

Thursday, August 8, 2013: 8:20 AM

101G, Minneapolis Convention Center

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Background/Question/Methods

Enzymes activities are a useful metric of bog microbial community function because they are the direct agents of decomposition for specific substrates in peat. Enzymatic depolymerization like other biochemical reactions is sensitive to temperature, however not all extracellular enzymes have the same response to temperature and may vary due to environmental factors and with microbial community composition. The Spruce and Peatland Under Climate and Environmental Change (SPRUCE) project will be a temperature and CO₂ manipulation experiment at Marcell Experimental Forest, MN. During enclosure construction we are assessing baseline enzyme activities and kinetics to understand how they vary across space and time to predict how enzymes might respond to the SPRUCE warming manipulation. We investigated the effect of temperature fluctuations, due to depth and season, on the temperature response of enzymes involved in carbon, nitrogen, and phosphorus cycling from peat.

Peat was collected from Marcell Experimental Forest, MN in February, July and August 2012. Three cores were extracted from 0-200cm below the bog surface and split into 10 or 25cm increments. Enzymes activities were assayed at multiple temperatures, from 2 to 65°C. The Arrhenius equation and Q₁₀ were used to estimate the temperature response for each enzyme at each depth and season.

Results/Conclusions

All three enzyme metrics, activity, temperature sensitivity, and stoichiometry decreased with depth, but no response was noted by season. With increasing depth there was decreasing microbial biomass, stable year around temperatures, and smaller peat carbon:nitrogen ratios; all three of these variables may have affected our enzyme metrics. Microorganisms produce enzymes, so a reduction in biomass with depth would likely result in reduced potential enzyme activity. Temperatures are stable below 100cm, less than a 5°C change throughout the year, possibly resulting in communities and enzymes specialized to specific temperature ranges, thus lowering temperature sensitivity. Total nitrogen increases with depth whereas total carbon remains the same, resulting in a lowered peat C:N. This occurs with a concomitant decline in the enzyme C:N mineralization ratio (β-glucosidase : (N-acetyl glucosaminidase+leucine amino peptidase)). Enzyme type was another significant variable, with proteases having lower temperature responses compared to other hydrolytic enzymes. For proteases, E_a<20, whereas the other hydrolytic enzymes involved in C and P depolymerization were more responsive to temperature, with E_a = 20-60. The lack of a temperature response in protease activity indicates a possibility for decoupling of N cycling from C and P cycling in the bog with warming.

Thursday, August 8, 2013

Exhibit Hall B, Minneapolis Convention Center

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Background/Question/Methods

Populus has become of great interest to bioenergy researchers for the production of cellulose-derived biofuels. The genetically diverse and clonal nature of *Populus* allows it to grow within a wide range of temperate habitat types. The ease that *Populus* clones can be propagated, tractable genome and fast growth rates have made it a leading candidate for bioenergy and fibre production and a model system for forest genetics. Our goal is to understand the microbiome associated with *Populus*, the host genotypic and environmental characteristics that effect the composition of the microbiome, and the role of the microbiome in plant health and productivity. The aim of the current study is to further parse the degree to which plant species vs other local environmental factors influences microbiome assembly in the habitats in which they co-occur

Native *P. deltoides* samples were collected within the lower Caney Fork River basin in Tennessee. At each site *P. deltoides* three adjacent heterospecific tree species were sampled. Replicate samples of bulk soil and root samples for rhizosphere, and endophytes were collected from each tree. High throughput sequencing data was generated for both bacterial and fungal communities via 454 pyro-sequencing. Denoising and quality filtering was performed via Ampliconnoise and ChimeraSlayer respectively. Taxonomic assignment, OTU picking, and all other downstream analyses were performed using QIIME.

Results/Conclusions

A total of 64 bacterial communities (399,674 reads) and 39 fungal communities (120,461 reads) remained after quality filtering and removal of singeltons. Initial phylogenetic and OTU-based analyses show minimal community differences between *P. deltoides* and adjacent heterospecifics for both bacterial and fungal communities. However, some specific differences in endophytic communities between species as apparent. For example *P. deltoides* have a significantly higher proportion of *Pseudomonas* (Bonferroni p-val < 0.001) compared to heterospecific endophytic communities. Bulk soil and rhizosphere samples contained higher relative abundances of Acidobacteria and Proteobacteria, while endophyte communities contained higher relative abundances of Actinobacteria. Although analysis of fungal community data is ongoing, we have observed increased representation of fungi from the Chytridiomycota and Mortierellomycotina (Bonferroni p-val < 0.001) in soil and rhizosphere communities compared to endophytic communities. With the exception of increased relative abundance of *Pseudomonas* within the root system, *P. deltoids* does not appear to affect the overall composition of fungal and bacterial communities differently than adjacent heterospecific trees. These results suggest that local soil properties and processes may predominately affect microbial community assembly.

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Soil chemical and microbiological properties mapping at an abandoned small-arms firing range in Oak Ridge, TN

Friday, August 9, 2013

Exhibit Hall B, Minneapolis Convention Center

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Background/Question/Methods

Lead (Pb) contaminated soils represent severe environmental problems as well as a significant hazard to human health. Prolonged exposure to high levels of toxic metals exerts considerable selective pressure on the soil microbial community and alters soil and ecosystem health. The objective of this study is to understand how the total level of Pb contamination has affected the soil chemistry and fungal community at an abandoned small-arms firing range in east Tennessee. 92 soil samples were collected in a spatially explicit sampling design across two ecosystem types, grassland and forested, surrounding the backstop at the abandoned firing range. Soils were analyzed via qPCR for total fungi and bacteria and fungal:bacterial ratios were calculated. Soil pH, total Pb, extractable Pb, total C and N, nitrate N, organic matter, phosphate, sulfate, and water content were all determined across the site and site maps, or interpolations, were created using ArcGIS 10.1.

Results/Conclusions

Soil Total Pb concentrations values range from below detection to well over 9,000 ppm or mg Pb kg⁻¹ dry soil. Highest values are observed to the northwest of the firing backstop and geographically coincide with an elevated earthen berm behind the backstop. However, high Total and extractable Pb was also detected at sampling locations of lower elevation along the first row both to the north and south of the backstop. Fungal:Bacterial ratios ranged from below 1.0 to over 6.3, and displayed a patchy distribution. However several soils with high fungal abundance occur transecting the forested area in a line straight south. Carbon:Nitrogen ratios were roughly 10.0 across most of the site, but ranged up to over 45.0 within the forested area.

Pb appears to be moving from behind the backstop to lower elevations and towards the local water source which could pose a hazard to downstream biota. Based on previous work at this site which revealed fungal species including *Phanerochaete flavido-alba* present and capable of Pb-mineral dissolution, the transect of high fungal numbers which directly corresponds with the direction of Pb movement, could be a contributing factor to Pb movement across the site. The highest levels of Pb also correspond to areas of carbon accumulation, potentially indicating decreased overall soil microbial activities due to Pb toxicity. Further examination of the soil fungal community for specific genera and functions implicated by previous work in Pb-mineral dissolution and movement is currently being explored.