

Abstract

Economic and medicinal importance of (*Momordica charantia* L.) karela caused performing a lot of research on their genetic diversity. Retrotransposon are main mobile elements in the plant genome and can move through the genome by an intermediate RNA. In this research, IRAP and REMAP markers were employed for identification of retrotransposon insertion and genetic diversity of 11 karela seeds collected from different regions. After DNA extraction by Dellaporta method, PCR was performed using designed primers. Collected data were analyzed using the Genealex software. Most retrotransposons were active in the genome and produced 71 polymorphic locations by 6 IRAP primers and 103 polymorphic locations using 12 REMAP primers. The expected heterozygosity average for IRAP was (He) 0.24 and for REMAP was (He) 0.31. Cluster analysis based on REMAP and IRAP data, Dice similarity coefficient and complete linkage algorithm, classified 11 genotypes in 5 main groups. Genetic variation analysis indicated 66% variation within and 34% variation among group in IRAP, and 61% variation within and 39% variation REMAP. Minimum genetic similarity in IRAP was observed in Durga seed of Hong Kong and Konarak seeds, in REMAP were in Long green and Durga India baby, and in REMAP-IRAP was in Konarakseed and Durga India baby. Finally, it is suggested to use Durga India baby and Konarak seeds as crossing parents in breeding program.

Keywords: Karela, genetic diversity, retrotransposon, IRAP, REMAP



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**Investigation on genetic variation of Biter guord (*Momordica
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