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“Development on the margin”

## The Role of Plant Defense Proteins During Early Symbiotic and Pathogenic Infection in Model Legume *Medicago truncatula*

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### Abstract

Legumes are among the most economically important crop families playing a vital role in human and animal diet as excellent sources of protein, vitamins, minerals and other nutrients. Grain legumes including chickpea, pigeon pea, soybean, dry beans, etc, form an extremely essential protein source for millions of poor families in semi-arid and tropical regions of many Asian and African countries. Legumes are unique in establishing rhizobial bacteria association which allows nitrogen fixation, production of protein-rich food and hence able to grow in nitrogen starved soils. Legumes are also capable of establishing symbiotic association with arbuscular mycorrhizal fungi. However, their pathogenic interactions with oomycete root rot pathogens like *Aphanomyces euteiches* often lead to major yield losses worldwide. The infection physiology involves protein-protein interactions between the pathogen and the host plant, where the latter generates symbiotic and pathogenic specific cellular responses. Our research study focuses on the two plant response mechanisms using the model legume *Medicago truncatula*.

We characterised the early host plant response upon infection by symbiotic (*Sino rhizobium meliloti* and *Glomus intraradices*) and pathogenic (*Aphanomyces euteiches*) microorganisms in wild type and transgenic plants lines deficient of a candidate signalling protein MtRac1 involved in host plant defense and symbiosis. Phenotypic comparisons of MtRac1-deficient plant cultures with wild type plants shows significant differences indicating the role of this protein in plant growth. Our results on gene expression analysis via semi-quantitative RT-PCR show significant expression of MtRac1 in wild type plants and transformed vector control cultures upon infection but not in Rac1 deficient cultures. Furthermore, analysis on evaluation of infection profiles, proteomic analysis and mass spectrometry to identify protein patterns activated in the plant cells will confirm the role of initial defense proteins against microbial infections. These results contributes to the development of new practices for control of soil borne pathogens and provides an outlook to investigations on opportunities for disease resistance development in legumes and in plant breeding to capture possibilities of raising crop yield, nutritional quality, limited pesticide use and over all poverty alleviation.

**Keywords:** *Aphanomyces euteiches*, arbuscular mycorrhizal symbiosis, *Medicago truncatula*, plant defense proteins, *Rhizobia* bacteria symbiosis