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Plant Biology

Building a community: Plants can choose their root's neighbours

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ABSTRACT

Hidden from the eye, plant roots interact with a diverse community of microorganisms living around them. These interactions can have a considerable effect on the health and growth of the plant. Still, our knowledge of how plants modulate them is limited. This study looks at root-specific metabolites, showing some can affect the composition of root-microbiota.

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Root microbiota is the term for the community of microorganisms living in and around plant roots. The microorganisms making up the root-microbiota include multiple species of bacteria, fungi, and archaea, forming a complex network of interaction with the plant's roots. These interactions could either be advantageous or harmful to the plant. Some microorganisms can produce compounds that are beneficial to the plant, such as nitrogen-fixating bacteria. In contrast, others can be harmful by either competing with beneficial bacteria or as pathogens attacking the plant directly. As a result, the composition of the microbiota is essential for the growth, development, and health of plants.

It is estimated that around 20% of the sugars produced by the plant through photosynthesis are used by the root microbiota. Thus, promoting beneficial root-microbiota interactions could help in increasing yield and supporting more sustainable agriculture. However, our current understanding of how plants form, maintain, and modulate the composition of their microbiota is relatively limited.

In this study, researchers used the model plant Arabidopsis thaliana to study how specific metabolites produced by the plant can affect its root-microbiota. This study focuses on a group of compounds called triterepenes, which are plant metabolites involved in signaling and pathogen response. Many of the genes in the triterepenes metabolic pathway express primarily in roots, making triterepenes good candidates for regulating plant to root-microbiota interactions.

The researchers focused on three Arabidopsis-specific metabolites produced in this pathway: thalianin, thalianyl fatty acid esters, and arabidin. They identified the essential genes controlling the biosynthesis of these metabolites. Then, they showed that Arabidopsis plants mutated in these genes accumulated less of these metabolites.

Next, the researchers grew there Arabidopsis plants in soil and compared the composition of the root-microbiota. The results show that the root-microbiota of Arabidopsis plants mutated in these genes were different in composition compared to that of wild-type plants. Such an evidence supports the hypothesis that triterepenes are involved in regulating plant to root-microbiota interactions.

Next, the researchers performed an analysis of the root-microbiota of rice and wheat, which do not produce the arbidopsis-specific metabolites thalianin, thalianyl fatty acid esters, and arabidin. By comparing the composition of the root-microbiota in these species, the researchers showed that some of the bacteria species that were depleted Arabidopsis mutant plants unable to synthesis these metabolites were also less abundant in the root-microbiota of rice and wheat plants, which do not produce them normally.

Finally, the researchers isolated 19 strains of bacteria from Arabidopsis root-microbiota samples, which could be grown in liquid media under lab conditions. When grown in the presence of these Arabidopsis-specific metabolites, some bacteria strains proliferated at an altered rate. Interestingly, some of the species affected belong to the same group of bacteria depleted or accumulated in the root-microbiota of Arabidopsis mutant plants. This trend observed both *in vitro and in vivo* indicates these root metabolites act selectively on specific bacteria strains promoting or inhibiting the proliferation of specific bacteria.

This study provides an interesting preliminary view into the nature of root-microbiota interactions, but also opens up many venues for future research.

Arabidopsis roots produce hundreds of metabolites, the biological significance of some of which is currently unknown. This study proposes an additional way of studying the role of these compounds- not by exploring the direct effect on the plant, but rather by studying the root-microbiota. Moreover, studying root-metabolites and their impact on root-microbiota in other plant species can also provide valuable information. Arabidopsis is a useful model organism for plant research. Still, for agricultural purposes, we must understand the interaction between plant and root microbiota in major crop species- rice, corn, wheat, etc.

It is also interesting to note that in this study, the changes in the composition of the microbiota were not reported to affect root morphology or architecture. The significance of enrichment in specific microorganisms in the microbiota remains unknown. Considering the energetic investment of the plant in maintaining its microbiota, it is likely that some changes in microbiota composition would result in morphological changes. Studying these could increase our understanding of the significance of the interaction between plant roots and specific bacteria strains.

Finally, many bacteria can be detected by analysis of the genetic material found in soil (such as ribosomal RNA fragments), but fail to grow under lab conditions. Understanding how plants foster specific root-bacteria interactions could reveal the conditions these bacteria require to survive, allowing us to study them directly.