

Exploring Genetic Diversity of Some Iranian Watermelon (*Citrullus vulgaris*) Accessions in Urmia Climatic Conditions

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Received: 15 October, 2015

Accepted: 4 January, 2017

Abstract

Background and Objectives

Watermelon (*Citrullus lanatus* Thunb) belongs to the genus Cucurbita and the family Cucurbitaceae. The aim of the present study was to evaluate the level of genetic variation among Iranian watermelon accessions originating from different regions of the country by morphological traits.

Materials and Methods

Sixteen accessions together with two commercial watermelon cultivars were planted in completely randomized block design with three replications in Agricultural Research Center of Urmia in 2013. Fifteen traits including leaf length, leaf width, plant length, number of fruit per plant, fruit length, fruit width, fruit weight, fruit mass, fruit skin, 100 seed weight, seed length, seed width, pH, TSS and yield were assessed on the studied accessions. During fruit ripening, four fruits from each plot were randomly selected and the traits were measured according to International Board for Plant Genetic Resources Institute descriptor. The TSS was assessed by using refractometer and the pH by using pH meter.

Results

Analysis of variance showed that there is a meaningful difference between genotypes for all studied traits except for pH, stem length and number of fruits per plant. According to the results, fruit yield ranged from 24626 kg h⁻¹ in Charleston Gray genotype to 13444 kg h⁻¹ in Hamedan 817 accession. The percentage of TSS varied from 9.27% in Crimson sweet genotype to 5.1% in Khorasan 806 accession and fruit pH varied from 5.63 in Hamedan 817 accession to 4.78 in Charleston Gray genotype. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all studied traits, indicating the significant effects of environmental effects. The highest positive correlation (0.968) was observed between pulp weight and fruit weight and the highest negative one (-0.815) was observed between TSS and seed length. The highest heritability was seen for 100 seed weight and the lowest one for pH. Cluster analysis with Ward method, classified the studied accessions in to three different groups. The maximum distance was observed between genotypes of groups 1 and 3.

Discussions

The results revealed a rather high level of genetic polymorphism and wide genetic variation between accessions, which offer valuable information for conservation and management of genetic resources and utilizing them in watermelon breeding programs. The genetic distance between accessions is a valuable parameter to conserve and use a given germplasm in breeding activities. It was proved that crosses between unrelated and genetically distant parents will show more power hybrid than crosses between genotypes closely related.

Keywords: *Correlation, General heritability, Genetic diversity, Morphological traits, Watermelon.*