

Genomic Heterogeneity within Cowpea Bradyrhizobia Isolated from Ghanaian Soils

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Abstract

Bradyrhizobia isolated from nodules of cowpea grown in 20 different Ghanaian soils were characterized on the basis of the 16S rRNA gene. RFLP groups established by four tetrameric restriction endonucleases were used to construct a phylogenetic tree which showed their genetic relatedness. The fast growing isolates produced 9 phylogenetic clusters while the slow growing isolates produced 11. Distribution among the isolates in the 11 clusters of the slow growing isolates was highly unbalanced with one cluster containing more than 50% of the total number of isolates. Diversity assessed using cluster divergence between both the fast and slow growing isolates was high, reaching 80%.

Introduction

Characterization of rhizobial strains naturally associated with the roots of legumes has been recommended as an effective approach to successful management of the legume-*Rhizobium* symbiosis (Richardson *et al.*, 1995; Mpepereki *et al.*, 1997). An array of different methods including host range analysis, serology, antibiotic resistance and biochemical analysis is available for the characterization of rhizobial strains. Currently, however, attention has focused on PCR-based genomic fingerprint methods, which have been shown to be effective for differentiating complex genomes (De Bruijn, 1992; Martinez-Romero, and Caballero-Melgado, 1996; Sessitsch *et al.*, 1997; Laguerre *et al.*, 1994). Indeed DNA sequence analysis of 16S rRNA regions has revealed much greater diversity than previously recognised (Moyer *et al.*, 1996) leading to important revisions in the taxonomy and systematics of the rhizobia.

Although African soils may harbour a large diversity of rhizobial populations, information on

diversity is limited. Cowpea rhizobia indigenous to Nigerian soils are probably the only group that has been studied (Fred *et al.*, 1932; Sinclair and Eaglesham, 1984). Assessing the diversity of West African cowpea bradyrhizobia using physiological and biochemical characteristics, (Fred *et al.*, 1932), found some traits common to all or most of the isolates, some related to geographical origin and some colony morphology. The indigenous cowpea rhizobia strains in Zimbabwean soils showed considerable cultural and physiological diversity that included unique types belonging to several as yet undefined species (Mpepereki *et al.*, 1997). Studies on fast growing rhizobia of *Sesbania* and *Acacia* species obtained from soils in Senegal has led to the description of two fast growing species, *Sinorhizobium saheli* and *S. teranga* (Nei and Li, 1979). In Ghana, the diversity of rhizobial populations of different legumes has not been examined. We present here analysis of the genomic diversity of rhizobial strains, isolated from nodules of cowpea plants grown in a wide range of Ghanaian soils.