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Metabolomic studies of model legume *Medicago truncatula*

We want to use a metabolomics approach to further examine the well characterised interactions between two model organisms - the legume *Medicago truncatula* and the soil bacteria *Sinorhizobium meliloti*. This approach enables the role of specific genes, gene products and signalling molecules regulating growth and development to be assessed. These signals include those regulating and co-ordinating the proliferating meristemic cells (root, shoot, flower and nodules) and their differentiation. Similarly, the extracellular signal molecules, called quorum sensing signals, co-ordinate bacterial colonisation of hosts will be examined for their effects on the plant. *Rhizobium* bacteria without these molecules fail to induce nodules on legume roots. Environmental conditions (eg soil nitrate, moisture and salt levels) also influence root architecture, mainly by regulating the initiation or suppression of lateral roots, or variation of root length, spacing and number. Roots are ideal for studying the effects of growth-promoting and -inhibiting compounds because it is possible to measure the location of differentiation events

As a basis for this work the Genomic Interactions Group (GIG) in the Research School of Biological Sciences has compiled proteome reference maps for the plant symbiont *Sinorhizobium meliloti* and the barrel medic plant (*Medicago truncatula*) (<http://semele.anu.edu.au/>) using peptide mass finger printing (PMF) of proteins isolated from 2D-gels. By identifying proteins on the scale of the proteome (upwards of thousands of proteins, depending on the state of the cells being analysed), using technologies of 2D-gels and high throughput mass spectrometry, it is now becoming possible for biologists to start building complex maps of cell function and to take a global view of cellular processes.

The next great question is what all these genes and their protein products do in the cell. Some clues may be garnered through homology analysis but ultimately the answer requires some kind of biochemical analysis; a profiling of the cellular metabolites, also known as metabolomics. Metabolomics can yield important information about the function of the translated proteins but is a much more challenging endeavour as it covers many different classes of chemical compounds (eg fatty acids, mono- and polysaccharides, steroids, flavonoids, terpenes, pigments, phytohormones etc), unlike proteomics, transcriptomics or genomics where one is looking at either nucleic acids or proteins and where it is possible to confirm sequences of nucleic acids against sequences of amino acids and vice versa. Nevertheless, the task can be made manageable by targeting particular classes of compounds for analysis by hyphenated techniques such as GC/MS or LC/MS. Analysis of key metabolites will test predictions about the dynamic fluctuations of the metabolic state from proteome analyses.