

## Abstract

One hundred maize inbred lines and eighty four hybrids were characterized for resistance to maize stem borer and post-harvest insect pests. This was achieved using genetic distance and population structure based on simple sequence repeat (SSR) markers and biophysical traits. The test materials were evaluated for stem borer, maize weevil and larger grain borer (LGB) resistance. Leaf samples were harvested from 10 healthy plants per genotype and bulked. Genomic DNA was extracted using a modified version of mini-prep Cetyl Trimethyl Ammonium Bromide (CTAB) method. The samples were genotyped with 55 SSRs makers. Univariate analysis of variance was done using the general linear model procedure of SAS statistical package. Rodgers genetic distance was calculated for all data sets as a measure of genetic distance using NTSYS-pc for Windows. The distance matrices were used to generate phenograms using the unweighted pair group method based on arithmetic average (UPGMA) method in MEGA5. The genotypes were assigned into different populations using population structure software. The data was further subjected to discriminant and principal component analysis to group the gnotyoes. Analysis of molecular variance within and among the different populations was done using arlequin. There were significant differences ( $P \leq 0.001$ ) for all the biophysical traits evaluated. The SSR marker data estimated successfully the close relationship among different hybrids and inbred lines within clusters. Comparisons of the different multivariate analyses revealed high concordance among the different approaches of analyses. The results of this study can be directly used by breeding programs to develop resistant genotypes.