
Genetic Diversity in Snake Gourd Genotypes Revealed by RAPD

Markers

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Rashid, M. H., Khan, ASM. M. R., Yasmin, R., Ishtiaque, S. and Chaki, A. K. (2016). Genetic diversity in snake gourd genotypes revealed by RAPD markers. *International Journal of Agricultural Technology* 12(1):125-144.

Abstract A genetic analysis of 21 diverse Bangladeshi snake gourd (*Trichosanthes anguina* L) genotypes was performed using Random Amplified Polymorphic DNA (RAPD) markers. Out of 14 random primers screened three were selected, which produced 34 amplicons, among them 33 (95.83%) was considered polymorphic providing an average of 11 amplicons per primer. RAPD amplicons per primer ranged from 8 (OPA-05) to 15 (OPC-02) and varied in size from 150 bp to 1450 bp. The Nei's index of diversity for each primer ranged from 0.0907 to 0.4898 with an average of 0.3356 whereas the Shannon's index of diversity for each primer ranged from 0.1914 to 0.6920 with an average of 0.5051. The UPGMA constructed based on RAPD analysis in 21 snake gourd genotypes in where two major groups were found. Cluster II had 18 genotypes whereas cluster one only had three. The highest genetic distance 0.9614 was estimated between the genotypes TA0021 and TA0002, while the lowest genetic distance 0.1252 was estimated between the genotypes TA0005 and TA0003. RAPD analysis showed an effective tool in estimating genetic variation in snake gourd genotypes. Examined *T. anguina* genotypes were genetically diverse and this variation stressed the need of genetic study and crop improvement of the species.

Key word: Genetic variation, RAPD marker, Snake gourd, UPGMA

Introduction

Commonly known as cucurbits or gourds, under the family Cucurbitaceae includes a large number of cultivated species of global or local economic importance (Robinson and Decker-Walters, 1997). Snake gourd (*Trichosanthes anguina* L) is one of the cucurbitaceous vine crop growing mostly in tropical and sub-tropical regions. The diverse morphological characters of *T. anguina* in Bangladesh provide relatively

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