



Research article

Genetic relationships among maize inbred lines as revealed by start codon targeted (SCoT) analysis

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Abstract

Maize (*Zea mays* L.), is a cereal crop with a remarkable potential for production, it is the third most important grain crop after wheat and rice. Molecular analysis is frequently used by maize breeders for selecting promising inbred lines to develop hybrid combination. In the present study 8 yellow maize inbred lines (Gm730, Gm 731, Gm 739, Gm 743, Gm 744, Gm 745, Gm 746 and Gm 749) developed by Maize Research Program, Field Crops Research Institute (FCRI), Agricultural Research Center (ARC), Egypt were analyzed using 10 Start codon targeted (SCoT) markers. These primers produced total 136 fragments across 8 maize inbred lines, of which 74 (54.4%) were polymorphic with an average of 7.4 polymorphic fragments per primer and number of amplified fragments ranged from 4 (SCoT- 07) to 13 (SCoT- 08). The genetic similarity between pairs of inbred lines ranged from 78 to 91. The highest genetic similarity was between inbred lines Gm 745 and Gm746. While the lowest genetic similarity was between inbred lines Gm 730 and Gm 749 and between inbred line Gm 731 and both of inbred lines Gm 739 and Gm 749. The dendrogram of eight maize inbred lines based on SCoT markers using UPGMA comprised two main clusters; the first cluster grouped two inbred lines; Gm 730 and Gm 731 which derived from the same genetic source. The second cluster divided into two sub clusters; one sub- cluster contains one inbred line (Gm 739). While the other sub-cluster grouped the other five inbred lines in two groups. In general, Cluster analysis based on SCoT data grouped inbred lines largely consistent with their pedigree. This present study showed effectiveness of employing SCoT markers in analysis of maize genotypes, and it would be a promising marker for further studies in population genetics, genetic diversity and genotypes improvement.