

## ESTIMATING THE CONTRIBUTION OF THE SOIL MICROBIAL COMMUNITY TO THE CROP ROTATION EFFECT

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Crop rotation has many benefits including, increased yield, decreased disease pressure, and decreased soil nutrient depletion. While the benefits of crop rotation are well established, the underlying drivers behind these benefits remain unclear. The soil microbial community plays an essential role in plant health by fostering soil nutrient cycling, availability and uptake. Plants and microbes are known to communicate with each other in the soil and plants can alter their microbial community based on the composition of their root exudates. Due to this, the soil microbial community could be significantly altered based on crop type planted and may play a key role in the crop rotation effect. The goal of this study was to determine the contribution of the microbial community to the corn soy crop rotation effect in south central Wisconsin. We measured the bacterial and fungal community composition and structure under continuous corn, continuous soybean, annual corn-soybean and a five-year corn-soybean monocropping rotation systems. Soil sampling occurred in the at planting, mid-season (approximately R1), and at harvest by collecting and pooling 5 soil cores (0-15 cm) from the middle rows of each plot. Extracted soil DNA was subjected to Illumina MiSeq amplicon sequencing for the bacterial V3-V4 region of the 16S rRNA and fungal ITS2 region 18S rRNA. Sequence data were processed using the Mothur (version 1.40.5) standard operation protocol and R statistical software (version 1.0.143) was used to analyze and visualize the data. Additionally, we estimated the carbon utilization diversity of the soil microbial community based on crop rotation scheme at planting, mid-season and harvest using Biolog EcoPlates plates. Preliminary results from the 2016 planting time-point show significant differences in beta diversity between bacterial communities of continuous corn, continuous soybean and annual rotations (PERMANOVA,  $p < 0.05$ ). Bacterial and fungal sequencing data from the additional 2016, 2017 and 2018 time points are in process.

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