Abstract

The increasing interest in the use of rhizobia as biofertilizers in smallholder agricultural farming systems of the Sub-Saharan Africa has prompted the identification of a large number of tropical rhizobia strains and led to studies on their diversity. Inoculants containing diverse strains of rhizobia have been developed for use as biofertilizers to promote soil fertility and symbiotic nitrogen fixation in legumes. In spite of this success, there is paucity of data on rhizobia diversity and genetic variation associated with the newly released and improved mid-altitude climbing (MAC) bean lines (*Phaseolus vulgaris* L.). In this study, 41 rhizobia isolates were obtained from the root nodules of MAC 13 and MAC 64 climbing beans grown in upper and lower midland agro-ecological zones of Eastern Kenya. Eastern Kenya was chosen because of its high production potential of diverse common bean cultivars. The rhizobia isolates were characterized phenotypically on the basis of colony morphology, growth and biochemical features. Rhizobia diversity from the different regions of Eastern Kenya was determined based on the amplified ribosomal DNA restriction analysis (ARDRA) of PCR amplified 16S rRNA genes using *Msp* I, *EcoR* I, and *Hae* III restriction enzymes. Notably, native rhizobia isolates were morphologically diverse and grouped into nine different morphotypes. Correspondingly, the analysis of molecular variance based on restriction digestion of 16S rRNA genes showed that the largest proportion of significant ($p < 0.05$) genetic variation was distributed within the rhizobia population (97.5%) than among rhizobia populations (1.5%) in the four agro-ecological zones. The high degree of morphological and genotypic diversity of rhizobia within Eastern Kenya shows that the region harbors novel rhizobia strains worth exploiting to obtain strains efficient in biological nitrogen fixation with *P. vulgaris* L. Genetic sequence analysis of the isolates and testing for their symbiotic properties should be carried out to ascertain their identity and functionality in diverse environments.