

Abstract

The genetic diversity of 65 accessions of sorghum [*Sorghum bicolor* (L.) Moench] collected from various farmers and germplasm lines from ICRISAT-Kenya were analyzed. Simple sequence repeats (SSR) markers were used in order to determine the extent and distribution of its genetic diversity. Twenty-nine (29) SSRs markers were polymorphic and a total of 192 alleles were detected which showed diversity. The number of alleles per primer ranged from 2 to 17, with an average of 6.62. The range of polymorphism information content (*PIC*) ranged from 0.03 to 0.86, with total average of 0.82. According to the results analyzed, estimates of the mean allelic pattern across the two populations was generated; expected heterozygosity (*He*; 0.45, 0.54), average observed alleles (*Na*; 3.40, 6.20), number of private allele (0.23, 3.03), and Shannon information index (*I*; 0.85, 1.13) for farmer and ICRISAT-Kenya germplasm, respectively. The expected heterozygosity (*He*) varied from 0 to 0.26 with an average of 0.05. The Neighbor-joining phenogram based on Nei's genetic distance grouped the 65 accessions into three main groups. The analysis of molecular variance (AMOVA) revealed that 99% of the total genetic variation was within accessions in a population whereas the genetic variation among populations in accessions accounted for 1% of the total genetic variation. Genetic diversity in ICRISAT sorghum material compared to the farmer's collection suggested little infiltration of improved germplasm to the farmers.