

## Nitrogen Addition Impacts on Structure and Function of the Switchgrass Root-associated Diazotrophic Community

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**Project Goals: This work aims to improve our understanding of plant-microbe interactions in switchgrass (*Panicum virgatum*) bioenergy cropping systems and their impact on soil biogeochemistry. In particular, we aim to address the role of associative nitrogen fixing organisms (diazotrophs) in meeting switchgrass nitrogen demands.**

Associative nitrogen fixation (ANF), the biological conversion of atmospheric dinitrogen gas to bioavailable forms by heterotrophic bacteria, is an important terrestrial N source that occurs under diverse environmental conditions.<sup>1</sup> ANF likely occurs predominately in the rhizosphere, where labile carbon (C) is readily accessible and competition for N between plants and soil microorganisms reduces N availability.<sup>1</sup> Switchgrass, an important bioenergy crop, harbors a diverse community of diazotrophic bacteria in association with its roots and may rely on these organisms as a significant N source when grown on marginal lands.<sup>2,3</sup> It is increasingly clear that diazotrophs are present and fixing N in association with switchgrass, however the impact of soil N availability on these potential N contributions, particularly in fertilized cropping systems, is not known.

In order to understand how soil N availability may impact switchgrass-diazotroph associations and potential N contributions from ANF, we evaluated the switchgrass root-associated diazotroph community and potential ANF rates under long-term and short-term fertilizer N additions.<sup>4</sup> We grew switchgrass in three Michigan marginal land soils in the greenhouse under these N addition treatments for four months before harvest. At harvest, belowground material was subsampled for *nifH* functional gene sequencing and potential ANF rates. In a separate experiment, we also examined the impact of N availability and diazotroph presence (inoculation with *Azotobacter vinelandii*) on switchgrass rhizosphere metabolite chemistry, using data from hydroponically grown switchgrass.<sup>5</sup> Switchgrass seedlings were grown for two-weeks in ¼ strength Hoagland's nutrient solution under high or low N availability. Growth media was then collected and rhizosphere metabolite chemistry was measured via NMR.

We found the switchgrass rhizosphere to exert strong selective pressure on the root-associated diazotroph community. Beta diversity of diazotroph communities in the three Michigan field soils suggest these communities were initially distinct ( $R^2 = 0.543$ ,  $p = 0.001$ ), but the root-associated communities showed little evidence of these site histories ( $R^2 = 0.073$ ,  $p = 0.015$ ). Long-term N addition was not a strong driver of diazotroph community structure ( $R^2 = 0.037$ ,  $p = 0.043$ ), but communities tended to separate by short-term N treatment ( $R^2 = 0.0799$ ,  $p = 0.001$ ). This response to short-term N may be driven by changes in root exudate chemistry as we observed significant differences in switchgrass rhizosphere metabolites under high vs. low N availability. In particular, we noted that high N rhizospheres tended to be dominated by carbohydrates (55.1 %), while organic acids (28.7 %) were the most abundant compounds in low N rhizospheres. Our findings indicate that N availability is likely a driver of diazotroph community structure as well as the forms of C available in the rhizosphere. However, N availability was not a driver of ANF rates in our study. ANF rates were overall highly variable across field soils and N additions, ranging from below detection to over  $10 \mu\text{g N fixed g}^{-1}$  rhizosphere  $\text{day}^{-1}$ , suggestive of ANF as a hot spot/hot moment process. And while we find evidence for potential association between specific diazotroph community members and ANF rates, community composition was not generally a driver of ANF.

## References

1. Smercina, D. N., Evans, S. E., Friesen, M. L., & Tiemann, L. K. (2019). To fix or not to fix: controls on free-living nitrogen fixation in the rhizosphere. *Appl. Environ. Microbiol.*, 85(6), e02546-18.
2. Ruan, L., Bhardwaj, A. K., Hamilton, S. K., & Robertson, G. P. (2016). Nitrogen fertilization challenges the climate benefit of cellulosic biofuels. *Environmental Research Letters*, 11(6), 064007.
3. Roley, S. S., Duncan, D. S., Liang, D., Garoutte, A., Jackson, R. D., Tiedje, J. M., & Robertson, G. P. (2018). Associative nitrogen fixation (ANF) in switchgrass (*Panicum virgatum*) across a nitrogen input gradient. *PloS one*, 13(6), e0197320.
4. Smercina, D. N., Evans, S. E., Friesen, M. L., & Tiemann, L. K. (2020). Impacts of nitrogen addition on switchgrass root-associated diazotrophic community structure and function. *FEMS Microbiology Ecology*, 96(12), fiae208.
5. Smercina, D. N., Bowsheer, A. W., Evans, S. E., Friesen, M. L., Eder, E. K., Hoyt, D. W., & Tiemann, L. K. (2020). Switchgrass rhizosphere metabolite chemistry driven by nitrogen availability. *Phytobiomes Journal*, PBIOMES-09.

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