How much does the plant control its microbiome? Partitioning the effects of host and environment on rhizosphere microbiome assembly during plant development

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Résumé

Background. The feedback between a developing plant and belowground microorganisms contributes to plant microbiome assembly and supports host health. However, environmental microbiomes naturally change over time, even in the absence of host shaping. Temporal changes in the microbiome are attributed to both deterministic drivers (e.g., selection) and stochastic fluctuations. Due to the collinearity of time and plant development, it has been so far impossible to separate host versus temporal influences on the microbiome.

Objectives. We discovered a method to delay the development of common bean plants without notable impact on mature plants. This allowed for an independent investigation of the belowground plant microbiome over the two typically co-occurring trajectories: plant growth stage and time.

Methods. We induced a 2-3 week growth delay to Phaseolus vulgaris L. (var. Red Hawk) bean seeds. Growth-delayed and control seeds were grown in environmental chambers. For the growth stage trajectory, plants were destructively harvested at growth stages V1, V2, V3, V4, (first trifoliate, second, etc.), R1 (first open flowers), R4 (half of the seed pods fully developed), and R7 (seed pods dry). For the time series trajectory, plants were harvested at days 3, 7, 14, 21, 35, 49, and 63 days-since-planting. Rhizoplane and rhizosphere bacterial microbiomes were profiled from each plant using 16S rRNA gene amplicon sequencing. Plant root and shoot biomass, plant height, nodule counts, and root structure were measured.

Results. There was a strong alignment in the bacterial communities by plant growth stage, which explained more microbiome variance than time. The rhizoplane communities were more strongly influenced by plant growth than the rhizosphere. However, most of the observed taxa were shaped by neutral processes rather than by plant selection. Plant-selected taxa included members of genera previously reported to be plant-beneficial, such as Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium, Pseudolabrys, Duganella, Paenibacillus, Bacillus, Thermoactinomyces and Gaiella. A time-lag-informed network analysis revealed associations between bacterial taxa over time and by growth stage, as the microbiome

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assembled to its observed mature state.

Conclusions. This work quantifies the plant influence on the rhizoplane and rhizosphere bacterial microbiome assembly. It distinguished a minority of plant-responsive taxa from those taxa that changed over the time, but without attribution to host developmental cues. This study provides insights into the ecological mechanisms of belowground plant microbiome assembly and has implications for applied microbiome research in agriculture and conservation.

Mots-Clés: disturbance ecology, plant microbiome, community assembly