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Recent Evolutionary History of the Soil Microbiome Influences Plant Drought Tolerance

Nichole Ginnan^{1,2}, Valeria Custodio³, Gabriel Castrillo³, Maggie Wagner^{1,2}

¹University of Kansas, Lawrence, KS, USA. ²Kansas Biological Survey and Center for Ecological Research, Lawrence, KS, USA. ³University of Nottingham, Sutton Bonington, United Kingdom

Abstract

Soil microbes can evolve independently in free-living environments or closely intertwined with a plant host. It is unclear whether, or how, a host affects the evolution of microbiomes, and vice versa. We explore this in the context of plant/microbial adaptation to a model stress: water limitation. We performed a mesocosm experiment with six pristine prairie soils collected from across a steep precipitation gradient. Under simulated drought conditions, soil communities from historically dry sites increased root/shoot mass of *Tripsacum dactyloides* (gamagrass), a native prairie grass and relative of maize, as compared to soil communities from wet sites. This suggests that soil microbes are adapted to local precipitation levels and those adaptations impact plant drought tolerance. Next, we experimentally evolved (EE) these soil microbiomes for 5 months in one of four treatments: a factorial combination of +/- water-stress and +/- plant host (gamagrass). EE rhizosphere/soil microbiomes were then inoculated onto maize and gamagrass seedlings to test the functional consequences of microbiome evolutionary history on plant phenotypes under drought. Preliminary results indicate that microbiomes evolved with a host and in well-watered conditions improved gamagrass drought tolerance, relative to those that evolved without a host, under drought stress, or both. In contrast, EE microbiomes did not significantly affect maize phenotypes. This suggests that plant-microbiome interactions are more beneficial to plants when they share an evolutionary history with their microbes, but stressful conditions may lead to the breakdown of these relationships. Metagenomic and transcriptomic analyses are underway to unravel the mechanisms driving these phenotypes.

