

GENOMIC ARRANGEMENT OF *NOD* GENE SEQUENCES OF *BRADYRHIZOBIUM* ISOLATES FROM TGX SOYBEAN GENOTYPES IN RELATION TO *BRADYRHIZOBIUM* USDA110

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Soybean nodulates with specific rhizobia and usually requires inoculation with *Bradyrhizobium japonicum* strains. Several varieties (e.g., Malayan and Orba) introduced to Africa (Pulver et al., 1982;) were however adequately nodulated in soils that had no previous inoculation with *B. japonicum* while cultivars from North America were poorly nodulated. The freely nodulating soybean genotypes, termed promiscuous, however, had poor agronomic characteristics. The International Institute of Tropical Agriculture (IITA) selected soybean genotypes that combined the free nodulating traits of the promiscuous genotypes and the improved agronomic characteristics of the North American genotypes. The resultant TGx genotypes, widely cultivated in western and eastern Africa have poor yields due to ineffective nodulation (Okereke and Eaglesham, 1992). This observation led to the suggestion that the TGx soybean genotypes would benefit from *B. japonicum* inoculation. It is therefore important that the genetic relatedness of the indigenous rhizobia nodulating these soybean genotypes to recommended inoculum strains (e.g., *B. japonicum* USDA 110) needs to be elucidated.

A total of 258 *Bradyrhizobium* isolates obtained from TGx genotypes were examined for their symbiotic effectiveness and genetic diversity in relation to *B. japonicum* USDA 110. The genomic arrangement of *nod* gene sequences of *Bradyrhizobium* isolates was examined by PCR protocols. RFLP group analysis was done based on the *EcoRI*- and *PstI*- restriction digests of the genomic DNAs hybridized with *nodD*<sub>2</sub>, *nolA*, *nodY*, *nodDYABC*, *nodS*, *nodU*, and *nodIJ* gene probes from *B. japonicum* USDA 110 and *nodK* from *B. elkanii* strain USDA 94. The expected proportion of nucleotide substitutions in and around the probed *nod* gene sequences were derived using the equation 6b of Upholt (1977).

The *Bradyrhizobium* isolates were placed into four symbiotic phenotype groups: SymI (41%), ineffective on both soybean genotypes; SymII (20%), effective on both soybean cultivars; SymIII (5%) caused rhizobitoxine-induced chlorosis on the soybean genotypes; and SymIV (33%), effective on TGx soybean genotype but ineffective on N. American soybean cultivar Clark IV. The % divergence of *Bradyrhizobium* isolates from *B. japonicum* USDA110 ranged from 1.8 to >18.1. Clustering did not directly correspond to symbiotic phenotype groups. The results indicate that TGx soybeans are nodulated by diverse *Bradyrhizobium* strains; some strains are closely related to *B. japonicum*, some to *B. elkanii* while others are divergent from conventional soybean bradyrhizobia.

#### References

- Okereke GU, Eaglesham ARJ (1992) *Agronomie Africaine* 2, 123-136.  
 Pulver EL et al (1982) *Crop Sci.* 22, 1065-1070.  
 Upholt WB (1977) *Nucleic Acid Res.* 4, 1257-1265.