PLANT SCIENCE

Multikingdom diffusion barrier control

Plant microbiomes modulate selective nutrient uptake by regulating diffusion barriers

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Despite their differences in evolutionary history, both plants and animals have evolved specialized barrier systems to control their interaction with the external world. Such barriers are crucial for selective nutrient uptake. In the animal gut, epithelial cells that are firmly connected by tight junctions play a key role. In plants, nutrient uptake occurs in the root, where a cell layer called the endodermis plays a similar role to the gut epithelium. The diffusion barriers around the endodermis separate the inside of the plant from the outside and allow the endodermal cells to determine which nutrients are taken up. As in the animal gut, the root microbiome is influential for nutrient uptake. On page 143 of this issue, Salas-González *et al.* (*1*) reveal an interplay of the developing endodermis and microbes that is tightly related to a plant's ability to take up nutrients efficiently.

Land plants acquire their nutrients and water from the soil through their root system. To allow for selective nutrient uptake, barriers have evolved that inhibit passive diffusion through the cell walls. The key diffusion barriers for nutrient uptake are formed around the endodermis and consist of impregnating layers of hydrophobic polymers. One of these layers, the Casparian strip, is made of lignin, which is a cross-linked polymer deposited in the cell walls of the endodermis. It gives rise to a ring that encompasses the endodermal cell layer and seals the cell wall space (*2*). The other diffusion barrier is the lipophilic polyester polymer suberin, which is deposited at the inner surface of the cell walls and effectively covers the entire surface of the endodermal cells (*3*). Together, these layers seal the outside of the root from the inside, thereby forcing any nutrient to pass by cellular uptake and subjecting them to homeostatic mechanisms, thus enabling the plant to have control over the nutrients it takes up. Thus, the endodermis has a function similar to that of the gut epithelium in animals, but the barrier function is conferred by lignin and suberin layers as opposed to tight junctions in the gut epithelia.

The diffusion barriers at the endodermis can be modulated by nutrient concentrations (*4*). For instance, there is increased deposition of suberin in response to high-salt conditions. Conversely, nutrient-deficient conditions for several minerals, such as iron or zinc, lead to reduced suberin deposition. This is reminiscent of nutrient-dependent modulation of the permeability of endothelial barrier function in the animal gut. For instance, glutamine increases intestinal barrier function, (*5*) whereas dietary fats can decrease barrier function (*6*).

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Now, the discovery of Salas-González *et al.* adds another layer of regulation of the diffusion barriers in plant roots and illuminates the pathways underpinning this regulation. They show that particular bacterial strains within the root microbiome have the capacity to change the composition and function of the endodermal diffusion barriers through the repression of the abscisic acid hormone signaling pathway, which is a main player in the response of plants to environmental stresses. This modulation can improve plant health in stressful conditions. Again, this finding is reminiscent of mechanisms in animal guts, even though the molecular mechanisms underpinning it are mostly unknown. In animal guts, microbes have been shown to regulate the barrier function of the epithelium, which is accompanied by stress-protective effects (*7*). Therefore, the dynamic relations of barriers in plant and animal systems seem to share a number of fundamental properties.

Studying host-nutrient-microbiome interactions using experimental perturbations requires a large number of experiments, because the matrix of experimental conditions grows large very quickly. The *Arabidopsis* system used by Salas-González *et al.* offers a number of specific advantages. *Arabidopsis* is a self-fertilizing species, thereby giving rise to multiple isogenic progeny that can be used to systematically study the causes and mechanisms of the interplay of host genotypes, nutrition, and microbial effects on diffusion barriers and their consequences on organismal health. Moreover, a large array of mutants is available, including mutants that are defective in the formation of the diffusion barriers or that are involved in plant-microbe interactions or nutrient sensing and homeostasis. Use of such mutants could reveal whether specific microbe-derived molecules or metabolites, or combinations of molecular signals and nutrient concentrations, trigger the impact on barrier formation.

The work by Salas-Gonzáles *et al.* has revealed an important facet of the complex interplay of selective nutrient uptake, nutrients, and microbes. In addition to the fundamental principles that such studies in this area can provide, there are agricultural prospects, too. Plant nutrition is highly relevant to our need to feed a growing global population by developing crops with high nutritional value. The latter is a particular challenge, because nutrient deficiencies still affect a notable fraction of the global human population (e.g., iron deficiency) and carbon fertilization by the increasing carbon dioxide concentrations in the atmosphere is projected to lead to a reduction of key nutrients in food crops (*8*). Tailoring root microbiomes to fine-tune nutrient uptake for maximizing yield and plant nutritional quality might provide an opportunity to address these issues in a way that is faster to roll out and that might require less effort than engineering crop genetics. ■

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