

Ton Bisseling is a professor in the Laboratory of Molecular Biology, Department of Plant Sciences, Wageningen University, Wageningen, Netherlands. E-mail: ton.bisseling@wur.nl

Jeffery L. Dangl is the John N. Couch Professor of Biology and associate director of the Carolina Center for Genome Science, University of North Carolina, Chapel Hill. E-mail: dangl@email.unc.edu

Paul Schulze-Lefert is the director of the Department of Plant-Microbe Interactions at the Max Planck Institute for Plant Breeding Research, Cologne, Germany, and honorary professor at the University of Cologne, Germany. E-mail: schlef@mpiz-koeln.mpg.de

Next-Generation Communication

IN THE PAST DECADE, THERE HAVE BEEN MAJOR ADVANCES IN OUR UNDERSTANDING OF THE molecular interplay between plants and various classes of microbial pathogens (bacteria, fungi, oomycetes, viruses, and nematodes) and microbial symbionts (rhizobia or mycorrhizal fungi). These fundamental insights, reviewed in a special section in this issue (p. 741), provide a conceptual framework for rational human intervention through the breeding or engineering of crops for durable and broad-spectrum disease resistance. However, such engineered plants will eventually be deployed into soils of varying geochemistry that harbor a staggering diversity of microbes. Many of these microbes can associate intimately with crops or other plants in natural habitats. A deeper understanding of plant-associated microbial communities is likely to offer exciting opportunities for controlling plant growth and pathogen burden in sustainable agricultural settings over the next two decades.

Genetics and molecular biology, and a focus on well-characterized model systems, uncovered the logic of an elaborate plant innate immune system. Additionally, the cellular signaling networks that determine legume nodule symbioses and mycorrhizal associations overlap, suggesting that molecular components of these “legume-specific” networks have clear non-legume counterparts. These findings revitalize prospects for the development of low-input agriculture, in which nitrogen-fixing bacteria and mycorrhizal-stimulated phosphate release are harnessed to reduce or replace the need for nitrogen- and phosphate-based fertilizers. But parasitic and symbiotic associations between plants and microbes are merely the two extreme outcomes of a continuum of interorganismal interactions affecting plant productivity. Remarkably little is understood about plant-microbe interactions that are, at first glance, symptomless. Complex communities of poorly studied plant-associated microbes are an untapped reservoir that can promote plant health and productivity.

One gram of soil typically contains $\sim 10^{10}$ bacteria. Microbial DNA fingerprints from plant roots (the rhizosphere) or aerial organs (the phyllosphere) have uncovered specific microbial communities—microbiomes—thriving on the surface of or within healthy plant tissue. For instance, rhizosphere microbiomes attached to, and within the first few millimeters away from, the root surface are distinct from those in bulk soil, suggesting specific colonization events. Moreover, rhizosphere microbiomes of bacteria and fungi typically differ between plant species. The organic carbon flux from roots promotes the growth of microbial decomposers that, in turn, recycle plant nutrients for root uptake by transpiration-driven water fluxes. Seedlings exude 30 to 40%, and adult plants 20%, of photosynthetically fixed carbon into the rhizosphere in the form of poorly characterized rhizodeposits. This extrusion of nutrients outside the plant raises fundamental questions: Do plants feed and structure microbial rhizosphere communities to their advantage, and if so, how? Is the taxonomic diversity of microbiota related to the functional diversity of food webs? Can the notoriously low heritability of plant growth be accounted for by large environmental interactions with microbial assemblages in the rhizosphere, which are in turn influenced by soil types? Purified isolates of rhizosphere-derived bacteria or fungi can promote plant growth, and a subset of rhizobacteria can suppress the growth of other soil-borne pathogens. Thus, the rhizosphere microbiome is likely to tune both maximal plant growth-promoting and protective functions.

Profiling techniques currently used to assess microbial population structure discriminate genetic fingerprints only at the species level. Advanced DNA sequencing technologies applied to rhizosphere and phyllosphere samples could overcome this limitation to define interspecies community structures. Ironically, very few studies have investigated the microbial populations inhabiting either *Arabidopsis thaliana* or model legumes. These model plants, and selected major crops such as corn and rice, provide superb genetic and genomic platforms for dissecting the organization and functions of rhizosphere and phyllosphere communities, and for identifying the plant loci that contribute to their formation.

– Ton Bisseling, Jeffery L. Dangl, Paul Schulze-Lefert

