

THE CHALLENGES OF MINERAL NUTRITION IN PLANTS FACING ENVIRONMENTAL STRESSES: MOLECULAR ASPECTS

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Understanding mineral homeostasis in plants is essential for global food security. On one hand, mineral disorders can cause significant crop yield losses. On the other, these studies can allow the development of strategies for biofortification, which is the enrichment of staple crops with essential nutrients. Plant mineral nutrition is a critical issue since often management practices such as fertilizer application cannot alleviate nutritional disorders. Besides, under stressful conditions, plants can modify their mineral homeostasis, changing the proportion of mineral concentration in edible parts. Therefore deciphering how plants regulate mineral homeostasis could contribute to the development of new varieties enriched in beneficial elements while minimizing the concentrations of undesired elements. This symposium will discuss the recent advances in mineral nutrition in plants and how environmental stress can impact it. Professors Michael Frei from the University of Bonn, Hannetz Roschttardt from the Universidad Católica de Chile, and Felipe Ricachenevsky from the Universidade Federal de Santa Maria are the invited speaker in this symposium.

GENETIC APPROACHES TO ADAPT RICE PRODUCTION TO IRON TOXICITY

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Fe toxicity is one of the major mineral disorders affecting rice (*Oryza sativa* L.) in flooded soils. Therefore we explored genetic variation for breeding novel varieties tolerating high levels of Fe. To this aim, we dissected genetic variation in Fe tolerance using bi-parental mapping of quantitative trait loci (QTL), and genome-wide association study. Candidate genes were further explored using gene knockout and overexpression lines. For example, we demonstrated that the potassium ion channel *OsAKT1* is involved in Fe tolerance, as potassium homeostasis affects Fe uptake in Fe toxic conditions. Several additional candidate genes are currently being investigated using mutants generated by genome editing (CRISPR/cas9). We also characterized physiological mechanisms of Fe tolerance, including redox homeostasis. The antioxidant ascorbic acid developed pro-oxidant activity in the presence of high levels of Fe by stimulating Fenton reactions leading to the production of hydroxyl radicals. More recently we have explored rice wild relatives as a source of novel genetic variation in Fe tolerance. As the species *Oryza meridionalis* and

Oryza rufipogon showed high Fe tolerance in screening experiments, interspecific chromosome segment substitution lines (CSSL) with *O. sativa* background were screened to identify novel QTL and physiological mechanisms underlying the ability to tolerate extremely high levels of Fe in foliar tissue. In conclusion, our work demonstrated substantial scope for mining genetic diversity for the breeding of rice adapted to Fe toxicity.

THE DIVERSE IRON DISTRIBUTION IN EUDICOTYLEDONEAE SEEDS: FROM *Arabidopsis* TO QUINOA

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Increased iron content in seeds is an important agronomic trait. This is due to the relevance of this element in seed production, embryo development, and seedling germination and growth, as well as in human nutrition. Seeds accumulate iron during embryo maturation stages of embryogenesis. Using *Arabidopsis thaliana* as model plant, it has been described that mature embryos accumulate iron within a specific cell layer, the endodermis. This distribution pattern is conserved in most of the members of Brassicales plants, with the exception of the basal *Vasconcellea pubescens* that also shows elevated amounts of iron in cortex cells. To determine whether the *V. pubescens* iron distribution is an indicative of a wider pattern in non-Brassicales Eudicotyledoneae, we studied iron distribution pattern in different embryos belonging to plant species from different Orders from Eudicotyledoneae and one basal from Magnoliidae. Our results indicate that iron distribution in *A. thaliana* embryo is an extreme case of apomorphic character found in Brassicales, not-extensive to the rest of Eudicotyledoneae.

WHO CONTROLS THE IONOME? MULTIPLE APPROACHES TO IDENTIFY GENES REGULATING ELEMENTAL VARIATION IN *Arabidopsis* AND RICE

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Plants are sessile organisms, and as such they must efficiently search nutrients in the soil. To understand the mechanisms involved in such control, the ionome is a useful concept for plant nutrition: it is defined as the inorganic composition of an organism, its organs, tissues or single cells. Ionomics is the integrated study of an organism's nutrients and trace elements, and consist in multi-element methods that allow us to study the ionome. Our work is focused in understanding which genes control the ionome in model and non-model species, and how we can access plant genetic diversity to improve plant and human nutrition. Three approaches will be showed: 1) How we have been using multiparent inbred lines to identify alleles that determine *Arabidopsis thaliana* ionome natural variation, and how this allowed us to characterize a new rare allele for Zn leaf accumulation; 2) How the leaf and seed ionome vary in the *Oryza* genus, which is composed of 25 species, most of them wild, and how some phenotypes are fixed in some species. We will focus on sodium (Na) accumulating wild rice species which is also salt stress tolerant, and how we are using wild rice introgression lines to transfer the trait into cultivated rice; 3) How we are performing a large-scale rice mutant panel screening for seed ionomics phenotypes, using ~1000 fast-neutron generated lines with high coverage genomic sequence. This approach is allowing for fast identification of causative mutations, as well as providing a good community resource.
