Abstract

An understanding of the extent, distribution and patterns of genetic variation is useful for estimation of any possible loss of genetic diversity and assessment of genetic variability and its potential use in breeding programs, including establishment of heterotic groups. This study assessed patterns of genetic diversity and relationships among 30 West African sorghum accessions using 22 microsatellite markers. Population structure and within population genetic diversity was also assessed using the same markers. Genotypic data was generated using the ABI Prism 3730 and alleles called and sized using genemapper software version 3.7. Molecular data was analyzed using DARwin 4.0, powermarker 3.0 and Arlequin version 3.11. The average marker quality index was 0.27 while a mean PIC of 0.54 was observed across the 22 SSR markers. Among the 30 accessions, the markers detect a total of 146 alleles with an average of 6.6 alleles per marker. Results from the various statistical analyses performed revealed a wide range of polymorphism from 22.7 to 86.4%. The mean heterozygosity was relatively low at 0.28 while the average Nei's genetic diversity among the 30 populations was 0.57. The within population Nei's genetic diversity assessed from 49 individuals in 10 populations was lower at 0.54 and the average heterozygosity was also lower at 0.21. Cluster and principal coordinate analysis of the 30 populations revealed two distinct groups independent of their geographic origins The examination of the hierarchical partitioning of genetic variation by AMOVA demonstrated that genetic differentiation was significant at $P < 0.00$. Of the total diversity, 8.9% was attributed to country differences, 54.11% was attributed to population differences within the countries while 36.99% was attributed to differences within populations. The F_{ST} value (0.63) indicated a very high genetic differentiation as expected for selfing species. This study demonstrates the utility of SSR markers in detecting polymorphism, estimating genetic diversity and establishment of genetic clusters for heterotic studies.