

Response of Total (DNA) and Metabolically Active (RNA) Microbial Communities in *Miscanthus x giganteus* Cultivated Soil to Different Nitrogen Fertilization Rates

Background/objective

Miscanthus x giganteus (*M x g*) is a promising perennial bioenergy feedstock, notable for its high yields and low nitrogen (N) requirements in comparison to other bioenergy crops. While N-fixing bacteria in the *M x g* rhizobiome are understood to contribute substantially to the plant's N needs, it has not been possible to differentiate the activity of various components of the microbial community using existing DNA-based methods. This study addresses this gap by comparing the miscanthus rhizobiome community as identified via DNA- and RNA-based analyses.

Approach

- ❖ Extracted DNA and RNA from 217 soil samples collected at the Long-term Assessment of Miscanthus Productivity and Sustainability (LAMPS) site in Iowa.
- ❖ Performed 16S SSU rRNA amplicon sequencing and characterized microbial community structure.

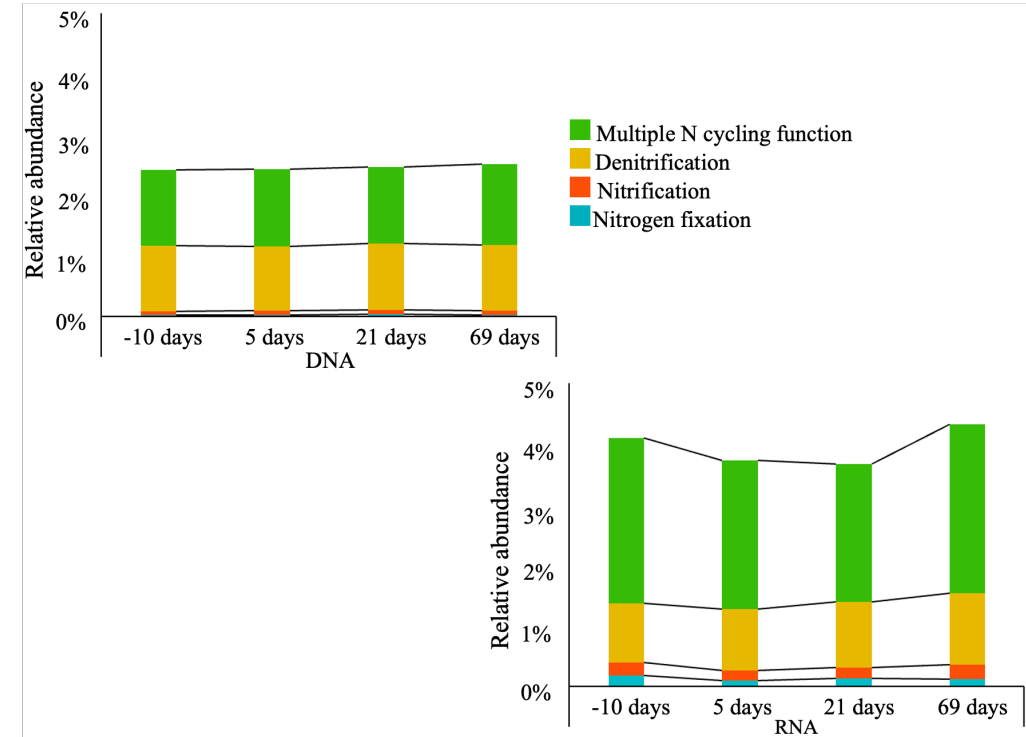
Results

- ❖ Results from DNA- and RNA-based analyses showed 90% overlap in community membership.
- ❖ Only RNA-based analyses showed seasonal response of N-cycling bacteria to fertilization, with abundance of N-cycling bacteria being up to 7x higher in RNA-based than DNA-based analyses.

Significance

RNA-based characterization can be an important complement to DNA-based approaches for understanding the role of the soil microbiome in providing N for key bioenergy grasses such as *M x g*.

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Relative abundance of bacterial communities associated with various N-cycling functions identified using DNA-based (top) and RNA-based (bottom) methods. Y-axis indicates time from fertilizer application.