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Bacterial Taxa and Metabolic Pathways Influenced By Nitrogen Fertilization and Landscape Positions Udayakumar Sekaran¹, Dheeman Saha², Laura White¹, Senthil Subramanian¹, and Sandeep Kumar¹ ¹Department of Agronomy, Horticulture and Plant Science, South Dakota State University, Brookings, SD. ²The University of New Mexico, Albuquerque, NM

Background

- Interest in the production of renewable energy from plants has increased in the last decade
- **Crop biomass can be used as an alternate source**
- Switchgrass (Panicum virgatum) is a warm season C4-perennial crop gaining in popularity for bio-fuel on marginal lands (Gelfand et al., 2013)
- Proper nitrogen (N) management and landscape positions (slope) are key factors in impacting the production of switchgrass
- Little is known about the fertilizer management and soil health under



switchgrass.

Thus, the objective of this study was to assess the responses of soil microbial communities and metabolic activities relevant to C, N, P and S cycling in soils to N management using a next-generation sequencing approach and landscape positions in switchgrass.



Figure 1: Steps of extracting Gene Sequencing and Operational Taxonomic Units (OTU) abundance information



Figure 3. Bacterial composition of different treatments at phylum level. Each bar represents the relative abundance (%) of each bacterial taxon at a) Shoulder and Footslope landscape position, b) High N_Shoulder, High N_Footslope, Low N_Shoulder, Low N_Footslope, Medium N_Shoulder, and Medium N_Footslope treatments.





WORKFLOW

Figure 4. PCA plots of metabolic pathway enrichment patterns indicating largest difference influenced by field position (left), and the interaction in low nitrogen rates. The 1st PC is 95.9% and the 2nd PC is 2.0%.

Conclusions

- Phylum level relative abundance shown in Fig-3 indicates that there were large differences in bacterial composition among samples.
- The clustering patterns base on relative enrichment of the most variant metabolic pathway (KEGG) IDs in Fig-4 indicated that field position had the largest impact on enrichment of metabolic pathway IDs.
- **Evaluation of major contributors to the PC1 axis identified various metabolic** pathways largely different between the samples.





Figure 2. Flowchart for data analysis stages of DNA sequencing files using QIIME-2 and PICRUSt

platforms.

Reference Gelfand I, Sahajpal R, Zhang X, Izaurralde RC, Gross KL, Robertson GP (2013) Sustainable bioenergy

production from marginal lands in the US Midwest. Nature, 493, 514.

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