

## Spatiotemporal dynamics of a microbiome on *Panicum hallii* under drought stress

Esther Singer<sup>1,2,\*</sup> (esinger@lbl.gov), Joseph Edwards<sup>3</sup>, Joel Reyes-Cabrera<sup>4</sup>, Tanja Woyke<sup>1</sup>,  
**Thomas E. Juenger**<sup>3</sup>

<sup>1</sup>Joint Genome Institute, Berkeley, CA; <sup>2</sup>Lawrence Berkeley National Laboratory, Berkeley, CA;  
<sup>3</sup>University of Texas, Austin, TX; and <sup>4</sup>Eastern New Mexico University, Portales, NM

[https://sites.cns.utexas.edu/juenger\\_lab/switchgrass](https://sites.cns.utexas.edu/juenger_lab/switchgrass)

### Project Goals: Short statement of goals.

**Our project aimed at establishing a high-throughput pipeline for characterizing diversity and community composition of the switchgrass and *Panicum hallii* microbiome. The pipeline we aimed to establish includes the optimization of 1) sampling techniques of various plant tissue types, 2) sample processing protocols as well as 3) the streamlined analysis of large 16S rRNA and ITS amplicon sequence datasets. The results of this project contribute essential information for the exploration of plant-microbe-soil interactions across continental scale environmental gradients.**

Abstract text. Please limit to 2 pages.

Part of the DOE's strategy to ensure American energy independence is to produce biofuels from dedicated biomass crops. Achieving DOE's ambitious goal of displacing 30% of 2004 gasoline demand with biofuels by 2030 will require major increases in plant productivity. Switchgrass (*Panicum virgatum*) has been championed as a promising bioenergy species, but widespread commercial use has partly been challenged by its genetic complexity. *Panicum hallii* is a close relative of agronomic switchgrass with a diploid genome and seed-to-seed time of 8 weeks, offering researchers a model system for exploring *Panicum* genetics, genomics, and adaptation for agronomic improvement. Furthermore, plant microbiomes are known to influence many aspects of plant health. We present biogeochemical dynamics including amplicon and shotgun sequencing data, soil chemistry and metabolite profiles as well as plant phenotypic characteristics. Interestingly, we observe significant impacts of soil depth on rhizosphere microbiome, but not on bulk soil communities. Drought treatment did not significantly change microbial community composition or soil chemistry. Plant development stages significantly affected individual bacterial species within depth horizons. This study is rare in its comprehensive biogeochemical characterization of environment and biological players and provides a framework for soil ecosystem science conducted in future EcoPod experiments. All data is integrated in an interactive we application that is publicly available.

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