Friday, September 28, 2018
9:00-9:30 a.m.

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Drought and host selection influence bacterial community dynamics in the grass root microbiome

Drought stress is a major obstacle to crop productivity, and the severity and frequency of drought are expected to increase in the coming century. Certain root-associated bacteria have been shown to mitigate the negative effects of drought stress on plant growth, and manipulation of the crop microbiome is an emerging strategy for overcoming drought stress in agricultural systems, yet the effect of drought on the development of the root microbiome is poorly understood. Through 16S rRNA amplicon and metatranscriptome sequencing, as well as root metabolomics, we demonstrate that drought delays the development of the early root microbiome and causes increased abundance and activity of monoderm bacteria, which lack an outer cell membrane and contain thick cell walls. Our data suggest that altered plant metabolism and increased activity of bacterial ATP-binding cassette (ABC) transporter genes are correlated with these shifts in community composition. Finally, inoculation experiments with monoderm isolates indicate that increased colonization of the root during drought can positively impact plant growth. Collectively, these results demonstrate the role that drought plays in restructuring the root microbiome and highlight the importance of temporal sampling when studying plant-associated microbiomes.