

Analysis of the Genetic Diversity and Variety Identification of Bitter Gourd (*Momordica charantia* L.) by ISSR Markers¹

Chia-Hsing Huang² Chii-Jeng Wang² Jong-Ho Chyuan³

Abstract

For identification and genetic diversity of bitter gourd, 27 ISSR markers were chosen to perform a genetic analysis of 38 diverse bitter gourd accessions. The 247 amplicons yielded from ISSR-PCR analysis and 115 polymorphic were included. Each primer produced 4.25 polymorphic bands in average. Numbers of polymorphic amplicon were 0 to 9 and each size of products ranged from 150 to 2700 bp. The lowest and highest genetic similarity coefficients were 0.508 and 0.938, respectively. The phylogenetic analysis indicating that similarity between wild varieties and general cultivars is relative far, but the similarity among general cultivars is very near. The 18 accessions including Taiwan cultivars and descendants of South-East Asia cultivars were chosen for variety identification study. The results show that discrimination for the 18 accessions just needs 6 ISSR primers and these primers are effective and convenient for bitter gourd identification. Genetic diversity of wild varieties from Taiwan is higher than the other accessions. These data will be a good reference for bitter gourd breeders.

keywords : bitter gourd, variety identification, ISSR (Inter Simple Sequence Repeat) .

1. Research article No.219 of Hualien District Agricultural Research and Extension Station.

2. Assistant researcher. Division of Crop Improvement of Hualien DARES.

3. Associate researcher. Division of Crop Improvement of Hualien DARES.