

Mariana Murillo-Roos

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

In the Plant Microbiosis Lab, our research investigates how and why diverse communities of plant-associated microorganisms form as well as their implications in order to improve plant-associated microbiota management. Microbe-microbe interactions play key roles in microbiome organization, so we are particularly interested in studying their basis and mechanisms to bridge the disconnect between evolutionary (binary plant-microbe interactions) and ecological (plant-associated microbial diversity) understandings of plant microbiota. Plant colonizers face scarce nutrients and resources, conditions under which resource distribution can regulate characteristics of microbe-microbe interactions. In this project, we will investigate how resource availability constrains development of microbe-microbe interactions and in turn microbial community structures. We will employ a convenient model system: Distantly related plant taxa have evolved C4 photosynthetic pathways independently, resulting in similar changes to resource distribution.

To investigate interactions in detail, we will utilize a “revolving lab-door” approach, working with both natural and synthetic microbial communities. Microbiota will first be characterized in naturally colonized, distantly related plant genera which have both C3 and either C4 or C3/C4 intermediate species. Inferred “interaction” networks will identify highly interactive keystone species and their interaction partners. High-throughput isolation of these microbiota will allow a more concrete investigation of formation of observed interactions as a function of resource distribution using “synthetic” microbial communities. Specifically, we will look at how host-controlled resource distribution constrains colonization and how colonization itself alters resources leading to development of structured microbe-microbe interaction networks.

Publications

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*, [Details PubMed](#)

Mayer T, Mari A, Almario J, Murillo-Roos M, Syed M Abdullah H, Dombrowski N, Hacquard S, Kemen

EM, Agler MT (2021) Obtaining deeper insights into microbiome diversity using a simple method to block host and nontargets in amplicon sequencing. *Mol Ecol Resour* 21(6), 1952-1965. [Details](#) [PubMed](#)

Supervisor

[Matthew Agler](#)

Start of PhD

March 19, 2018

Doctoral Disputation

July 6, 2023