

ABSTRACT

An insight on diversity and relationships among germplasm is important in any breeding program for crop improvement. The main objectives of our study were to: (i) determine the level of genetic diversity within mid altitude maize inbred lines resistant to weevils, aflatoxin accumulation and drought, (ii) to suggest potential heterotic groups using their genetic structures and distance based on cluster analysis with the aim to generate broad based source germplasm for mid altitude maize breeding program with combined traits of importance against Aflatoxin accumulation. In this study, 25 SSR markers were used to finger print forty two maize inbred lines to assess the genetic diversity, genetic relationships, and their population structure. A total of 184 alleles were identified at all the loci with an average of 7.36 and a range between two and 19 alleles per locus. The major allele frequency varied from 0.17 to 0.90 with an average of 0.49 while the minor allele frequency varied from 0.10 to 0.83 with an average of 0.51. The gene diversity values varied from 0.18 to 0.92 with an average of 0.65. Average heterozygosity percentage of the inbred lines was 4%, ranging from 0% to 2%, indicating the low level of heterozygosity within the inbred lines. The average polymorphism information content (PIC) was 0.61. A dendrogram constructed using unweighted Neighbour Joining algorithm suggested three heterotic groups among the inbred lines. The three heterotic patterns based on the SSR markers need to be verified by field testing to confirm what appears to be promising alternative heterotic patterns. The fixed pattern detected using SSR markers could potentially contribute towards effective utilization of the inbred lines for the exploitation of heterosis and formation of genetically diverse sources population.