Relic DNA dynamics mask the resilience of switchgrass bacterial communities to extreme drying rewetting

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Project Goals: We characterized the active and 'relic' (inactive or dead cells) microbiome of switchgrass and corn soils over a short-term disturbance. We measured the abundance and composition of living and relic bacterial communities before and after an extreme rewetting event (80mm of rain after 28 days of drought). Measuring both changes in viable taxa and relic DNA provides valuable information about the bacterial taxa most resilient to drying rewetting and the sensitivity of different soil bacterial communities to drying rewetting.

The soil microbiome is likely to be an important contributor to the sustainability of cellulosic bioenergy feedstocks. Future climates are expected to have more variable rainfall, including longer droughts and intensified rainfall events. Plant-microbe interactions can increase the resilience of cellulosic energy crops to extreme drying rewetting events, but bacterial responses to short-term disturbances like drying rewetting can be context-dependent and difficult to characterize. Specifically, DNA-based characterizations include dead or dormant cells, obscuring responses of the live community. Here, we asked 1) how do viable bacteria respond to drying rewetting and does this differ between corn and switchgrass soil? 2) Does the inclusion of relic DNA mask responses and 3) how does the composition of viable communities relate to relic DNA pools across a disturbance? To address these questions, we quantified changes in the size and composition of the viable bacterial community and relic DNA pools using the chemical treatment propidium monoazide (PMA) on soil samples collected at three time points; 6 hours before, 1 hour after, and 18 hours after an extreme drying rewetting event (80mm of rain every 28 days). We found that viable bacterial taxa and relic DNA in corn and switchgrass soil responded differently to extreme drying rewetting. In corn soil, we observed an increase in relic DNA 1-hr after extreme rewetting, and a simultaneous decrease in the relative abundance of viable bacteria. In switchgrass soil, we observed the opposite trend, an increase in the relative abundance of living bacteria, associated with a rapid decrease in relic DNA after rewetting. When we completed the analyses without controlling for relic DNA, we found that the increase in relic DNA in corn soil masked the sensitivity of corn bacterial communities to extreme rewetting, while the decrease in relic DNA in switchgrass soil masked the resiliency of switchgrass bacterial communities to extreme rewetting. To improve our understanding of the sources of relic DNA, we also looked at the number of taxa that appeared in both the viable community and the relic DNA community and found that 72% of taxa were present in both the living and relic communities. Furthermore, among the top 25% most abundant taxa, 100% were present in both the living and relic communities. However, only 55% of living taxa were present before and after extreme drying rewetting. Together, our results indicate

that relic DNA dynamics differ by soil cropping system and can mask important responses to disturbance that are critical for the sustainable production of cellulosic bioenergy crops in future climates.

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