



ABSTRACT

*“Molecular and physiological basis of plant nutrition:
Insights into the responses to magnesium and nitrate
availability”*

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Crop nutrition can be manipulated through agronomy and genetics, to optimize biomass allocation and thereby crop yields, and the delivery of essential mineral nutrients to humans and livestock. Our primary research goal is to dissect and exploit the physiological and genetic bases for plant mineral nutrient use efficiency (NUE). (i) The first focus is on magnesium, which is an essential element in plant cell biology but also the fourth most common cation in the human body and half of its dietary intake is from plant origin. Hypomagnesaemia in the human body is recognized as a global clinical problem. Our primary interest is to identify genes involved in Mg homeostasis in the model species *Arabidopsis thaliana*. To achieve this goal, our experimental outlines are to use natural and mutant-induced changes in Mg content and to identify transcriptome changes associated with Mg depletion and restoration. (ii) The second focus is on nitrate since it is the major nutritional determinant of root morphology, and because of its agronomic significance in determining yield and seed set. Modifying root system architecture (RSA) is one of the strategies aimed at developing plants that capture nutrients more efficiently, which are suited for sustainable farming with less fertilizer inputs. Learning about mechanisms of lateral roots (LRs) growth stimulation or repression by nitrate availability will help to draw strategies to modify RSA. Low nitrate levels in the soil stimulate lateral root development, which substantially increases the root surface area available for acquisition. Conversely, homogeneous high levels of nitrate inhibit lateral root elongation. We are trying to gain better knowledge about these nitrate-dependent changes in root morphology of *Arabidopsis*. Forward genetic dissections (mutant screens) and genome-wide association mapping are currently used to identify key genes that determine RSA and root biomass allocation. Our applied ambition is to transfer the benefits from *Arabidopsis* research to *Brassica* crops. Comparative genomics through a model-to-crop pipeline will allow key genes controlling root architecture traits and mineral content to be studied in crop systems.