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Estimating the contribution of soil microbial communities to the crop rotation effect
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Crop rotation has been practiced for thousands of years due to the many agronomic benefits associated with rotating between different crops. These advantages include increased yield, decreased disease pressure and decreased nutrient amendments. While the benefits of crop rotation have been well established, the primary drivers behind it remain unclear. The soil microbiome is a key component to plant health and plants can tailor the microbial community they recruit based on the composition of their root exudates. Due to this fact, the soil microbiome could be changing significantly with crop rotation and playing a key role in the rotation effect. To determine if the contribution of the microbial community to the corn-soy crop rotation effect, we measured the bacterial and fungal richness and diversity under four corn-soy rotation schemes (continuous corn, continuous soy, annual corn-soy rotation and a five-year corn-soy rotation) at Arlington Agricultural Research Center in Arlington, WI. The aim of this study was to determine how the soil microbial communities and community functions respond to different lengths of corn-soy rotations and if specific OTUs correlate with high yield. We evaluated the soil microbial communities for beta diversity, alpha diversity, and richness based on rotation scheme using an Illumina 2x250 Miseq run, targeting the bacterial V4 region of the 16S rRNA and fungal ITS2 region of the 18S rRNA. This study provides growers with data on the best corn-soy rotation sequence to foster microbial communities associated with high yield.