

Abstract:

The Great Lakes region of Central Africa is a major producer of common beans in Africa. The region is known for high population density and small average farm size. The common bean represents the most important legume crop of the region, grown on over a third of the cultivated land area, and the per capita consumption is among the highest in the world for the food crop. The objective of this study was to evaluate the genetic diversity in a collection of 365 genotypes from the Great Lakes region of Central Africa, including a large group of landraces from Rwanda as well as varieties from primary centers of diversity and from neighboring countries of Central Africa, such as the Democratic Republic of Congo and Uganda, using 30 fluorescently labeled microsatellite markers and automated allele detection. In addition, the landraces were evaluated for their seed iron and zinc concentration to determine if genetic diversity influenced nutritional quality. Principal coordinate and neighborjoining analyses allowed the separation of the landraces into 132 Andean and 195 Mesoamerican (or Middle American) genotypes with 32 landraces and 6 varieties intermediate between the gene pools and representing inter-gene pool introgression in terms of seed characteristics and alleles. Genetic diversity and the number of alleles were high for the collection, reflecting the preference for a wide range of seed types in the region and no strong commercial class preference, although red, red mottled and brown seeded beans were common. Observed heterozygosity was also high and may be explained by the common practice of maintaining seed and plant mixtures, a coping strategy practiced by Central African farmers to reduce the effects of abiotic and biotic stresses. Finally, nutritional quality differed between the gene pools with respect to seed iron and zinc concentration, while genotypes from the intermediate group were notably high in both minerals. In conclusion, this study has shown that Central African varieties of common bean are a source of wide genetic diversity with variable nutritional quality that can be used in crop improvement programs for the region.