

Assessment of genetic diversity of sorghum (*sorghum bicolor*) accessions from Tanzania using ssr markers: implications for conservation

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Abstract:

Plant genetic resources are a key component of global biodiversity from which humanity derives most of its food and other essential goods and services. An understanding of the extent, distribution, and patterns of genetic variation is useful for several purposes, including selection for conservation, estimation of any possible loss of genetic diversity prior to conservation programs, understanding the genetic variability available and its potential use in breeding programs, and estimating the relative strengths of the evolutionary forces shaping natural populations. Sorghum is a subsistent and staple crop for many people living across Africa especially those in marginal arid and semi-arid tropics. The study aimed to assess the genetic diversity within as well as among 96 accessions of sorghum germplasm collected from diverse regions of Tanzania using microsatellite markers. This entailed DNA extraction whereby the CTAB method was employed, DNA quality and purity check was done and then the DNA was normalized to ensure uniformity in the amount of DNA samples used and then polymerase chain reaction was done using the 12 microsatellites. Data analysis was then carried out and different softwares were used in the data analysis and this included the genemapper version 3.7 software, allelobin software, powermarker version 3.25 software and Darwin version 5.0 software, all these were used for different stages of the analysis. The area of study included Dodoma, Morogoro, Babati, Kilimanjaro and Mtwara regions. The molecular markers revealed that there was considerable amount of genetic diversity among the Tanzania sorghum and this is indicated by the high number of alleles and the clusters generated. There are so many sub clusters dividing from the main clusters and this suggests that there is high level of diversity in these Tanzanians accessions. However this diversity was not divided according to the geographical regions and there was no appreciable diversity within the sorghum accessions but the sorghum accessions clustered according to their genotype i.e. the sorghum landraces clustered together and the varieties also clustered together. Geographical Information Systems was also used. GIS was used in this study whereby maps showing the collecting localities and the environmental conditions for those localities were generated using a combination of different GIS and computer software.