Investigating the Interplay between the Phyllosphere Microbiome, Epicuticular Wax, and Root Mucilage on Sorghum Resilience to Water and Nitrogen Limitation.

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Project Goals:

The research goal of this project is to determine the taxonomic, phylogenetic, and functional diversity of the microbiome of the sorghum aerial root mucilage and epicuticular wax, and how it changes under plant stress. Our overarching objective is to understand how sorghum interacts with the mucilage and wax microbiome and to determine plant-interactions that can be leveraged to support sorghum resilience and productivity.

Abstract:

Sorghum (*Sorghum bicolor)* produces several exudates on its external aerial surfaces (epiphytic phyllosphere). In particular, sorghum accumulates high levels of epicuticular wax on stems over its development, and it also grows aerial roots that produce protective sugar-rich mucilage. The epicuticular wax supports tolerance to sorghum water limitation. However, the functional role of the sorghum aerial root mucilage is still unclear, though it has been shown that diazotrophs colonize the mucilage of maize aerial roots and can provide substantial fixed nitrogen for the host. Here, we hypothesize that the wax and mucilage are suitable environments for specialized microbiomes that support sorghum resilience to stress from water limitation and nitrogen limitation, respectively. We applied 16S rRNA gene amplicon sequencing to study the bacterial communities associated with the aerial root mucilage from N-fertilized and non-fertilized sorghum plants at two-time points, and the epicuticular wax from plants under non-limiting and limiting water conditions. Our initial results showed that Proteobacteria, Bacteroidetes and Firmicutes are the dominant phyla in the mucilage compartment regardless of the fertilization treatment. However, differential abundance analysis revealed specific bacterial taxa significantly more abundant on the mucilage of N-fertilized plants compared with non-fertilized treatment and vice versa. Similarly, we found that Proteobacteria, and Firmicutes are the dominant bacterial group in the epicuticular wax compartment. In parallel, we are building a large bacterial collection by targeting a wide range of traits, including nitrogen-fixation, phosphate-solubilization, methanol-utilization, and others to evaluate the functional diversity of the bacterial communities in sorghum aerial root mucilage and epicuticular wax. The outcome of this work will inform understanding of the interplay between the phyllosphere microbiome and plant exudates for sorghum resilience and productivity, and supports our long-term goal of translating our findings into sorghum cultivation for biofuel production and crop adaptation to drought.

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