

Abstract

Genetic diversity plays an important role in selection of parental stocks in plant breeding. Sorghum [*Sorghum bicolor* (L.) Moench] breeding initiatives have been constrained by lack of information on genetic diversity of cultivated accessions which would otherwise guide in the choice of heterotic parents for hybridization. This study was carried out to determine genetic diversity of sorghum accessions collected from Africa and ICRISAT using simple sequence repeats (SSR) of microsatellite marker. Thirty sorghum SSR markers were used to assess the genetic diversity of 134 sorghum accessions. The number of alleles per microsatellite locus in the 134 sorghum accessions ranged between 2 to 22, with a total of 259 different alleles having been amplified. The greatest number of alleles was found at the locus 3590e705f67911e0b58c0010185a4b14 with 22 alleles. The average Polymorphism Information Content (PIC) for all the assayed sorghum accessions was 0.55. Expected heterozygosity of population ranged between 2.91 for Sudan and 1.58 for Central Africa. Pairwise population comparisons for genetic identity were derived based on *Nei's*. Genetic identity of the populations ranged from 0.36 for Central Africa and Northern Africa to 0.93 between Eastern Africa and Rwanda. Analysis of Molecular Variance (AMOVA) revealed that 75% of the molecular variation in sorghum accessions was due to within individual populations while 25% of the total variation was partitioned among populations. There was low population differentiation due to either continuous exchange of genes between sorghum populations largely by germplasm exchange or no intense selection processes. The diversity observed within sorghum accession from Sudan and East African region could be useful in improvement of sorghum for various traits.