

Breeding plants with more beneficial bacteria to feed the world won't be simple, study says

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With the human population expected to climb from 7.4 billion to more than 11 billion people by 2100, some scientists hope that manipulating the plant microbiome could open up new ways to meet the growing

demand for food.

But breeding more beneficial communities of microbes in and on crop [plants](#) may be easier in some [plant tissues](#) and growing conditions than others, finds a study led by researchers at Duke University.

The results appear July 12 in *Nature Communications*.

Mention the microbiome, and most people think of the vast army of [microscopic bacteria](#) and fungi that thrive inside the human body, helping us digest our food and fight infection.

But plants are also home to millions of microbes that have a huge impact on plant health and growth. Beneficial bacteria that live in and on roots and leaves can help plants take up minerals and nutrients from the soil, fend off pathogens and withstand salt, heat and drought.

Previous studies have shown that a plant's genes can shape its microbiome in the lab, but far fewer studies have measured the extent to which the plant microbiome is under genetic control in the field.

"There can be thousands of different kinds of bacteria within a single leaf," said first author Maggie Wagner, who was a graduate student at Duke at the time of the study. "The question is: what factors influence the microbes that end up living inside the plant?"

To disentangle the relative effects of a plant's genes, environment and other factors, Wagner and colleagues used DNA sequencing to analyze the microbiome of a spindly wildflower called *Boechera stricta* where it grows wild in the Rocky Mountains.

Genetically identical lines of the plant were germinated from seed in greenhouses at Duke and then transplanted as seedlings into three

experimental gardens in central Idaho.

Two to four years later, the researchers returned to harvest the plants. They sequenced the bacterial DNA in the roots and leaves of 440 individuals.

When they compared the bacterial sequences they found to databases of known microbes, the researchers detected nearly 4,000 types of bacteria living inside the plants.

Proteobacteria and Actinobacteria were the most common bacterial groups. Roots harbored two to ten times more types of bacteria than leaves.

Environmental differences among sites and between years—such as soil pH, moisture and temperature—had the biggest influence on the plants' bacterial makeup.

On average, 5 percent or less of the variation in microbial diversity was controlled by plant genetics. The influence of plant genes was stronger in the leaves than in the roots, and varied significantly from one site to another.

"There's a lot of interest in harnessing the power of microbiomes for plant health, especially for [crop plants](#)," said Wagner, now a postdoctoral researcher in the Department of Plant Pathology at North Carolina State University.

Agricultural companies are already coating seeds with beneficial [microbes](#) or adding them to the soil to boost the production of crops like soybean and corn and reduce our reliance on fertilizers and pesticides.

These results support the idea that it is also possible to use traditional

plant breeding to shape the plant microbiome. But at least for crops in the same plant family as *Boechera*, such as cabbage and broccoli, breeding a better microbiome may be easier in leaves than roots, and a microbial community that breeds true in one location or set of growing conditions may not be reliably inherited in others.

"Microbiomes could be a very useful tool for improving agricultural productivity in the face of population growth and climate change," Wagner said, "but designing an effective breeding program could be a lot harder than some people think it is."

More information: Maggie R. Wagner et al, Host genotype and age shape the leaf and root microbiomes of a wild perennial plant, *Nature Communications* (2016). [DOI: 10.1038/NCOMMS12151](https://doi.org/10.1038/NCOMMS12151)

Provided by Duke University

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