

A Systems Understanding of Nitrogen-Fixation on the Aerial Roots of Sorghum

Emily Reed,^{1*} Sadies Vela,^{1*} Vânia C. S. Pankievicz,² Saptarshi Pyne,² April MacIntyre,² Sushmita Roy,² **Jean-Michel Ané**,² Wilfred Vermerris^{1*} (wev@ufl.edu)

¹University of Florida, Gainesville, FL

²University of Wisconsin – Madison, Madison, WI

<https://sonar.bact.wisc.edu/>

Project Goals: The overall goal of this project is to understand better the molecular and cellular networks controlling biological nitrogen fixation in sorghum aerial roots using a combination of genetics, synthetic bacterial communities, and systems biology.

Since the Green Revolution, the intensive use of synthetic fertilizers is the most common strategy to alleviate the limitation of nitrogen (N) availability on crop yields. With the desire to produce bioenergy crops on low-productivity lands to avoid competition with food production, the heavy use of fertilizer that will be necessary to ensure reasonable yields raises the cost of production and increases the environmental footprint of producing bioenergy crops. Sorghum is an attractive bioenergy crop due to its ability to produce high biomass yields with limited inputs and to withstand biotic and abiotic stresses. To further enhance sorghum's bioenergy potential, we are investigating the mechanisms that enable specific sorghum accessions to support symbiotic interactions with N-fixing microbes in the mucilage of their aerial roots. This symbiosis allows them to obtain a significant amount of N from the air, reducing the need for chemical fertilizers. Specifically, we are investigating the genetic basis of aerial root formation using a genome-wide association study of two panels of genetically diverse genotypes. We are also determining the dependence of aerial root formation on factors such as rainfall and soil composition by planting select genotypes in different geographic locations and with varying levels of fertilizer. In parallel, we are using single-cell and bulk transcriptome profiling to investigate the sorghum gene regulatory networks that enable mucilage production and N-fixation and interactions of sorghum with diverse microbial species. From this analysis, we expect to infer cell-type-specific gene regulatory networks and critical regulatory genes that drive the dynamics of these processes. Candidate genes that are important to enable biological nitrogen fixation (BNF) will be tested through reverse genetics approaches. Furthermore, breeding populations derived from crossing bioenergy sorghums with accessions that support BNF are under development. As a result of these activities, we will enhance our understanding of BNF in sorghum and have genetic tools at our disposal to enable the commercial development of N-fixing bioenergy sorghums to display high biomass productivity on marginal lands, with a reduction in inputs.

The authors gratefully acknowledge funding from the U.S. Department of Energy (BER) grant no. DE-SC0021052.