

Plants control microbiome diversity inside leaves to promote health

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In a new study, published in the journal *Nature*, Michigan State University scientists show how plant genes select which microbes get to live inside their leaves in order to stay healthy.

This is the first study to show a causal relationship between [plant health](#) and assembly of the microbial community in the phyllosphere—the total above-ground portions of [plants](#). The work suggests that organisms, from plants to animals, may share a similar strategy to control their microbiomes.

Microbiome studies are a hot topic in human health science. When scientists mention that human '[gut bacteria](#)' should be well balanced, they refer to the [gut microbiome](#), the [genetic material](#) of all the microbes living in human digestive systems.

"The field of large-scale plant microbiome study is only about a decade old," said Sheng Yang He, lead co-author of the study, a member of the MSU-DOE Plant Research Laboratory and a Howard Hughes Medical Institute Investigator. "We want to know if plants need a properly assembled phyllosphere microbiome.

Plant genes: Gatekeepers of microbes

"In nature, plants are bombarded by zillions of microbes," said He, a University Distinguished Professor who holds joint appointments in the Department of Plant Biology and the Department of Microbiology and Molecular Genetics in the MSU College of Natural Science. "If everything is allowed to grow in the plants, it would probably be a mess. We want to know if the numbers and types of microbes matter, if there is a perfect composition of microbes. If so, do plants have a genetic system to host and nurture the right microbiome?"

It seems plants do. The newly discovered mechanism involves two genetic networks. One involves the plant [immune system](#) and the other controls hydration levels inside leaves. Both networks work together to select which microbes survive inside of plant leaves.

"When we remove both networks from a plant, the microbiome composition inside the leaves changes," He said. "The numbers and mix of bacteria types are abnormal, and our team sees symptoms of tissue damage in plants."

"The symptoms are conceptually like those associated with inflammatory bowel disease in humans," he said. "This is probably because the genes involved are ancient, in evolutionary terms. These genes are found in most plants, while some even have similarities to those involved in animal immunity. "

According to the scientists in the He lab, this may be the first time dysbiosis-associated sickness is formally described in the plant kingdom. The fact it seems conceptually similar to human health suggests a fundamental process in life.

Developing new tech to determine causality

The reason it is difficult to find causality in microbiome studies is because it is practically impossible to cut through the noise of zillions of microbes.

The He lab has worked around this problem by developing a germ-free growth chamber they call the gnotobiotic system—an environment for rearing organisms in which all the microorganisms are either known or excluded.

"Very few people have grown a sterile plant in sterile, organic-rich material," He said. "Our system uses a peat-based soil-like substrate, basically greenhouse potting soil. We use heat and pressure to kill all the germs in the soil, and the plants can grow under this germ-free condition."

Researchers can then introduce microbes in a controlled fashion, into this environment.

"You can add one, two, or even a community of bacteria," He said. "In our study, we extracted a community of bacteria from dysbiotic, or sick, plants and introduced them to our healthy plants, and vice-versa. We found that both the microbiome composition and the plant genetic systems are required for plant health."

For example, a plant with defective genetics could not take advantage of a microbiome transplanted from a healthy plant. The microbiome slowly reverted to the state that caused sickness.

On the other end, a healthy plant exposed to a sick plant's microbiome also suffered. Although it had the genetic tools to select the right microbes, microbe availability was limited and abnormal. The plant couldn't fix the situation.

Microbe levels and composition matter

It turns out that increased microbiome diversity correlates with plant health. Somehow, [plant genes](#) are gatekeepers that encourage this diversity.

The sick plants in the study had 100 times more microbes in a leaf, compared to a healthy plant. But the population was less diverse. To figure out why, the scientists did thousands of one-on-one bacteria face-offs to tease out which strains were aggressive.

In the sick plants, proteobacteria strains—many of which are harmful to plants—jumped from two-thirds the composition of a healthy microbiome to 96% in the abnormal population. Firmicutes strains, many which may be helpful to plants, went down in numbers.

"Perhaps, when the population of microbiome is abnormally higher in that sick plant, the microbes are physically too close to each other," He said. "Suddenly, they fight over resources, and the aggressive—in this case harmful—ones unfortunately win. Healthy plants seem to prevent this takeover from happening."

The big picture: Supporting plant health

The study is yet another example of how diversity is important to support healthy living systems. Each type of microbe might impart different benefits to plants, such as increased immunity, stress tolerance or nutrient absorption.

Scientists such as He want to be able to manipulate the plant [genetic system](#) to reconfigure the plant [microbiome](#). Plants could become more efficient at selecting their microbial partners and experience improved plant health, resilience, and productivity.

"Our field is still young," He said. "Microbiome research tends to focus on human gut bacteria. But many more bacteria live on plant leaves, the lungs of our planet. It would be wonderful to understand how [microbes](#) impact the health of the phyllosphere in natural ecosystems and crop fields."

More information: Tao Chen et al. A plant genetic network for preventing dysbiosis in the phyllosphere, *Nature* (2020). [DOI: 10.1038/s41586-020-2185-0](https://doi.org/10.1038/s41586-020-2185-0)

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