

Genetic Diversity and Population Structure of Watermelon (*Citrullus lanatus*) Germplasm Using Microsatellite Markers

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[Introduction]

There have been growing interests in breeding of watermelon genus *Citrullus* for economic benefits. However, there is limited information on the scope and utilization of its genetic variation which is the basis for the germplasm management and its further utilization. The objective of the present study was to determine the genetic relationship among 50 watermelon accessions by using SSR markers.

[Materials and Methods]

Fifty watermelon germplasm conserved at the National Agrobiodiversity Center (NAC) (<http://genebank.rda.go.kr>) were selected for analyzing their genetic diversity and population structure. A total of 51 microsatellite markers were used for generating genotypic data.

[Results and Discussion]

The allele number and polymorphic information content (PIC) of total accessions per locus ranged from 2 to 8 (mean = 3.55) and from 0.136 to 0.762 (mean = 0.455), respectively. A high level of gene diversity [Nei's gene diversity index (Nei) = 0.53] and a low observed heterozygosity (H_o = 0.13) were revealed within the samples. Structure analysis consisted of grouping the 50 accessions into two main populations (Pop I and Pop II) and an admixture group. Among the 50 watermelon accessions, 38 were assigned to a single cluster and 12 were considered as admixed. These results will be very useful in facilitating efficient use of genetic variations in watermelon *Citrullus* breeding and optimizing the accessions in genome-wide association studies.

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