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## Genetic assessment of watermelon (*Citrullus lanatus*) varieties using SSR markers developed from *Cucurbit* species

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### Objectives

The objective of this study was to evaluate applicability of SSR markers developed in *cucurbit* species in order to investigate genetic characterization of watermelon (*Citrullus lanatus*).

### Materials and Methods

#### 1. Materials

- Varieties: 24 varieties including 'Samboggul'

#### 2. Methods

- SSR marker: 296 SSR markers developed from *cucurbit* species
- Silver Staining: DNA silver staining kit (Promega Cat. Q4132)
- Data analysis: NTSYSpc version 2.10b (Rohlf, 1998).

### Results and Discussion

Cross-species application of SSR markers developed in melon and cucumber was examined for watermelon (*Citrullus lanatus*) in order to investigate genetic characterization. Seventy SSR loci out of 208 SSRs from melon and 61 SSRs from cucumber were detected in watermelon varieties. Of the 70 primers, sixteen revealed polymorphism in 24 tested varieties. Additionally, nine polymorphic primer sets were selected from 27 SSRs derived from watermelon. A total of 92 polymorphic amplified fragments were obtained by using 25 SSR markers. Average polymorphism information content (PIC) was 0.43, ranging from 0.15 to 0.86. A total of 92 SSR loci were used to calculate Jaccard's distance coefficients for cluster analysis using UPGMA. Clustering group of varieties based on the SSR analysis was divided 4 groups corresponding to varietal types. However, several varieties in the marketing varieties group could not be distinguished. This suggests that genetic diversity is low in the companies' breeding lines and there has been little introgression into the gene pool of watermelons because of the limited number of polymorphic SSR markers. These results could be utilized to a reliable means for genetic distance of the watermelon varieties and to a useful tool for breeders to introduce valuable wild watermelon genes into varieties.

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