



The Soil Ecology Society Biennial Meeting 2019

POSTER PRESENTATIONS



**SOIL
ECOLOGY
SOCIETY**

MICROBIAL COMMUNITY-LEVEL PHYSIOLOGICAL PROFILES, LABILE C FORMS AND
OXIDOREDUCTASE ACTIVITIES IN FLOODPLAIN FOREST SOILS

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ABSTRACT

River regulations came into force in southern Moravia in the 1970s and several reservoirs were constructed at the confluence of the Morava and Dyje rivers, thereby reducing the incidence of flooding and lowering the water table. These changes strongly impacted the floodplain forests: the vegetation changed and the sites became relatively dry. This study investigated how the reduced flooding affected the labile components of the organic matter and soil microbial activity.

Samples of a Fluvisol were collected at depths of 0-5, 5-15 and 15-30 cm in two experimental plots established in a typical hardwood floodplain forest (Lanžhot, Czech Republic), where flooding has rarely occurred in the past 40 years. Microbial community-level physiological profiling (CLPPs) was conducted with Biolog EcoPlates™. Hot water soluble C, carbohydrates and polyphenols, labile C and microbial biomass C were also analysed.

Substrates such as mannitol, N-acetyl glucosamine, galacturonic, 4-hydroxybenzoic acid, galactonic acid, lactone and arginine were generally more efficiently degraded in the soil surface than in deeper layers. The communities in the 5-15 and 15-30 cm layers showed a greater capacity to degrade xylose, methylpyruvate, α -ketobutyric acid and asparagine. The contents of all C forms, biomass-C and oxidoreductase activities decreased sharply with depth, as usually observed in terrestrial ecosystems. However, although the dehydrogenase and catalase activities per unit of labile C also decreased with depth, the activities per unit of total soil C or microbial biomass C remained relatively constant or even increased in the deepest soil layer, reflecting the typical vertical distribution in floodplain soils.

CYANOBACTERIAL COMMUNITIES INHABITING ALVARs OF DRUMMOND ISLAND,
MICHIGAN

AUTHORS

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ABSTRACT

Little is known about the microbial communities associated with alvar habitats. Alvars are areas of calcareous bedrock, typically calcite or dolomite, with little to no soil or organic matter. The development of soil facilitates the transition from bare substrate to an environment that can support vascular plant growth. Alvar rock samples and soil crust samples were collected from two sites on Drummond Island, Michigan. Samples were subject to microscopy to characterize the alvar material. Samples were enriched using liquid media and cyanobacteria were identified using microscopy and 16S rRNA sequencing. Geochemical analysis of the alvar samples revealed that the two sites differ in the degree of weathering, but are geologically similar. Scanning electron microscopy with energy dispersive spectroscopy showed that both sites contain Mg making them both dolomite substrates. Endolithic and soil crust cyanobacteria were successfully cultivated from both alvar sites using a liquid cyanobacterial growth medium, BG-11. Lithic samples and soil crust enrichments were imaged using light and scanning electron microscopy revealing a diverse array of cyanobacterial species. Liquid enrichments primarily contained *Leptolyngbya*, *Pleurocapsa*, *Microcoleus*, *Nostoc*, *Calothrix* and *Phormidium* spp. Molecular analysis of unenriched samples found similar species along with *Microsystis*, *Oscillatoria*, and *Spirulina* spp. 16S rRNA sequences revealed that a number of the organisms detected had closest relatives from species found in Antarctic and Colorado Plateau environments. Overall, the results of microscopy and molecular detection revealed a diverse array of cyanobacteria that likely play an important role in developing and stabilizing the delicate soils of the alvar.

IMPACT OF CHICKEN-LIVESTOCK INTEGRATION IN THE SOIL MICROBIOME OF
CURRENT AND SUBSEQUENT YEAR CROPS

AUTHORS

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ABSTRACT

Integration of livestock into crop management practices is of increased interest in diversified farming systems. Livestock presence affects soil fertility, as well as the composition and function of the soil microbiome. Soil microorganisms perform different roles in nutrient cycling and plant health; however, livestock integration could raise food safety concerns, in particular if combined with vegetable production. In this work, soil microbiome responses to chicken-livestock rotations is being studied, within the context of small to mid-scale diversified farms. The study system integrates chicken-pasture grazing into a three-year pasture-pasture-vegetable rotation. Within this system, we aim at understanding the balance between beneficial and harmful soil microorganisms at different stages of the rotation. We hypothesize that 1) chicken grazing results in a bacterial-dominated environment, 2) bacterial communities in chicken grazed soils are more diverse, and 3) the effects of chicken grazing are observed in subsequent vegetable crops. Changes in bacterial and fungal biomass, and fungal:bacteria ratios were measured in the studied soils, based on the use of bacterial and fungal-specific DNA markers. Overall, pasture plots, regardless of chicken grazing, had a significantly higher bacterial and fungal biomass than vegetable plots. A tendency toward a lower fungal biomass, and lower fungal:bacteria ratio was observed when comparing plots with and without chickens. Bacterial diversity and community composition are being surveyed using amplicon sequencing of ribosomal genes. The results of the amplicon survey will determine the effect that chicken grazing has on the soil microbiome and will explore potential food safety concerns within crop-livestock rotations.

IMPACT OF CLIMATE ADAPTIVE SOIL HEALTH MANAGEMENT PRACTICES ON
NITROGEN CYCLING

AUTHORS

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ABSTRACT

Biological soil health management is imperative in order to understand biological nutrient cycling related to soil fertility and environmental impact. Biological soil health indicators related to nitrogen cycling were measured from a wide range of agro-ecosystems including long-term USDA organic certified plots affiliated with North Dakota State University (3 yrs since certification), Pennsylvania State University (6 yrs since certification) and Washington State University (12 yrs since certification). Results reveal the effect of climate adaptive soil health management practices like reduced tillage, incorporation of animal wastes, cover cropping and crop rotations on soil microbial communities and their function, novel soil health indicators and greenhouse gas emissions. This study emphasizes the fact that “organic does not always mean sustainable” and soil management and climate plays a pivotal role in building a healthy soil that has the potential to provide ecosystem services.

QUANTITATIVE RESPONSES OF AMMONIUM-OXIDATION DOMINATE N₂O EMISSIONS
IN BIOENERGY CROP

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ABSTRACT

The N fertilization feeding microbial key transformations to released nitrous oxide (N₂O) a potent greenhouse gas and predominantly produced from agriculture soils. A field experiment was conducted to compare the effects of different N-sources on soil microbes their activities and N₂O emission from bioenergy crop (*Saccharum officinarum* L.) grown on region of Southern Brazil. Quantitative PCR (qPCR) analysis of key functional genes involved in N₂O formation and reduction (*amoA*, *nxB*, *nirK*, *nirS*, and *nosZ*) was measured. The biomass production diminished from 23.2-to-32.5 Mg ha⁻¹, when urea (UR) is applied compared to other N-sources. The intensity of gases emitter when using the UR were 6.8-fold higher than ammonium nitrate (AN) and ammonium sulphate (AS). Ammonia-oxidizing bacteria (AOB) revealed significant contribution to the N₂O emissions, but not archaea (AOA). Urea elevated AOB population, enhanced N₂O emissions and load higher emission factor 2.19%. Collectively, our data indicate that UR enriched AOB community consequently enhanced N₂O fluxes and support the hypothesis the main N₂O source in this system appeared to be via nitrification. Conversely, MAP could affect the microbial nitrogen transformation process and reduce N₂O emissions from cane fields.

USING META-ANALYSIS TO UNDERSTAND THE EFFECTS OF RANGELAND
MANAGEMENT PRACTICES ON SOIL PROPERTIES AND PLANT-RELATED OUTCOMES IN
CALIFORNIA

AUTHORS

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ABSTRACT

In California, as elsewhere, soils are becoming a central focus of rangeland management because of their relationship to ecosystem values and services. For example, rangeland soil management is called upon by the California 2030 Natural and Working Lands Climate Change Implementation Plan as a climate mitigation strategy, and funding through The Healthy Soils Program aims to maximize this outcome. To determine whether desired on-site and public services can be achieved with widely-used management practices in California—riparian restoration, oak establishment, compost application, and grazing—we conducted a meta-analysis assessing how these practices affect a suite of soil properties and plant-related metrics throughout the state. We extracted data on any reported soil parameter that is “dynamic” and therefore potentially relevant to soil health. We also extracted data on aboveground forage production, forage nitrogen content, and herbaceous species richness. Our search resulted in a total of 399 individual soil observations compiled from 33 publications and 64 individual plant community observations from 26 publications. The presence of oaks had the largest and most consistent effect on soil properties, with soil organic carbon, microbial biomass, and other measures of soil fertility increasing beneath oak canopies. The presence of grazing increased compaction and total N, and decreased pH. In contrast, compost applications did not significantly affect any of the measured soil parameters, but did boost forage production. These relationships were supported by varying levels of evidence (number of observations and studies) in the literature, which we will use to highlight priority areas for future research.

HERBIVORY WITH FIRE EXCLUSION REDUCES SOIL CARBON DIOXIDE EMISSIONS FROM
SOUTH AFRICAN GRASSLAND SOILS.

AUTHORS

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ABSTRACT

Herbivory and fire are common disturbances in grasslands and may alter the composition and quantity of detritus inputs into the soil, potentially influencing soil CO₂ emission rates. We sought to establish how these two disturbances independently and interactively affect the dynamics of CO₂ emissions in grassland soils by measuring soil respiration from savanna basaltic loam, granitic sand and grassland basaltic loam soils. Herbivory was expected to increase soil carbon sequestration resulting in the formation of more stable forms of soil carbon bonded to soil mineral nutrients, thus becoming unavailable to soil microbes. Contrastingly, fire would cause immediate mineralisation of soil nutrients with the majority of nutrients lost via volatilization, thus leading to the formation of less stable forms of soil carbon that are easily accessible to soil microbes, hence increased soil respiration. CO₂ fluxes were found to be consistently lower in control sites without herbivory or fire in all soil types. CO₂ fluxes were highest in sites with both herbivory and fire, with mean fluxes of 3.5, 0.9 and 2.3 $\mu\text{mol m}^{-2} \text{s}^{-1}$ ($P < 0.001$), from the three soil types, respectively. Grassland sites subject only to fire-disturbance had higher CO₂ fluxes than sites subject only to herbivory-disturbance ($P < 0.001$). In savanna soils, neither herbivory nor fire significantly influenced soil CO₂ emissions. As expected, herbivory lowered CO₂ fluxes but only in grassland sites with higher soil carbon content, while emission rates increased due to the twofold effect of having both herbivory and fire in all three soil types.

HEAVY METALS ALONG AN URBAN-RURAL GRADIENT FROM A MAJOR CITY IN NEW JERSEY AND PHYTO-REMEDICATION CHARACTERISTIC OF TWO PLANTS IN THE PRESENCE AND ABSENCE OF COMMERCIAL MYCORRHIZAL INOCULATION.

AUTHORS

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ABSTRACT

Urbanization dramatically alters natural environments through the processes associated with anthropogenic activities. A byproduct of highly urbanized areas is the increased emissions of heavy metal pollutants. The objectives of this study were (i) to analyze soil concentrations of Zn, Cu, Pb, and Fe from 30 soil samples from an urban – rural gradient in southern New Jersey, USA, (ii) assess the microbial function (ECOLOG) along the gradient and (iii) assess metal phyto-remediation by clover and switchgrass in the presence and absence of commercial mycorrhizal inoculation. Contrary to expectations, suburban soils had lower levels of heavy metals than either urban or rural soils and had a significantly different resource utilization profile by the microbial community. Uptake of metals by switchgrass was greater than clover due to greater overall biomass. The pattern on metal distribution within the plant varied by metal and mycorrhizal addition with Zn and Cu accumulation mainly in the root and increasing with mycorrhizal inoculation and Fe accumulating most in the shoot. For Pb there was a shift from accumulate in the shoot to accumulation in the root with the addition of mycorrhiza and, with switchgrass, a greater overall accumulation in plants not inoculated with mycorrhizae.

COMPARISON OF BIOCRUST-ASSOCIATED FUNGAL COMMUNITIES AT GRASSLAND
SITES IN NEW MEXICO

AUTHORS

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ABSTRACT

Understanding nutrient cycling in drylands is critical for promoting productivity in arid regions that cover ~40% of Earth's terrestrial surface. In drylands, biological activity is constrained by the pulsed inputs of water, which is the key driver of ecosystem productivity. Studies of dryland ecosystems indicate that fungal metabolism can dominate N transformations in the soil, and fungi that can operate at low soil moisture levels and mineralize nutrients could play a crucial role in translocating nutrients in these systems. Two prior studies reported that 25-50% of fungal taxa are shared between biocrusts and plant roots in grasslands, but data remain scant on the proportion of biocrust fungi that overlap with those inhabiting soil or roots.

Compositional comparisons of dryland fungal communities in these microsites will help expand our knowledge of these taxa and their potential roles in driving biocrust-plant nutrient dynamics. Biocrusts and plant (*Bouteloua eriopoda*) roots were sampled from previously established experimental sites in New Mexico, biocrust soil DNA was extracted and PCR-amplified with fungus-specific primers, and Illumina MiSeq sequenced. To visualize fungal root colonization, roots were also stained and microscopically assayed. Biocrust and root fungal communities shared OTUs and were dominated by Ascomycetes in the order Pleosporales. Dark-septate hyphae colonized 53% of root length, whereas aseptate hyphae (Glomeromycota, basal fungi) colonized 33%. This study supplements the microbial community characterization of dryland ecosystems and identifies potential fungal candidates that mediate nutrient and/or water transfers between plants and biocrusts.

NITROGEN CYCLING IS AFFECTED BY INTERSEEDING COVER CROPS INTO CORN

AUTHORS

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ABSTRACT

The soil microbial community is responsible for various nitrogen (N) transformation that impact crop productivity and environmental sustainability. Interseeded cover crops have the potential to impact microbial activity by affecting the amount and diversity of organic inputs to the soil. The goal of our research is to observe the effects of interseeding cover crops into corn on the activity of the soil microbial community and on crop yield and N status. We used four interseeded cover crop treatments and measured various soil nutrient-cycling processes, including nitrification potential, denitrification potential, and extracellular enzyme activity. Our preliminary results indicate that interseeded cover crops decrease the activity of enzymes associated with N-mineralization, with a greater proportion of N remaining in organic (dissolved organic N) rather than inorganic forms. In addition, with interseeded cover crops we see reduced potential for N loss via nitrification and denitrification, resulting in elevated corn tissue N. Our research suggests that interseeding cover crops can help retain N in the agroecosystem by slowing the rate of N transformations, increasing plant uptake of N, and reducing N-loss pathways. It remains to be determined whether such effects are driven by changes in the composition of the microbial community or reflect physiological responses of the microbial community to soil nutrient status.

HOW DO INVASIVE PLANTS IMPACT RIPARIAN SOIL NITROGEN CYCLING? A CASE STUDY FROM A LARGE-SCALE RUSSIAN OLIVE REMOVAL PROJECT IN THE MIDDLE RIO GRANDE

AUTHORS

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ABSTRACT

Biological invasions are a consequence of anthropogenic global change and represent a world-wide environmental and economic problem. Riparian ecosystems are especially prone for the invasion of alien species due to the natural corridors they represent. While most research focus on salt cedar (*Tamarix* sp.) in western US and its impacts on hydrologic processes, less effort has been invested into researching the effects of Russian olive (*Elaeagnus angustifolia*), which is an invasive, N₂-fixing species. Recent soil incubation experiments suggest that decomposing Russian olive litter expedites N cycling. We will examine the effects of Russian olive on nitrogen cycling in a large-scale restoration project. Our study area is set in a middle Río Grande riparian corridor, in central New Mexico. The experimental design consists of study plots ($n = 3$ per stand) in a native cottonwood (*Populus fremontii*) stand, Russian olive stand where trees have been mechanically removed, and Russian olive stands where the trees will not be removed. This design allows us to evaluate N cycling differences between native, invaded stands, and stands managed for restoration. From each plot we will analyze soil ammonium and nitrate contents, and microbial physiological profiles. We will present preliminary results showing latent differences in soil NO₃⁻ and NH₄⁺, soil respiration, N₂O flux and microbial community-level physiological profiles across our study sites. This project will provide information about the legacy effects of invasive woody N₂-fixing species on N cycling compared to native stands, in addition to the immediate effects of invasive species removal on N dynamics.

LOW TEMPERATURE SENSITIVITY OF AUTOTROPHIC AND HETEROTROPHIC SOIL
RESPIRATION COMPONENTS UNDER ARTIFICIAL WARMING.

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ABSTRACT

Soil respiration (R_{soil}) is the second largest terrestrial CO₂ flux being the greatest ecosystem C release to the atmosphere. R_{soil} is associated with organic matter decomposition, nutrient cycling and gross primary productivity. R_{soil} is often modeled as a function of soil temperature and moisture using mainly data from Temperate ecosystems. However, little is known about the sensitivity of autotrophic (R_a) and heterotrophic (R_h) components of R_{soil} to temperature in Tropical systems. We investigated the effects of a 2°C temperature (eT) increase over ambient air (aT) on an established tropical pasture in Brazil, dominated by the legume *Stylosanthes capitata* (C₃) and by the 'Guinea grass' *Panicum maximum* (C₄) with a temperature free-air controlled enhancement system. We used δ¹³C in fluxes and used a partitioning mixing model to untangle the contributions of C₃, C₄ and heterotrophs to total R_{soil} . There was a 20% increase in R_{soil} driven by changes in rates of R_a which had a strong diel effect. Nighttime R_a was responsible for 10% of total from the total R_{soil} under aT, and less than 30% under eT. Both R_a and R_h showed little sensitivity to soil temperature. At daytime C₄-C was responsible for more than 90% of R_{soil} regardless of the temperature. During the nighttime C₃-C contributed by 25% of total autotrophic-C respired by the soil. Our results indicate that plant diurnal activity may dominate R_{soil} in this moist tropical pasture exposed to increased ambient temperature.

LAND USE CHANGE EFFECTS ON SOIL MICROORGANISMS IN TROPICAL ECOSYSTEMS:
A META-ANALYSIS

AUTHORS

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ABSTRACT

Tropical regions are experiencing fast rates of land change impacting biogeochemical cycles and carbon stocks in the soil. Land conversion from forest to agriculture or grazing can affect soil microorganism through shifts in plant communities and soil properties. Changes in microbial traits can potentially impact nutrient cycling – specifically carbon, nitrogen, and phosphorus. The objective of this work was to synthesize trends and document knowledge gaps of how microorganisms are affected by land use change in tropical regions. We searched for literature relevant to land use and microorganism traits in tropical ecosystems. Then, we selected paired comparisons from two or more land uses, classified them by rainfall class and calculated the response ratio. We found that conversion from forest to agriculture in dry ecosystems increased microbial biomass and enzyme activities in the soil. In moist and wet environments, the conversion of forest to any other land use showed losses in most of the microbial traits. Overall, microbial abundance and functionality was reduced by changes from forest to other land uses. Losses in soil microbial traits may implicate that human disturbances are negatively impacting soil microorganism. Observed declines in microbial traits from forest to agriculture, pasture, plantation, and secondary forest could affect carbon, nitrogen and phosphorus cycles. Understanding microbial traits responses to land use change have implications for soil fertility management, ecosystem productivity, and improving our ability to predict feedbacks between tropical ecosystems and future disturbances.

THE IMPACT OF SOUTHERN PINE BARK BEETLE ON THE DECOMPOSITION AND
FUNGAL SUCCESS OF PITCH PINE WOOD IN THE NJ PINE BARRENS.

AUTHORS

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ABSTRACT

With a change in climate patterns, warmer winters in New Jersey, USA have allowed Southern pine bark beetles to invade pines in the NJ pine barrens. The pine barrens is an ecologically unique and protected area in New Jersey, so the impacts of bark beetles in this system is of great concern for conservation. Since bark beetles in general import the fungi they depend on to help feed their larvae, we are addressing three aspects of introduction of fungi into wood, which will ultimately join the decomposer pool as beetles kill their host tree. We look at (i) does the introduction of beetle fungi affect the rate of wood decay, (ii) does this unique fungal introduction influence the subsequent succession of decomposer fungi into this decaying wood and (iii) does the natural tree defense response to damage, of resin production influence the rate of wood decomposition and the succession of fungi effecting that decomposition. Wood and bark invaded by beetles has a slower decomposition rate than wood and bark not influenced by beetles. Using community DNA analysis, there are significant differences in the fungal community developing on decomposing beetle infested wood and bark to un-infested material. The presence of resin significantly decreases wood decomposition.

SEEING THE UNSEEN, BACTERIAL DRIVERS OF DECOMPOSITION IN ALFALFA SOILS
FERTILIZED WITH HIGH ORGANIC MATTER AMENDMENTS

AUTHORS

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ABSTRACT

Addressing the growing demand for food from a burgeoning population requires agricultural methods that sustainably support increases in crop production while maintaining environmental health. Agricultural practices that include the use of compost, in lieu of mineral fertilizers, have been shown to reduce environmental impacts and improve soil health. Producers seeking to improve sustainability through compost use are challenged by the chemical form and availability of nutrients in organic amendments, limiting their ability to predict when nutrients will be available to crops. To better understand nutrient dynamics in soils amended with organic fertilizers, we compared the soil microbial community response to amendments with differing carbon and nitrogen content. Composted horse manure was chosen to represent an organic high carbon amendment, and alfalfa hay was chosen to represent a high nitrogen amendment. Amended soils were incubated for 97 days and destructively sampled on seven progressively longer incubation intervals. DNA was extracted for 16s rRNA gene characterization, additionally, measurements of nitrate and other soil health characteristics were made. Our results showed significant shifts in soil microbial communities to both time and amendment. Nutrient release was tightly associated with amendment composition, with alfalfa showing the greatest release of plant available nutrients. We observed complex interactions between soils and amendments, with specific bacteria associated with both nitrogen and carbon metabolism. These bacteria are targets for further characterization and may contribute to the adoption of high organic matter fertilizers, contributing to the sustainability of agricultural production.

DEFICIT IRRIGATION REDUCES ABSOLUTE, BUT NOT YIELD-SCALED GREENHOUSE GAS EMISSIONS

AUTHORS

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ABSTRACT

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 water productivity and contribute to farmers' capacity to adapt to a changing climate. Strategic deficit irrigation (SDI) aims to reduce crop water usage with minimal impacts on crop yield, and may have important implications for climate change mitigation. We tested SDI practices in a replicated corn field trial near Greeley, Colorado. Three treatments were applied based on target percent of maximum crop evapotranspiration (ET) during key growth stages. Greenhouse gas (GHG) fluxes of nitrous oxide (N₂O) and carbon dioxide (CO₂) emissions were assessed on a regular basis during the growing season. In comparison to the 100% ET treatment, cumulative N₂O-N emissions were reduced by 15 and 40% in the 65% ET and 40% ET treatments respectively. Cumulative CO₂-C emission were reduced by 7 and 22% in the 65%ET and 40% ET treatments respectively. Soil temperature was a significant driver of both N₂O and CO₂ fluxes. Reduced surface moisture conditions under DI can reduce GHG emissions but also have a significant impact on yield. While the 100% ET treatment had the highest absolute emissions, it also had lower yield-scaled global warming potential in comparison to the deficit irrigation treatments. These results suggest that while SDI is effective at reducing water use and GHG emissions from agriculture, yield should be considered when assessing SDI as a climate-smart solution.

EVOLUTION OF SOIL CARBON UNDER AN AGRICULTURAL CHRONOSEQUENCE IN THE
DESERT OF AREQUIPA, PERÚ

AUTHORS

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ABSTRACT

Accumulation of organic matter in agricultural soils can enhance soil structure, water holding capacity, and nutrient retention, thus providing an important indication of soil productivity. As agriculture expands into marginal sandy soils, we need to understand how increases in soil organic carbon can impact yield. To quantify soil carbon accumulation and impact on sandy soil productivity, we selected an agricultural chronosequence in the desert of Majes, Perú. The region plans to expand its viticulture industry; an examination of soil productivity within vineyards provides key information to growers. In collaboration with the research station of the Universidad Nacional de San Agustín as part of the Arequipa Nexus Institute, we selected three vineyards established for 5, 10, or 35 years to create a pilot chronosequence. We sampled soils at two depths along a grid between and within the vine rows to measure soil organic carbon, total carbon, and inorganic carbon content. To assess biologic activity in the field, we installed a set of gas wells at two depths to measure CO₂ and O₂ production. Preliminary results at 25 cm show that the oldest vineyard produced 3.5 times more CO₂ than the youngest vineyard, indicative of higher root activity. Further, to characterize the soil biogeochemistry, we will conduct a field assessment of soil carbon using visible and near infrared spectroscopy (VNIR) correlations. By comparing the VNIR spectrum with laboratory carbon measurements, we aim to create a rapid field assessment to map soil biogeochemistry across the region for future agricultural development.

BEYOND SALT CHEMISTRY: HOW THE WHOLE SOIL-PLANT-INSECT SYSTEM RESPONDS TO SALINITY

AUTHORS

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ABSTRACT

Soils in the Northern Great Plains can host high salt concentrations, resulting from geologic origin, and strongly tied to landscape climate and hydrology patterns. We know that high salt concentrations in topsoil directly impact plant productivity and crop yield. However, our field and greenhouse studies have also revealed that salinity alters additional ecosystem properties. Specifically, soils within saline patches tend to have reduced structural development, higher water content, and elevated soil nutrient concentrations. Thus, salt-affected soils provide poor plant growing conditions and provide habitat for soil organisms that is physically and chemically different than nearby non-saline soils. These changes are associated with our observations of shifts in soil biological communities (broad taxonomic microbial groups and earthworms), and we are investigating how these saline soil communities participate in plant-soil feedbacks. Salinity causes additional changes aboveground, including helping herbivorous insect pests develop and maintain healthier populations on plant hosts (*Zea mays* and *Glycine max*) when grown in increasingly saline soils. Moreover, herbivorous pests like soybean aphids (*Aphis glycines*) prefer plants grown in highly-saline soils. Given that soil salinity occurs within a suite of soil conditions that influence soil function, and that plant salt stress can be exacerbated by insect pests, saline patches are a good candidate for zone soil management and targeted pest management. We expect that efforts to improve soil quality in saline soils will alleviate biotic and abiotic threats to crop production.

THE USE OF PLANT HYPERSPECTRAL SIGNATURES TO LOOK BELOWGROUND AT THE
SANTA RITA EXPERIMENTAL RANGE

AUTHORS

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ABSTRACT

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 spread and 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 nutrient cycling, soil functioning, and other ecosystem services. This project offers a novel approach to answering these questions by combining remotely sensed data from an open-access data platform to infer foliar chemistry with measures of soil biogeochemistry 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.

AUTHORS

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ABSTRACT

Microplastic pollution is an issue of major global concern in marine and freshwater systems, yet has only recently received any attention in soil. Current work indicates widespread presence of microplastics in riparian, urban, and agricultural soils, and have demonstrated deleterious effects on soil organisms similar to those described in marine systems. However, if we are to understand the potential threat of microplastic pollution to soil biodiversity and its associated ecosystem processes, a number of fundamental research questions must be addressed. These include: development of methods to detect microplastic ingestion by terrestrial invertebrates, determination of the effects of land use practices on microplastic occurrence in soils, and assessment of how microbial colonization affects palatability of microplastics to soil detritivores. We will discuss plans for and current progress on forthcoming research using Michigan agricultural soils as a model system.

AUTHORS

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ABSTRACT

Robust, predictive models of elemental cycling in terrestrial ecosystems and contaminant fate and transport in the subsurface require understanding and identification of key microbial, biogeochemical and hydrologic processes that control species reactivity, cycling, and mobility across multiple spatial and temporal scales. The ability to identify and adequately probe dynamic processes at the molecular to pore scale provides mechanistic information needed to accurately represent these processes in computational reactive flow and transport models as well as community land models, an important goal of many soil ecologists who address the nation's sustainability challenges. Linking experimental and theoretical approaches from molecular to field scale requires the convergence of diverse experimental and computational techniques and collaboration with experts from multiple disciplines.

EMSL, a DOE national user facility in Richland WA, provides integrated experimental, computational, and modeling and simulation resources and expertise for scientific studies and discovery in soil ecology to users free of charge. This poster highlights six integrated research platforms that are particularly relevant for such research: multi-omics including proteomics, metabolomics and transcriptomics; subcellular bioimaging and structural analysis; cell spatial and temporal dynamics; isotope and chemical analysis; plant, soil and subsurface transport; and theory, simulation, data analytics and visualization.

RESPONSE OF BACTERIAL AND NEMATODE COMMUNITIES TO COMPOST
AMENDMENT IN AN ALMOND PRODUCTION SYSTEM

AUTHORS

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ABSTRACT

Municipal compost, produced from yard trimmings, food scraps and other inputs may increase soil organic carbon (SOC) and improve soil health. It is not well understood, though, which composts result in greater SOC pools and how soil biology responds to increments of SOC. The goals of this project were: 1) to measure the effects of compost on bacterial and nematode diversity and 2) to examine the relationship between nematodes, bacterial communities and SOC processing. In an almond production system, two different compost blends were compared to a fertilized standard and non-fertilized control. Soil sampling occurred three times per summer during the first two years. Carbon pools, such as permanganate-oxidizable carbon (POXC) and total C were measured. Bacterial phylogenetic diversity was assessed using high-throughput sequencing and bacterial soil functions inferred from taxonomy. Nematodes were extracted from soil and identified to genus microscopically.

Both composts increased various measures of SOC. Bacterial communities for each compost blend were distinct from each other and from controls and fertilized plots. In year one, compost treatments had more reads of bacteria with possible cellulolysis and xylanolysis potential, indicating likely SOC processing. Nematode communities responded more strongly to treatments in year two. The relative abundance of bacterial-feeding nematodes was higher with compost compared to fertilizer, while compost decreased the relative abundance of fungal-feeding nematodes. Path analysis indicated that soil organic matter influenced microbial composition which, in turn, influenced nematode communities. Certain nematode groups, such as the bacterial-feeder, *Prismatolaimus*, were correlated with POXC.

ARBUSCULAR MYCORRHIZAL COLONIZATION AND MUTUALISM: THE ROLES OF
STRESS, DISTURBANCE, AND LIFE HISTORY TRAITS

AUTHORS

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Dr. Rebecca Bunn - Western Washington University

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ABSTRACT

Plants can survive in a wide variety of environments from tundra, to frequently grazed pastures, to undisturbed forests. Using frameworks to classify species by life history traits can be useful for understanding this diversity and the implications these species play in ecosystem functions. Grime's C-S-R (Competitor, Stress tolerators, and Ruderal) Framework is one such system used for grouping terrestrial plants by their functional traits that facilitate their survival under stress and disturbance. Stress is defined as prolonged harsh environmental conditions and disturbance is defined as events responsible for biomass loss. This two-axis framework classifies three major life history strategies: 1) Competitors that succeed in low stress and undisturbed environments, 2) Stress tolerators that can subsist in longstanding adverse conditions, and 3) Ruderals that can survive frequent disturbances. It has been proposed that Grime's framework could also be applied to arbuscular mycorrhizal fungi (AMF) – soil fungi that form mutualist relationships with plant's roots. Most AMF species in the *Gigasporaceae* family have life history strategies consistent with competitors, *Acaulosporaceae* with stress tolerators, and *Glomeraceae* with ruderals. In this experiment we aim to test this hypothesis by inoculating corn (*Zea mays*) with isolates of either *Gigasporaceae*, *Acaulosporaceae*, or *Glomeraceae* and subjecting them to four physical treatments: shade (stress), replacement of the host (disturbance one), replacement of the host and sieving (disturbance two), or control (low-stress, undisturbed). Conclusions will be based on 1) the AMF family survival after four months and 2) relative benefit provided to the host.

USING KNOWLEDGE OF ECOSYSTEM PRODUCTIVITY TO PREDICT THE WATER
BALANCE

AUTHORS

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ABSTRACT

Net Primary Productivity (NPP) of an ecosystem is heavily dependent on water throughflow and soil depth. Percolation concepts can be used to show that soil depth is proportional to a power of the infiltration (equal to the run-off, Q , when overland flow can be neglected) near 1. NPP has been shown using percolation to be proportional to a power near 2 of the transpiration, which for existing calculations of the water balance has been approximated as evapotranspiration, ET . Each of these relationships have been tested on meta-data sets involving thousands of individual measurements. Writing NPP as $ET^2(P-ET)$ allows an optimization, with respect to the water fluxes that yields $ET = (2/3) P$, equal to a rule of thumb. Using the exact predicted powers, the result is $ET = 0.623P$, very close to the measured global average of 0.63 or 0.64. Further, the single parameter theory, which is the root fractal dimension, generates the variability of observed results when actual root measurements are used.

BIOSOLIDS FROM SEWAGE TREATMENT PLANTS ARE NOT DETRIMENTAL TO
EARTHWORM POPULATIONS IN TEMPERATE CORN AGROECOSYSTEMS

AUTHORS

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ABSTRACT

Biosolids from sewage treatment plants are an organic amendment that can improve soil fertility and increase organic matter content, but it may contain organic and inorganic constituents that are toxic to soil fauna. It is important to confirm that biosolids applied to agricultural land does not reduce the abundance, biomass and diversity of earthworm populations, given the importance of these ecosystem engineers to soil functions. The objective of this study was to investigate the influence of biosolid application on earthworm populations in a temperate corn agroecosystem. Earthworms were collected from experimental field plots (randomized complete block design with four replicates) that were amended with three types of biosolids (lime stabilized, composted and mesophilic anaerobic digested, all applied at a rate of 120 kg N/ha) through two application methods (surface spreading or incorporated) for two consecutive years. We also collected earthworms from fertilized (urea at 120 kg N/ha) and unfertilized control plots. The earthworm collection method involved digging soil blocks of 25×25×25cm, hand-sorting to retrieve surface-dwelling earthworms and using 0.5% formaldehyde solution to expel deep-dwelling earthworms from the soil pit. Earthworms were preserved in 5 % formalin solution, then identified, counted and weighed. Earthworm abundance and biomass was influenced by the biosolid type but not by the application method. More earthworms with larger biomass were obtained from lime-stabilized > mesophilic anaerobic digested > composted biosolids > fertilized controls. Overall, larger earthworm populations in biosolid treatments than without, suggests that biosolids have no adverse effect on earthworms.

PHYLOGENETIC NICHE CONSERVATION THEORY MAY EXPLAIN THE FUNCTIONAL
REDUNDANCY OF SOIL MICROBIOTA

AUTHORS

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ABSTRACT

Functional redundancy in soil microbial communities seems to contradict the notion that individual species have distinct metabolic niches in multi-species communities. The objective of this study was to use phylogenetic niche conservatism theory as an explanation for the functional redundancy of soil microbiota. Phylogenetic niche conservatism is defined as the tendency for lineages to retain ancestral functional characteristics through evolutionary time-scales. The present-day soil microbiota is the result of a community assembly process that started when prokaryotes first appeared on Earth. For billions of years, microbiota have retained a highly conserved set of core genes that control the essential redox and biogeochemical reactions for life. These genes are passed from microbe to microbe at the planetary scale, primarily by horizontal gene transfer, contributes to functional redundancy. Within a specific soil, the heterogeneous matrix provides an infinite number of sets of diverse environmental conditions, i.e., niches that leads to divergence of microbial species. Phylogenetic niche conservatism theory predicts that two or more microbial species diverging from the same clade will have overlapping niches, implying that they are functionally redundant in some of their metabolic processes. Therefore, endogenous genetic factors that constrain the adaptation of individuals, and thus populations, to changing environmental conditions are responsible for the observed phylogenetic niche conservatism. Furthermore, the degree of functional redundancy is proportional to the complexity of the considered function. We present a conceptual model that identifies six patterns of functional redundancy in soil microbial communities, consistent with phylogenetic niche conservatism theory.

DECOMPOSITION OF RESIDUES AND RESIDUE MIXTURES DEPENDS ON MANAGEMENT INTENSITY AND SOIL HEALTH

AUTHORS

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ABSTRACT

Cropping system diversity can impact microbially-mediated processes and ecosystem functions in agroecosystems, yet we still know little about how microbial activity responds to crop diversity. Increasing aboveground diversity in row crop agriculture can be done by lengthening crop rotations or through addition of cover crops (CC). To investigate the relationship between microbial activity and crop residue type/diversity, we collected soils from three farms with varying levels of management intensity and soil health. We incubated soils for 70 d after adding four common CC residues (legumes and grasses) individually and in mixtures. This approach allows us to investigate additive/non-additive effects of residue mixtures during early stages of decomposition. We hypothesized that as CC diversity increased, so should microbial activity and N-mineralization. Furthermore, this response would be larger than that predicted by individual residues. We find significant differences in total CO₂ respiration between farms and CC treatments. Respiration rates were greatest with leguminous versus grass residues, which is expected because legumes have much lower C:N ratios. Overall, we see large differences in magnitude of decomposition dynamics between farms, but not always between residue types. Soils from a farm with soil health improvement management practices exhibited non-additive antagonistic effects for CO₂ respiration with increased CC diversity. Generally, farms with more recent shifts to soil health improvement showed non-additive synergistic effects on decomposition and N availability with increasing residue diversity. Our results indicate microbial communities in agroecosystems with degraded soils and depleted SOM stocks respond more rapidly and synergistically to increased CC diversity.

NATURAL TRANSFORMATION OF EXTRACELLULAR DNA IN SOIL

AUTHORS

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Sarah Evans - Michigan State University

ABSTRACT

Bacteria have the unique ability to evolve by transferring genes between and within species. This process, called horizontal gene transfer (HGT), is often cited as a driving force in bacterial diversification and can facilitate evolution. One mechanism of HGT, known as natural transformation involves the uptake and integration of extracellular DNA (exoDNA) into a recipient's genome. Transformation is unique from other mechanisms of HGT because it relies on exogenous or exoDNA. ExoDNA is abundant in soil, but also highly variable, suggesting availability of this genetic source could influence rates of transformation – and evolution – in soil. However, controls on rates of transformation have only been extensively studied in laboratory model systems. Here we combine a novel system for studying transformation in soil with in situ measurements of soil exoDNA, to better understand the contribution of transformation to bacterial evolution. We find that on average, across multiple soil types, 60% of DNA is exoDNA and that transformation increases with higher concentrations of exoDNA. We also find that transformation is influenced by environmental factors such as nutrient availability, salinity and soil moisture. Previous transformation studies have focused on HGT across distant bacterial lineages, but here we show that transformation of antibiotic resistant alleles from closely related species has the potential to promote functional genetic diversity in microbial communities. The role of HGT in bacterial evolution in soil has historically been difficult to define, but here we provide experimental evidence of genome diversification through transformation.

A CHRONOSEQUENCE OF SOIL HEALTH UNDER TALLGRASS PRAIRIE RECONSTRUCTION IN CENTRAL MISSOURI

AUTHORS

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ABSTRACT

Changes in soil health with reconstruction time were examined using a chronosequence of formerly cultivated fields reconstructed to native tallgrass prairie in Central Missouri (0-13 yrs as of 2017), with one row-cropped field representing "0-yr". Two long-term reconstructed prairie sites (~25 yrs and ~45 yrs post-reconstruction) and one remnant prairie served as reference sites. A suite of soil health indicators including pH, wet aggregate stability (WAS), particle size, soil organic C/N, active C (permanganate oxidizable C) and N (total protein), mineralizable C and N (soil respiration and potentially mineralizable nitrogen), and enzyme activities involved in C, N, P, and S cycling were assessed. Several of the indicators followed a "bell-shaped" response curve from 0 to 13 yrs, with a peak around 9-yr. The ratios of active C to SOC and active N to TN declined with increasing time post-reconstruction, reflecting the conversion of active C/N pools to more stable C/N pools resulting from continued organic inputs in the reconstructed prairie. During the soil health restoration, the soil physical, chemical, and biochemical properties changed synergistically. The ten biochemical indicators were highly positively correlated to each other ($r = 0.78-0.99$). All biochemical indicators were positively correlated with WAS but negatively related to pH, which declined with increasing post-reconstruction time. We postulate that the apparent soil health decline observed in sites with greater than 9-yr reconstruction may be the result of a combination of historical management and site conditions. Further study, however, is required to understand the factors affecting reconstructed prairie soil health.

DECOMPOSITION RATES AND FIBER ANALYSES OF NORWAY AND SUGAR MAPLE LEAVES EXPERIENCING CONSPECIFIC AND HETEROSPECIFIC SOIL ENVIRONMENTS.

AUTHORS

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ABSTRACT

In the Northeastern United States, non-native Norway Maple (*Acer platanoides*) trees have been out-competing native Sugar Maple (*Acer saccharum*). Here we are testing the Home Field Advantage (HFA) hypothesis which states that litter decomposition is accelerated underneath a conspecific canopy (home) that underneath a heterospecific canopy (away).

We collected recently fallen litter using 40 litterfall traps placed under Norway and sugar maple trees growing in the Crum Woods of Swarthmore College. We set a reciprocal transplant decomposition experiment using 144 litterbags each containing 4 g of litter which were placed under three mature trees of each species. We measured mass loss at 4 time periods (average 64, 185, 427 and 595 days, respectively). Lignin, cellulose, hemicellulose and cell soluble content were determined with ANKOM 200 Fiber Analyzer. Total C:N of green tissue and litterfall were determined by dry combustion using a LECO TruSpec CHN.

After controlling for the potential effects of heterospecific and conspecific soils, there was no evidence for HFA for Norway maple litter as predicted. On the contrary, the litter of sugar maple was the one showing evidence of HFA. However, it is not clear how to reconcile the higher nitrogen content found in Norway maple litter which facilitates its decomposition with the higher content of lignin and hemicellulose which makes it more recalcitrant. Overall, the slower decomposition rates shown by sugar maple litter both at home and under the canopies of Norway maple might help explain why they are being outcompeted in the Northeastern United States.

LINKING MICROBIAL FUNCTION AND SOIL HEALTH WITH TILLAGE AND PESTICIDE SEED TREATMENT

AUTHORS

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ABSTRACT

Soil microbial communities mediate many ecosystem functions, such as carbon cycling. Agricultural management practices can drastically alter soil physical, chemical, and biological properties. However, we are only just beginning to understand the effect of these practices on soil microbial communities and ecosystem functions. Soil tillage causes shifts in soil microbial communities. However, research is often limited to comparisons between full-till and no-till practices. Strip-tillage offers some of the benefits of tillage while potentially minimizing negative impacts. The effect of pesticides on soil microbial function is less understood. In particular, there is limited research investigating pesticide seed treatments and microbial communities. We sampled from a field experiment with a corn-soy-corn rotation with three tillage treatments (full-till, strip-till, and no-till) and two pesticide treatments (seeds treated with pesticides and seeds without) in a fully factorial design. A seventh treatment contained alfalfa hay as an additional control. To fully explore the relationship between management and soil microbial function, we determined differences in multiple soil chemical, physical and biological properties. Soil microbial community structure was assessed by sequencing the 16S and ITS amplicons. The ability of microbial communities to perform carbon cycling functions was assessed with a MicroResp assay. Microbial function (carbon, nitrogen and phosphorus cycling) was further analyzed with enzyme assays and by predicting functional genes in the community using PICRUSt. This work furthers our understanding on the effect of tillage and pesticides on soil microbial function.

EFFECTS OF PRESCRIBED BURNS ON LITTER DECOMPOSITION AND
MICROARTHROPOD COMMUNITIES IN NJ PINELANDS

AUTHORS

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ABSTRACT

Fire is an important disturbance to many ecosystems, including the NJ Pinelands which is a fire-adapted system. Prescribed burns are low-intensity and the leaf litter is only partially reduced by 10-40% during these burns. Fire has the potential to alter the decomposition process. For this study, we are particularly interested in the effects of fire on the litter-inhabiting microarthropod communities.

We are conducting a litterbag experiment following prescribed burns which occurred in April and June 2018, using composite sampled pine needles in 1mm mesh bags. The litterbags were collected at 3 months post-fire and remaining litterbags will be collected at 1 year, 1.5 year and 2 years. Litter remaining was calculated using a fresh to dry weight conversion, and microarthropods were extracted using a modified Tullgren Funnel. Soil respiration (IRGA), soil temperature, soil moisture and LOI were also monitored in the plots. To determine the immediate effects of the burn on the microarthropod communities, we collected pine needle samples within each plot immediately before and after each fire.

Soil respiration initially decreased following the June burn, but was not affected following the April burn. Preliminary analysis of microarthropod communities before and after the April burn indicate no change to overall biodiversity. However, mite biodiversity decreased ($p < 0.1$) immediately after the burn which is largely attributed to decreases in oribatid mite diversity. The project is ongoing, but will provide insight to if litter decomposition and associated microarthropod communities are affected by low-intensity prescribed burns.

MODELING EFFECTS OF CARBON QUALITY AND CARBON-NITROGEN STOICHIOMETRY
ON ECO-ENZYMATIC STOICHIOMETRY DURING PLANT LITTER DECOMPOSITION

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ABSTRACT

We developed an enzyme-based model of plant litter decomposition to evaluate the effects of litter N and lignin concentrations on patterns of decay. This model consisted of three substrate pools: 1) organic nitrogen-containing compounds (C_1), 2) cellulose (C_2), and 3) lignin (C_3), with each substrate pool degraded by a specific enzyme pool (E_i). Reverse Michaelis-Menten (RMM) equations were solved for values of E_2 and E_3 . Thus the balance of dC_2/dt and dC_3/dt provided estimates of total lignocellulose decay ($dC_{2,3}/dt = dC_2/dt + C_3/dt$), the size of the total lignocellulose-degrading enzyme pool ($E_{2,3} = E_2 + E_3$), and the net carbon use efficiency for lignocellulose ($CUE_{2,3} = dC_2/dt \cdot CUE_2 + C_3/dt \cdot CUE_3$). Finally, the allocation of enzymes (E_1) needed to degrade the N-containing pool (C_1) to meet the N-demand accompanying C released from the C-only pools ($C_{2,3}$) was determined by setting the C:N ratio of the microbial biomass equivalent to the ratio of the assimilable C released from $dC_1/dt + dC_{2,3}/dt$ to the N released from C_1 . Again, RMM formulae were used to estimate E_1 . Thus, this model estimates the allocation of E_1 , E_2 and E_3 to: 1) balance microbial C-N stoichiometric requirements, given both the chemical stoichiometry and recalcitrance of the decaying litter, and 2) maximize microbial growth with the attendant mineralization of excess N released from C_1 . Results indicated that the latter model was more consistent with observations. Moreover, relative allocations of C- and N- acquiring enzymes bracketed observations, given uncertainty in the onset of lignin decay.

USING SEPARATION TECHNIQUES TO EXPLORE THE LOCATION OF EXOENZYME
ACTIVITY WITHIN THE MATRIX OF ARCTIC SOILS

AUTHORS

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ABSTRACT

Microbial processes such as extracellular enzyme (exoenzyme) production are a major driver of decomposition, and a current topic of interest in Arctic soils due to the effects of climate warming. While enzyme activity levels are often assessed, the specific location of these exoenzymes within the soil matrix is not clear. Identifying the locations of different soil exoenzymes is needed to improve our understanding of microbial functioning. Using soil cores obtained from Barrow, Alaska, we addressed two questions: 1) are enzymes free-floating in the soil pore water? 2) are enzyme activities associated with particles such as cells, clays, tannins, or the organic matter substrates themselves? For free-floating enzymes, we assayed enzyme activities in soil pore lysimeter samples. We also examined soil cores with blending, filtration and sonication techniques in various combinations and assessed hydrolytic and oxidative enzyme activities. The soil pore water assays showed little to no enzyme activity ($< 0.05 \text{ nmol g soil}^{-1} \text{ hr}^{-1}$) indicating that free-floating enzymes are not abundant in these samples. In the soil cores, our results showed activity was present for most of the hydrolytic enzymes and there were several clear differences among treatments. In the sonication + blending treatment, five of six hydrolytic enzymes showed higher activity compared to blending only (standard treatment) or sonication only, suggesting that enzymes are bound to solid portions of the soil. Furthermore, higher activities in unfiltered and filtered through $50 \mu\text{m}$ relative to $2 \mu\text{m}$ suggested that the enzymes were preferentially bound to larger particles in the soil.

LITTER QUALITY AND SOIL FAUNA AS DRIVERS OF SOIL RESTORATION IN
AGROFORESTRY SYSTEMS OF SAPUCAIA-RJ, BRAZIL

AUTHORS

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ABSTRACT

Litter inputs and associated biological activity are essential for restoring nutrient cycling and a range of key soil functions in degraded ecosystems. The objective of this research was to evaluate litter dwelling soil arthropod communities and their relationship with the litter layer and soil restoration in agroforestry systems in Sapucaia-RJ, Brazil. Soil macroinvertebrates and litter samples were collected under five management systems: three types of agroforestry systems, degraded pasture and a nearby forest system. Sampling occurred in April and September of 2018 using pitfall traps and a quadrat (25 x 25 cm) for determination of litter biomass. Litter samples were evaluated for total C and N as well as other macronutrients and micronutrients. Soil macroinvertebrate community diversity and abundance were assessed and their relationships with litter chemical characteristics explored via correlation analysis. Overall abundance of invertebrate communities was highest in the pasture, and this was associated with large numbers of Formicidae and overall low values of diversity. Diptera and Entomobryomorpha were the most common taxa in the forest and agroforestry systems. Preliminary results suggest that macroinvertebrate diversity was positively correlated with macro- and micronutrients in the litter layer. However, soil fauna abundance was negatively correlated with litter nutrient concentrations for the April sampling, while no relation was observed in September 2018. The quality of litter in agroforestry systems appears to influence soil invertebrate communities, with important implications for restoration processes in these agricultural systems.

STIMULATING SOIL RESPIRATION BELOW FREEZING

AUTHORS

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ABSTRACT

Arctic soils contain large carbon stores predicted to decompose faster as temperatures rise, and there is the potential for increased microbial respiration to exacerbate warming. Soil respiration has mostly been measured in warmer months, but recent studies suggest that winter fluxes are also significant. Soil temperature, carbon and nutrient availability are predicted to control Arctic overwinter respiration. However, determining the nature and extent of substrate limitation in frozen soils is not possible following the traditional approach of observing responses to additions of aqueous solution (e.g. of glucose) below freezing. My objective was to develop a method to add carbon and/or nutrients to a frozen Arctic tundra soil to determine the extent of carbon and nutrient limitation to winter respiration.

I attempted to stimulate respiration in an Arctic tundra soil with glucose and/or nitrogen and phosphorus added as dry powder or suspended in glycerol and incubated between -3 and -7 deg. C for 25 days. Glycerol additions consistently increased soil respiration over the entire incubation, regardless of glucose and/or nutrient additions. This is likely because the soils were effectively thawed by the glycerol, possibly leading to greater substrate and nutrient availability. In contrast, powder additions left soils frozen and stimulated respiration, but to a smaller degree than glycerol, and quickly decreased, likely due to diffusional constraints in frozen soils. These results suggest that dry powder additions are an effective but constrained alternative to aqueous solutions to determine substrate limitations to respiration in frozen soils.

DO DECOMPOSING AMF AND EMF NECROMASS CONTRIBUTE DIFFERENTLY TO THE
FORMATION OF MINERAL ASSOCIATED SOIL ORGANIC MATTER?

AUTHORS

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ABSTRACT

Active soil microbial biomass is small relative to total soil organic matter (SOM) stocks. However, it has become clear that microbial necromass (residue of biomass) is a significant contributor to SOM, in particular to mineral associated organic matter (MAOM). Plants allocate large quantities of carbon (C) belowground through mycorrhizal associations, yet little is known about MAOM formation from arbuscular (AMF) versus ectomycorrhizal fungal (EMF) necromass. Through an experimental incubation of dual labeled (^{13}C and ^{15}N) AMF and EMF necromass, we evaluate the efficiency of MAOM formation from both AMF and EMF necromass. The fungal necromass was grown in an isotopic labeling chamber and collected in fungal in-growth bags. Chemical analysis of the necromass indicates that the EMF has double the nitrogen concentration of the AMF and Fourier-transformed mid-infrared spectroscopy indicates that the EMF has a higher amide and chitin content than the AMF. Using these indicators of litter quality we hypothesize that the EMF will actually form MAOM more efficiently than the AMF. The isotopic label in the necromass allows us to trace the mycorrhizal-derived C in CO_2 and SOM. Physical fractionation of SOM after aggregate dispersion will allow us to quantify MAOM (<53 μm) from hyphal necromass. These data will provide a comparison of MAOM formation efficiency from AMF and EMF and help elucidate metrics of mycorrhizal litter quality that relate to stabilization of SOM.

ON THE EDGE OF OPPORTUNITY: EVALUATING MICROBIAL FUNCTIONAL DYNAMICS
AT THE EDGES OF PRAIRIE MONOLITHS AND RESTORATION TARGETS

AUTHORS

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ABSTRACT

Benefits of microbial additions to restore ecosystem functions not only relies on microbial establishment and spread, but that they can function similarly in novel environments. The ability of microbes from undisturbed systems to reinstate beneficial functions in degraded systems remains understudied. To explore these potential benefits, we transplanted tallgrass prairie monoliths into recipient sites that varied in land use history and time since disturbance. We examined if the presence of prairie microbial communities altered recipient site functions. We assessed changes in microbial extracellular enzyme activity (EEA) and microbial biomass carbon (MBC), in relationship to soil carbon and nutrients. Because nutrient environments and carbon resources of recipient sites differ the most from prairies just after disturbance, we hypothesized that the strength of response at the monolith-recipient site edge should be greatest in sites most recently disturbed. We identified four clear patterns of microbial EEA across these edges: analogues edges, resistant edges, directionally resistant edges, or synergistic edges (edge function is not predicted by monolith or recipient site function). Specific patterns differed with regards to both the recipient site and the target enzyme. For example, patterns of BGase activity differed across land use history, whereas NAGase showed similar patterns regardless of recipient site. These results show that ecosystem recovery may benefit from the introduction of microbes from undisturbed sites, but that response depends on specific function and the disturbance history of the recipient site. This study highlights the functional role of soil microbes in ecological restoration.

SOIL MICROBIAL RESPONSES TO ALTERED PRECIPITATION REGIMES ACROSS A
SOUTHWESTERN UNITED STATES ELEVATION GRADIENT

AUTHORS

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ABSTRACT

Microbes play an important role in soil carbon (C) cycling. Future microbial activity patterns may be affected by climate, given predictions for warmer temperatures and altered precipitation regimes in the next century. Little is known about the short- versus long-term soil microbial community responses to altered precipitation in dryland systems. Soil organic carbon (SOC) is a critical component of the global C cycle, accounting for several times more C than plant or atmospheric pools. Assessing microbial biomass and C respiration rates under current and potential future precipitation patterns will help understand how SOC pools might change with climate change. We investigated how soil microbial communities are influenced by changes to both long- and short-term precipitation patterns across a 1000 m elevation gradient in northern Arizona, where precipitation increases with elevation. We manipulated precipitation (50% addition and 50% exclusion of ambient rainfall) at five sites across the gradient. We extracted microbial biomass carbon (MBC) from soil and used a portable gas exchange system to measure soil CO₂ flux at each site. MBC and respiration rates were greatest at the three highest elevation sites and lowest at the two lowest elevation sites. Within sites, precipitation treatments did not change MBC, but respiration rates differed among the precipitation treatments at the lowest elevation site with higher respiration rates in the precipitation addition plots. Our results suggest that soil C cycling in drier systems may be more sensitive to short-term precipitation change than wetter systems.

EFFECT OF SEASON AND SITE CONDITIONS ON SOIL MICROBIAL COMMUNITY
ACTIVITIES IN HIGH-ELEVATION MIXED CONIFER FOREST

AUTHORS

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ABSTRACT

Soil microbial communities are sensitive to changes in temperature, precipitation, and snow cover along with disturbances such as wildfire. Understanding the responses of resident microbiota to these variations in environmental conditions is crucial due to their essential role in the carbon (C) storage and nutrient cycling functions of watersheds in the southwestern United States. Bacteria and fungi transform compounds in the soil and are responsible for the biogeochemical cycling of C and nutrients such as nitrogen (N) and phosphorus (P). In this study, we quantified trends in soil microbial community dynamics over both spatial and temporal scales in the Jemez River Basin Critical Zone Observatory (CZO). The high elevation, sub-alpine field site experiences a bimodal precipitation regime; much of its precipitation occurs during the summer monsoon rains and winter snow. We sampled twelve sites at two depths with respect to landscape position, depth, and aspect over the course of a year at four time intervals during snowmelt, pre-, during-, and post-monsoon. Our results demonstrate that season, depth, and dissolved C and N (DOC and DON) concentrations influence potential extracellular enzyme activities (EEA) in the soil. Activities were highest in the post-monsoon season, corresponding to low DOC and DON. EEA decreased with soil depth and microbial biomass and EEA were both positively correlated with DOC and DON. These results suggest pulse-driven patterns in resource availability and have important implications for these high elevation ecosystems that are experiencing greater variability in summer monsoons, winter snowpack, and fire disturbance.

WHO BENEFITS FROM BIOCHAR? ECOLOGICAL AND BIOGEOCHEMICAL INTERACTIONS
IN A PERENNIAL CROPPING SYSTEM

AUTHORS

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ABSTRACT

Biochar is a relatively stable form of charcoal used as a soil amendment that has been proposed as a means of simultaneously sequestering carbon and improving soil health. Biochar can improve soil properties and increase desirable microbial activities in ways that can benefit plant growth. However, there are well documented instances of biochar having no effects or even negative effects on plant performance, suggesting context-dependencies with soil type and plant species identity. Therefore, it is essential to test a wide range of crop-soil-biochar combinations before recommending field application to growers. Here, we report on the first three seasons of a ten-year field experiment to evaluate the impacts of two biochar types on soil physical, chemical, and microbial properties in a Christmas tree cropping system on Marlette fine sand. We found general increases in soil moisture, pH, enzyme activities associated with C, N, and P acquisition, and microbial biomass N and C with concurrent decreases in bulk density and bioavailable N. Effects on DOC:DON ratio varied between biochar types. Tree seedlings exhibited negative growth responses to biochar while weeds exhibited positive responses, suggesting that biochar may promote undesirable competitive effects. Our results demonstrate that the impact of biochar amendment on soil health and crop performance may be mediated by interactions with soil microbial communities. These findings reiterate past results with regards to soil properties, but point towards idiosyncrasies in plant responses, indicating that decisions to apply biochar should take into account soil health goals as they relate to specific cropping systems.

THE PROBLEM OF DEFORESTATION LEADING TO SOIL EROSION

AUTHORS

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ABSTRACT

One problem of the region is the rapid depletion of its forest cover. Mass deforestation for economic reasons is carried out in a reckless way. Shifting cultivators, due to population pressures, move into newly opened areas and begin to practice swidden (slash and burn) agriculture. Then the forest areas of generally fragile, sloping soils, are subject to intensive agriculture practices, which rapidly degrade the land.

Soil Erosion

The greatest problem man will encounter when forest trees are extensively cut without replanting, combined with improper farming of fragile, sloping lands is soil erosion. The erosion of topsoil—the thin upper crust on the earth's surface in which man plants his food crops—is an extremely serious problem in Asia.

Importance of Topsoil

Soil is the result of gradual weathering of plants, rock, and minerals. Its formation is a very slow process that in some estimates takes place at the rate of 2.5 cm per century. Topsoil is rich and fertile because of its organic matter content. Plants and animals die, decay, and are incorporated into the soil, making it fertile and capable of supporting the growth of food crop.

AUTHORS

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ABSTRACT

Little is known about the impacts of root stage distributions on plant-soil feedbacks, soil resource cycling, or projections of plant growth. A plant's proportion of biomass in later stage roots and resource uptake efficiency are typically inverse with growth enhanced by maintaining high-uptake capable early stage roots. There are trade-offs in senescence scheduling for root stages, but circumstance can skew distributions towards later stages. Direct examination of the impacts of different stage distributions is experimentally intractable.

We apply a stage-based matrix population model using varying resource acquisition, survivorship, transportation capacity, and maintenance costs for root stages to analyze stage distribution across a plant's life. A simulated perennial plant expands into a 2-dimensional soil environment. Growth and ageing feedbacks integrate resource acquisition by roots and carbon production from photosynthesis. The objective is to explore the effects of stage distribution on plant growth, resource cycling, and root turnover, and determine the conditions for which stage distribution dynamics tends towards stability, cycles or non-periodic fluctuations.

A parameter space search indicates greatest plant growth – sum of root and leaf biomass – is associated with distributions heavily skewed towards early stages. This arises from allocation strategies favoring new root growth over root maintenance leading to a near complete turnover of roots. A regression tree analysis indicates root and leaf photosynthetic conversion rates and allocation strategy were the strongest predictors of plant growth. A spatial analysis of root stage distribution will indicate how changing spatial arrangement of root stages impacts growth and resource cycling.

DEPLETED FUNCTIONAL POTENTIAL IN C, N, P, AND S CYCLING GENES OF SOIL
MICROBIAL COMMUNITIES WITH TROPICAL FOREST SUCCESSION

AUTHORS

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ABSTRACT

Land cover change can alter soil microbial community composition and activity, which can influence the functional potential of microorganisms to drive biogeochemical processes in soils. We investigated whether observed shifts in soil microbial community composition were accompanied by changes in their functional potential. We measured abundance of genes involved in soil biogeochemical processes along a tropical forest successional gradient using the GeoChip 3.0 functional gene microarray. We found differences in signal intensities of genes involved in carbon (C), nitrogen (N), phosphorus (P), and sulfur (S) cycling between pastures, early successional (40 years old), and late successional (90 years old) forests. Specifically, signal intensities of genes involved in C degradation (glucanases and chitinases, among others), N cycling (*amoA*, *gdh*, *nifH*, *nrfA*), P utilization (*ppx*), and sulfite reduction (*dsrA*) were consistently lower in late successional forests compared to early successional forests. Nonmetric multidimensional scaling of total signal intensities for each gene revealed that late successional forests were functionally distinct from early successional forests and pastures. The majority of gene probes were present across all land cover types, and yet the number of unique gene probes for C, N, P, and S cycling genes were consistently lower in late successional forest soils compared to early successional forest and pasture soils. We observed a decrease in the fungal-to-bacteria ratio in late successional forest soils, but did not observe any difference in extracellular enzyme activity between land covers. Taken together, our results suggest that these tropical soil microbial communities may lose function with forest succession.

MYCORRHIZAL FEEDBACKS IN THE RHIZOSPHERE AND THEIR ROLE IN THE
MAINTENANCE OF BIODIVERSITY.

AUTHORS

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ABSTRACT

The mechanisms contributing to the maintenance of species diversity remains a key area of interest in ecology. Previous research has shown links between rhizosphere processes and species diversity, with positive soil feedbacks leading to a loss of species diversity and negative feedback effects driving a more diverse community. North American prairie systems are an ecosystem strongly shaped by arbuscular mycorrhizal (AM) fungal mutualisms. Many studies have shown that the abundance of and the composition within AM fungal communities have significant impacts on prairie plant community composition. Late successional prairie species do not establish well under conventional restoration practices, and previous studies have shown that responsiveness to AM fungi correlates more with successional stage than with phylogenetic relatedness. A greenhouse experiment was conducted measuring the changes of soil AM fungal composition associated with specific host plants through the use of next-gen sequencing for both unfertilized and phosphorus fertilized pots. This experiment was designed to evaluate the effect of host plant identity on AM fungal composition as well as those effects across phylogenetic relationships and life history characteristics. The differential AM fungal communities were then used as inocula in a test of plant species fitness impacts from their own soil community and those of their competitors. We are able to test the phylogenetic and life history characteristics impacts on these fitness relationships. Preliminary results show strong differences across families in the strength and direction of feedback effects when plants are grown with conspecific associated soil communities.

EFFECTS OF AGRILUS PLANIPENNIS AND LONICERA MAACKII ON FUNGAL DRIVEN
DECOMPOSITION IN MIDWESTERN FORESTS

AUTHORS

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ABSTRACT

Midwestern forests are currently invaded by emerald ash borer (EAB, *Agrilus planipennis*) and Amur honeysuckle (*Lonicera maackii*). EAB induced loss of ash (*Fraxinus* spp.) trees coupled with the gain of honeysuckle is changing understory plant composition, likely altering forest nutrient cycling. Few studies have investigated their interactive effect on microbial processes like fungal driven decomposition due to variation in leaf litter. To assess these changes, we ran two independent 100-day decomposition culture experiments (monoculture and dilution cultures). Fungi from three fungal guilds (white rot (WR), brown rot (BR) and ectomycorrhizal (ECM)) were cultured on litter from eight species of trees/shrubs commonly found within Midwestern forests. Each monoculture contained litter from a single species with a single fungal species while dilution cultures consisted of 50:50 mixtures of native and *L. maackii* litter. We measured litter decay rate, fungal hyphal growth, and fungal biomass. In monoculture, *L. maackii* had the fastest decomposition rate ($P < 0.0001$). In dilution cultures, *L. maackii* increased native species decomposition rates compared to their respective monocultures ($P < 0.0001$). Litter with ECM and WR had similar, faster decay than BR ($P < 0.0001$). BR had the fastest hyphal growth rate followed by WR and ECM ($P < 0.0001$). WR had the largest fungal biomass followed by BR and ECM ($P < 0.0001$). Dilution cultures had higher fungal biomass than their respective monocultures. These results suggest that *L. maackii* causes an increased litter decay rate that is possibly driven by an increase in fungal growth across fungal guilds.

BIOENERGY CROP RESIDUES ALTER DECOMPOSITION DYNAMICS OF SOIL ORGANIC MATTER

AUTHORS

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ABSTRACT

We sought to understand patterns of soil carbon dynamics in bioenergy cropping systems using a laboratory soil incubation. We characterized differences in respiration for soils amended with bioenergy crop residues. We used soils from fields dominated by the C3 grass smooth brome (*Bromus inermis*) and residues from C4 bioenergy crops, corn (*Zea mays*) and switchgrass (*Panicum virgatum*). We added 0.45 g of either corn or switchgrass roots, shoots, or roots and shoots to 30 g of soil. We assessed respiration rates for 39 days, and found that across both species, residue addition of any kind stimulated total respiration compared to control soils with no residue additions. Total C respired was highest in soils amended with shoots; 32% greater than soil plus roots and 17% greater than soil plus roots and shoots. Across all treatments, residue additions increased peptidase activity and decreased chitinase activity. Isotope analyses indicated that across all treatments, residues were the primary source of C respired, and addition of residues suppressed respiration from soil organic C, relative to soil only controls. Addition of labile C in the form of ¹³C-labeled glucose and pyruvic acid from days 36-39 did not alter patterns of respiration among residue types, indicating no strong priming effect. This incubation has revealed that patterns of soil C accrual are affected by crop residue inputs but not by additions of common root exudates. A better understanding of patterns of soil C dynamics is necessary to achieve the potential of making bioenergy crops a C-neutral energy source.

PLANT-SOIL FEEDBACKS IN METAL CONTAMINATED SOILS

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ABSTRACT

Microorganisms living on roots are critical to the health and growth of plants. When the environment is degraded such as in urban brownfields, the tipping point between beneficial microbes and pathogenic microbes will determine plant growth and the long-term re-greening of degraded environments. We examine the effect of plant-soil feedbacks in two heavy metal contaminated soils from the brownfield portion of Liberty State Park (LSP) in Jersey City, NJ, USA and in a non-contaminated reference soil. We established a microbial enrichment phase of the experiment in which we planted rye grass into 7 replicates of each soil (21 pots) and, we also held 7 control replicates of each soil (21 pots) that were not planted. In preparation for the measurement phase, we used the same soil that was previously planted in the enrichment phase, but in this phase, we planted all (42) pots (experimental planted and non-planted controls) to see how the enriched microbes affected plant growth. At harvest, all plants were dry weighed and soil assessed for phosphatase activity, a measure of soil microbial activity. Our results showed that contaminated soils showed less of a decline in plant growth compared with the control soils when grown in previously enriched soil. When the soil was not contaminated, plant growth was limited by enrichment. We find that the outcome of plant-soil feedbacks may vary depending on the abiotic constraints of the soil.

SHOTGUN METAGENOMIC ANALYSIS OF MICROBIAL SOIL ORGANIC MATTER
DECOMPOSITION AND NUTRIENT CYCLING IN AN ARCTIC SNOW FENCE EXPERIMENT

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ABSTRACT

Arctic soils contain approximately 50% of the Earth's soil organic carbon. There is growing concern that rising global temperatures may lead to increased microbial metabolism and carbon mineralization rates, feeding back into warming temperatures through the release of CO₂ and CH₄. Additionally, soil organic matter (SOM) decomposition and nutrient mineralization facilitate shifts in plant community composition, altering soil chemistry via litter inputs and rhizodeposits. Here we collected soil samples from a long-term snow fence experiment located in a moist acidic tundra ecosystem in Northern Alaska, designed to mimic anticipated increases in precipitation and temperature in the Arctic. Using metagenomic shotgun sequencing, we analyzed soil microbial community responses to increased snow depth and associated environmental shifts. We focused on the community's genetic capacity to produce enzymes required for SOM decomposition and nutrient cycling, which will influence the fate of carbon stored in this ecosystem. We found that soil microbial communities under deeper snowpack have higher bacteria:fungi relative abundance ratios, decreased relative abundance of genes encoding enzymes for the breakdown of hemicellulose, chitin, and starch, and increased relative abundance of genes required for nitrogen fixation, ammonification, and nitrate reduction, but only past a snow-depth threshold 50-100% greater than the control. These results suggest predicted increased snowfall and soil temperatures in the Arctic may 1) increase soil nutrient availability, potentially facilitating plant community shifts, and 2) decrease fungal abundance leading to reduced SOM decomposition potential and the re-accrual of soil carbon in this ecosystem over time.

EFFECT OF SALINITY ON SOIL NEMATODE HABITAT AND COMMUNITY STRUCTURE

AUTHORS

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ABSTRACT

Soil salinity is a naturally-occurring problem in the Northern Great Plains that affects crop productivity and presumably influences belowground organisms. We expect that soils with moderate concentrations of salts alter the structure and function of soil food webs and related soil properties. Our main objective is to determine if soils with moderate salt concentrations (2.0-4.0 dS/m) have different microbial and nematode communities compared to soils with lower salt accumulations (< 1.0 dS/m). To answer our research question, we are assessing microbial community structure (phospholipid fatty acid analysis) and nematode abundance and feeding group composition (sucrose flotation) in soils across naturally-occurring salinity gradients in row-crop fields. Additionally, we are measuring a set of soil properties that aim to quantify potential food sources and habitat characteristics that may influence nematode communities. Microbial and nematode abundance and composition are expected to be statistically different in soils affected by salinity than those in non-saline soils. Preliminary data indicate that microbial abundance, active carbon, soil moisture content, and nitrogen and phosphorus nutrient pools are higher in saline soils than in non-saline soils. We expect that these differences will correspond to differences in nematode abundance and feeding group distribution across salinity gradients. Researching potential changes in nematode communities will be valuable in better understanding their role in soil health. Gaining knowledge on the interaction of soil nematodes within an environment under salinity stress will allow us to better use these organisms as soil health indicators and understand barriers to plant production in these problem soils.

SOIL MICROBIAL DYNAMICS OF MIDWEST PRAIRIE STRIPS

AUTHORS

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ABSTRACT

Increasingly, agricultural producers are turning to conservation-oriented practices to mitigate deterioration of soil quality and ensure enduring productivity. One such practice is the adoption of prairie strips - zones of prairie grasses and wildflowers planted intermittently within monoculture row crop fields. Prairie strips have been shown to improve soil quality by reducing nutrient loss and removing harmful insecticides. Soil microbes are integral to these processes; however, it is unclear how soil microbial communities shift in response to prairie strip establishment. Research indicates that microbiota in prairie strip soil may have the ability to disperse and provide measurable benefits to row crop plants. In particular, a recent study demonstrated that fungal microbiota in prairie soil can confer higher productivity and constitutive herbivory resistance to neighboring plants over distances of multiple meters. Prairie strips may provide similar benefits to row crop plants by facilitating the dispersal of beneficial microbes outward from prairie soil. **Here I propose a project to investigate the soil microbial dynamics of prairie strips established at three agricultural sites in the Midwest.** I will collect soil samples from each site and analyze them for bacterial and fungal community composition along with key soil health metrics. By analyzing soil microbial communities within and adjacent to newly established prairie strips, I hope to elucidate how microbes disperse and function in diversified row crop systems.

N AND P LIMITATION ON FINE ROOT PRODUCTION IN DIFFERENT TREE SPECIES IN
NORTHERN HARDWOOD FORESTS

AUTHORS

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ABSTRACT

Colimitation of forest productivity by nitrogen (N) and phosphorus (P) could arise from the different nutrient limitation status among tree species. Belowground fine root production is sensitive to soil nutrient availability, and can respond to limitation status of individual tree species. Studying allocation to fine root production by individual species can be quite challenging in mixed forests, owing to the difficulty in separating fine roots by species in root mixtures. We refined a simple method to quantitatively describe root community composition by amplifying the *trnL* intron region of plant plastid DNA. We then examined the fine root allocation of individual tree species in response to elevated N and P in a long-term factorial N×P fertilization experiment in northern hardwood forests in central New Hampshire, USA. After 6-year's fertilization, soil cores were collected and separated into Oe, Oa, and mineral horizons. Roots were isolated from the cores by hand and species composition was analyzed. We found that N limited the fine root production of red maple and sugar maple, and that N and P co-limited the fine root production of American beech. Most fine root responses occurred in mid-aged and mature rather than in young stands.

ROBBING THE PHOSPHORUS VAULT: CAN TROPICAL RAINFOREST TREES ACCESS AND
USE "UNAVAILABLE" P?

AUTHORS

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ABSTRACT

Tropical rainforests often grow on phosphorus (P) poor soils where most soil P is thought to reside in pools that are largely unavailable to biota. This low P status can be exacerbated by deforestation and land conversion. For example, disturbances that commonly occur in tropical forests often remove substantial quantities of biomass or drive losses of soil organic P. These losses of P, combined with reduced soil P availability due to strong geochemical sorption, could have profound impacts forest regeneration following disturbance. However, Richter and others (2006) observed a substantial increase in biomass P over the course forest regeneration in a pine plantation seemingly supplied by the soil residual P pool, often presumed to be unavailable to biota. Here, we tested the hypothesis that the residual P pool supports forest growth in regenerating tropical forest ecosystems by measuring shifts in soil P pools in a secondary successional chronosequence. We found a significant decline of soil residual P over the course of the first 25 years of forest regeneration, suggesting that this pool can function as a P source to biota on decadal timescales. This decline in residual P coincided with a period of increasing bioavailable soil P and the ~20-year period of forest biomass aggradation in this system. These data support our hypothesis, suggesting that soil residual P may be more available to biota than previously assumed and may play a critical role in defining how tropical forests respond not just to deforestation, but to global environmental change more broadly.

SEASONAL NUTRIENT CYCLING TRENDS IN A CHIHUAHUAN DESERT ECOSYSTEM

AUTHORS

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ABSTRACT

In arid soils, patches under shrub canopies often function as “islands of fertility” concentrating nutrients and keeping a constant soil temperature and moisture in comparison to unvegetated ground. To better understand finer temporal changes in this resource-island framework, we set out to address the following questions: (1) Does the resource island pattern of nutrient concentrations, microbial biomass, and enzyme activity hold in a bajada landscape within the Chihuahuan desert? And (2) How these soil spatial patterns vary in response to rainfall? To address these questions, we collected soil from beneath creosote bush, honey mesquite, and unvegetated soil to measure soil nutrient concentration (N and P), microbial biomass, and exoenzyme potential activity at six time points during June and July of 2015 across several natural rainfall pulses. Overall trends in nutrients and microbial biomass C and N were consistent with islands of fertility throughout our sampling period with higher concentrations below mesquite followed by creosote followed by bare soil. The one notable exception was %C in the bulk soil which was similar among all three cover types. Rainfall did not alter these relative patterns among cover types, but magnitudes of these variables increased after the first intense rainfall event. Hydrolytic enzymes were consistent with islands of fertility in contrast to oxidative enzymes which were more homogeneous throughout patch types with no particular response to rainfall. In conclusion, most soil characteristics we measured followed islands of fertility throughout the summer. While nutrients responded to rainfall events, microbial biomass and enzyme activities were relatively constant.

EFFECTS OF N-DEPOSITION ON MILLIPEDES: AN INVESTIGATION OF MILLIPEDE-MICROBIAL INTERACTIONS

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ABSTRACT

Nitrogen deposition in natural systems is an ongoing problem resulting from fossil fuel combustion and industrial pollution. This is a widespread problem, extending far beyond cities where much of the nitrogen species are generated. How increased N inputs affect soil fauna is understudied. We investigated this using a mesocosm experimental approach to understand how increased soil nitrate affects millipede survival, and how millipedes impact nitrogen cycling processes. Mesocosms were set up in a full factorial design of millipedes (with and without one individual of Xystodesmidae: *Cherokia georgiana georgiana*) and three levels of soil nitrate (ambient, +10 kg/ha, and +20 kg/ha). Mesocosms consisted of small plastic containers with sieved soil and leaf litter. Nitrate levels were measured at the start of the experiment and after 5, 10, 20, and 30 days, after which the experiment was terminated. Nitrification potential was measured at the start and end of the experiment. In addition, soil, litter, and fecal samples collected at two time points (10 and 30 days) were used to elucidate the effects of and interactions between millipede presence and N-addition on microbial communities (bacteria and fungi via Illumina MiSeq). In general, faunal effects on microbial communities are just beginning to be explored. Millipede microbiomes have been little explored, with most research restricted to the gut fauna. Our analyses compared microbial communities across treatments as well as among soil, litter, and fecal material. This work allows an in-depth understanding of how millipedes impact N-cycling and microbial community interactions.

BASIC BIOLOGY OF XYSTODESMID MILLIPEDES: SOIL MOISTURE

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ABSTRACT

Crossley's shaving lotion, a corollary of Occam's razor, states that temperature and moisture are the most likely explanatory variables in soil systems. With this in mind, we began an investigation of the soil moisture requirements of the millipede family Xystodesmidae, a diverse and conspicuous component of the Southeastern US soil fauna. Millipedes are particularly prone to desiccation: they have few lipids in their cuticle and respire through spiracles, which they cannot close as insects' spiracles do. We collected *Cherokia georgiana georgiana* from a mixed pine-hardwood forest in Middle Georgia and measured soil moisture at each specific collection location. Millipede survival was then assessed in the lab at 7.1%, 8.5%, and 10.7% soil moisture, based on these field measurements. Experimental units were large plastic containers that each held 40 g of leaf matter and 3,000 g of sieved soil. Soil moisture was maintained by weighing containers daily and adding water as needed. Containers were incubated at 20°C until mortality of all individuals. Five *Cherokia* were used in each treatment. We repeated the experiment using the larger *Cleptoria rileyi*. For both species, 8.5% soil moisture led to the longest survival rates.

COMPOSTED BIOSOLIDS STIMULATE NITROGEN-DEGRADING ENZYME ACTIVITIES IN
AGRICULTURAL SOIL

AUTHORS

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ABSTRACT

Biosolids generated by municipal wastewater facilities are nutrient-rich residues that may be used as fertilizer after sanitation and stabilization. Biosolids incorporated into soil may stimulate carbon and nitrogen mineralization potential but the magnitude could depend on the type of biosolid treatments varying in nutrient availability. Our objective of this study was to evaluate the response of soil extracellular enzymes, indicators of microbial activity and carbon and nitrogen mineralization potential, to differences in biosolid treatments. At the McGill Lods Agronomy Research Centre in Quebec, Canada, corn plots were amended for two years with three types of biosolids, (composted, lime stabilized, and mesophilic anaerobic digested) as well as fertilized (urea) and unfertilized controls. We measured the activity of carbon- and nitrogen-acquiring enzymes from soil samples (0-5 cm) collected from each treatment after corn harvest. Fertilizer had no significant effects on total carbon acquiring enzymes, but composted biosolids increased total nitrogen acquisition enzymes and had 59% higher leucine aminopeptidase activity, as well as 170% higher phenol oxidase activity relative to the unfertilized control. Peroxidase activity increased significantly in the lime stabilized biosolids plots compared to the unfertilized control. Nitrogen-acquiring enzyme activity was positively correlated ($P < 0.05$) with soil ammonium concentration, suggesting a higher nitrogen mineralization potential. These findings indicate composted biosolid strongly stimulated nitrogen acquisition enzymes which may contribute to higher plant available nitrogen. Composted biosolids had the strongest effect on enzymes compared to all other treatment, and we suspect this is because of large input of both organic C and N.

LEAF LITTER LABILITY IS IN THE EYES OF THE DECOMPOSER

AUTHORS

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ABSTRACT

Decomposition models generally focus on interactions between litter quality and microbial decomposition rates, predicting positive correlations between the two. However, microbes are not the only decomposers. Soil macroinvertebrates play an essential role in decomposition by initially fragmenting and digesting plant litter. Without macroinvertebrates, microbes prefer purportedly-labile (lower lignin content) plant litter, such as *Cornus florida*, over supposedly-recalcitrant (higher lignin content) litter, such as *Quercus rubra*. *With* macroinvertebrates litter mass loss rates are expected to increase, especially with labile litter, whose consumption is expected to increase more than recalcitrant litter, but the effects of litter quality on macroinvertebrate litter decomposition have yet to be quantified.

C.florida and *Q.rubra* litter were fed to *Narceus americanus* millipedes and individual body mass, respiration, litter consumption and frass production rates were recorded daily. Frass was then analyzed for carbon and nutrient content, including total extractable nitrogen (N) and phenolics, to determine millipede growth efficiency as a function of litter quality.

Surprisingly, both litter consumption (*Q.rubra*: 214 mg/day; *C.florida*:201 mg/day) and frass production rates (*Q.rubra*: 49.4 mg/day; *C.florida*: 22.9 mg/day) were higher when consuming recalcitrant litter. Lower extractable N concentrations in frass suggest possible N limitation when consuming *C.florida*. Additionally, mortality rates in millipedes consuming *Q.rubra* were half of those with supposedly more labile *C.florida*, perhaps due to relatively high concentrations of extractable phenolics in *C.florida* litter(487% higher). Overall, these results indicate that litter decomposed faster by microbes is not necessarily favored by macroinvertebrates, and the factors controlling litter quality may differ between microbes and macroinvertebrates.

EVIDENCE THAT FIRE FREQUENCY AFFECTS PEDOGENESIS OVER DECADAL TIME
SCALES

AUTHORS

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ABSTRACT

Fire has recently been proposed as a seventh soil forming factor to complement Jenny's seminal equation of soil forming factors. Though fire influences the other soil forming factors and often mediates their interactions, it has not yet been experimentally demonstrated that fire influences pedogenesis. Further, it is not clear on what time scale fire might influence pedogenic processes. We had the unique opportunity to investigate this further using a long-term fire frequency study located on the Osceola National Forest in northern Florida, USA (Spodosols). There, four fire frequency treatments (burned every: 1 year, 2 years, and 4 years; and unburned) have been maintained for the last sixty years (0.8 ha plots, n=6). We measured the depths of the respective A/E and E/B horizon boundaries in each treatment to determine the effect of fire frequency on horizon depth. We found that the boundary of the A/E horizon and the E/B horizon is shallower in the unburned stands relative to any of the fire treatments. These results suggest that fire alters soil horizonation, which is a byproduct of pedogenic forces, and that this alteration becomes clearly noticeable in only sixty years.

RELATIVE CONTRIBUTIONS OF TERMITES AND FUNGI TO WOOD DECAY AT THREE
SITES IN THE SOUTHEASTERN USA

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ABSTRACT

Dead wood represents a major store of terrestrial carbon and contributes resources to a diverse assemblage of microbial and invertebrate decomposers, upon which many subsequent trophic groups are dependent. The relative contribution to wood decay from fungi and termites is unknown despite the importance of such questions for the development of global decomposition models. Further, it is not clear how the relative importance of these two groups varies with climate and elevation. To investigate these questions, we measured mass loss from a common substrate (blocks of Monterey pine wood) in three physiographic regions of the southeastern USA (Coastal Plain, Piedmont, and Southern Appalachian Mountains) that represent a broad gradient in elevation and climate. At each location, we set out blocks of wood enveloped in mesh, which allowed access to the wood by fungi alone, or allowed access by both termites and fungi. Here, we discuss results from two years of decomposition. This information will be useful for providing estimates for wood decay at three different climates and elevations in the southeastern USA and will be contributed to a larger global study of wood decay.

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ABSTRACT

Sustainable agriculture practices are known to improve the structure and functional capabilities of soil microbial communities over time. This study describes the consistency of long-term no-till practices in an irrigated cotton system and contrasts it with a conventional-tilled cotton system in a semi-arid environment in West Texas. Stability analysis was used to investigate the treatment by environment interactions for microbial biomass carbon (MBC) and NO₃-N levels measured across the growing season from 2016 to 2018 under both types of production systems. Slopes of the regressions of MBC against environmental mean were < 1 in the no-till system for 2016 and in conventional system for 2018, indicating that the system is homeostatic towards environmental conditions. In contrast, 2017 no-till and conventional systems, and 2018 no-till, the > 1 slope infers that MBC levels increase as environmental conditions improve. Regressions for NO₃-N indicated homeostatic systems in 2017 no-till and conventional systems, and in 2018 no-till system (slope < 1). However, slopes were > 1 on the 2016 no-till and the 2018 conventional system indicating more variability through the season for each observed year. Although variation in stability was observed in both systems, no-till fields appear to have lower magnitude of variability and have the capability to respond more positively to environmental factors than the conventional production system. Despite both systems being irrigated, yearly differences in environmental conditions in this semi-arid environment does impact soil microbial dynamics in these cotton production systems.

LOCALLY EFFECTIVE MICROBES AND SOIL AMENDMENTS INFLUENCE THE
RHIZOSPHERE COMMUNITY AND PROMOTE PHYTOSTABILIZATION OF MINES

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ABSTRACT

The 76-acre Formosa Mine in Southern Oregon has been designated as a USEPA Superfund site. Formosa was added to the USEPA's National Priorities List because acid mine drainage has severely degraded 18 miles of river and negatively impacted the local steelhead fishery. Although phytostabilization is one pathway to remediate the Formosa site, hostile edaphic conditions are a major impediment to plant establishment. At many mine sites, the microbial-mineral interactions spawn a biogeochemical cycle that perpetuates and increases soil acidity. If the fundamental goal is to establish a permanent ground cover, it will ultimately be important to shift the microbial community structure from one dominated by autotrophs to a community that has a diverse heterotrophic demographic. One strategy to accelerate phytostabilization is to engender a major shift in the microbial community by adding locally effective microbes (LEM) to soil amendments prior to site remediation. The purpose of these studies was to assess feasibility of culturing LEM from forest soils adjacent to the Formosa mine, and inoculating a biochar/biosolid/lime amendment with LEM. The inoculated media was added to mine soil and planted with a native grass. The results of this greenhouse study determined that the addition of LEM did shift the microbial community over four months and demonstrated that biochar/biosolid mixtures provide may propel mine remediation efforts.

RHIZOSPHERE VERSUS BULK SOIL MICROBIAL PROCESSES UNDER CONTRASTING CROP ROTATIONS

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ABSTRACT

Sustainable agricultural management needs to regenerate soil organic matter (SOM) while ensuring profitability. Increasing the quantity and quality of C inputs may increase SOM accrual by increasing efficient microbial transformation of plant inputs, and their subsequent mineral stabilization. The point-of-entry of plant inputs (through roots or above-ground litter) may also determine their fate because of the different microbial abundance and community they encounter.

We tested whether increasing plant input quantity and quality to the soil could increase soil C and N in rhizosphere and bulk soil while also comparing their microbial communities. We sampled soils from a wheat-fallow rotation (low-C input), and continuous wheat-corn-millet rotations (high-C input) with and without an additional legume crop (high-quality input) in Akron, CO. We found no crop rotation effects on soil C and N, possibly due to high soil texture variability across plots. Soil C and N, however, were consistently higher in the rhizosphere than bulk soil. The rhizosphere soil also had the highest microbial activity and biomass, which was positively related to the amount of root biomass, suggesting crop productivity stimulates microbial activity in rhizosphere, but not in bulk soil. Our results confirm that the rhizosphere, due to its richer and highly active microbial community, is instrumental to C and N cycling, and suggest distinguishing rhizosphere biogeochemistry from bulk in soil C models could improve predictions of the fate of soil C. Additionally, management that increases the fraction of rhizosphere soil may enhance C and N cycling.

USING CROP RESIDUE AND NO-TILL TO MANAGE SOIL MICROBIAL DYNAMICS IN A
DRYLAND COTTON SYSTEM IN WEST TEXAS

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ABSTRACT

Conventional agriculture under increasing climate variability on the Southern High Plains can have negative impacts on soil processes leading to a decline in overall soil health. Thus, consideration of conservation practices that can increase soil health for dryland agriculture will be critical. We assessed the effects of crop residue in combination with no-till on soil microbial activities in a dryland cotton production system in West Texas (2014-2017). Three treatments were established 1) using erosion blankets (shade), 2) Sorghum residue or wheat residue (stubble) and 3) control (no stubble) with 6 replicates plots (8 x 7 m) in each treatment and control. In 2016-2017 shade treatment was not included. Soil samples were collected before planting and over the growth season to evaluate environmental, nutrients, and microbial parameters. Results showed over the four years that stubble reduced daily soil temperature range (DTR_{soil}) by approximately 6 °C on average at 0 cm and approximately 2.5 °C at 15 cm during the hottest months. The reduction in daily soil temperature range increased microbial activities. Overall, microbial biomass carbon increased by 31 % in the stubble with respect to the controls. Enzyme activities increased by 42 % in stubble on average with respect to the control and the proportion of fungi was higher in all years in comparison with bacteria under stubble. The implementation of conservation management practices can mitigate climate variability with the reduction in (DTR_{soil}) and positively affect the dynamics of microbial communities and their contribution to soil productivity.

IMPACT OF FIRE AND HERBIVORY ON SOIL MICROBIAL POPULATIONS IN MESIC AND SEMI-ARID SAVANNA ECOSYSTEMS OF SOUTH AFRICA.

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ABSTRACT

Fire and herbivory are amongst the most important ecosystem drivers shaping South African savannas. They are globally important consumers of above-ground biomass and affect belowground systems both directly and indirectly. Soil microbial communities mediate approximately 85%–90% of soil organic matter (OM) decomposition and may thus limit nutrient cycling and ecosystem productivity. In this study, we use two long term herbivore exclosures and burning trials (Nkuhlu and Letaba) along rivers in Kruger National Park, South Africa, to assess the impact of fire and herbivory on soil microbial communities. Soil microbial biomass C (SMBC) was similar between sites, *ca.* 9.8 $\mu\text{g SMBC g}^{-1}$ dry soil ($p = 0.407$) despite Letaba being drier and warmer than Nkuhlu. The riverine vegetation zone had 33 and 48 % higher SMBC compared to the upslope open-canopy vegetation at Letaba and Nkuhlu, respectively. There was an interaction ($p=0.027$) between fire and herbivory in determining SMBC in the riparian zone at Letaba. In contrast, there was no interaction in the riparian zone at Nkuhlu, although fire positively ($p = 0.003$) influenced SMBC. Linear regression models on soil parameters indicated that fire and herbivory impacted SMBC through their influence on edaphic conditions. The soil microbial populations were controlled mainly by the SOM content and composition in Nkuhlu, and by the pH, soil texture and available Ca and Na in Letaba. Biodiversity results will also be discussed as part of a multivariate approach.

INVESTIGATING THE EFFECTS OF SOIL MICROBES ON SEEDLING SUCCESS AND
ENDOPHYTE COLONIZATION

AUTHORS

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ABSTRACT

Interactions between plants and soil microbes are critical to ecosystem functioning and the maintenance of plant productivity in both unmanaged and agricultural ecosystems. However, despite the ubiquity of plant-microbe interactions and the well-established effects of some soil microbes on plant health, the specific nature of potential plant-microbe interactions remains unknown for the vast majority of soil bacteria and fungi. While some plant growth promoting interactions are mediated by soil-dwelling microbes, many bacteria and fungi can reside in plant tissues and function as endophytes. Here I investigate potential “probiotic” soil microbes in wheat (*Triticum aestivum*).

With a collection of over 200 natural and agricultural soils, I have established a laboratory-based platform to study the effects and dynamics of natural soil microbial communities in the early life of wheat using a culture-independent approach (via marker gene sequencing) combined with an *in-vitro* seedling germination assay. This project is designed to answer the following questions: Q1: To what extent do native soil microbial communities influence wheat seed germination success? Q2: Across a large range of soil types with distinct soil microbial communities, what are the specific microbial taxa, or combinations of taxa, that promote germination success? Q3: Across this same range of soils, are there specific microbial lineages that are consistently recruited into the host plant tissue and become endophytes? By combining a diversity of source soils with a controlled experimental design, this work provides important insight into the effects of soil-dwelling microbes on the health and microbiome of an agriculturally important crop.

DYNAMICS OF MINERAL N AND SOIL ORGANIC C IN MINERAL AND ORGANICALLY
FERTILIZED SYSTEMS

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ABSTRACT

Nitrogen fertilizer increases crop yields, but improper management is associated with environmental liabilities. A potential liability relates to the disputed response—loss versus gain—of soil organic C to N fertilizer application. The argument for SOC loss implicates increased mineral N availability to increased turnover rates. The argument for SOC gain implicates increased mineral N availability to increased crop residue inputs. This study compared the impact of two fertilizer sources of N—mineral (MNF; NO_3NH_4) and organic (ONF; animal manure)—on mineral N dynamics (availability, net mineralization, and mineralization rate), residue inputs and SOC change. In the MNF, both crop yield and residue inputs were greater than in the ONF. However, in the ONF, animal manure contributed to greater net organic C and N inputs. Also, in the ONF, net N mineralization was generally greater and mineralization rates increased each year, compared to the MNF. Neither treatment affected total soil N, although in the ONF mineral soil N was generally greater under corn and soybean crops than in the MNF. In the MNF, SOC was lost despite greater crop residue inputs and lower available and mineralized N. In the ONF, SOC was maintained probably because of the greater net residue and manure C and N inputs. This study did not support either argument in that SOC loss nor gain was not linked to mineral N availability and its impact on turnover rates or crop residue production. However, this study did establish that SOC maintenance was linked to animal manure inputs.

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ABSTRACT

Application of decomposable organic residues like manure and crop litter is generally beneficial to earthworms. There is interest to apply biochar, a carbonaceous product of pyrolysis, to temperate agricultural soils. The slow decomposition rate, ash content and the presence of combustion byproducts in biochar could be detrimental to earthworms. The objective of this study was to describe the earthworm populations in biochar-amended soils on a dairy farm in the St. Francis River watershed, Quebec. Earthworms were collected from replicated field plots under cereal production. Site "A" received three biochar types at two application rates (5 and 10 t biochar ha⁻¹) plus an unamended control (0 t biochar ha⁻¹), while Site "B" received biochar (7.5 t biochar ha⁻¹), dairy slurry manure (10 t slurry ha⁻¹) or a combination of biochar and dairy slurry manure, plus an unamended control. Earthworms were collected by handsorting and formaldehyde expulsion from soil pits on 5 October 2010 and 2 October 2011. Three species, *Aporrectodea turgida*, *Aporrectodea tuberculata* and *Lumbricus rubellus*, were found. *Aporrectodea* spp. was the dominant genus. Biochar sources, rates and application with dairy slurry did not affect the earthworm population, which had 52 to 218 individuals m⁻² in 2010 and 4 to 96 individuals m⁻² in 2011. The seasonal difference in earthworm populations was attributed to a late summer drought in 2011. The similarity in earthworm abundance and biomass in biochar-amended soils as other agricultural soils in this region leads to the conclusion that earthworm populations are stable in temperate biochar-amended soils.

RESTORATION OF SOIL MICROBIAL COMMUNITIES IN PRAIRIE CONSERVATION CORRIDORS

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ABSTRACT

Tallgrass prairie ecosystems are one of the most endangered ecosystems in North America. Due to this loss there is substantial interest in restoring tallgrass prairies in the Midwest and Great Plains regions to recover aboveground ecosystem services. However, most prairie restorations focus on improving plant community and animal diversity, with little focus on how restoration impacts soil microbial communities. Soil microorganisms provide important ecosystem services such as controls over nutrient cycling and carbon sequestration, as well as improving establishment of late successional plants. Traditional aboveground-focused restoration practices do not restore soil microbial communities to one that resembles a remnant prairie soil community, but instead restores to a new community that still reflects the legacy of agriculture. To incorporate microbially-focused restoration strategies into standard restoration practices, methods must be affordable, easy to implement and effective. The objective of this study was to determine if inoculation with a recalcitrant substrate or a microbial community enhanced the restoration process. We tested several possible treatments to improve microbial restoration using a field-level inoculation experiment. We added biochar and remnant prairie soil amendments alone, as well as a combination of the two amendments to plots within a new prairie conservation corridor in southwest Michigan. We sampled soil in the experimental plots in August 2018 and examined changes in bacterial 16S rRNA amplicon-based community composition using an Illumina Mi-Seq approach. We also determined soil respiration and extracellular enzyme activities for key enzymes involved in carbon degradation.

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ABSTRACT

Global fire regimes are changing, with shifts in wildfire duration, frequency, and severity predicted for North American forests over the next 100 years. Fires can result in dramatic changes to C stocks, through the combustion of biomass and organic soil horizons, as well as through the production of pyrogenic organic matter. In addition, fires can restructure plant and microbial communities within the ecosystem, which can have long-lasting effects on ecosystem functions. We investigated the effects of fire on soil microbial communities (bacteria and fungi), plants, and soils in an unprecedentedly extreme fire season in the boreal forest of Canada's Northwest Territories, using field surveys, remote sensing, and high-throughput sequencing. We asked (1) What factors structure the soil microbial communities post-fire? and (2) Which specific taxa respond positively to fires? We found that pH, vegetation, and fire are strong predictors of soil microbial community composition. In addition, abundant key taxa were identified as fire responders, including the fungus *Penicillium sp.*, and the bacteria *Massilia sp.*, and *Arthrobacter sp.* These results suggest that accounting for burn severity could improve our understanding of soil microbial response to fires, with potentially important implications for ecosystem functions.

CROP DIVERSIFICATION AND SOIL ORGANIC MATTER DYNAMICS: EVIDENCE FROM
ON-FARM TRIALS IN CENTRAL MALAWI

AUTHORS

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ABSTRACT

Crop diversification through intercropping and rotation has been observed to increase soil organic matter (SOM) more rapidly and to a greater degree than continuous monocrops. Crop plants add root exudates and residues to soil, and a diversity of these inputs across space and time affects SOM dynamics. Within cropping systems, the time frame for building SOM and for changes in factors that regulate SOM, such as soil aggregation, is not well understood. A study of five on-farm, legume diversification trials in central Malawi examined the effects of different cropping systems on SOM after six years of trial establishment. The five study treatments were (1) continuous maize plus fertilizer, (2) maize/groundnut rotation, (3) pigeonpea/maize rotation, (4) doubled-up legume rotation - groundnut-pigeonpea intercrop rotated with maize, and (5) maize-pigeonpea intercrop. An in-situ soil carbon dioxide (CO₂) respiration “burst” test was conducted using a portable respiration meter to measure CO₂ efflux before and two hours after adding water to a PVC ring set into the soil. Soil respiration rates did not differ significantly across treatments. Soil cores taken at each site were dry-sieved into aggregate size classes: mega-aggregates (>2 mm), macroaggregates (0.25-2 mm), microaggregates (0.053-0.25 mm) and a silt/clay fraction (<0.053mm). The proportion of macroaggregates differed by treatments 1, 3, and 4 at two of the trial sites. Bulk density, gravimetric moisture, and water infiltration rates, other factors relating to SOM dynamics, did not vary across treatments. Results indicate that a long time frame is necessary to detect crop diversification effects on SOM.

LONICERA MAACKII INCREASES RATES OF NUTRIENT TURNOVER DURING COARSE
WOODY DEBRIS DECAY

AUTHORS

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ABSTRACT

Increasing carbon emissions alter the stability of ecosystem processes, such as decomposition. During decay, microorganisms release enzymes, catalyzing nutrient turnover reactions. One factor altering decomposition in forests is invasive species. Amur honeysuckle (*Lonicera maackii*) has overtaken many Midwestern US forests, therefore monitoring decay dynamics under honeysuckle invasion is essential for understanding nutrient cycling in this region. We placed *Quercus rubra* and *Pinus radiata* blocks in a honeysuckle invaded forest for one year and calculated decay rate to determine environmental and enzymatic drivers of decomposition. We measured honeysuckle size and abundance within a meter radius of the decaying blocks as well as soil moisture and canopy coverage to determine if they altered decay rate. We also measured activities of β -glucosidase, phosphatase and leucine aminopeptidase as a proxy for nutrient turnover. Larger honeysuckle shrubs increased phosphatase and β -glucosidase activities for both substrates and increased leucine aminopeptidase and phosphatase activities in pine wood, suggesting that honeysuckle directly increases the rates of nutrient turnover. Larger honeysuckle shrubs increased wood moisture, and β -glucosidase and leucine aminopeptidase increased with wood moisture. This suggests that honeysuckle indirectly increased rates of nutrient cycling. Phosphatase activity increased with moisture on pine but decreased with moisture on oak, perhaps due to alleviated moisture limitation on recalcitrant pine wood. These results indicate that honeysuckle may prime native woody debris for faster decomposition and nutrient turnover, despite not directly changing decay rates. This could become especially important in late-stage decay where there could be perceptible differences in decay rates caused by honeysuckle.

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ABSTRACT

We investigated soil fauna communities in vacant lots of Baltimore City under different plant species composition. To determine the connection between above- and belowground biodiversity, we sampled nematodes, ground beetles, isopods, millipedes and earthworms. Additionally, we collected data on site history and analyzed the soil physical and chemical properties on 25 vacant lots. In general, parcel-to-parcel variability of both biotic and abiotic data was high. Fungal and bacterial feeding nematode abundance showed some treatment effect, but overall, plant manipulations did not explain community structure of the soil fauna. Earthworm density varied between 26-240 individuals m⁻², but biomass was low, 2-40 g m⁻². High frequency of *Lumbricus castaneus* and *Allolobophora chlorotica* indicate an early successional community in most vacant lots. Soil organic matter (range from 3.4 to 8.5%), pH (5.6-7.2), nutrient and metal contents varied among parcels, however proximity of parcels influenced soil properties. Parcels closer together were more similar than far apart in abiotic properties, such as Na, K, Ca, Si, and Zn concentrations, indicating similar age or management. After one year of plant community establishment, these abiotic factors as well as location and age of vacant lots might be more important to soil fauna recovery, than vegetation structure. Future monitoring will reveal if linkages between above- and belowground communities change over time.

INFLUENCES OF BIOENERGY CROPPING SYSTEM IDENTITY AND MANAGEMENT ON MICROARTHROPOD COMMUNITIES

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ABSTRACT

Bioenergy production shows promise as a cost-effective climate change mitigation strategy, but uncertainties remain regarding the impact of land conversion to bioenergy cropping systems on soil carbon stocks. There is growing evidence that soil microarthropods strongly influence soil carbon dynamics by increasing litter degradation rates and regulating soil microbial communities, with potential feedbacks on net primary productivity and SOM accrual. Microarthropods are generally disfavored by agricultural intensification, but it is not clear how microarthropod community structure varies across different bioenergy cropping systems. Understanding how bioenergy crop identity and management regime impact microarthropod communities and their interactions with other biota can help inform the implementation of bioenergy systems that maximize SOM accrual. To address this, microarthropod surveys were conducted in energy sorghum, switchgrass, and restored prairie cropping systems between July and August 2018. We predicted that microarthropod abundance and diversity would be greatest in undisturbed restored prairie polycultures and lowest in conventionally-managed energy sorghum, with intermediate levels in switchgrass monocultures. Preliminary results indicate that total microarthropod abundance and that of major microarthropod groups (collembolans, oribatid mites, non-oribatid mites) were generally similar in switchgrass and restored prairie and significantly reduced in energy sorghum. Next steps include identifying microarthropods to lower taxonomic resolutions to assess changes in community composition across cropping systems. This work will inform future research manipulating microarthropod community composition to evaluate impacts on soil microbes and bioenergy crops with implications on SOM accrual.

LARGELY INCREASED NITROUS OXIDE EMISSION FROM GLOBAL LIVESTOCK SECTOR
DURING 1860-2014: A GEOSPATIAL-TEMPORAL ANALYSIS

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ABSTRACT

The atmospheric concentration of nitrous oxide (N₂O), one of major greenhouse gases, has increased over 121% compared with the preindustrial level, and most of the increase arises from anthropogenic activities. The shift of human diet and the ever-increasing human population pose a huge pressure on the demand of growing livestock population. Of particular interest is how changes in livestock population could alter the environmental health through emissions of greenhouse gases, especially nitrous oxide. Moreover, the quantification of livestock induced nitrous oxide emission with global coverage that characterize consecutive inter-annual variations during historical period is lacking. Thus, in this study, we tried to quantify the magnitude, temporal and spatial variations of livestock-induced nitrous oxide emission during 1860-2014. We include both direct and indirect emission of nitrous oxide from managed soils. We also further analyze the relative contribution of major livestock types on nitrous oxide emission. The results indicated that there was a significant increasing trend of livestock-induced nitrous oxide during 1860-2014. Changes in nitrous oxide emission exhibited highly spatial variability and concentrated in several hotspots during the study period. Less meat consumption is not only good for human health, but also favors for environment-friendly development.