

Large scale study identifies core microbial community for maize rhizosphere

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In the PNAS study of the maize rhizosphere, heritable microbes associated with maize roots were identified through a large scale, multi-year, and multi-site field study. Credit: Lawrence Berkeley National Laboratory

A plant's health is affected not only by conditions such as water and temperature, but by the microorganisms that live around its roots. The rhizosphere microbiome, as this microbial community is known, regulates nutrient availability to the plant from the soil, and can impact

plant growth and yields.

Published the week of June 25, 2018 in the *Proceedings of the National Academy of Sciences (PNAS)*, researchers report on the results of a large-scale field study that partially replicates earlier trials to identify soil microbes that colonize [plants](#) and which can be associated with particular traits. The work was conducted by an international team led by scientists at the Max Planck Institute for Developmental Biology (MPI), the Howard Hughes Medical Institute at the University of North Carolina at Chapel Hill (UNC), and Cornell University, and includes researchers at the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), a DOE Office of Science User Facility.

"This is an extremely large and thorough temporal survey of the maize rhizosphere microbiota," noted study senior author Ruth Ley of MPI. "The dataset constitutes a rich resource for soil microbiologists and potentially plant breeders, once we zero in on the microbial traits that we'd like to breed for, to reduce dependence on fossil fuels in agriculture."

The study builds on a [previous study](#), also reported in *PNAS*, in which the team used 500 samples from 27 maize lines growing in five fields across three states. All of those samples were collected at a single time point. This time around, the team collected nearly 5,000 samples from a subset of the same maize lines growing in just one field over an entire growing season. "Scaling from 500 to 5,000 is challenging for sample processing and the bioinformatics is also quite challenging, as we had over half a billion 16S sequences," Ley said. "First author Tony Walters did a brilliant job with this."

The information allowed the team to associate abundances of microbial populations with plant genotype, while also distinguishing the effects of conditions such as plant age and weather. The large-scale field study

allowed them to identify 143 heritable microbes, whose population variations across samples were partially driven by differences in plant genotype. Additionally, the team identified a core rhizosphere microbiome consisting of seven operational taxonomic units (OTUs), all within the Proteobacteria phylum, found in every single sample.

"Scaling up allowed us to understand the relative importance of plant genetics, environment, and time," said Cornell University's Ed Buckler, whose team provided expertise on maize genetics and the field trials. "We knew each mattered, but this really provides perspective on how much each matters."

The work was conducted as part of the JGI's Rhizosphere Grand Challenge pilot projects involving maize and the model plant *Arabidopsis*. These projects highlighted JGI's capabilities and expertise that could be harnessed for scientific grand challenges assigned to the DOE's Office of Biological and Environmental Research back in 2010.

"The overarching goal of the Rhizosphere Grand Challenge as it was conceived was to determine the major drivers of microbial community composition in plant-associated [microbial communities](#), e.g., plant compartment, soil type, plant age, and plant genotype," said JGI User Programs Deputy Susannah Tringe. "The previous paper used 454 pyrotag sequencing to demonstrate effects of plant genotype on microbial community structure in the rhizosphere, but lacked the statistical power to make specific genotype-phenotype links. The current study used Illumina tag sequencing, all done at JGI, for deeper sampling and much higher temporal resolution for improved statistical analysis."

Jeff Dangl, Howard Hughes Medical Institute investigator and the UNC John N. Couch Professor of Biology, was one of the original designers of the Rhizosphere Grand Challenge along with Tringe, Ley and Buckler, and offered a final thought on the work: "This is another case of team

science driving discovery, under the inspiration of a champion for the project," he said. "First author Tony Walters fearlessly took on this project and drove it forward. But without JGI's 16S sequencing platform, and without the development by Rob Knight and his group of new computational tools to specifically handle such a huge dataset, it would never have been completed."

More information: William A. Walters et al, Large-scale replicated field study of maize rhizosphere identifies heritable microbes, *Proceedings of the National Academy of Sciences* (2018). [DOI: 10.1073/pnas.1800918115](https://doi.org/10.1073/pnas.1800918115)

Provided by Lawrence Berkeley National Laboratory

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