

Conversion of Natural Grassland into Biofuel Crops (Switchgrass, *Panicum virgatum* L.) is Associated with Reduction in Methane Consumption

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Project Goals: Switchgrass (SG; *Panicum virgatum* L.) is a perennial C₄ grass native to the tallgrass prairies and a promising feedstock in the U.S. for bioenergy production. Capable of abundant biomass yield with minimal fertilizer or water, SG can survive on marginal soils, and even thrive once established. We hypothesize that successful establishment and sustainable cultivation of SG in marginal soils is in part enabled by beneficial plant-microbial interactions. We are investigating the succession of rhizosphere microbial communities, and ecosystem-scale effects of high- and low-performing SG plants grown in nutrient-limited soils in southern Oklahoma. The outcome of this research will provide a better genomic basis for SG cultivation in marginal soils, expand our knowledge of the interactions between soil microbiomes, plants and ecosystems, and ultimately guide efforts for translation into agronomic row crops.

SG has been shown to input carbon (C) into the soil, and thus has the potential to increase C sequestration and to improve soil productivity over long-term cultivation. However, to fully evaluate the sustainability of SG-based biofuel production, it is crucial to understand the impacts of SG establishment on biotic and abiotic characteristics of nutrient-poor soils. Here, we aim to characterize the ecosystem-scale consequences of SG cultivation in comparison with native annual grassland fallows at two sites in Oklahoma. We hypothesize that SG sustainability relates to improvements of soil quality mediated by its influence on the soil microbial communities and the activation of beneficial plant-microbe interactions. This will ultimately result in measurable effects on key ecosystem functions such as C sequestration and greenhouse gas (GHG) production. To understand the impact of SG establishment on soil characteristics and microbiology, we setup multi-year monthly field measurements of greenhouse gases fluxes (CO₂ and CH₄), soil chemical properties, and characterization of soil microbial communities' structure and function.

We selected two study sites in southern Oklahoma that are marginally suitable for row-crop cultivation. These two sites, a silt-loam soil close to the Red River (RR) and a clay loam soil (3rd Street Farm, 3S), share a low N and P nutrient availability but differ in other physio-chemical variables (pH, soil texture, soil organic matter (SOM) content). At both sites, two plots (27 x 22m) were established: a native annual grassland fallow (FL) and a SG plot contacting 500 genetically distinct seedlings (Alamo variety) in a honeycomb design. During the first two growing seasons following SG planting, these four plots were monitored monthly. We measured topsoil chemistry (plant-available P and N, and SOM content), GHG fluxes (CO₂ and CH₄), and microbial

community composition (16S rRNA genes). GHG concentrations were measured with a high sensitivity (parts-per-billion), high resolution (every 2s) cavity ring down spectrometer (Picarro G2508 analyzer). Five-minute resolution meteorological data such as soil temperature, air temperature, soil moisture, and precipitation were provided by the Oklahoma Mesonet network (<http://climate.ok.gov/index.php/climate>). We found that SG significantly increased plant-available P levels, SOM content, and soil C/N at the RR site when compared to the FL. No significant changes in soil chemistry were observed between SG and FL plots at the 3S site. Similar seasonal microbial successional patterns were observed for all plots, but community structures differed between sites and plot types. SG cultivation did not influence significantly annual CO₂ fluxes compared to the FL plots. However, SG significantly reduced the annual CH₄ consumption, potentially impacting ecosystem carbon balance. A machine learning approach was used to identify important factors for predicting soil trace gas dynamics and we found that soil temperature, soil moisture, and month of the year were the most influential variables. Further investigations are underway to elucidate linkages between the microbial communities (by time-series) and GHG emissions. These data are also being used to parameterize an ecosystem model.

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