

Abstract

Lack of genetic diversity data for Kenyan sorghum germplasm makes it difficult to manage and utilize its genetic resources. The main objective of this study was to assess the extent and structure of variability in sorghum landraces from Kenya using Simple Sequence Repeat (SSR) markers. Genotypic data was used to characterize genetic diversity in 148 sorghum accessions from western, Turkana, coast and eastern regions of Kenya. The accessions were genotyped as bulks using 39 SSR markers. The procedures used were DNA extraction, DNA amplification (PCR) and capillary electrophoresis. Average PIC value of 0.536 was observed indicating high levels of polymorphism. Gene diversity index range was 0.03 – 0.91 with a mean of 0.57 per locus. A total of 349 alleles were observed with an average of 8.9 alleles per locus. The average heterozygosity level per locus was low at 0.237. Analysis of molecular variance showed all variation components to be highly significant ($P < 0.001$). The variability within accessions among the populations was 56.4%, within individual accessions was 38.85% and among geographical origins was 4.8%. A low level of genetic differentiation ($F_{ST} = 0.048$), a high inbreeding level ($F_{IS} = 0.59$), and a high value of heterozygosity deficiency ($F_{IT} = 0.61$) were observed showing an increased degree of allele fixation. Breeders' and western material had the highest diversity (6.48 and 6.28 alleles/accession respectively). Turkana sorghum diversity was lowest (4.44 alleles/accession). Cluster analysis grouped the accessions into three groups with a genetic distance (GD) range of 0.4 to 0.8. Results show a high diversity among Kenyan sorghum germplasm that can be used in future crop improvement. However the different populations have a closely related genetic background. There is need for a broader characterization including molecular mapping; many loci are linked to important traits.