

Genetic diversity of breeding Maize inbred lines determined by SSR markers

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Maize (*Zea mays* L.) is an important cereal crop of India as well as world. Undoubtedly, the concerted efforts of plant breeders and their breeding strategies have helped to increase the production and productivity two to three folds in many crops including maize. Hybrid cultivars have played a vital role in increasing acreage and productivity of maize. The success in identifying heterosis in hybrid maize breeding depends on the availability of reliable genetic diversity among maize inbred lines. Molecular markers have proven to be a valuable tool for genetic diversity analysis of many crop species. SSRs are currently considered as the molecular markers of choice and are rapidly being adapted by plant researchers. SSR based molecular diversity analysis of 27 maize inbred lines had produced 23 polymorphic alleles

from ten markers with an average of 2.3 alleles per locus and mean polymorphic information content (PIC) of 0.45. The dendrograms generated with hierarchical Unweighted Pair Group Method with Arithmetic mean (UPGMA) cluster analysis revealed five major clusters at 0.62 similarity coefficient. Interestingly, UMI 1266-7 and UMI 1265-6 were close even at 0.79 similarity index which is quite obvious from the similarity in their parentage. In the present study, parents of the hybrids that found to possess significantly high mean performance for grain yield were distinctly apart in the marker based classification. Hence, these preliminary results revealed that SSR marker based molecular diversity analysis could be much useful in classifying the maize inbreds.