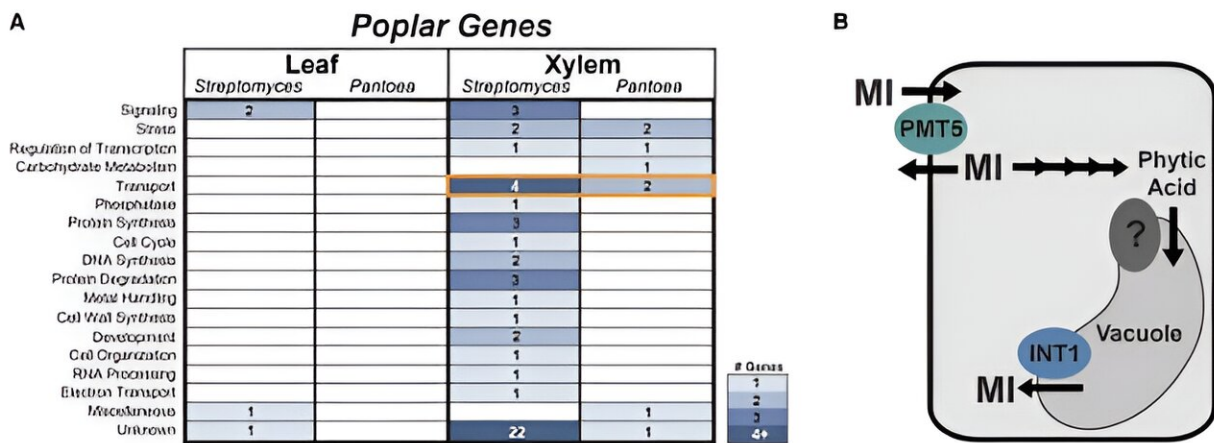


# Signaling across kingdoms to build the plant microbiome

October 19 2023



GWAS sub-networks identify putative poplar genes influencing diverse microbial interactions. Credit: *Current Biology* (2023). DOI: [10.1016/j.cub.2023.06.057](https://doi.org/10.1016/j.cub.2023.06.057)

Microorganisms that live on or in plant tissues form what is known as a plant microbiome. This interface plays an important role in plants' survival due to the existence of beneficial microorganisms. Plants grown in distinct environments can have similar microbiomes or can change over time depending on environmental factors. This complex microbial community assembles and changes by exchanging signals between the host and microbes.

In a recent study, researchers have gathered and filtered a large amount of data using a combination of computational approaches to identify new mechanisms. They then used experiments to validate these mechanisms. This [data mining](#) led to the discovery of a host transport mechanism and a chemical signal that influences beneficial bacterial colonization of plants' roots.

The research is [published](#) in the journal *Current Biology*.

Across the tree of life, microbiomes come together through a complex dialogue between [host plants](#) and their microbial partners. This research adds to scientific knowledge about these dialogues. The study highlighted a unique role for how host plants transport a molecule that influences how microbes colonize microbiomes.

The work used an experimental approach to filter large datasets. This approach will improve researchers' ability to identify new chemical signals. Understanding signaling molecules that are involved with increasing colonization by beneficial microbes will help scientists examine new ways to help plants resist pathogens and reduce the effects of environmental stress.

To be able to identify microbial taxa in any sequence dataset, researchers built kmer profiles from every publicly available sequenced genome. Using these kmer profiles with their ParaKraken codebase on the Summit supercomputer at the Oak Ridge National Laboratory, they analyzed meta-transcriptomic sequencing data from leaf and xylem tissue from approximately 500 *Populus trichocarpa* genotypes grown in a common garden.

This approach allowed the researchers to detect thousands of species of microbes living in these [plant tissues](#). They used the abundance of each species as a phenotype for a [genome-wide association study](#) to determine

which [plant genes](#) were likely affecting the colonization of each microbial species. This resulted in a rich view of the processes that the host plant uses to select for specific microbial species in its microbiome.

The researchers found that two different microbial species were both affected by both of the myo-inositol transporters in plant xylem (stem) tissue. To study this finding further, they used the model plant species *Arabidopsis thaliana* (a small mustard weed) to do so. They used existing lines of *Arabidopsis* in which these myo-inositol transporters had been deleted, and measured the colonization levels of *Arabidopsis* seedling roots in the knockout lines versus a control that contained the genes in a laboratory-based assay where the seedlings were grown on agar plates.

They found that the *Arabidopsis* lines without myo-inositol transporters had significantly reduced levels of colonization. Furthermore, colonization levels were restored when the researchers added myo-inositol to the growth medium in the agar plates. They found that the bacterial colonization is controlled by the same genes in both the stem tissue in trees grown under field conditions and in the roots of mustard weed seedlings grown in the laboratory.

This remarkable finding points to the strong conservation of this mechanism across very different types of plants. The researchers further investigated the mode of action of myo-inositol, which is known to be an internal signaling molecule in plants. Surprisingly, they found that knocking out genes in the plant signaling cascade did not affect colonization levels in *Arabidopsis* roots.

Myo-inositol is a type of sugar that some bacteria can use as a [food source](#), so the researchers knocked out the catabolic pathway for myo-inositol in the bacteria and found that this also did not affect [colonization](#). However, the researchers did discover that myo-inositol significantly affected the motility (swimming capability) of the bacteria.

Thus, it appears that plants are using myo-inositol in a role that has never been studied before, specifically as a cross-kingdom signaling molecule. The plant thus appears to be pumping myo-inositol out of its tissues to trigger specific bacteria to swim towards plant roots and colonize them.

This research has discovered and confirmed a conserved role for the transport of the plant metabolite myo-inositol as a eukaryotic-derived signaling molecule to modulate microbial activities.

**More information:** Bridget S. O'Banion et al, Plant myo-inositol transport influences bacterial colonization phenotypes, *Current Biology* (2023). [DOI: 10.1016/j.cub.2023.06.057](https://doi.org/10.1016/j.cub.2023.06.057)

Provided by US Department of Energy

Citation: Signaling across kingdoms to build the plant microbiome (2023, October 19) retrieved 27 April 2024 from <https://phys.org/news/2023-10-kingdoms-microbiome.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.