

S2T2**Stress-specialized phyllosphere exudates select for distinct microbiome members in sorghum epicuticular wax and aerial root mucilage**

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Abstract

Bioenergy sorghum produces several exudates on its external aerial surfaces to adapt to abiotic stress. Sorghum accumulates elevated levels of epicuticular wax on its stems and leaves to prevent water loss. Also, sorghum produces sugar-rich mucilage on its aerial roots, likely to facilitate nutrient acquisition. We hypothesized that these phyllospheric exudates selectively enrich for specific microbiome members that support host resilience. Here, we assessed the microbiome associated with the epicuticular wax from sorghum plants under non-limiting and limiting water conditions, and the aerial root mucilage from N-fertilized and non-fertilized plants. Our study included two different developmental points over two growing seasons and two field sites in Michigan and Texas. In parallel, we isolated and characterized hundreds of bacterial isolates from wax and mucilage.

We found that the dominant microbial phyla in the wax were Proteobacteria and Firmicutes, and Sphingomonadaceae and Rhizobiaceae families were the major taxa regardless of water availability to plants. The dominant bacterial phyla in the mucilage were Proteobacteria, Bacteroidetes, and Firmicutes. The mucilage-associated microbiome contained described diazotroph bacterial species and exhibited changes over time. We characterized 200 bacterial isolates with putative plant-beneficial traits. By sequencing the genome of several isolates, we observed that the wax isolates harbors genes associated with stress tolerance, and the mucilage isolates are enriched in plant-growth promotion genes. We also found that the Ascomycota and Basidiomycota phyla dominate the mucilage fungal community.

This work integrates data from both cultivation-independent and -dependent approaches to gain deeper insights into phyllosphere dynamics, functions, and host-beneficial phenotypes.

