This study further suggests that competition for resources, rather than resource partitioning through environmental heterogeneity, likely has a greater influence on plant diversity.

## Fungal responses to an invasive plant in a warmer, fertilized forest

\*Mark Anthony<sup>1</sup>, Serita Frey<sup>1</sup>, Kristina Stinson<sup>2</sup>

<sup>1</sup>University of New Hampshire, United States

<sup>2</sup>University of Massachusetts, United States

Global change is altering the availability of soil resources that can promote successful plant invasions. The effects of invasion on sensitive soil microorganisms might therefore be amplified in a global change context, feeding back to further alter soil resource availability. In this study, we measured the impacts of *Alliaria petiolata* (garlic mustard) invasion on fungal functional guilds (saprotrophs, ectomycorrhizae, arbuscular mycorrhizae, and pathotrophs) in the context of simulated N deposition ( $5 \text{ g N m}^{-2} \text{ yr}^{-1}$ ), soil warming ( $+5^\circ\text{C}$ ), and their interaction. To do this, we initiated an experimental invasion within warmed and N amended plots at the Soil Warming  $\times$  Nitrogen Addition Study at the Harvard Forest Long-term Ecological Research (LTER) site in Petersham, MA. Two year after invasion, soil was collected and analyzed for fungal community structure and soil resource availability (water, organic C and N, inorganic N, fine root contents). We found clear effects of simulated N deposition, soil warming, and their interaction on labile organic C pools, inorganic N availability, and the quantity and spatial distribution of fine roots. Fungal communities were most significantly reassembled in invaded  $\times$  fertilized  $\times$  warmed plots, a response accompanied by greater C mineralization and the redistribution of fine roots from mineral soil into the organic horizon. Conversely, the effect of invasion on the arbuscular mycorrhizal community was buffered in plots with fertilizer and heat. Our results suggest that impacts of invasion on fungi can be both enhanced (general fungal response) and ameliorated (mycorrhizal response) in the context of global change.

## **Investigating deficit irrigation impacts on belowground processes and climate change mitigation potential**

\*Nora Flynn<sup>1</sup>, Louise Comas<sup>2</sup>, Catherine Stewart<sup>2</sup>, Steven Fonte<sup>1</sup>

<sup>1</sup>Colorado State University, United States

<sup>2</sup>USDA - Agricultural Research Service, United States

The pressure of rising global food demand in combination with increasingly limited water and land resources requires the development of farm management practices that improve plant-water productivity and contribute to farmers' capacity to adapt to a changing climate. Deficit irrigation (DI) is a strategy to reduce crop water usage with minimal impacts on crop yield, and may have important implications for climate change mitigation. Deeper root growth and reduced surface moisture under DI are likely to impact soil biological activity, which in turn regulates greenhouse gas emissions, organic matter turnover and nutrient dynamics, yet the impacts of DI remain poorly understood. To better understand DI impacts on microbial processes and its potential to mitigate global warming, we evaluated greenhouse gas emissions and multiple soil physical, biological and chemical properties under different DI intensities in a replicated corn field trial near Greeley, Colorado. Treatments differed based on target percent of maximum crop evapotranspiration (ET). The lowest ET treatment (40% of ET in late vegetative and maturation stages) exhibited reduced N<sub>2</sub>O emissions in comparison to well-watered treatments. Additionally, the 40% ET treatment resulted in significantly greater root proliferation at depth (below 40 cm) than the full ET treatment, and significantly greater microbial abundance at depth. These results suggest that DI may help to mitigate climate change via reduced N<sub>2</sub>O emission and altered soil microbial activity.

## **Using extracellular polymeric substances (EPS) from bacteria to make soils more drought-adapted**

\*Joseph Blankinship<sup>1</sup>, Kenneth Marchus<sup>2</sup>, Joshua Schimel<sup>2</sup>

<sup>1</sup>University of Arizona, United States

<sup>2</sup>University of California Santa Barbara, United States

Crops—and plants in all ecosystems—depend on healthy soils that can supply water and nutrients even when it is not raining (or irrigating). One possible strategy for helping agriculture adapt to drought is to learn from soil bacteria. When soils dry out, bacteria are known to release extracellular polymeric substances (EPS) into the soil environment that act as superb sponges to increase water retention and as pipes to increase availability of soluble resources. However, nothing is known about the link between soil EPS and plant health. What if we could augment EPS in soil during drought as a way of helping crops adapt? This question was studied using soils from Sea Smoke Vineyard near Lompoc, California. Pinot noir grapevines were grown in a greenhouse with soils of varying amounts of xanthan gum. Xanthan gum is a bacterial EPS polysaccharide that is organically certified and commercially produced. We captured close-up images showing how strands of xanthan gum connect dry soil particles that were otherwise hydrologically disconnected. Laboratory tests showed that a xanthan gum concentration of at least 0.5% (by mass) was needed to increase soil water-holding capacity and aggregate stability. And greenhouse trials with xanthan gum in vineyard soils showed a 40% increase in water-use efficiency without sacrificing nitrogen supply or plant health. If xanthan gum can successfully sustain nutrient availability while reducing irrigation demand, then bacterial EPS (whether amended or naturally secreted) could be a viable strategy for dealing with water scarcity in arid land agriculture.

## **The influence of Japanese stiltgrass on soil microbes, edaphic properties, and tree regeneration in a nitrogen saturated environment**

\*Tyler Rippel, Pasquale Succi, Samantha Chapman

Villanova University, United States

Many northeastern deciduous forests suffer from poor seedling regeneration due to soil impacts from invasive understory plants and nitrogen deposition. Specifically, Japanese stiltgrass (*Microstegium vimineum*), a non-native invasive grass that is widely spread throughout eastern America, can inhibit native tree succession through a variety of soil influences such as altering pH. In a highly invaded Pennsylvania forest which has N saturated soils, we investigated the following two novel questions: (1) Does Japanese stiltgrass influence nitrogen cycling in nitrogen saturated environments? (2) Does Japanese stiltgrass invasion have a stronger influence on soil dynamics important for tree regeneration than overstory tree community composition? We examined plots with and without Japanese stilt grass in wetlands, grasslands and successional forests. We assessed multiple plant traits, soil pH, soil nutrient pools and availability, and amoA gene abundance in five replicates of each community type. In plots with Japanese stiltgrass, we found a ubiquitous increase in bulk pH and rhizosphere pH. Soil NO<sup>3</sup>-was 36% higher in plots that had Japanese stiltgrass, indicating that nitrification may be increased even in these nitrogen saturated soils. Our findings suggest that Japanese stiltgrass controls N cycling within wetlands, grasslands, and successional forests possibly by raising pH to induce increased nitrification rates. These results implicate that forest management may have to account for altered N cycling and the legacy effect of increased nitrate in soils. Our results suggest that forest managers may need to account for altered N cycling and the legacy effect of increased nitrate in invaded forest soils.

## **Consequences of changing rainfall patterns on nitrous oxide fluxes in cropping systems**

\*Kate Glanville, G. Philip Robertson

Michigan State University, United States

In the US Midwest, the dry intervals between precipitation events and the amount of precipitation falling in single events are increasing and predicted to increase further with all greenhouse gas emissions scenarios. N<sub>2</sub>O fluxes are closely linked with soil moisture, causing changing rainfall patterns to very likely influence N<sub>2</sub>O fluxes. Since the majority of anthropogenic N<sub>2</sub>O production is from agricultural soils, in which fluxes are largely controlled by oxygen, nitrate, and carbon availability, it is important to understand the effects of changing rainfall patterns on production. Our objective is to test the hypothesis that changing rainfall patterns strongly alter N<sub>2</sub>O fluxes in agricultural soils as modulated by cropping system and landscape position.

We used rainfall manipulation shelters to create soils exposed to same amounts of rainfall delivered at different intervals (3-day, 2-week, and 4-week). The initial phase of this experiment was conducted for 10-weeks in a no-till continuous-corn system in place from 2008 at the Kellogg Biological Station Long-Term Ecological Research site. Results from the first field season show cumulative N<sub>2</sub>O fluxes were four times higher when rainfall occurred in 4-week rather than sub weekly or 2-week intervals. Results will also be reported from the 2016 field season and related to changes in denitrifier enzyme activity and nitrate availability. Understanding patterns and mechanisms for N<sub>2</sub>O fluxes from the soil is important for developing mitigation practices and parameterizing biogeochemical models.

## **Prescription side effects: Controlled burning alters resource stoichiometry in a Midwestern forest soil**

\*Meghan Midgley<sup>1</sup>, Quinn Taylor<sup>2</sup>

<sup>1</sup>The Morton Arboretum, United States

<sup>2</sup>University of San Diego, United States

In eastern deciduous forests, burning is a common forest management technique used to control invasive understory plants, such as buckthorn and thistle, and promote oak regeneration. However, little is known about how controlled burns impact soil properties. As alterations to soil biogeochemistry affect plant growth and competition, changes in the soil may enhance or dampen the desired impacts of controlled burning. In this study, we assessed the impacts of controlled burning on soil biogeochemistry by comparing adjacent annually burned and historically unburned forests in The Morton Arboretum's East Woods.

We found that high-frequency controlled burning fundamentally altered the carbon : nitrogen : phosphorus (C:N:P) stoichiometry of extracellular enzyme activities, microbial biomass, and soluble C and nutrients. In particular, burning decreased microbial biomass C:P ( $P= 0.049$ ) and increased the abundance of C- and N-degrading enzymes relative to P-degrading enzymes ( $P = 0.044$  and  $<0.01$ , respectively), indicating that burning increased P incorporation into microbial biomass while simultaneously decreasing microbial P demand relative to C and N demand. As fire volatilizes C and N at lower temperatures than P and increased soil pH ( $P < 0.01$ ), these changes in microbial biomass and enzyme stoichiometry are likely driven by increased P availability relative to C and N availability. Thus, important side effects of burning are changes in resource stoichiometry – a shift towards C- and N-limitation and away from P-limitation. The consequences of these shifts for plant community composition remain a critical unknown for predicting the restoration outcomes of controlled burning.

## **Linking soil C and N cycling and trace gas fluxes with soil bacterial communities along a gradient of simple to complex crop rotations**

\*Brendan O'Neill<sup>1</sup>, Thomas Schmidt<sup>2</sup>, G. Philip Robertson<sup>1</sup>, Sasha Kravchenko<sup>1</sup>, Stuart Grandy<sup>3</sup>

<sup>1</sup>Michigan State University, United States

<sup>2</sup>University of Michigan, United States

<sup>3</sup>University of New Hampshire, United States

Increasing rotational complexity in agroecosystems can have multiple belowground effects but linkages between nutrient cycling pathways and the microbial communities that carry out these processes remain poorly understood. We tracked soil carbon (C) and nitrogen (N), trace gas fluxes and soil microbial communities along a gradient of increasing cropping system complexity from continuous grain monocultures to up to five plant species in 3-year rotations – including winter cover crops – in treatments that have not received external inputs. Rotations with a history of cover crops respired at least 20% more CO<sub>2</sub>, had greater potential C and N mineralization rates, and shifted patterns in microbial enzyme potentials, compared to all other rotations without cover crops. Denitrification was also different under cover crops with greater nitrous oxide emissions, a reduction in denitrification potential, and a shift in the phylogeny of genes for nitrite reductase (*nirK*). Finally, crop rotational composition had no effect on soil bacterial richness or diversity, but bacterial community composition significantly diverged in rotations with cover crops compared to those without. Differences in community composition were strongest between taxa of the *Proteobacteria* in the rotations with cover crops and *Acidobacteria* in rotations without cover. Our results show that even amid a range of the quality and quantity of plant inputs from different rotation, cover crops exerted an overriding effect on soil C and N dynamics, trace gas fluxes, and the physiology of organisms carrying out nutrient cycling.

## **Edaphic manipulation of the soil community of biofuel switchgrass (*Panicum virgatum*) in three soils**

\*Joni Baumgarten, John Dighton

Rutgers University, United States

*Panicum virgatum* is a potential biofuel crop that is tolerant of many different soils. Previous experiments by the authors have shown that the soil community and *P. virgatum* are resilient to nitrogen fertilizer additions in good agricultural soil. However, in less nutrient-rich soils where biofuel crops should be grown to prevent competition with food crops, *P. virgatum* may show a greater response to changes in the soil conditions. We ask: does *P. virgatum* growth respond to soil manipulations (adding nitrogen fertilizer and commercial mycorrhizal inoculum) differently in three different soils—good agricultural soil, marginal agricultural soil, and sand from the New Jersey Pine Barrens, where switchgrass grows in disturbed sites. We conducted a 3x2x2 factorial design greenhouse experiment to test the hypothesis that switchgrass biomass yields will respond to manipulations of the soil community in one growing season.

Results differed by soil type, but not by fertilizer or mycorrhizal inoculum treatments. Principle Components Analysis of well color development in the Biolog MicroPlates shows differences due to soil type but not by other treatments. Soil arthropod morphospecies differed by soil type but not by other treatments. Nematode numbers differed significantly ( $p=0.000006$ ) by soil type, but not by other factors. Mycorrhizal colonization did not differ by soil type or treatment. There were differences in root mass by soil type ( $p=0.0044$  level), and by fertilizer ( $p=0.09$ ). Above-ground biomass differed significantly by soil type but not by the other treatments. These results show the resilience of the soil community to perturbation across all soil types.

## **Environmental controls on free-living nitrogen fixation and nitrogen mineralization**

\*Darian Smercina, Lisa Tiemann, Sarah Evans, Maren Friesen

Michigan State University, United States

Plant accessible nitrogen (N) is controlled by N fixation (N-fix) and N mineralization (N-min), yet there is no consensus on the link between N-fix and N-min rates in soils. To better understand the dynamics of N-fix versus N-min, we used six marginal land (low soil N) sites, across Michigan and Wisconsin, planted with switchgrass (*Panicum virgatum*) monocultures. Split plots received fertilizer N at all sites. During the 2016 growing season, we measured potential N-fix and net N-min rates, and assessed several plant characteristics and soil biological and chemical properties including plant tissue carbon (C) and N, root mass, photosynthetic efficiency ( $q_L$ ,  $q_P$ ,  $\Phi_{II}$ , LEF), soil microbial biomass C and N, extracellular enzyme activities, plant available N (PA-N), and soil moisture. At peak growing season, N-fix positively correlated with plant available ammonium (PA-NH<sub>4</sub>) across all sites. N-fix rates did not differ between sites or between sub-plots, regardless of fertilization. Two Michigan sites, Lux Arbor (LUX) and Lake City (LC), were sampled monthly during the growing season. Averaged across 6 months, LC N-fix rates were significantly greater than LUX N-fix rates. At LC, N-fix positively correlated with soil moisture and PA-NH<sub>4</sub>, while N-fix at LUX negatively correlated with urease activity. Across all sites and sample dates, net N-min was negative, indicating N immobilization, and positively correlated with soil moisture and peptidase enzyme activities. These data demonstrate high variability in the most dominant pathways for plant accessible N. Ongoing analyses will elucidate whether plant characteristics or other soil variables are driving this variability.

## **SES Service Awardee – Deborah Neher**

### **Soil health – what progress have we made in the past 25 years?**

University of Vermont

My career in soil health began in 1990 as a member of the Agricultural Lands component of the Environmental Monitoring and Assessment Program. I dedicated the past 25 years of my career to evaluating soil invertebrates (nematodes, protozoa and microarthropods) as biological indicators of soil health. During that time, my research went through phases of evaluating sampling designs and statistical reliability of indices, calibration steps, and ecological interpretation. This research provided the necessary empirical support for choosing nematode communities as one of 16 indicators to monitor the condition of farmlands in the US by the H. John Heinz III Center for Science, Economics and Environment, State of the Nation's Ecosystem report last published in 2008. Political and economic environments were not conducive to bringing the Heinz proposal to full implementation. In the meantime, scientists at Cornell University developed a Comprehensive Assessment of Soil Health test and the USDA Natural Resource Conservation Service established a Soil Health Assessment program. Consequently, soil health is now a widely used term but seems to represent a selective memory of the science performed. Rather than repeat history, it is time to refresh memories and tell the story of soil health research and achievements.

## Appendix II

# SOIL ECOLOGY SOCIETY BIENNIAL ORAL PRESENTATION ABSTRACTS

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Thursday June 8th

PARALLEL ORAL SESSION F  
Ballroom D

## **Pathways and patterns of plant litter chemistry throughout decomposition**

\*Becky Ball<sup>1</sup>, Kyle Wickings<sup>2</sup>, Lynn Christenson<sup>3</sup>

<sup>1</sup>Arizona State University, United States

<sup>2</sup>Cornell University, United States

<sup>3</sup>Vassar College, United States

Decomposition of plant litter is a fundamental ecological process, integral to energy flow in foodwebs, biogeochemistry and soil formation. Most studies of plant litter decomposition typically measure only initial litter chemistry and assume that initial chemical differences determine decomposition dynamics in later stages of decay. However, initial differences in macronutrients do not always predict how litter will behave throughout decomposition. The less-frequently measured parameters, including micronutrients, phenolics and structural compounds can alter the decomposition process, and changes in their relative abundance may be important. Litter decomposition is a key regulator of C and nutrient cycling; thus, a more comprehensive understanding of this process is imperative. We tested the hypothesis that initial differences in litter chemistry among species will not persist in later stages of decomposition, with chemical content either diverging or converging throughout decomposition as determined by the local biotic and abiotic environments. To do so, we have compiled archived litter samples from across the U.S. from a broad range of plant species and ecosystems to identify patterns of changes in litter chemistry during decomposition. On these existing samples, we analyzed a comprehensive set of litter chemistry measurements across studies including macro- and micronutrients, fiber and other labile and recalcitrant plant compounds known to impact decomposition (polysaccharides, protein- and non-protein-derived N-bearing compounds, lignin, lipids, and phenols) across a consistent set of decay stages. Results support our hypothesis, with both divergence and convergence of litter chemistry occurring over time, and the relationship with plant functional group and ecosystem will be explored.

## **Augmentation of basal resources in a soil food web changes patterns of intraguild predation and decomposition rate**

\*Monica Farfan, David Wise

University of Illinois at Chicago, United States

Predation between generalist predators that consume shared prey on a lower trophic level is termed intraguild predation (IGP). We investigated how augmentation of the resource base of a forest-soil food web alters the dynamics of an IGP module consisting of two size classes of predaceous mites and shared fungivorous prey (fungivorous mites and Collembola). Because changes in this IGP module could alter decomposition rates by affecting fungal grazing, we also examined effects of resource enhancement on the rate of decomposition of a standardized substrate. In the two-year experiment, basal resources were augmented by adding artificial detritus to increase saprophytic fungi. During each field season, 150 fenced 1-m<sup>2</sup> plots received bi-weekly detrital enhancements at one of three rates: High (4x), Low (1x), or None (0x); 50 unfenced, non-enhanced plots served as a Reference treatment. Detrital enhancement increased densities of fungivorous prey and Parasitidae, a family of predaceous mites. The High rate changed the dominant fungivorous taxon from Tydeidae to Tarsonemidae, a mite family specializing on thin-walled fungal hyphae, which were likely more abundant in that treatment. Path analyses revealed a complex pattern of changes in the IGP module in response to detrital addition. One emergent pattern was the tendency for resource enhancement to increase the degree to which increases in the smaller IG-Prey positively affected densities of the larger IG-Predators. Decomposition rate was highest in the High treatment, probably because saprophytic fungi were more abundant in those plots, and because fungivores had a negative impact on decomposition in the Low treatment.

## **Microarthropods in bedded pack: A source for biocontrol of biting fly pests on dairy farms?**

Michael LeDuc, Tucker Andrews, Thomas Weicht, \*Deborah Neher

University of Vermont / Plant and Soil Science, United States

Bedded pack dairy systems use straw or wood chips to bed cows throughout the cold Vermont winter. Layers of bedding and manure accumulate for up to 8 months, begin to compost, generating heat that comforts the cows housed indoors. Microarthropods were extracted from bedded pack samples using Tullgren funnels. Summer bedded pack contained communities of mite (mesostigmata, astigmata and oribatida) and pseudoscorpions. Two genera of mesostigmata are in the family Uropodidae. The limited literature on published ecology indicates these mites can survive on a variety of fungi, but likely feed on preferentially on fly larvae. Likewise, the pseudoscorpions are also likely predators on fly larvae in the system. On each of five farms sites, we have identified two mites, Macrochelidae *Glyphtholaspis* sp. and Parasitidae *Eugamasus* sp., that have potential to act as fly predators. Preferential feeding trials, currently underway, have confirmed the predation of *Glyphtholaspis*- sp. on *Musca* larva. Other important mite taxa include Acaridae *Rhizoglyphus*. Future research will test the hypothesis that these fly predators may be a biocontrol mechanism for managing flies that vector the bacteria that cause mastitis.

## **Soil microbial communities and gas dynamics contribute to arbuscular mycorrhizal nitrogen uptake and transfer to plants**

\*Rachel Hestrin<sup>1</sup>, Maria Harrison<sup>2</sup>, Johannes Lehmann<sup>1</sup>

<sup>1</sup>Cornell University, United States

<sup>2</sup>Boyce Thompson Institute; Cornell University, United States

Arbuscular mycorrhizal fungi (AMF) associate with most terrestrial plants and influence ecosystem ecology and biogeochemistry. There is evidence that AMF play a role in soil nitrogen cycling, in part by taking up nitrogen and transferring it to plants. However, many aspects of this process are poorly understood, including the factors that control plant and fungal access to nitrogen stored in soil organic matter. Soil microbial communities sampled from different cropping systems were added to microcosms and incubations to assess microbial contributions to nitrogen uptake from organic matter. Stable isotopes were used to track nitrogen movement from organic matter into AMF and host plants. Results show that AMF can increase total plant biomass and nitrogen content fourfold, but that both AMF and free-living microbes compete with plants for nitrogen from organic matter. Surprisingly, gaseous nitrogen species also contribute significantly to plant nitrogen content. This research links interactions between plants, mycorrhizal symbionts, and free-living microbes with terrestrial carbon and nitrogen dynamics.

## **Invasive root herbivores accelerate soil carbon inputs and soil organic matter decomposition**

\*Huijie Gan<sup>1</sup>, Chao Liang<sup>2</sup>, Kyle Wickings<sup>1</sup>

<sup>1</sup>Cornell University, United States

<sup>2</sup>Institute of Applied Ecology, Chinese Academy of Sciences, China

Increasing evidence reveals that C inputs originated from roots are more likely to be preserved in soils compared to plant litter from aboveground. Despite awareness of the importance of root inputs for soil biogeochemical processes, our understanding of how biotic plant stressors such as root herbivores alter the input and cycling of root-derived carbon remains limited. To test the hypothesis that root herbivory alters soil microbial activity and C cycling, we carried out three separate experiments; a lab incubation, a manipulative field study, and a large-scale field survey. Collectively, our studies indicate that at high densities, root herbivores reduced total organic C in soils and such reductions are associated with increases in microbial biomass and hydrolytic enzyme activities. In contrast, root feeding appears to have little impact on microbial necromass in soils. We further propose a conceptual framework illustrating the role of belowground herbivores in soil C cycling, and discuss implications of large change in population dynamics of root herbivores, due to climate change or invasive species, for soil organic matter dynamics and soil C sequestration.

## **Oribatid mites as a tool to assess soil recovery after oil sands mining**

\*Brittany McAdams<sup>1</sup>, Sylvie Quideau<sup>1</sup>, Mathew Swallow<sup>2</sup>, Lisa Lumley<sup>3</sup>

<sup>1</sup>University of Alberta, Canada

<sup>2</sup>Mt. Royal University, Canada

<sup>3</sup>Royal Alberta Museum, Canada

Bitumen extraction via surface mining has disrupted nearly 1000 km<sup>2</sup> of boreal forest habitat in Alberta, Canada, requiring forest ecosystems to be reconstructed from the ground up. Previous work has investigated the influence of vegetation and reclamation materials on soil microbial communities, soil organic matter quality, and nutrient cycling. Little attention has been paid to the reestablishment of soil mesofauna to measure soil development. Oribatid mites play a key role in the boreal forest floor where they dominate the detritivore community and participate in the comminution of litter. Insight into the stage of development and quality of forest floors undergoing reclamation may be found through using oribatid mites as bioindicators. The objectives of this study were to (1) assess oribatid mite community composition with time since reclamation (8-31 yrs) and (2) investigate the application of community analyses ( $\geq 0.3$  mm) as a bioindicator of forest floor development. We used a chronosequence of aspen and spruce stands undergoing reclamation and compared them to the undisturbed forest matrix. Species-level identification revealed the presence of a novel forest floor at sites undergoing reclamation had the biggest impact on oribatid mite reestablishment. Reclaimed stands with a novel forest floor thickness  $\geq 2$  cm had similar oribatid mite species richness and diversity to that of undisturbed stands. Assemblages in stands undergoing reclamation remained different from assemblages found in undisturbed stands. Evidence of bioindicator potential was seen in the shift in relative abundance from common to rare species with the development of a novel forest floor.

## **Is soil pore water an exchange depot for nutrients in Arctic tussock tundra soils?**

\*Anthony Darrouzet-Nardi<sup>1</sup>, Michael Weintraub<sup>2</sup>, Jane Martinez<sup>1</sup>, Daniela Aguirre<sup>1</sup>

<sup>1</sup>University of Texas at El Paso, United States

<sup>2</sup>University of Toledo Dept. of Environmental Sciences, United States

Moist acidic tussock tundra soils in Arctic ecosystems maintain high moisture content (~80% by mass) throughout the roughly three-month-long summer growing season (May-July). In this wet environment, soil pore water may serve as a well-mixed medium, or exchange depot, in which enzymatic decomposition of soil organic matter takes place and nutrients are exchanged between plants and microbes. Alternatively, biogeochemical activities may be more localized in microsites within the soil separated by the complex physical structure of the soil matrix. Here we evaluate these alternative hypotheses using comparisons of both seasonal nutrient dynamics and soil ecoenzyme activities in soil pore water and soil extractions. Differences in concentrations between pore water and extractions show that nutrients in the soil pore water are typically low with the exception of a flush of nutrients at the beginning of the season, suggesting that nutrients are exchanged via soil pore water during soil thaw but that cycling is more localized during the growing season. In contrast, analyses of sugar concentrations in soil pore water show that they follow seasonal trends associated with plant production. The finding of more localized nutrient cycling activity is corroborated by low ecoenzyme activities in soil pore water compared with the larger solid particles in the soil. Taken together, these data suggest that some biogeochemical processes such as root exudation and nutrient turnover at thaw are facilitated by a well-mixed soil pore water pool while others such as microbial uptake of decomposition products are more localized.

## **A Serengeti without arbuscular mycorrhizas: Quantifying interactions between migratory mammals and fungal symbionts**

\*Bo Stevens<sup>1</sup>, Jeffrey Propster<sup>1</sup>, Gail Wilson<sup>2</sup>, Andrew Abraham<sup>1</sup>, Chase Ridenour<sup>1</sup>, Chris Doughty<sup>1</sup>, Nancy Johnson<sup>1</sup>

<sup>1</sup>Northern Arizona University, United States

<sup>2</sup>Oklahoma State University, United States

Both mycorrhizas and grazing mammals influence phosphorus (P) availability and primary productivity of grassland ecosystems. Grasses are estimated to obtain as much as 90% of their P from arbuscular mycorrhizas, and these symbioses are particularly important in acquiring P from the highly weathered soils which typically occur in tropical grasslands, such as the Serengeti. Large, migratory ungulates have been shown to translocate nutrients and increase the availability of P for grassland vegetation. The P content of vegetation and the abundance of arbuscular mycorrhizal (AM) fungi are highest in regions with the highest soil P. The concentration of P in plant tissues may influence the migratory patterns of ungulates in the Serengeti; during the gestation period, when nutritional requirements are increased, grazing mammals seek areas containing plants with higher P concentrations. The purpose of this study was to analyze the interactive roles of AM fungi and mammalian grazers on the P cycle and primary production in the Serengeti. Bayesian linear regressions were used to infer the primary factors that influence AM fungal abundance in the experimental plots. The best model indicated that total soil P was the strongest predictor of AM fungal biomass, it was significantly and positively correlated with the AM fungal biomass in grazed plots, but not in ungrazed plots. Biomass measurements of AM fungi were combined with published data on the abundance and physiology of large ungulates in a customized Madingley model to simulate P dynamics and net primary production of the Serengeti ecosystem.

## **Pulse size, frequency and soil-litter mixing alter the control of cumulative precipitation over litter decomposition in drylands**

\*François-Xavier Joly, Heather Throop

School of Earth and Space Exploration - Arizona State University, United States

It has traditionally been considered that macroclimate is the predominant driver of litter decomposition rates. However, in drylands, cumulative monthly or yearly precipitation typically fails to predict these rates. In these systems, the windows of opportunity for decomposer activity may rather depend on the precipitation size and frequency and local factors affecting litter desiccation, such as soil-litter mixing. We used a full-factorial microcosm experiment to disentangle the relative importance of cumulative precipitation, pulse frequency, and soil-litter mixing on litter decomposition. Decomposition saturated with increasing cumulative precipitation when pulses were large and infrequent, suggesting that litter moisture no longer increased and/or microbial activity was no longer limited by water availability above a certain pulse size. Greater precipitation pulse frequency thus increased decomposition, suggesting that periods of microbial activity depend more on precipitation frequency than quantity. Soil-litter mixing consistently increased decomposition, with greatest relative increase (+194%) under the driest conditions. In a follow-up experiment, we investigated how pulse size altered the dynamic of litter moisture and litter microbial respiration. We found that both litter moisture and microbial respiration saturated with increasing pulse size, confirming the existence of a pulse size threshold above which litter moisture and consequent microbial activity are no longer limited by water availability. Collectively, our results highlight the need to incorporate soil-litter mixing as key driver of decomposition in drylands, and to consider precipitation at finer temporal scale, particularly in the context of climate change that affects the size and frequency of precipitation events.

## **Peatland microbial community response to altered climate tempered by plant – soil interactions**

\*Ashley Keiser<sup>1</sup>, Montana Smith<sup>2</sup>, Sheryl Bell<sup>2</sup>, Kirsten Hofmockel<sup>2</sup>

<sup>1</sup>Iowa State University, United States

<sup>2</sup>Pacific Northwest National Laboratory, Department of Energy, United States

Under future climate change scenarios, boreal peatlands can expect warmer, longer growing seasons and alterations to the already fluctuating water tables. With combined increases in atmospheric CO<sub>2</sub> concentrations and temperature, we can further expect increased sphagnum growth in these peatlands, and thus, the potential for increased, labile root exudates during the growing season. Increased availability of labile root exudates may further stimulate an increase in microbial biomass and, indirectly, microbial cell turnover, which provides bio-available carbon (C) and nitrogen (N) compounds for microbial degradation and assimilation. Using experimental microcosms, we explored how the interaction between belowground labile carbon compound inputs and altered climate impact peatland C cycling. There was a significant interaction between moisture and temperature, with the greatest cumulative C mineralized at high temperature but low moisture. However, the magnitude of the response to climate varied by substrate addition. For example, glycine-amended communities had the greatest cumulative carbon mineralized at low temperatures, but the lowest at high temperatures. Glycine treatments also sustained high levels of respiration across the duration of the study resulting in the most narrow differences in cumulative mineralization among climate treatments, and thus, appear least sensitive to temperature increases. Collectively, our results indicate that moisture alone, through potential future alterations in the water table, does not alter decomposition. An interaction between increased temperatures and moisture fluctuations may cause future increases in decomposition, and thus, increased CO<sub>2</sub> respiration from peatland ecosystems, but this may be tempered by belowground carbon inputs.

## **The effect of C decomposition environment on plant detritus C in soil organic matter**

\*Anna Cates, Thea Whitman, Randall Jackson

University of Wisconsin-Madison, United States

While it is established that increasing temperature and moisture increases the rate of soil C mineralization, we do not know whether these factors alter the chemical quality or physical protection of the remaining soil C. By incubating <sup>13</sup>C-depleted plant biomass and soil under varying temperature and moisture, we are tracking the fate of the plant <sup>13</sup>C in soil pools, as well as microbial activity over the course of decomposition. At destructive sampling early, intermediate, and late in decomposition, we are fractionating soils into size-based aggregates, estimating microbial biomass C and efficiency, assaying extracellular enzyme activity (EEA), and examining microbial community composition via 16s sequencing. When 25% of biomass was decomposed, we observed three times the CO<sub>2</sub> efflux rate and twice the sum of EEA at 30 °C than 22 °C. CO<sub>2</sub> efflux rate is greater at 65% water-filled pore space (WFPS) than 45% WFPS at 30 °C, but the opposite is true at 22 °C. Microbial biomass and C use efficiency were over 80% higher at 22 °C and 45% WFPS than all other treatments. Preliminary data suggests more macroaggregates were formed at 22°C, but microaggregates were not affected. Current theoretical and computational models assume that if C is mineralized rapidly, total soil C stocks will decline over time. However, if physical protection of C remaining is altered by temperature and moisture during decomposition, mean residence times of soil C pools should be adjusted accordingly to better predict how changing environmental factors affect the long-term stabilization of soil C.

## Organic N cycling in agroecosystems

\*Kirsten Hofmockel<sup>1</sup>, Alison King<sup>2</sup>

<sup>1</sup>Pacific Northwest National Laboratory, Department of Energy, United States

<sup>2</sup>Iowa State University, United States

Diversifying cropping systems often entails altering other management practices, such as tillage regime or nitrogen (N) source that together can influence plant-microbe-soil interactions. We hypothesized that compared to conventional systems, the integrated effects of crop rotation, N source, and tillage in diversified cropping systems will promote microbially-mediated soil C and N cycling while attenuating inorganic N pools. To test this hypothesis, we studied a cropping systems trial in its 10th year in Iowa, USA, which tested a 2-yr cropping system of corn/soybean managed with conventional fertilizer N inputs and conservation tillage, to 3-yr and 4-yr diversified cropping systems managed with composted manure, reduced N fertilizer inputs, and periodic moldboard ploughing. We assayed soil microbial biomass, soil extractable NH<sub>4</sub> and NO<sub>3</sub>, gross proteolytic activity, and potential enzyme activity of six hydrolytic enzymes eight times during the growing season. At the 0–20 cm depth, native protease activity in the 4-yr cropping system was greater than in the 2-yr cropping system by a factor of 7.9, whereas dissolved inorganic N pools did not differ between cropping systems ( $P = 0.292$ ). At the 0–20 cm depth, MBC and MBN the 4-yr cropping system exceeded those in the 2-yr cropping system by factors of 1.51 and 1.57. Our findings suggest that diversified crop cropping systems, even when periodically moldboard ploughed, support higher levels of microbial biomass, which coincides with greater production of bioavailable N from SOM, and a deeper microbially active layer than conventional corn/soy systems that comprise much of the Midwestern US landscape.