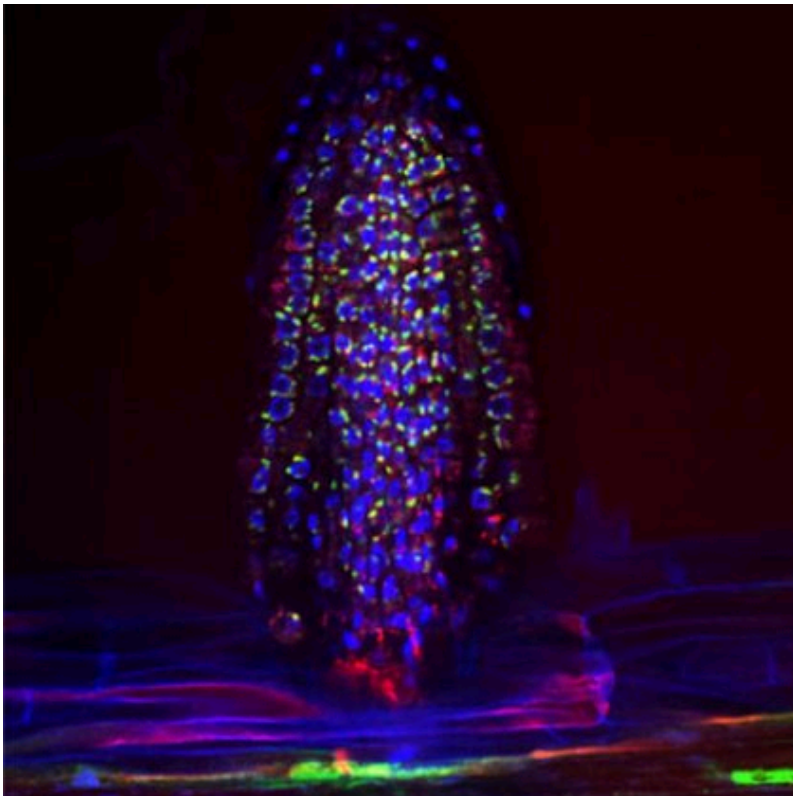


International plant research could reduce our reliance on pesticides and fertilisers



A fluorescent micrograph capturing the presence of bacteria (shown in green) on the surface of an emerging *Arabidopsis* lateral root (plant nuclei shown in blue). (Sarah Lebeis/University of North Carolina)

3 August 2012

The findings of an international plant study, involving Queensland scientists, may help to end agricultural reliance on high pesticide and fertiliser application.

The study sheds light on how microbial communities (microbiomes) living in and on plant roots can boost plant health, growth and defense against pests.

Led by the University of North Carolina and the US Department of Energy Joint Genome Institute, the research studied the microbiome in soil around the roots of more than 600 *Arabidopsis thaliana* plants.

The team, which included The University of Queensland Professor Philip Hugenholtz, investigated how the microbiome helps shuttle nutrients and information into and out of the roots within the soil matrix.

The findings, published on the cover of international scientific journal *Nature* (August 2, 2012

issue), suggest that high resolution knowledge of the plant root microbiome could help develop a strategy of community-based plant probiotics to augment or even replace fertilisers and pesticides and improve plant health.

Co-author Susannah Tringe, head of DOE JGI's Metagenome Program, said the microbiome can be viewed as an extension of the plant's genome.

"We can't really know a plant genome's full functional capacity until we also understand the functional capacity and the drivers governing assembly of its associated microbiome," she said.

"In the same way that microbes play critical roles in and around our own bodies, we are adopting this concept of host-associated metagenomics in plant genomics as well, as it will ultimately lead to predictive interventions that will increase plant health and productivity, disease resistance and carbon capture."

Senior author Jeff Dangl of Howard Hughes Medical Institute (HHMI) said the study provided a deeper and more fine-tuned indication of how host plants and soil microbes shape the shared microbiome.

"We defined microbial taxa that are reproducibly attracted to plant roots, and which ones the plant allows to penetrate into the roots, presumably in exchange for nutritional or other benefits," he said.

Co-author, Phil Hugenholtz from the Australian Centre for Ecogenomics at UQ added that the human microbiome had been the poster child for the application of genomic methods to host-associated ecosystems.

"However plants have a long and impressive history in furthering our understanding of host-microbe interactions," Professor Hugenholtz said.

"I believe that this work and a sister publication in the same issue foreshadow tremendous advances in the study of plant-microbe interactions in the coming years."

The researchers grew the tiny, weedy plant, *Arabidopsis thaliana* in two different soil types, then full plant root systems were removed from their pots and shaken to remove non-rhizosphere soil.

Rhizosphere soil (the area of soil that surrounds the roots of a plant) was then washed off and collected, and finally the roots themselves were frozen and ground up to access the microbes deep inside.

The researchers then isolated DNA from these three compartments—soil, rhizosphere and endophytes—and looked at the 16S rRNA gene, a diagnostic tag that can help distinguish between microbial species.

In a computational tour de force, the researchers sifted through massive amounts of sequence data from the soil, the root-soil interface and the root-cell compartment—over 1,200 samples constituting some two billion bases of high quality DNA code.

The team also involved scientists from University of Bremen, Germany and Cornell University, America,

The team is now engaged in an even larger-scale, long-term study supported by the HHMI, the Gordon and Betty Moore Foundation, the National Science Foundation and the DOE Office of Science to define the root-associated microbiomes of three important model plant species across a wide diversity of geographical locations and ecological conditions.

[The Nature article can be viewed here.](#)

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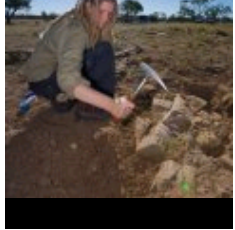
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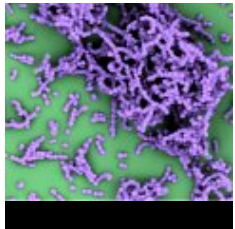


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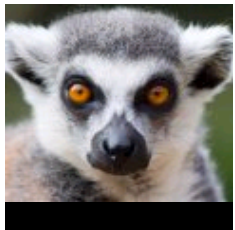


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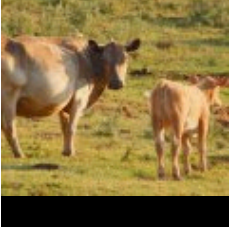


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