Variation in Microbial Communities and Nitrogen Transformation Rates among Switchgrass Varieties

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Overview

Switchgrass (*Panicum virgatum*) is a C4 perennial grass with unique nitrogen (N) conservation strategies that give it potential as a low-input bioenergy crop. A recent study found that a higher-yielding switchgrass variety associated with a larger and more active community of free-living N-fixers (diazotrophs) than a lower-yielding variety.[1] Root morphology, also shown to vary among switchgrass varieties, is known to influence root exudation rates, which directly impact the amount of carbon (C) available to energetically-demanding N-fixation. We are investigating the relationship between root morphology, microbial community structure, and N-fixation potential across 12 switchgrass varieties (including upland and lowland ecotypes), at the Great Lakes Bioenergy Research Center at Kellogg Biological Station in southwest Michigan. Preliminary results suggest that switchgrass ecotypes differ in root morphology and N-fixation, but that bacterial community compositions do not differ. Discerning what plant characteristics support diazotrophic communities has large implications for the development of low-input agricultural systems.

Questions & Background

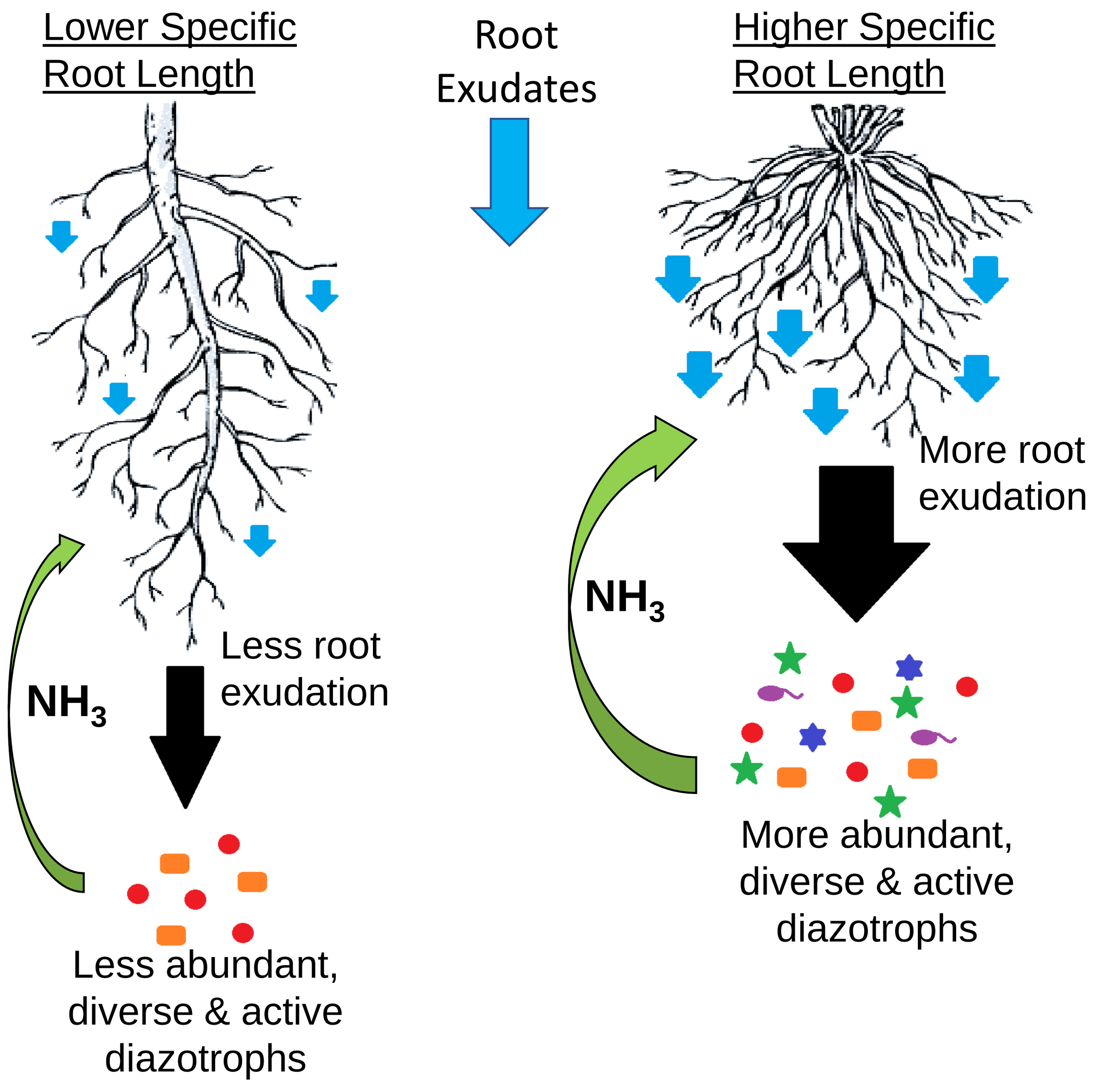
1) Does diazotrophic community abundance and activity differ among switchgrass varieties?

- Switchgrass varieties differ in N-requirements. Preliminary work suggests this may be driven by associations with diazotrophs.[1,2,3]

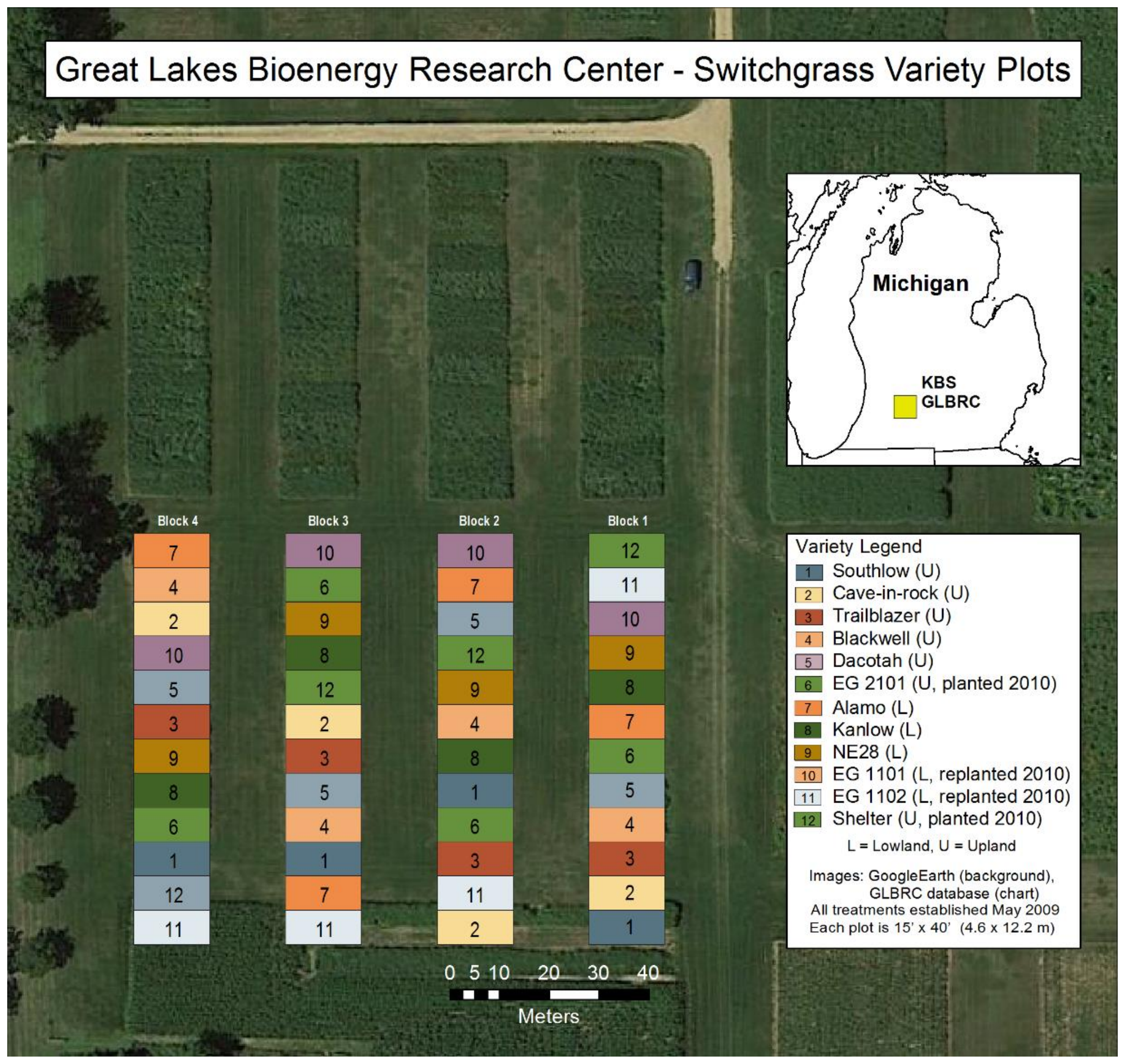
2) If so, can differences in diazotrophic communities be explained by variation in root architecture among the varieties?

- Specific root length (total root length/total root dry mass) is positively correlated with root exudation[4,5]
- Diazotrophs are C-limited and are highly dependent on root exudation to fuel N-fixation.

Hypothesis: Varieties with higher SRL associate with more active and abundant diazotroph communities due to larger surface area for root exudation.

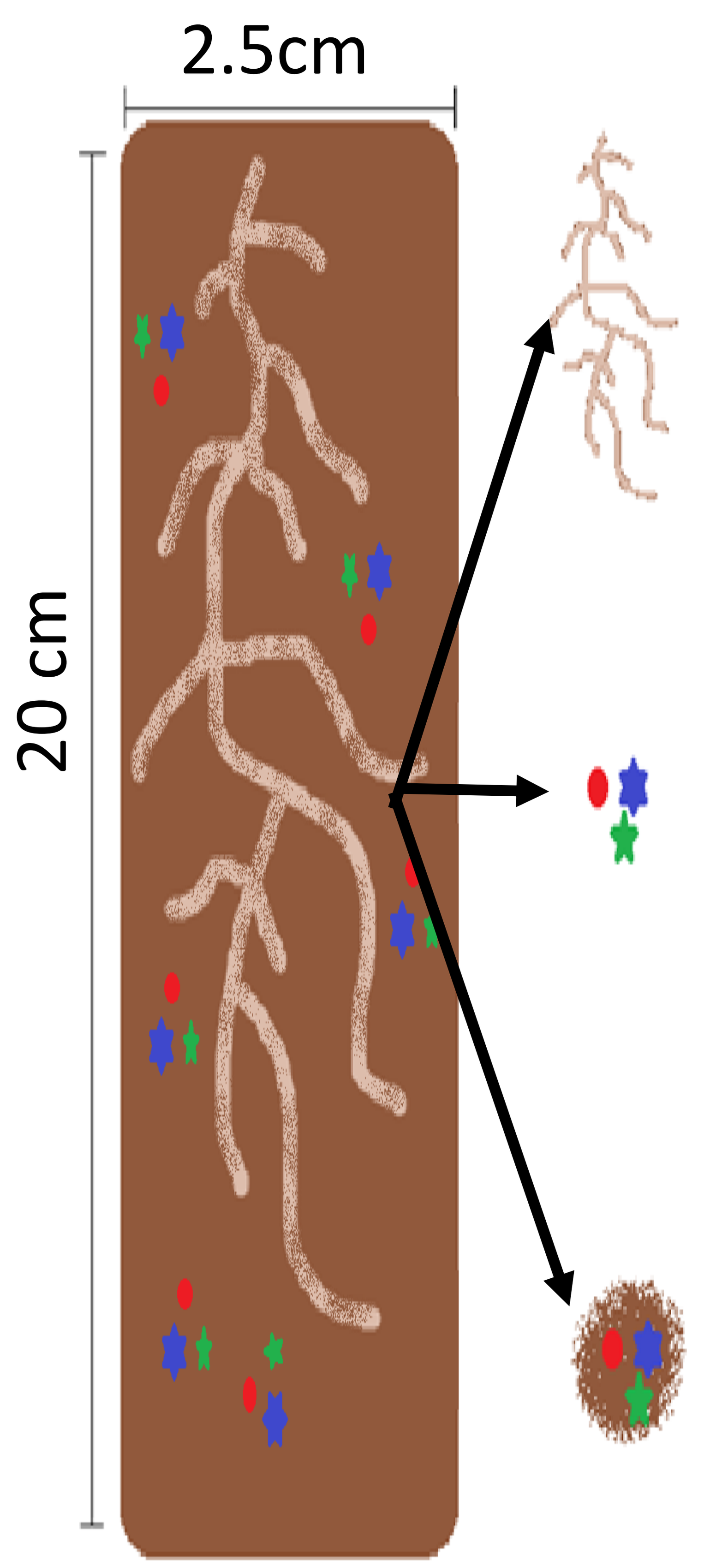


Study Site



Methods

- 3 pseudorep cores per block, n = 12 soil cores per variety
- Cores taken summer 2016 at time of flowering for each variety



- Sieve & scan roots: Specific Root Length (total root length/ total root dry mass)

- Microbial biomass
- Bacterial & Fungal Community Analysis (16S/ITS amplicon sequencing)
- Abundance of diazotrophs (*nifH* & *nifD* wafergen)

- N-mineralization potential
- N-fixation potential
- Total soil C & N

Preliminary Findings

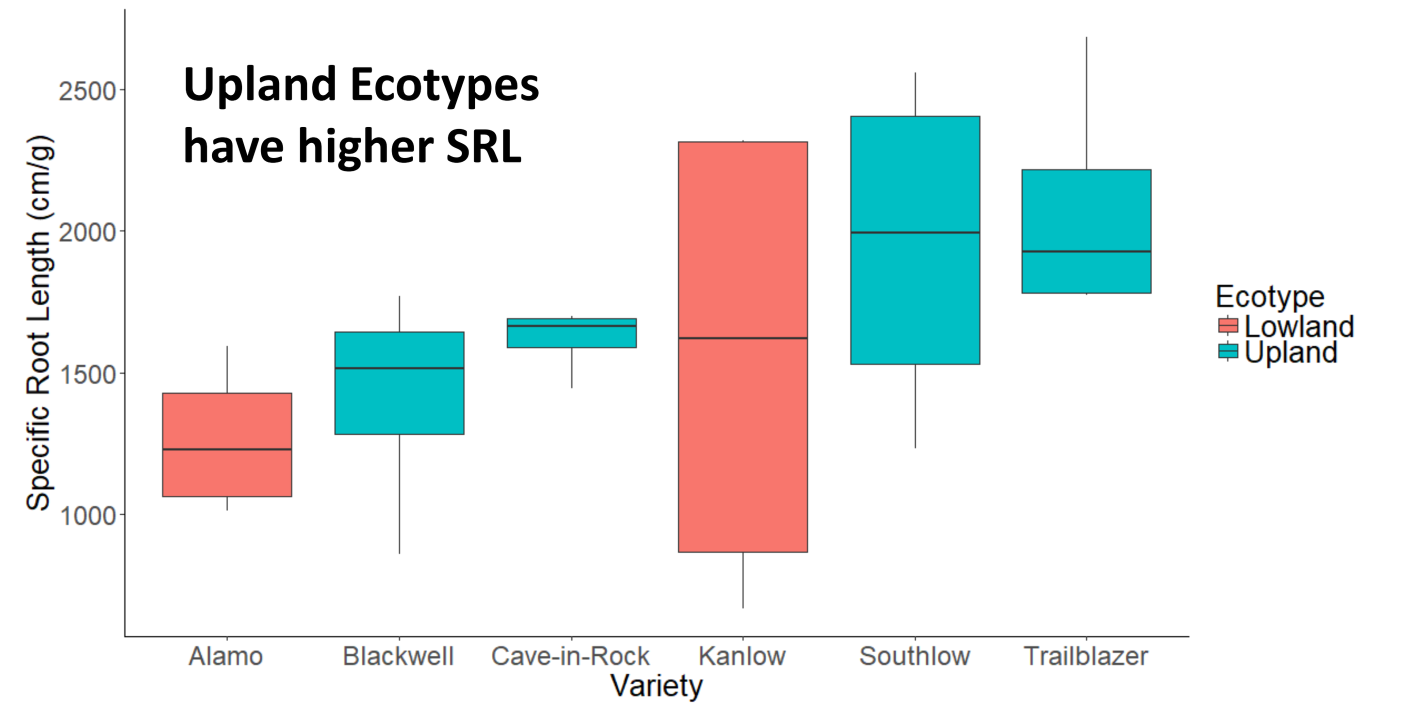


Figure 1. Specific Root Length (total root length (cm)/total root dry mass (g) by Switchgrass Variety (n = 4, avg. of 3 pseudoreps).
Two extreme outliers (IQR*3) removed and ln(SRL) used for statistical analysis.
1-way ANOVA (variety effect): $P = 0.2962$; T-test (ecotype effect): $P = 0.09246$.

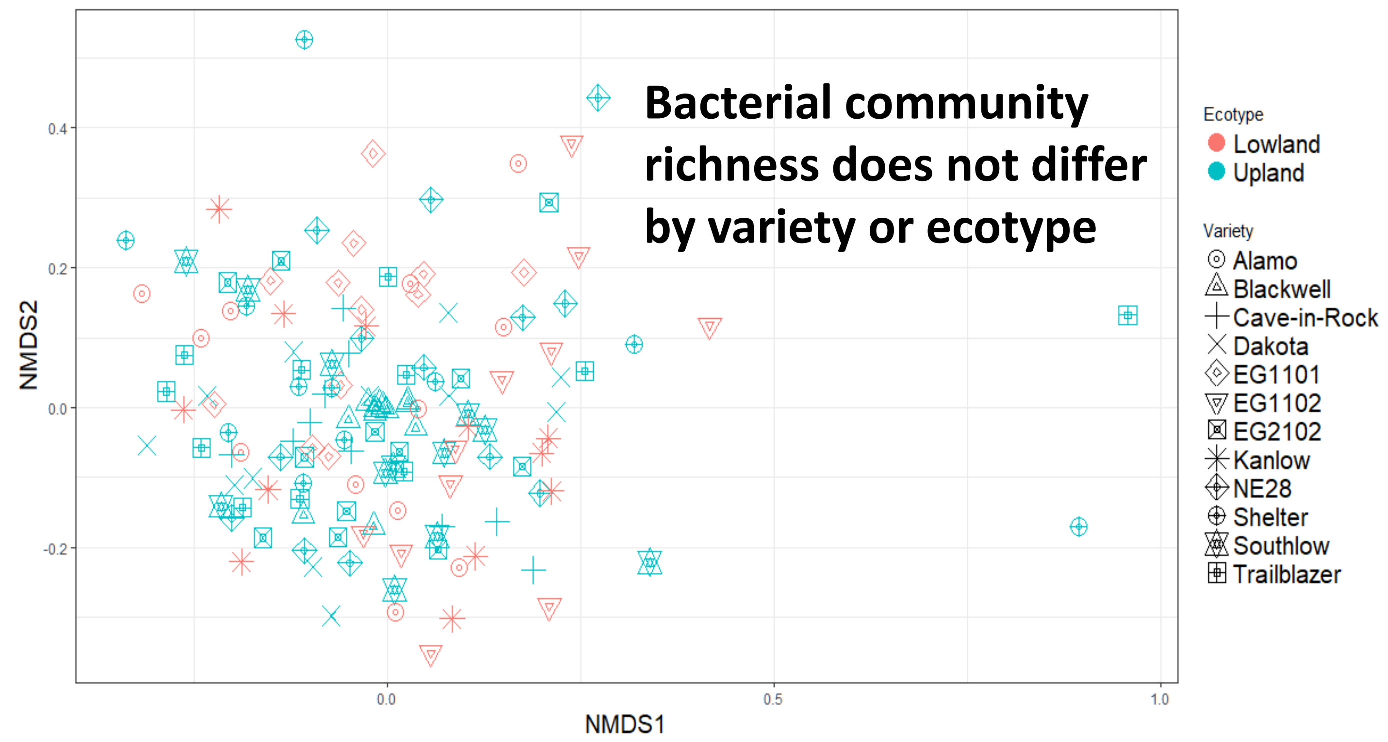


Figure 2. 16s amplicon sequences from switchgrass variety rhizosphere soils. Data pruned for only bacteria, low sequence samples and taxa, converted to presence/absence. Bray-Curtis Distance Metric, NMDS Plot. Permanova (By Variety): $P < 0.001$, $R^2 = 0.103$; Beta-Dispersion: $P < 0.001$

Future Directions

- Are root endophyte communities more highly selected by varieties than rhizosphere communities?
- If the microbial communities differ among varieties, how critical are "home" microbes to a variety's success or N-demands? (plant-soil feedback)

References & Acknowledgements

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1. Rodrigues et al 2016, GCB Bioenergy 2. Aspinwall et al 2013, New Phytologist; 3. Stahlheber et al 2016, in press; 4. de Graaff et al 2013, Soil Biology and Biogeochemistry; 5. Adkins et al 2016, Geoderma