

Abstract

While soybean is an exotic crop introduced in Kenya early last century, promiscuous (TGx) varieties which nodulate with indigenous rhizobia have only recently been introduced. Since farmers in Kenya generally cannot afford or access fertilizer or inoculants, the identification of effective indigenous *Bradyrhizobium* strains which nodulate promiscuous soybean could be useful in the development of inoculant strains. Genetic diversity and phylogeny of indigenous *Bradyrhizobium* strains nodulating seven introduced promiscuous soybean varieties grown in two different sites in Kenya was assayed using the Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) of the 16S-23S rDNA intergenic spacer region and 16S rRNA gene sequencing. PCR-RFLP analysis directly applied on 289 nodules using *Msp* I distinguished 18 intergenic spacer groups (IGS) I–XVIII. Predominant IGS groups were I, III, II, IV and VI which constituted 43.9%, 24.6%, 8.3% 7.6% and 6.9% respectively of all the analyzed nodules from the two sites while IGS group VII, IX, X, XI, XII, XIV, XVI, XVII, XVIII each constituted 1% or less. The IGS groups were specific to sites and treatments but not varieties. Phylogenetic analysis of the 16S rRNA gene sequences showed that all indigenous strains belong to the genus *Bradyrhizobium*. *Bradyrhizobium elkanii*, *Bradyrhizobium* spp and *Bradyrhizobium japonicum* related strains were the most predominant and accounted for 37.9%, 34.5%, and 20.7% respectively while *B. yuanmigense* related accounted for 6.9% of all strains identified in the two combined sites. The diversity identified in *Bradyrhizobium* populations in the two sites represent a valuable genetic resource that has potential utility for the selection of more competitive and effective strains to improve biological nitrogen fixation and thus increase soybean yields at low cost.