

Cross-feeding niches among commensal leaf bacteria are shaped by the interaction of strain-level diversity and resource availability.

Murillo-Roos M, Abdullah HSM, Debbar M, Ueberschaar N, Agler MT (2022) Cross-feeding niches among commensal leaf bacteria are shaped by the interaction of strain-level diversity and resource availability. *ISME J* , [PubMed](#)

ILRS Authors

[Mariana Murillo-Roos](#)

Projects

Community resource availability as a driver of convergent microbe-microbe interaction types and microbial community structures

[Details](#)

Abstract

Leaf microbiomes play crucial roles in plant health, making it important to understand the origins and functional relevance of their diversity. High strain-level leaf bacterial genetic diversity is known to be relevant for interactions with hosts, but little is known about its relevance for interactions with the multitude of diverse co-colonizing microorganisms. In leaves, nutrients like amino acids are major regulators of microbial growth and activity. Using metabolomics of leaf apoplast fluid, we found that different species of the plant genus *Flaveria* considerably differ in the concentrations of high-cost amino acids. We investigated how these differences affect bacterial community diversity and assembly by enriching leaf bacteria in vitro with only sucrose or sucrose + amino acids as possible carbon sources. Enrichments from *F. robusta* were dominated by *Pantoea* sp. and *Pseudomonas* sp., regardless of carbon source. The latter was unable to grow on sucrose alone but persisted in the sucrose-only enrichment thanks to exchange of diverse metabolites from *Pantoea* sp. Individual *Pseudomonas* strains in the enrichments had high genetic similarity but still displayed clear niche partitioning, enabling distinct strains to cross-feed in parallel. *Pantoea* strains were also closely related, but individuals enriched from *F. trinervia* fed *Pseudomonas* more poorly than those from *F. robusta*. This can be explained in part by the plant environment, since some cross-feeding interactions were selected for, when experimentally evolved in a poor (sucrose-only) environment but selected against in a rich (sucrose + amino acids) one. Together, our work shows that leaf bacterial diversity is functionally relevant in cross-feeding interactions and strongly suggests that the leaf resource environment can shape these interactions and thereby indirectly drive bacterial diversity.

Identifier

doi: 10.1038/s41396-022-01271-2 PMID: 35768644

