

THE AUTHOR FILE

Jeff Dangl

Better surveys of microbial friends and foes

Like humans, plants are teeming with microbes. Some microbes are neutral, some are beneficial and others are up to no good. Sequencing technology allows metagenomics researchers to count and



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classify microbes, helping them discern pals from enemies in plants, human body cavities or entire ecosystems.

Now, Jeff Dangl and his group at the University of North Carolina (UNC) at Chapel Hill have created a way to improve this census-taking. “The potential of this

method is to reduce costs and improve accuracy and depth,” he says.

Commonly, scientists take a microbial survey by sequencing a unique identifier, the conserved 16S ribosomal RNA gene of every microbe in a sample. But challenges get in the way of using these identifiers to characterize microbial communities.

Dangl and his team designed a unique tag for each 16S gene copy. Using this tag removes many of the errors that arise in sequencing and avoids the biases introduced in amplifying the genes during sample preparation. The researchers also found a way to de-emphasize genetic material from host organisms, which can contaminate metagenomics surveys. Dangl credits his graduate students, Derek Lundberg and Scott Yourstone, and Piotr Mieczkowski, who directs UNC’s high-throughput sequencing facility, as the team who “cooked up these improvements.” The approach can also help to study the interaction of plants and their microbial co-inhabitants, an area of research that has long interested Dangl, a biologist and Howard Hughes Medical Institute investigator.

In bridging plant biology, microbiology and immunology, Dangl has garnered cross-disciplinary respect. He is “simply a powerhouse” who pulls everyone along with him towards a goal, says Susannah Tringe, who directs the metagenomics program at the US Department of Energy’s Joint Genome Institute. “Whenever an advisory committee is being put together, it seems like his name comes up—because he can not only quickly understand the science but immediately process the implications and make insightful suggestions.”

Plant geneticist Jeff Bennetzen of the University of Georgia enjoys talking science with Dangl “because he is willing to roam freely in the world of ideas,” which takes a project beyond its next obvious steps.

While earning his PhD at Stanford University, Dangl got hooked on immunology. Then he forged a link few others did, connecting immunology to his passion for plants and their pathogens. He was following one of his mentors’ maxims, which is to pursue one’s curiosity and the path not taken: to look at problems from oblique angles, guided by people who have different training, skill sets and perspectives. “I was fascinated that an organism with no circulating cells and no ability to run and hide from pathogens could evolve,” Dangl says.

After finishing his PhD program, Dangl jumped at an offer to do research at the Max Planck Institute for Plant Breeding Research (MPIZ) in Cologne, Germany. He studied the molecular mechanisms underpinning plants’ reactions to pathogens—a completely new field in the 1980s when molecular genetics was just emerging as a powerful tool.

He and his wife, who is also a scientist, spent 9 years total in Cologne, first at the MPIZ and then at the Max Delbrück Institute. They were first postdoctoral fellows and then junior group leaders in what he calls “a mecca for plant biology.” Although they both had job offers to stay in Cologne or work in France, “the lure of home, and distance from family and friends on the West Coast, tipped the balance,” he says. They both landed faculty posts at UNC.

Besides his commitment to science, Dangl’s heart beats for the arts. When writing, he might listen to Chet Baker or Miles Davis. For fun, his choices include The Grateful Dead, Neil Young, Death Cab for Cutie and Billy Bragg.

“I was an English major in university and still read incessantly,” he says. His list of favorite contemporary novelists includes Haruki Murakami, Salman Rushdie, Ian McEwan and Zadie Smith. He adds Jorge Luis Borges and Gabriel García Márquez as old favorites he often revisits.

Vivien Marx

Lundberg, D.S., Yourstone, S., Mieczkowski, M., Jones, C.D. & Dangl, J.L. Practical innovations for high-throughput amplicon sequencing. *Nat. Methods* **10**, 999–1002 (2013).

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