

HIGHLY SPECIFIC HOSTS IN THE LISTIA SECTION OF THE LEGUME GENUS *LOTONONIS* ARE NODULATED BY METHYLOBACTERIA AND BY NOVEL ISOLATES THAT ARE A NEW GENUS OF ROOT NODULE BACTERIA

Julie K. Ardley, Graham W. O'Hara*, Wayne G. Reeve*, Ron J. Yates*, Michael J. Dilworth, John G. Howieson*

Centre for *Rhizobium* Studies, Murdoch University, Murdoch W. A. 6150, Australia; J.Ardley@murdoch.edu.au

Symbiotic specificity and nodule morphology are characteristics that can be used as taxonomic markers in the legume genus *Lotononis* and that support its division into two separate genera. *Lotononis* (from the Crotalariaeae tribe in the Genistoid clade of the sub-family Fabaceae) is of mainly southern African origin, comprising some 150 species of herbs and small shrubs. Our work has shown that *Lotononis* is nodulated by phylogenetically diverse root nodule bacteria and that different specificity groups exist within the genus. *Lotononis* is currently divided into 15 taxonomic sections. Species in the Listia section (*L. angolensis*, *L. bainesii*, *L. listii*, *L. marlothii*, *L. subulata* and *L. solitudinis*) form collar nodules and are highly specific in their ability to nodulate with root nodule bacteria (RNB). Species from other sections within *Lotononis* form indeterminate nodules and RNB isolated from these hosts belong to species of *Bradyrhizobium*, *Sinorhizobium*, *Mesorhizobium* and non-pigmented *Methylobacterium*, based on sequence analysis of the 16S rRNA gene. These RNB are unable to nodulate species in the Listia section. All studied Listia section species form effective nitrogen-fixing symbioses with pink-pigmented methylobacteria, except *L. angolensis*, where the nodules are ineffective. These methylobacteria also form ineffective nodules on *Lotononis* species outside the Listia section. Interestingly, none of these methylobacteria strains that we have tested is able to utilize methanol. *L. angolensis*, which grows in more tropical areas of Africa than the other Listia species, forms effective nodules with a group of as yet uncharacterized bacterial strains. Our phenotypic and genetic analysis of the alphaproteobacterial *L. angolensis* symbionts indicates that they form a lineage that is distinct from currently described RNB and constitutes a new genus. *L. angolensis* isolates are typically pink-pigmented, fast growing and mucilaginous. The optimum growth temperature is 41°C. A phylogenetic tree based on the sequence of a nearly full-length portion of the 16S rRNA gene grouped the *L. angolensis* isolates with a number of other RNB that have not yet been fully described. These include North American *Lupinus texensis* symbionts, a strain isolated from *Phaseolus vulgaris* in Ethiopia and an isolate from *Indigofera tinctoria* in tropical northern Australia. Closely related non-symbiotic bacteria include species of *Balneiomonas*, *Bosea*, *Chelatococcus* and *Microvirga*. The *L. angolensis* isolates are unable to nodulate *L. bainesii* or *L. listii*, but have formed effective symbioses with other *Lotononis* species.

Ms Ardley is the recipient of a Murdoch University Research Studentship.

EVALUATION OF COWPEA BREEDING LINES FOR NITROGEN FIXATION AT ARC-GRAIN CROPS INSTITUTE, POTCHEFSTROOM, SOUTH AFRICA

Joseph A. N. Asiwe*¹, Alphonsus Belane**, Felix D. Dakora**

*ARC-Grain Crops Institute, Private Mail Bag X1251, Potchefstroom 2520, South Africa **Tshwane University of Technology, Pretoria, South Africa

Cowpea, *Vigna unguiculata* (L.) Walp, is one of the important grain legumes in South Africa. It is an important source of cheap plant protein to most poor families, provides regular income to farmers for the sale of grain and fodder, and a good source of animal fodder. In addition, cowpea is good for the sustainability of soil fertility through biological nitrogen fixation. The amount of biologically fixed nitrogen can be enhanced by different methods, including inoculation with proven strains, screening for improved microbial and host-plant materials, and introduction of improved cultural practices. Cowpea breeding program in attempt to enhance the genetic diversity of its gene bank, has introduced many exotic cowpea lines. The agronomic potentials of these lines to fix atmospheric nitrogen as to meet their nitrogen requirements and or contribute to nitrogen enrichment of the soil have not been studied. This paper reports the results of screening conducted to identify cowpea lines that possess high potentials to fix atmospheric nitrogen. Thirty cowpea genotypes were screened in replicated trials at Taung, South Africa and Wa in Ghana, during 2005/06 cropping season using randomized complete block design. Data were collected on important parameters which included mass of root nodules, specific nodule activity, grain and dry fodder yields as well as hundred seed weight. Results showed that there was significant differences observed among the genotypes in all the variables at both locations, and that the performances of genotypes at Taung were significantly higher than those at Wa. Nodule mass per plant varied from 0.53 g to 3.33 g at Taung and 0.1g to 2.7g at Wa. Highest nodule mass was obtained from Bechuana white and IT82D-889 at Taung and from Wa, respectively, while Machananyiko (61.5 µgN-fixed.mg nod DM⁻¹.d⁻¹) and Pan 311 (96.90 µgN-fixed.mg nod DM⁻¹.d⁻¹) had the highest specific nodule activities Taung and Wa respectively. IT90K-59 (3388 kg ha⁻¹) and Soronko (1019 kg ha⁻¹) produced the highest grain yield at Taung and Wa respectively. Highest fodder yields were obtained from Valanga (8260kg ha⁻¹) at Taung and TVu 11424 (1720 kg ha⁻¹) at Wa. Highest mass of hundred seeds was obtained from CH14 (16.40 g) and Brown eye (18.23 g) at Taung and Wa, respectively. The implications of these on their nitrogen fixation are discussed in the paper. The best promising lines are selected for further laboratory studies and hybridization in the cowpea improvement programme.

This work was funded by McKnight Foundation, USA.