**The incompatible interaction between Medicago truncatula A17 and Sinorhizobium meliloti RM41 induces early nodule senesce**

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*Medicago truncatula* establishes nitrogen-fixing symbiosis with *Sinorhizobium* species *S. meliloti* and *S. medicae*. To identify the genetic determinants of the symbiotic process large-scale mutagenesis programs have been initiated in both partners using chemical mutagens, fast-neutron bombardment or transposable elements (1). These programs have helped to isolate a number of genes that are essential for the initiation and development of the symbiotic process. By exploring the natural variations existing among different ecotypes and strains of the plant and bacterial partners, respectively, one can identify genes/proteins that are required only under certain conditions, with certain partners and/or participate in the fine-tuning of the interaction (2-4).

We found that M. truncatula A17 ecotype that has a sequenced genome can establish effective symbiosis with a number of S. meliloti and medicae strains including the reference strain 1021, but it is ineffective with strain RM41. M. truncatula DZA315.16 and A20 ecotypes, however, form effective symbiosis with both bacteria. We have shown with microscopic analysis that although bacteriod development occurs in the incompatible nodules, final nodule differentiation is arrested and bacteroids that are unable to fix nitrogen disappear from the nodule cells that are repopulated by saprophytic bacteria.

We compared the transcriptome of 10 and 21 day old nodules formed on the roots of two M. truncatula ecotypes (A17 and DZA315.16) after inoculation with Rm41 to identify those bacterial and plant pathways that are differentially expressed in the effective and incompatible interactions. We could detect the early and elevated expression of senescence related genes (cysteine proteases, chitinases and phosphatases). In addition, several genes involved in defense response (resistance proteins) showed altered expression in the incompatible nodules. The increased expression of about 40 transport mechanism related bacterial genes in the inefficient nodules was also observed.

(1) Tadege et. al. (2009) Plant Physiol. 151:978-984.

(2) Tirichine et al. (2000) Plant Physiol. 123:845–851.

(3) Crook et al. (2012) Mol. Plant-Microbe Int. 25: 1026–1033.

(4) Liu et al. (2014) BMC Plant Biology 14:167