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Influence of phosphorus and sucrose in root morphology, biochemistry and physiology

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Phosphorus is one of the most limiting nutrients for crops in the world and the least efficiently used by plants. To increase the absorption capacity of Pi, plants need to adapt the biochemistry, physiology and morphology of their root system. An alternative to solve this problem is to explore the genetic diversity available and breed more Pi-absorption efficient cultivars in combination with soil management practices. Previously, we evaluated maize genotypes for their Pi uptake and use efficiency by verifying grain yield under contrasting levels of phosphorus. In this study, two contrasting genotypes were used to perform a detailed morphological parameters characterization of the root system of plants grown in nutrient solution. We have standardized the growth conditions in nutrient solution (time course and Pi concentration), as well as the parameters to be assessed. To help test the hypothesis that Pi and sucrose availability have a significance on root growth, we tested three different sucrose concentrations (0, 50 and 150 mM) in low and high Pi conditions (2.5 and 250 uM) on two maize contrasting lines. Concentration of sugars (sucrose, glucose and fructose), Pi, K, Ca, Mg and S were measured from maize roots and shoots, as well as the expression of genes involved in sugar metabolism, Pi response and root morphology. We showed that sucrose influenced maize development, modifying not only genetic and biochemical profiles, but also root morphology. Plants grown on sucrose showed a smaller number of fine roots that had higher sugar content, and the genes involved on these processes were also affected. The shoots from sucrose grown plants presented higher Pi and lower K and Ca content. We showed with this study that low Pi and no sucrose at 12 days after treatment are the most feasible conditions to distinguish maize contrasting genotypes for Pi use efficiency. Some root characteristics that are associated with P acquisition can be used for early screening of more efficient plants. This information is essential to accelerate the breeding process and to support advanced studies in molecular biology and physiology, culminating on the in the development of maize efficient cultivars that use less fertilizers.

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Towards deciphering plant-fungal dialogues

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The arbuscular mycorrhiza (AM) association results from a successful interaction between the majority of terrestrial plants and fungal symbiotic partners in the Glomeromycota. Host plants supply photosynthates to their AM fungal partners and, in return, AM fungi enhance the phosphate and nitrogen nutrition of their hosts. This bi-directional nutrient exchange is believed to take place at intracellular fungal structures, called the arbuscules, that form within the root cortical cells. Development of fungal arbuscules induces polarization of the colonized cell and is accompanied by the synthesis of an extensive periarbuscular membrane. This membrane remains in continuum with the peripheral plasma membrane and governs the molecular dialogue between fungus and plant. While there has been much progress in understanding signaling during the early phase of AM symbiosis development, the regulation of symbiosome development, and nutrient transport are largely unknown.

Proteomics is likely to be the best methodology to unravel the molecular components of the plant-fungus interactions. In a novel proteomics approach we aim at determining the molecular constituents of the periarbuscular membrane and the peripheral plasma membrane sub-domains of the polarized arbusculated cells.