



Dissecting *Medicago truncatula* leaves for the analysis of root formation in tissue culture.

Our Group focuses on the processes involved in plant meristem development and plant responses to bacterial infection. We are investigating the nodule meristem formed on legume roots by *Rhizobium* infection, the interaction of *Rhizobium* with rice plants and root biology.

Our research utilises two interacting, well-characterised model organisms—the legume *Medicago truncatula* and the soil bacteria *Sinorhizobium meliloti* as well as the interaction between *Rhizobium leguminosarum* bv. *trifolii* strain R4 and rice. With these we are able to assess the role of specific genes, gene products and signalling molecules that regulate growth and development.

One of our aims is to isolate and characterise novel peptide signal molecules that may act as regulators of proliferating meristemic cells and their differentiation. Knowledge of these peptide signals and the control of meristem communication is the key to manipulating plants for adaptation to the Australian environment and for the production of pharmaceuticals.

GENOMIC INTERACTIONS

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HIGHLIGHTS

- The *skl* mutant is an ethylene-insensitive hypernodulating legume mutant which lacks the ability to modulate auxin transport from the shoot to the root when inoculated with its symbiont *Sinorhizobium meliloti*. However, at the nodule initiation zone rhizobia reduced auxin transport in the *skl* mutant but the increased expression of the auxin efflux transporters resulted in higher nodule numbers. Proteomic analysis showed that in the rhizobia inoculated *skl* mutant, the levels of plant defense and stress response proteins were reduced, resulting in increased nodule numbers.
- *Rhizobium* strains can infect non-legume rice. Most *Rhizobium* strains initiate an infection through cracks at emerging lateral root regions, where they multiply briefly before inhibiting the growth of the rice seedlings. A few strains, however, continue to multiply in the intercellular spaces and colonise the root. This method of entry is not encoded for by either the symbiotic (pSym) or the tumour-inducing (Ti) plasmids.
- One strain of *R. leguminosarum* bv. *trifolii*, strain R4, could enhance the growth of some rice cultivars. R4 is a denitrifying strain, reducing nitrate to nitrogen gas and did not build up detectable levels of NO, which is toxic in rice tissues. Most *Rhizobium* strains are not denitrifiers and inhibit rice growth. Strain R4 is thus a candidate for engineering into a future biological nitrogen fixation system within these roots. When labeled with green fluorescent protein (gfp) as a visual marker, R4 could be seen to infect the root hairs near the base of growing lateral roots, form structures resembling infection threads inside rice root hairs and to colonize the intercellular spaces of the rice roots.
- Using a computational approach we have identified over 500 non-coding RNA genes in *Medicago truncatula* and over 1500 in *Lotus japonicus*. These have been contrasted with protein encoding genes and their characteristic features now enable us to predict non-coding RNA genes using a machine learning approach. We have also found that many of these RNAs encode microRNAs and have created the *Medicago*- and *Lotus* MIRAT (microRNA and target gene) databases available as web services.