## FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology



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## Soybean Nodulation: From Gene Mutation, via Gene Isolation to Functional Circuits

Legume plants (18,000 legume species exist) possess a complex root-developmental pathway, leading to nitrogenfixing nodulation. Rhizobium bacteria induce cortical cell proliferation, then invade concurrently the newly developed tissue to differentiate into nitrogen-fixing bacteroids. This nodule development is of global significance for agriculture and ecology. We have used a variety of analytical approaches to understand one key component of this symbiosis, namely the legume-specific process of 'Autoregulation of Nodulation' (AON). The symbiosis (both nodule induction and nitrogen fixation) is inhibited by nitrate. We used induced EMS mutagenesis of soybean to isolate nitrate-tolerant symbiosis (nts) mutants. They lacked AON. The mutant trait was controlled by a single genetic element, shown to be active in the shoot. Thus communication between root and shoot was assumed. We then developed complex DNA profiling and gene cloning techniques to first clone the mutated gene (2002). It encodes a LRR receptor kinase called GmNARK. GmNARK homologues are functional in other legumes such as pea, bean, Medicago truncatula (called SUNN) and Lotus japonicus (called HAR1). We then found interacting genes and signalling factors. GmNARK is modulated by GmKAPP (Kinase Associated Protein Phosphatase). GmNARK is also the receptor of inoculation for nitrate-induced, root-derived RIC peptides. These are 11-12 amino acids long, and triarabinossylated at a central proline (P7). These are an excellent example of systemic communication. GmNARK regulates the synthesis of a microRNA (miR2111) in the shoot. This RNA is essential for nodulation, interacts with the TML (Too much love) gene. GmNARK, once activated by CLE peptide (either GmRIC1 or GmRIC2), suppresses the synthesis of miR2111, thus inhibiting further nodule induction. We thus understand the overall AON control circuit, its signal peptide and microRNA, and the receptor kinases and transcription factors. Most importantly the data suggest that similar control circuits exist for other processes in plants.

## **Country or International Organization**

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