

ABSTRACT

Molecular marker information supported by quality morphological data facilitates the choice of suitable parents for applied breeding. The main aim of this study was to assess genetic diversity among 55 cultivated yield elite pigeonpea lines using 21 simple sequence repeat (SSR) markers that are well distributed across the genome. Among the 55 pigeonpea genotypes, 16 medium duration were selected and evaluated in the field for response to pod borer resistance in varied agro-ecological zones of Kenya during long rains of April-October cropping season. Twenty one primer pairs detected 80 alleles with a mean of 3.9 alleles per locus and polymorphism information content (PIC) ranging from 0.09 to 0.75 averaging to 0.39 suggesting a low genetic diversity. However, marker CcM1820 revealed the highest number of alleles (9) with a PIC value of 0.75. The genotype response to pod borer attack was significant ($P \leq 0.05$) with three genotypes (ICEAPs 01541, 01154-2 and 00902) revealing tolerance to pod borer. The markers based on Neighbor Joining, grouped the 55 genotypes into three main clusters based on parentage selection. Most genotypes developed from ICEAP 00068 as the maternal parent were grouped in Cluster I while cluster II comprised of improved genotypes and cluster III comprised genotypes developed from ICPL 87091 as maternal parent. The resistant genotypes identified in the field experiment were grouped in cluster I except ICEAP 00902 which grouped in cluster II. Future studies should focus on broadening genetic base by including more landraces and wild relatives to maximize selection and improve breeding work.