Understanding the plant microbiome

Sur Herrera Paredes
Curriculum in Bioinformatics and Computational Biology, Department of Biology, The University of North Carolina at Chapel Hill. USA. Current address: Department of Biology, Stanford University. USA. surh@stanford.edu

For decades, scientist have characterized plant-microbe interactions by focusing on relationships between one plant species and one microbial strain. This approach has been remarkably successful in elucidating molecular, physiological and ecological processes in various heavily studied model systems. However, in recent years, we realized that plants associate with a huge diversity of microbes. This realization raised important questions such as: What is the natural microbial diversity within plants? Is this diversity influenced by the soil? Which plant genes, if any, play a role in structuring their microbial diversity? What is the role of the environment? And, how all these factors interact with one another? Besides diversity, we also want to know what functions do these microbes perform for the plant? And, can we harness these functions for improving plant performance?

We characterized the bacterial diversity in and around Arabidopsis roots and showed that, while soil type is very important, the plant robustly selects a subset of soil taxa [1]. Further, we used plant mutant panels to demonstrate that the plant phytohormone salicylic acid, which controls plant immunity, modulates the abundance of specific bacteria in the root [2], and that an intact phosphate starvation response in Arabidopsis is required to assemble a wild-type root microbiome [3].

We realized that microbial diversity surveys in natural soils are limited by an inherent lack of genomic context. Therefore, we pioneered the use of complex but well-defined synthetic bacterial communities. With this approach, we showed that plants deficient in the salicylic acid pathway can no longer exclude many bacteria, and some of the inhibitory effect of salicylic acid is direct [2]. Moreover, we showed that the master transcriptional regulator of the plant phosphate starvation response is also a negative regulator of immunity [3], and that some bacterial communities can induce the activation of the plant phosphate starvation response [3, 4]. Finally, by systematically varying the bacterial community and nutritional composition that a plant encounters, we were able to directly infer which bacterial groups influence plant performance [4]. We used these inferences to design bacterial consortia that manipulate the plant [4].

Plant-microbe interactions are essential for plant health and, by extension, for human health. Each day, about one in nine people on Earth (~800 million people), most of them children, are hungry, which has devastating and long-lasting consequences. To abate hunger, we need a sustainable increase in agricultural productivity. Our work attempts to bring together the best of reductionist and systems-level approaches, providing key insights into plant microbiome function and manipulation, which will impact conservation, management and agriculture.

References:

1. D. S. Lundberg et al., Defining the core Arabidopsis thaliana root microbiome. Nature. 488, 86–90 (2012).
2. S. L. Lebeis et al., Salicylic acid modulates colonization of the root microbiome by

specific bacterial taxa. Science. 349, 860–864 (2015).
3. G. Castrillo et al., Root microbiota drive direct integration of phosphate stress and immunity. Nature. 543, 513–518 (2017).
4. S. Herrera Paredes et al., Design of synthetic bacterial communities for predictable plant phenotypes. PLOS Biol. 16, e2003962 (2018).

Acknowledgements:
The author was a Howard Hughes Medical Institute International Student Research Fellow and is a Simons Foundation fellow of the Life Sciences Research Foundation.

Competing interests:
The author collaborated with AgBiome LLC, a corporation whose goal is to use plant-associated microbes to improve plant productivity.