

Genetic variability, heritability and genetic advance for horticultural traits and mineral content in watermelon

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Received: October 2019 / Accepted: January 2020

Abstract

Genetic variability, heritability and genetic advance were studied in 102 germplasm of watermelon from different *Citrullus* species (*C. lanatus* var. *lanatus*, *C. lanatus* var. *citroides* and *C. colocynthis*) for yield attributing traits and different mineral content. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for node number of first male flower, yield per plant, average fruit weight, manganese, copper and zinc contents respectively. Moderate to high heritability coupled with high genetic advance as per cent of mean were found for average fruit weight, yield per plant, Zn and Mn content and high heritability with moderate genetic advance as per cent of mean were obtained for Mg and Na which reflected wide variability for traits of economic importance and further selection could improve the genotypes.

Keywords: PCV, GCV, Heritability, Genetic Advance, *Citrullus colocynthis*

Introduction

Watermelon is a morphologically diverse, out crossing horticultural crop of broad economic importance that belongs to the family Cucurbitaceae. The genus *Citrullus* has four diploid species ($2n=22$) that are widely grown in Africa, Asia and the Mediterranean region (Levi et al. 2001a). It has four species viz. *C. lanatus*, *C. ecirrhosus*, *C. colocynthis*, and *C. rehmii*). Commercially grown cultivars are classified as *C. lanatus* var. *lanatus*, and most of the wild accessions are *C. lanatus* var. *citroides* (Wehner et al., 2001). *C. lanatus* var. *citroides*, which is most common in central Africa, probably gave rise to domesticated *C. lanatus* var. *lanatus* (Robinson and Decker-Walters 1997). *Citrullus lanatus* var. *citroides*

Mansf. is also known as the citron or preserving melon. *Citrullus colocynthis* (L.) Schrad. a wild perennial species growing predominantly in Northern Africa and South Western Asia (Jarret et al. 1997). *Citrullus colocynthis* is considered as putative ancestral or progenitor species of watermelon which is generally found to be grown in India in north western plain in fallow lands / field and it is drought hardy and a wide diversity is found in Rajasthan and Gujarat. Globally, a lot of studies had been done on genetic variability parameters, heritability and genetic advance of watermelon genotypes from different species (Singh et al. 2013). Genetic variability plays an important role in a crop in selecting the best genotypes for making rapid improvement in yield and other desirable characters as well as to select the potential parent for hybridization programmes. Larger genetic variability increases the possibility of identification of genotype for novel traits of interest and ensures better chances of producing new forms which might be superior to the existing ones. Genetic parameters like coefficients of variation, heritability, predicted genetic advance and classification of germplasm are of paramount significance in formulating an appropriate breeding strategy aimed at exploiting the inherent variability of the breeding population. The main objective of this investigation was to find out genetic variability parameters, heritability and genetic advance in a broader germplasm of watermelon from different *Citrullus* species.

Materials and Methods

This investigation was carried out at the Research Farm of Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi during the *Spring Summer* season of 2015. The research farm at IARI, New Delhi is situated geographically at 228.61m (750 feet) altitude over mean sea level, with 28°08'N latitude and 77°12'E longitudes. The climate is sub-temperate and semi-arid type with alluvial soil, experiences

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very hot summers (above 40°C) and relatively dry and cool winters (below 5°C). The mean maximum daily temperature during the hot weather (April-July) ranges from 27.5°C to 45.8°C and the mean minimum temperature from 15.6°C to 31.0°C. The experiment was laid out in randomized block design with 102 genotypes with three replications. Majority of the germplasm are plant Introductions (PIs) and many from egusi watermelon types. Few accessions from *Citrullus lanatus* var. *citroides* and a *Citrullus colocynthis* genotype collected from Bikaner, India. The nursery was grown in polythene bags in polyhouse and 30 days old seedlings were transplanted. The plants were spaced at 2.5 m from row to row and 0.75 m from plant to plant within a row. The recommended package of practices was followed. Necessary plant protection measures were carried out uniformly to protect the germplasm lines. Data were recorded for 102 genotypes of watermelon for 16 yield traits and 8 mineral contents from five randomly selected plants/fruits of each replication for recording the data related to plant traits viz. Days to first male flower opening, Days to first female flower opening, Node number of first male flower, Node number of first female flower, Average fruit weight (kg), Number of fruits per plant, Yield per plant (kg), Fruit length (cm), Fruit diameter (cm), Rind thickness (cm), Seed length (cm), Seed width (cm), Yield per plant (kg), Total soluble solids (°brix), Days to harvest from pollination, Node to first fruit set and minerals like Sodium (Na), Potassium (K), Zinc (Zn), Manganese (Mn), Copper (Cu), Iron (Fe), Magnesium (Mg) and Calcium (Ca) respectively. Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957). Genetic advance as per cent mean was categorized into following groups as suggested by Johnson et al. (1955).

Result and Discussion

Analysis of variance showed that mean sum of squares was highly significant for 16 yield traits and 8 characters for mineral contents which indicated the presence of high magnitude of variability for all the yield contributing characters and mineral contents among the watermelon germplasm utilized for this study. The extent of genetic variation for a particular trait may be judged by the estimation of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for 16 fruit yield traits and mineral contents are presented in Table 1 and Table 2. Amongst the yield related characters, high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for node number of first male flower (58.38, 56.67), yield per plant (57.37, 52.76), and average fruit weight

(44.98, 43.79 g). Moderate range of PCV and GCV were found for number of fruits per plant (37.55, 34.09), rind thickness (37.72, 28.67), seed width (34.22, 28.75), days to first female flower opening (29.46, 29.07), node to first female flower (28.32, 27.45) and lower values were estimated for days to harvest from pollination (23.88, 22.94), node to first fruit set (25.27, 24.18), fruit diameter (25.50, 22.23), flesh thickness (26.58, 23.30) and seed length (25.30, 22.09). Similar results have also been reported by Shibukumar et al. (1995), Said and Fatiha (2015) and Choudhary et al. (2012). Out of 8 nutritional traits, high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for manganese (57.49, 55.79), copper (56.62, 55.95) and zinc (54.73, 53.69) content. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were in moderate range for iron (45.83, 45.17), sodium (45.44, 44.80), potassium (44.36, 43.82) and magnesium (38.82, 38.50) and the minimum phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were estimated for calcium (18.60, 18.37) content. Low estimates of phenotypic and genotypic coefficients of variation of mineral contents for calcium (18.60, 18.37) content earlier report by Said *et al.*, (2012). Relatively wide difference between the estimates of PCV and GCV were found for the characters namely rind thickness (37.72, 28.67), seed width (34.22, 28.75), fruit length (29.88, 26.83), flesh thickness (26.58, 23.30), fruit diameter (25.50, 22.23), seed length (25.30, 22.09), number of fruits per plant (37.55, 34.09), node number of first male flower (58.38, 56.67) and manganese content of fruit (57.49, 55.79). The difference between PCV and GCV was low for fruit yield related attributes like total soluble solids (TSS) (PCV 43.74 and GCV 43.44), days to first female flower (PCV 29.46 and GCV 29.07), days to first male flower opening (PCV 41.51 and GCV 40.13), node number of first male flower (PCV 58.38 and GCV 56.67), node number of first female flower (PCV 28.32 and GCV 27.45), node to first fruit set (PCV 25.27 and GCV 24.18), days to harvest from pollination (PCV 23.88 and GCV 22.94) and average fruit weight (PCV 44.98 and GCV 43.79).

Heritability estimate provides the information regarding the amount of transmissible genetic variation to total variation and determines genetic improvement and response to selection. The term heritability in broad sense was defined as the ratio of genetic variance to the total phenotypic variance (Lush, 1940; Jonson et al., 1955). Broad-sense heritability for 16 fruit yield traits and mineral contents are presented in table 1. Broad-sense heritability values for different traits varied from 57.77

to 98.67%. Rind thickness (57.77) was the least heritable trait while total soluble solids (98.67) was the most heritable trait. Amongst yield traits, high range of heritability was observed for days to first female flower opening (97.33), average fruit weight (97.22), node number of first female flower (93.93), days to first male flower opening (93.45), days to harvest from pollination (92.32) and node to first fruit set (91.55). Moderate range of heritability was found for number of fruits per plant (82.40), fruit length (80.60), flesh thickness (76.87), yield per plant (76.39), seed length (76.26), fruit diameter (76.04) and node number of first male flower (74.36). The low estimate of heritability was obtained for seed width (70.55%). Broad-sense heritability for mineral contents were presented in table 2. High range of heritability was observed for magnesium (98.39%), calcium (97.60), iron (97.14) and sodium (91.55). Moderate range of heritability was estimated for potassium (89.36), zinc (82.26) and low heritability was found in copper (78.36%). Similar results have also been reported by Sundaram *et al.* (2011) and Choudhary *et al.* (2012).

The highest value of genetic advance among yield traits was estimated for days to harvest from pollination

(27.74) followed by days to first female flower opening (20.15), days to first male flower opening (19.95), node number of first male flower (9.31), node to first fruit set (9.06), fruit length (6.61), node number of first male flower (6.29), fruit diameter (4.97), flesh thickness (4.63), total soluble solids (4.36), yield per plant (2.98), number of fruit per plant (2.84), average fruit weight (1.21), seed length (0.45), rind thickness (0.43) and seed width (0.32). Amongst mineral contents, potassium (2196.62) exhibited highest value of genetic advance followed by sodium (178.49), calcium (3.91), zinc, (3.42), magnesium (1.31), iron content (0.83) while the lowest value was recorded for manganese and copper content (0.02).

Genetic advance was worked out as per cent mean for all the characters and presented in Table 1. The highest value of genetic advance as per cent of mean among yield traits was obtained for yield per plant (90.28%), followed by average fruit weight (90.08), node number of first male flower (89.43) and total soluble solids (TSS) (88.91). Moderate range of genetic advance as per cent of mean was recorded for days to first male flower opening (79.92%), number fruits per plant (63.74), days to first female flower opening (59.07), node number of

Table 1: Estimates of variability, heritability, genetic advance and GA as per cent of mean for yield attributes in watermelon germplasm

S. No.	Character	Range	Grand Mean	PCV (%)	GCV (%)	h ² (%)	Genetic advance	GA as per cent of mean
1.	Days to first male flower opening	14.67-44	24.97	41.51	40.13	93.45	19.95	79.92
2.	Days to first female flower opening	21.33-55.33	34.12	29.46	29.07	97.33	20.15	59.07
3.	Node number of first male flower	2.33-19	7.03	58.38	56.67	74.36	6.29	89.43
4.	Node number of first female flower	9.67-31.67	16.99	28.32	27.45	93.93	9.31	54.80
5.	Node to first fruit set	11-31.67	19.02	25.27	24.18	91.55	9.06	47.66
6.	Number of fruits per plant	2.03-9.50	04.46	37.55	34.09	82.40	2.84	63.74
7.	Days to harvest from pollination	32.32-98.67	61.09	23.88	22.94	92.32	27.74	45.41
8.	Average fruit weight (kg)	0.25-7.50	1.34	44.98	43.79	97.22	1.21	90.08
9.	Fruit length (cm)	6.2-23.33	13.33	29.88	26.83	80.60	6.61	49.61
10.	Fruit diameter (cm)	7.2-21.33	12.43	25.50	22.23	76.04	4.97	39.94
11.	Flesh thickness (cm)	6-19.33	10.99	26.58	23.30	76.87	4.63	42.09
12.	Rind thickness (cm)	0.47-2.17	0.96	37.72	28.67	57.77	0.43	44.89
13.	Seed length (cm)	0.67-1.97	1.14	25.30	22.09	76.26	0.45	39.75
14.	Seed width(cm)	0.3-1.13	0.65	34.22	28.75	70.55	0.32	49.73
15.	Yield per plant (kg)	0.59-13.93	3.30	57.37	52.76	76.39	2.98	90.28
16.	TSS (°Brix)	1.5-11.90	4.90	43.74	43.44	98.67	4.36	88.91

Table 2: Estimates of variability, heritability, genetic advance and GA as per cent of mean for mineral contents in watermelon germplasm

S. No.	Character	Range	Grand Mean	PCV (%)	GCV (%)	h ² (%)	Genetic advance	GA as per cent of mean
1.	Sodium (mg/100g)	38-728.17	208.280	45.44	44.80	91.55	178.49	85.7
2.	Potassium (mg/100g)	369.93-8326.20	2690.00	44.36	43.82	89.36	2196.62	81.66
3.	Zinc (mg/100g)	0.03-18.11	3.520	54.73	53.69	86.26	3.42	97.25
4.	Manganese (mg/100g)	0.007-0.155	0.023	57.49	55.79	82.93	0.02	98.21
5.	Copper (mg/100g)	0.003-0.155	0.019	56.62	55.95	78.36	0.02	91.40
6.	Iron (mg/100g)	0.46-2.59	0.910	45.83	45.17	97.14	0.83	91.71
7.	Magnesium (mg/100g)	0.65-4.47	1.670	38.82	38.50	98.39	1.31	78.68
8.	Calcium (mg/100g)	7.55-19.92	10.450	18.60	18.37	97.60	3.91	37.40

first female flower (54.80), seed width (49.73), fruit length (49.61), node to first fruit set (47.66), days to harvest from pollination (45.41), rind thickness (44.89), flesh thickness (42.09), fruit diameter (39.94) and lowest genetic advance were observed for seed length (39.75%). Genetic advance was worked out as percent mean for mineral contents are presented in Table 2. The highest genetic advance as per cent of mean was estimated for manganese (98.21%), followed by zinc (97.25), iron (91.71), copper (91.40), sodium (85.70), potassium (81.66), magnesium content (78.68) and the lowest genetic advance as per cent of mean was estimated for calcium (37.40) content. The results of present study will be useful as it gives information about the groups where certain traits are more important allowing breeder to conduct specific breeding programme for higher yield, fruit quality and incorporate important mineral in the elite genotypes in watermelon by utilizing genotypes from different groups.

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तरबूज के विभिन्न प्रजातियों (सीट्रुलस लनैटस वार. लनैटस, सी. लनैटस वार. सीटरोइड्स एवं सी. कोलोसिन्थीस) में उपज घटकों एवं विभिन्न खनिज लवणों के आनुवांशिक विविधता, वंशागतत्व एवं आनुवांशिक उन्नयन का अध्ययन 102 जननद्रव्यों को समाहित कर किया गया। उच्च बाह्यदृश्य प्रारूप गुणांक विविधता एवं आनुवांशिक गुणांक विविधता पार्श्व गाँठ पर प्रथम नर पुष्प विकास, उपज प्रति पौध, औसत फल भार, मैग्नीज, तांबा एवं जिंक में क्रमशः पाया गया। मध्यम से उच्च वंशागतत्व के साथ-साथ उच्च आनुवांशिक उन्नयन-जैसा प्रतिशत मध्य औसत फल भार, उपज प्रति पौध, जिंक एवं मैग्नीज की मात्रा के लिए तथा उच्च वंशागतत्व के साथ मध्यम आनुवांशिक उन्नयन-जैसा प्रतिशत मध्य मैग्निशियम व सोडियम की मात्रा के लिए पाया गया जिससे आर्थिक महत्व वाले गुणों के प्रति वृहद् विविधता परिलक्षित होता है। इसके आधार पर आगे प्रभेद उन्नयन हेतु चयन प्रक्रिया में इन मूल्यों को सम्मिलित किया जा सकता है।

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