STMS based diversity analysis in chickpea (*Cicer arietinum* L.) for *Fusarium* wilt

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ABSTRACT : Thirty pairs of STMS primers were used for molecular characterization of 47 elite chickpea cultivars with difference in the level of resistance against *Fusarium* wilt. Out of 30, 26 were found to be polymorphic and produced 97 alleles across the 47 genotypes with an average of 3.73 alleles per locus. The highest numbers of alleles were observed in TA 125 (9 alleles). Based on the allele frequencies, the estimated PIC values ranged from 0.043 (TA72) to 0.826 (CaSTMS). The Jaccard's coefficient based genetic similarity matrix was utilized to prepared UPGMA dendrogram to visualize the clustering of genotypes. The dendrogram clearly showed three main clusters with 2 genotypes each in two clusters and the third cluster accommodated 91% genotypes. The clustering pattern indicated low level of genetic variability among the genotypes studied. The genotypes F5-33 and F5-38 with their coefficient values 4.17 differed from the genotypes ICRISAT 7806, HK 94-134 and F5-123 in respect of their coefficient values indicating that they are distantly related to each other. These genotypes can be cultivars with difference in the level of resistance against *Fusarium* wilt. These genotypes can be used in hybridization programme in order to generate mapping population for the *Fusarium* trait of interest and other molecular breeding programs.

Key Words : STMS, molecular characterization, diversity analysis, *Cicer arietinum*, *Fusarium* wilt.