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Bacterial community maintenance of plant root development

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Plants intimately associate with microbial communities collectively known as the plant microbiome. The microbiome contributes to plant processes such as development, nutrient acquisition and pathogen protection. The establishment of community assembly rules and community-host feedback patterns has been limited due to the complexity of natural microbial communities. Here, we applied a synthetic ecology approach to an amenable plant-microbiome mesocosm to unravel novel community-host and microbe-microbe interactions.

A. thaliana plants were inoculated across a gradient of phosphate, salinity, pH and temperature conditions with a genome-sequenced bacterial inoculum composed of 185 phylogenetically diverse isolates (SynCom). Colonization patterns across the fractions and conditions sampled were quantified using 16s amplicon sequencing. We used the correlation of these abundance profiles among all members of the community to split the SynCom into four modules which exhibited a characteristic colonization pattern and high phylogenetic coherence.

Subsequently, we measured plant molecular and morphological phenotypes when inoculated with each of these modules independently and in combination. Plant phenotypes induced by some modules were attenuated when co-inoculating with other modules exhibiting ecological epistasis between guilds in the community. Following our top-down approach, we identified a single genus that was responsible for dampening the effects that all other members of the community exerted over the root morphology of the plant.

This demonstrates that in the context of a complex community there are multiple interactions that strongly influence plant development and that a balanced microbiome is required to equilibrate these interactions and prevent host dysbiosis.