Abstract

Germplasm collection the first step for plant breeding., were analyzed using r simple sequence repeat (SSR) markers. Collectively 10 primers which contained different simple sequence repeat (microsatellite) were used as single primer, and tested for PCR amplification. 41 polymorphic bands were scored. To assess the genetic similarity among the masses of cluster analysis using Jaccard's similarity coefficient using UPGMA method was used. The average genetic distance between populations (using the Jaccard similarity coefficient) 74/0, and the mean polymorphic information content (PIC) 69/0, respectively. P8 primer highest PIC (8/0) respectively. Survey data Mvlkvy dendrogram cluster analysis showed high genetic diversity among the genotypes. The highest genetic distance between genotypes TN-94-218 and TN-94-186 and the lowest genetic distance between genotypes TN-94-154 and TN-94-163 accessions. According to the results and indicating the efficiency of this marker in separation of cultivars, collection and molecular evaluation of genotypes from different distribution regions of this genus can afford complementary information about its diversity and taxonomy.

Key words: Cucumber, Genetic diversity, SSR marker

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