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Genetic variability and correlation studies in various genotypes of watermelon [*Citrullus lanatus* (Thunb.) Mansf.]

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Abstract

The study was conducted to determine genetic variability and correlation involving 21 watermelon genotypes in a randomized block design with three replications. A considerable amount of variability was observed for qualitative and quantitative traits. Maximum phenotypic and genotypic variability was recorded for the seediness, followed by pericarp thickness and fruit weight. Most of the characters except cotyledon size, leaf blade ratio, emergence of first male flower, emergence of first female flower, days taken to fruit maturity, blooming period and seed length exhibited high estimates of heritability coupled with the high estimates of genetic advance. Number of fruits per vine had significant genotypic and phenotypic positive correlation with the traits leaf blade length, internodal length, number of primary branches and number of secondary branches. Based on yield and yield contributing characters, the genotypes viz., VRW-14, VRW-12, VRW-20 and VRW-17 were found promising for future improvement programme.

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Introduction

Watermelon (*Citrullus lanatus*), an important and widely cultivated cucurbit belongs to family *Cucurbitaceae*. According to Maggs-Kolling and Christiansen (2003), all *Citrullus spp* originated in the Kalahari region of Africa. Paris (2015) in his work on ethno-botany of watermelon, articulated multiple origin hypothesis for dessert watermelon but settled for north-eastern Africa as the origin of sweet watermelon. However, there was no consensus on its putative progenitor.

Cultivated watermelon has three species *Citrullus lanatus* var. *lanatus*, *C. lanatus* var. *citroides* and *C. mucospermus* (Fursa, 1972). *Citrullus colocynthis* and *Citrullus eccirrhosus* are two perennial wild species. *Praecitrullus fistulosus* (Stocks) Pangalo commonly called 'Tinda' from India and Pakistan is a related species. In India, watermelon occupied an area of about 99,000 ha with a production of about 20,98,000 MT (NHB 2019). Watermelon is a low-calorie

fruit and a rich source of citrulline (Rimando & Perkins-Veazie 2005), anti-carcinogenic functions like lycopene and β -carotene, a precursor of Vitamin A (Edwards et al. 2003). Lycopene content in watermelon varies from 40-120 $\mu\text{g/g}$ flesh weight, which is more than raw tomato and readily available to the human body as compared to tomato (Tadmor et al. 2005).

The genetic variability within species imparts uniqueness to adapt it to various kinds of evolutionary processes across the environments. Genetic base of watermelon has been shrinking due to exploitation of similar backgrounds in breeding programs (Hwang et al. 2011). Biodiversity is also declining rapidly due to human intervention, increasing urbanization and loss of habitat. Therefore, conservation of available genetic resources in watermelon has become utmost priority for future utilization in crop improvement programmes (Tanksley & McCouch 1997). Domestication events were focused more on desirable horticultural traits like big fruit, red flesh and sweetness but ignored undesirable traits which confer biotic and abiotic tolerance/resistance thereby narrowing the genetic base (Zamir 2001). A narrow genetic base leads to the lowering of allelic variation of genes in a population and hence loss of heterogeneity. This makes the crops with a narrow genetic base to be more susceptible to biotic and abiotic stresses. Hence wide variability ensures better opportunities to develop improved cultivars. The presence of adequate variability in the basic genetic material of any crop is a prerequisite for initiating a systematic breeding programme for the improvement of a crop. Study of such

variability among different germplasm of a crop helps to identify the most potential genotypes by using various genetic parameters like heritability, genetic advance and genetic coefficient of variation. Information on the nature and extent of genetic variability and the degree of transmission of character is of paramount importance in enhancing the efficiency of selection. The knowledge of correlations between various characters and their relative contribution to yield is useful for multiple character selection (Kehinde & Idehen 2008).

Materials and Methods

The present research was conducted at Research Farm of the Department of Vegetable Science, CCS HAU Hisar (Haryana) during the *Summer* season of 2020-21. Twenty-one watermelon genotypes (Table 1) were grown in a randomized block design with three replications. The experiment material was laid out with a plot size 6 x 2 m, maintaining crop spacing of 2m x 0.6 cm. The crop was raised as per the standard package of practices recommended by CCS HAU, Hisar. The observations for traits like germination percentage, cotyledon size, leaf blade length, leaf blade width, leaf blade ratio, petiole length, internode length, vine length, number of primary branches, number of secondary branches, days to emergence of first staminate flower, days to emergence of first pistillate flower, days taken to fruit maturity, blooming period, fruit length, fruit diameter, fruit weight, number of fruits per vine, pericarp thickness, total soluble solids of fruit flesh, seediness: number of seed per fruit, seed length, seed width were recorded on randomly selected five representative plants per plot in

each replication, while for days to emergence of first staminate flower, days to emergence of first pistillate flower, blooming periods, days

taken to fruit maturity were recorded on a whole plot basis.

Table 1. List of genotypes and their source

S. No.	Genotype	Crop	Variety	Source	Origin
1.	VRW-1, VRW-2, VRW-3, VRW-6, VRW-7, VRW-9, VRW-12, VRW-14, VRW-16, VRW-17, VRW-18, VRW-19, VRW-20, VRW-21, VRW-23, VRW-24, VRW-26	<i>Citrullus lanatus</i> var. <i>lanatus</i>	Germplasm	IIVR, Varanasi	India
2.	NSC-747 P, Misthi	<i>Citrullus lanatus</i> var. <i>lanatus</i>	F ₁ Hybrid	NSC, N. Delhi	India
3.	Durgapura Lal	<i>Citrullus lanatus</i> var. <i>lanatus</i>	Variety	RRS, Durgapura	India

The analysis of variance was performed as suggested by Panse and Sukhatme (1967). The GCV and PCV were estimated according to Burton (1952). The heritability in the broad sense was calculated as the ratio of genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was expressed in the form of a percentage (Hanson *et al.*, 1955). The genetic advance was worked out by adopting the following formula given by Johnson *et al.* (1955). Genetic advance as *per cent* of mean for each character was worked out by the following formula:

$$\text{GAM (\%)} = \frac{\text{GA}}{\bar{X}} \times 100$$

The genetic advance as *per cent* of mean was categorized below as:

0-10% = Low 10-20% = Moderate
>20% = High

Correlation coefficients at the phenotypic level and genotypic level were calculated using the variances and co- variances according to Al-Jibouri *et al.* (1958).

Results and Discussion

Range and mean performance

The wide ranges among the genotypes for yield contributing characters (Table 2) indicated the extent of variability present among the genotypes for characters under the investigation. A wide variation in germination percentage was observed, which ranged from 58.44 % to 91.00 %. The cotyledon size ranged from 2.29 cm to 2.94 cm. The leaf blade length and width ranged from 10.8 cm to 17.10 cm and 6.4 cm to 11.80 cm, respectively. The leaf blade ratio ranged from 1.45 to 2.00. The petiole length ranged from 6.17 cm to 9.88 cm. The internode length ranged from 7.39 cm to 14.62 cm. The vine length ranged from 2.51 m to 5.14 m. The number of primary and secondary branches ranged from 3.93 to 7.66 and 9.83 to 19.15, respectively. The days to emergence of first staminate and pistillate flower ranged from 38.33 days to 50.33 days and 46.33 days to

61.00 days, respectively. The days taken to fruit maturity ranged from 67.67 days to 99.0 days. The blooming period ranged from 91.67 days to 109.67 days. The fruit length and diameter were ranged from 16.38 cm to 28.03 cm and 12.36 cm to 24.49 cm, respectively. The fruit weight was ranged from 2.05 kg to 5.57 kg. The number of fruits per vine was ranged from 1.85 to 4.35. The pericarp thickness was ranged from 9.31 mm to 21.57 mm. A wide variation in total soluble solids of fruit flesh were observed, which ranged from 7.74 °Brix to 17.16 °Brix. A wide variation in the number of seeds per fruit (seediness) were observed, which ranged from 143.98 to 885.15. The seed length and width ranged from 6.90 cm to 8.60 cm and 3.10 cm to 4.90 cm. This indicated that a wide variation in yield contributing characters were observed for 21 genotypes in present study. The findings of yield contributing traits are in consonance with Maggs-Kolling et al. (2000), Goda (2007), Solmaz & Sari (2009), Huh et al. (2014), Hakimi & El Madidi (2015), Singh et al. (2018), Sadiq et al. (2019), Mohosina et al. (2020) and Biswas et al. (2020). The results for qualitative character (TSS) are in agreement with the finding of Maggs-Kolling et al. (2000), Solmaz & Sari (2009), Hakimi & El Madidi (2015), Singh et al. (2018) and Biswas et al. (2020). The results for seeds protein content are in similar with Maggs-Kolling et al. (2000), Razavi & Milani (2006), Goda (2007), Solmaz & Sari (2009) and Sari et al. (2017).

Genetic variability: Results about genetic variability revealed that the value of phenotypic coefficient of variation (PCV) was found higher than respective genotypic

coefficient of variation (GCV), which ensured the presence of environmental factor in the expression of genotypes. It was also observed that the value of PCV was not much higher than the respective value of GCV, which indicated the high heritability and stable nature of genotypes, hence selection is also effective. High estimates of PCV and GCV were observed for the trait seediness, followed by pericarp thickness, number of primary branches, fruit weight, TSS and number of fruits per vine which reflected wide variability for traits of economic importance, hence further selection could improve the genotypes. Similar results were reported by Kehinde & Idehen (2008), Ogbonna & Obi (2010), Olaniyi et al. (2011), Said & Fatiha (2015) and Nisha et al. (2018) for fruit weight and number of fruits per vine; Ndukauba et al. (2015) for number of primary branches and number of fruits per vine; Choudhary et al. (2012) and Mohosina et al. (2020) for pericarp thickness. Sundaram et al. (2011) and Anburani et al. (2019) also observed similar results for most of these characters in watermelon.

Moderate estimates of PCV and GCV were observed for germination percentage, leaf blade length, leaf blade width, petiole length, internode length, number of secondary branches, fruit length, fruit diameter and seed width. Similar results were reported by the Ndukauba *et al.* (2015) and Nisha et al. (2018) for fruit diameter; and Mohosina et al. (2020) for fruit length and fruit diameter. Low PCV and GCV were observed cotyledon size, leaf blade ratio, days to emergence of 1st staminate flower, days to emergence of first pistillate/female flower, days taken to fruit

maturity, blooming period and seed length. The results of these characters are in agreement with the findings of Fulgence et al. (2019) for days taken to fruit maturity; Mohosina et al. (2020) for days to emergence of first staminate/male flower and days to emergence of 1st pistillate flower. Sundaram et al. (2011) and Nisha et al. (2018) also reported that GCV and PCV values were low for days to emergence of first pistillate/female flower, whereas moderate for days to emergence of ^{first} staminate/male flower and days taken to fruit maturity.

Heritability and Genetic Advance: The high estimates of heritability were reported for the characters viz., seediness, followed by pericarp thickness, fruit weight, fruit length, number of fruits per vine, number of secondary branches, TSS, fruit diameter, germination percentage, number of primary branches, vine length, internode length, leaf blade width, seed width, petiole length, days taken to fruit maturity, leaf blade length, seed length, days to emergence of first staminate flower, days to emergence of first pistillate flower and cotyledon size. The results of heritability align with the findings of Lalta et al. (1998) and Adjoumani et al. (2016) for number of fruits per vine and fruit weight; Fulgence et al. (2019) for days taken to fruit maturity, fruit diameter, seed length and seed width; Rabou et al. (2021) for fruit length, fruit diameter, fruit weight, TSS, pericarp thickness and number of fruits per vine. These results are also validated by several other investigations by Nisha et al. (2018), Sundaram et al. (2011), Choudhary et al. (2012) and Anburani et al. (2019) for one or more characters in their respective genetic

materials. Earlier, the breeding approaches were based on the phenotypic performance of the genotypes. The high heritability estimates were effective for such breeding approaches, where prime concern was on phenotypes. Later Jain et al. (1999) reported that for selecting the superior genotypes, heritability value along with genetic advance was a better approach rather than heritability value alone. The finding of Panse (1957) stated that the high estimate of heritability coupled with high genetic advance showed the additive gene effects, which supports the findings of Jain et al. (1999).

The high estimates of genetic advance as *per cent* of mean (GAM) was observed for germination percentage, leaf blade length, leaf blade width, petiole length, internode length, vine length, number of primary branches, number of secondary branches, fruit length, fruit diameter, fruit weight, number of fruits per vine, pericarp thickness, TSS, seediness and seed width. The results of high heritability are similar to the findings of Thakur & Nandpuri (1974), Sidhu & Brar (1978), Ogbonna & Obi (2010), Choudhary et al. (2015) and Haldhar et al. (2016) for fruit weight, fruit yield per vine and seediness; Prasad et al. (1988) for pericarp thickness; Ndukauba et al. (2015) for vine length and seediness; Nisha et al. (2018) for fruit diameter, rind thickness, fruit weight and number of fruits per vine; and Anburani et al. (2019) for vine length, number of primary branches per plant, fruit length, fruit diameter, fruit weight and seediness. The moderate estimates of genetic advance as *per cent* of mean (GAM) was observed for cotyledon size, leaf blade ratio, days to emergence of first

staminate flower, days to emergence of 1st pistillate flower, days taken to fruit maturity and seed length, whereas, low estimate of genetic advance as *per cent* of mean (GAM) was observed for blooming period. The results are in agreement with the finding of Gill &

Kumar (1986) and Fulgence et al. (2019) for days taken to fruit maturity; and Nisha et al. (2018) for days to emergence of first staminate flower, days to emergence of first pistillate flower and days taken to fruit maturity.

Table 2. Variability parameters for different traits in 21 watermelon genotypes

Trait	Mean	Range	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	Genetic Advance (% of mean)
G%	72.38	58.44-91.00	97.58	15.81	16.00	23.28	32.16
CS	2.66	2.29-2.94	85.45	6.83	7.39	0.35	13.01
LBL	13.18	10.8-17.10	92.10	12.10	12.61	3.15	23.92
LBW	7.81	6.4-11.80	96.94	15.97	16.22	2.53	32.39
LBR	1.70	1.45-2.00	78.74	7.80	8.79	0.24	14.25
PL	7.25	6.17-9.88	95.77	12.74	13.01	1.86	25.68
NPB	5.94	3.93-7.66	97.46	20.01	20.27	2.42	40.69
NSB	14.94	9.83-19.15	98.25	19.44	19.61	5.93	39.70
IL	10.19	7.39-14.62	97.23	19.76	20.04	4.09	40.14
VL	3.95	2.51-5.14	97.37	20.26	20.54	1.63	41.19
EFSF	43.38	38.33-50.33	85.92	8.21	8.86	6.80	15.69
EFPF	53.21	46.33-61.00	85.89	7.68	8.28	7.80	14.66
BP	101.27	91.67-109.67	73.85	4.67	5.43	8.37	8.27
FL	22.07	16.38-28.03	98.81	17.21	17.31	7.78	35.23
FD	18.37	12.36-24.49	97.90	17.90	18.09	6.70	36.49
FW	3.79	2.05-5.57	99.09	27.77	27.89	2.16	56.94
DTFM	83.17	67.67-99	94.23	8.76	9.02	14.57	17.51
F/V	3.27	1.85-4.35	98.64	20.69	20.83	1.38	42.33
PT	13.65	9.31-21.57	99.21	29.66	29.78	8.31	60.87
TSS	11.63	7.74-17.16	97.98	21.12	21.34	5.01	43.07
SN	506.71	143.98-885.15	99.39	35.89	35.99	37.43	73.7
SL	7.68	6.90-8.60	87.64	6.35	6.78	0.94	12.25
SW	3.85	3.10-4.90	96.92	13.83	14.05	1.08	28.05

(G%: Germination percentage; CS: Cotyledon Size; LBL: Leaf blade length; LBW: Leaf blade width; LBR: Leaf blade ratio; PL: Petiole length; NPB: No. of primary branches; NSB: No. of secondary branches IL: Internode length; VL: Vine length; EFSF: Days to emergence of 1st staminate flower; EFPF: Days to emergence of 1st pistillate flower; BP: Blooming Period; FL: Fruit length; FD: Fruit diameter; FW: Fruit weight; DTFM: Days taken to fruit maturity; F/V: Fruits per vine; PT: Pericarp thickness; TSS: Total soluble solids of fruit flesh; SN: Seediness; SL: Seed length; SW: Seed width)

Correlation Coefficient Analysis: The results of genotypic and phenotypic correlation among the 23 characters under investigation were depicted in Table 3. Correlation analysis revealed that maximum positive association was recorded for the traits number of primary branches and number of secondary branches, while, the most negative correlation was observed for the character's vine length and leaf blade width and ratio. Number of fruits per vine had significant genotypic and phenotypic positive correlation with the traits leaf blade length, internode length, number of primary branches and number of secondary branches. Ndukauba et al. (2015) and Bhagyalekshmi et al. (2020) also observed a positive correlation between the number of fruits per vine with the number of primary branches per plant. Fruit weight recorded significant positive association with vine length, number of primary branches, number of secondary branches, days to fruit maturity, fruit length, fruit diameter, seediness and pericarp thickness. The above results are supported by the research work of Ndukauba et al. (2015) for number of primary branches, fruit diameter and seediness; El-Madidi & Hakimi (2005), Kumar & Wehner (2011), Hakimi & El-Madidi (2015) Haldhar et al. (2015) and Nasab et al. (2020) for fruit length and fruit diameter; Nisha et al. (2018) and Fulgence et al., (2019) for fruit diameter and seediness; and Bhagyalekshmi et al. (2020) for number of branches per vine, days taken to fruit maturity, fruit diameter, seediness and pericarp thickness. Mohosina et al. (2020) for fruit length, fruit diameter and pericarp thickness. Kehinde & Idehen (2008) obtained

similar results between number of fruits per vine and seediness.

Days to emergence of first pistillate flower had significant genotypic and phenotypic positive correlation with the traits petiole length, vine length, days to emergence of first staminate flower, days taken to fruit maturity and TSS, while significant negative correlation with blooming period, fruit diameter and seed width. Nisha et al. (2018) and Bhagyalekshmi et al. (2020) also found positive interrelationship of vine length and days taken to fruit maturity with days to emergence of first pistillate flower. Significant negative association of days emergence of first pistillate flower with fruit diameter was also reported by Mohosina et al. (2020). Days taken to fruit maturity had a significant genotypic and phenotypic positive correlation with the traits days to emergence of first staminate flower, days to emergence of first pistillate flower, fruit weight and TSS, while negatively correlated with germination percentage and pericarp thickness. All the correlations obtained except TSS align with the results of Bhagyalekshmi et al. (2020). Similar conclusions were also cited by Singh & Singh (1988), Sundaram et al. (2011), Nisha et al. (2018) and Samadia & Haldhar (2020) for one or more characters in their respective genetic materials.

The blooming period had a significant genotypic and phenotypic positive correlation with the traits of number of primary branches, number of secondary branches, fruit diameter and pericarp thickness while negatively correlated with days to emergence of first staminate flower, days to emergence of first pistillate flower and days taken to fruit

maturity. TSS had a significant genotypic and phenotypic positive correlation with the days to emergence of first staminate flower, days to emergence of first pistillate flower and days taken to fruit maturity, while negatively correlated with leaf blade length, leaf blade width, internode length and petiole length. Mulyani and Waluyo (2020) also performed a correlation analysis between yield component traits and the yield of watermelon genotypes and found similar associations for one or more

traits. The results of correlation analysis depicted that the traits leaf blade length, internode length, number of primary branches and number of secondary branches, vine length, days taken to fruit maturity, fruit length, fruit diameter, seediness and pericarp thickness are the major yield attributing characters. So, more emphasis should be given to the above characters while improving these genotypes.

Table 3. Genotypic (above diagonal) and phenotypic correlation coefficients (below diagonal) among different traits in watermelon

	G%	CS	LBL	LBW	LBR	PL	IL	VL	NPB	NSB	EFSF	EFPF	DTF M	BP	FL	FD	FW	F/V	PT	TSS	SN	SL	SW
G%	1.000	0.385 **	- 0.039	- 0.119	0.188	- 0.076	- 0.016	- 0.157	- 0.052	- 0.036	- 0.330 **	- 0.315 *	- 0.342 **	- 0.173	- 0.151	- 0.050	- 0.407 **	0.150	- 0.164	- 0.215	0.118	0.470 **	0.448 **
CS	0.342 **	1.000	- 0.030	0.126	- 0.340 **	- 0.055	- 0.007	0.201	0.179	0.197	- 0.034	- 0.098	- 0.012	- 0.021	0.199	0.343 **	0.194	0.086	- 0.151	- 0.139	0.012	1.020 **	0.891 **
LBL	- 0.045	- 0.039	1.000	0.855 **	- 0.044	0.318 **	0.919 **	0.070	- 0.061	- 0.018	0.249 *	0.203	- 0.011	- 0.199	0.027	- 0.208	- 0.107	0.498 **	0.235	- 0.472 **	0.374 **	- 0.086	- 0.165
LBW	- 0.114	0.103	0.818 **	1.000	- 0.564 **	0.341 **	0.736 **	0.332 **	0.151	0.162	0.297 *	0.234	0.203	- 0.069	0.203	- 0.004	0.149	0.292 *	0.110	- 0.375 **	0.311 *	0.036	- 0.083
LBR	0.150	0.250 *	0.013	- 0.531 **	1.000	- 0.178	0.017	0.539 **	0.417 **	0.374 **	0.256 *	- 0.219	0.440 **	- 0.221	0.394 **	0.333 **	0.486 **	0.226	0.097	- 0.019	- 0.020	- 0.209	- 0.097
PL	- 0.077	- 0.026	0.302 *	0.326 **	- 0.154	1.000	0.370 **	0.172	0.096	0.113	0.314 *	0.282 *	0.093	- 0.143	- 0.172	0.238	- 0.024	0.173	0.178	- 0.396 **	0.172	- 0.130	- 0.243
IL	- 0.019	- 0.007	0.868 **	0.714 **	0.001	0.364 **	1.000	0.125	- 0.023	0.043	0.257 *	0.205	- 0.080	- 0.153	- 0.007	- 0.138	- 0.112	0.428 **	0.289 *	- 0.462 **	0.192	- 0.074	- 0.159
VL	- 0.158	0.178	0.081	0.321 **	- 0.457 **	0.165	0.121	1.000	0.551 **	0.563 **	0.352 **	0.279 *	0.204	0.189	0.347 **	0.321 **	0.450 **	0.188	0.149	0.114	- 0.236	0.102	- 0.109
NPB	- 0.055	0.192	- 0.062	0.149	- 0.365 **	0.089	- 0.027	0.535 **	1.000	0.998 **	0.137	0.041	0.088	0.391 **	0.337 **	0.580 **	0.447 **	0.478 **	0.234	0.148	0.284 *	0.037	- 0.180
NSB	- 0.036	0.174	- 0.016	0.160	- 0.330 **	0.113	0.047	0.553 **	0.976 **	1.000	0.165	0.073	0.081	0.391 **	0.300 *	0.568 **	0.404 **	0.538 **	0.249 *	0.134	0.247 *	0.034	- 0.182
EFSF	- 0.293 *	- 0.043	0.226	0.281 *	- 0.237	0.265 *	0.231	0.316 *	0.134	0.164	1.000	1.041 **	0.748 **	- 0.438 **	0.253 *	- 0.204	0.225	0.141	- 0.068	0.327 **	0.124	- 0.143	- 0.261 *
EFPF	- 0.288	- 0.072	0.167	0.228	- 0.204	0.260 *	0.190	0.255 *	0.030	0.055	0.870 **	1.000	0.787 **	- 0.439	0.186	- 0.282	0.140	0.070	- 0.147	0.366 **	0.098	- 0.159	- 0.272

	*												**		*							*
DTF	-	-	-	0.202	-	0.086	-	0.184	0.086	0.083	0.673	0.696	1.000	-	0.303	-	0.412	-	-	0.433	-	-
M	0.325	0.015	0.026	0.414	0.086	0.064	0.184	0.086	0.083	0.673	0.696	1.000	0.351	0.303	0.064	0.412	0.163	0.247	0.433	0.076	0.070	0.160
	**			**							**	**		*		**	*	*	**	*		
BP	-	0.050	-	-	-	-	-	0.143	0.345	0.324	-	-	-	1.000	0.205	0.415	0.213	0.008	0.309	-	-	-
	0.134	0.050	0.174	0.063	0.114	0.083	0.119	0.143	0.345	0.324	0.360	0.321	0.281	1.000	0.205	0.415	0.213	0.008	0.309	0.172	0.013	0.169
									**	**	**	**	*			**			*			0.096
FL	-	0.180	0.026	0.196	-	-	-	0.338	0.336	0.293	0.234	0.177	0.298	0.186	1.000	0.417	0.846	-	0.467	-	0.069	0.076
	0.148	0.180	0.026	0.196	0.339	0.171	0.007	0.338	0.336	0.293	0.234	0.177	0.298	0.186	1.000	0.417	0.846	0.076	0.467	0.027	0.069	0.076
					**			**	**	*			*			**	**		**			0.054
FD	-	0.311	-	-	-	0.230	-	0.311	0.568	0.557	-	-	-	0.363	0.407	1.000	0.594	0.144	0.367	-	-	0.207
	0.047	0.311	0.201	0.001	0.302	0.230	0.138	0.311	0.568	0.557	0.176	0.277	0.061	0.363	0.407	1.000	0.594	0.144	0.367	0.086	0.024	0.074
		*			*			*	**	**		*		**	**		**		**			
FW	-	0.178	-	0.149	-	-	-	0.444	0.441	0.401	0.213	0.132	0.400	0.183	0.835	0.590	1.000	-	0.492	0.021	-	0.076
	0.400	0.178	0.105	0.149	0.438	0.023	0.114	0.444	0.441	0.401	0.213	0.132	0.400	0.183	0.835	0.590	1.000	0.133	0.492	0.021	0.076	0.048
	**				**			**	**	**			**		**	**			**			
F/V	0.146	0.062	0.469	0.286	0.188	0.159	0.416	0.185	0.469	0.531	0.136	0.051	-	-	-	0.147	-	1.000	0.151	-	0.358	-
	0.146	0.062	0.469	0.286	0.188	0.159	0.416	0.185	0.469	0.531	0.136	0.051	0.158	0.018	0.076	0.147	0.129	1.000	0.151	0.132	0.358	0.028
			**	*			**		**	**										**	**	0.183
PT	-	-	0.221	0.105	0.091	0.175	0.285	0.146	0.233	0.248	-	-	-	0.269	0.462	0.365	0.491	0.152	1.000	0.394	0.201	0.251
	0.163	0.135	0.221	0.105	0.091	0.175	0.285	0.146	0.233	0.248	0.068	0.141	0.236	0.269	0.462	0.365	0.491	0.152	1.000	0.394	0.201	0.251
							*			*				*	**	**	**			**	*	*
TSS	-	-	0.444	0.364	-	0.382	0.450	0.114	0.137	0.137	0.296	0.345	0.416	-	-	-	0.021	-	-	0.390	1.000	-
	0.209	0.139	0.444	0.364	0.012	0.382	0.450	0.114	0.137	0.137	0.296	0.345	0.416	0.164	0.028	0.093	0.021	0.128	0.390	1.000	0.131	0.110
			**	**		**	**				*	**	**						**			0.094
SN	0.119	0.010	0.361	0.304	-	0.169	0.190	-	0.279	0.244	0.116	0.082	-	-	0.066	-	-	0.355	0.199	-	1.000	-
	0.119	0.010	0.361	0.304	0.019	0.169	0.190	0.232	0.279	0.244	0.116	0.082	0.076	0.012	0.066	0.022	0.070	0.355	0.199	0.130	1.000	0.060
			**	*					*									**				0.096
SL	0.438	0.869	-	0.020	-	-	-	0.096	0.021	0.033	-	-	-	-	0.064	0.212	0.069	0.031	-	-	-	1.000
	0.438	0.869	0.070	0.020	0.159	0.123	0.064	0.096	0.021	0.033	0.093	0.168	0.069	0.113	0.064	0.212	0.069	0.031	0.236	0.109	0.058	1.000
	**	**																				0.957
																						**
SW	0.436	0.827	-	-	-	-	-	-	-	-	-	-	-	-	-	0.065	-	-	-	-	-	0.881
	0.436	0.827	0.150	0.085	0.075	0.223	0.149	0.110	0.173	0.175	0.238	0.248	0.146	0.052	0.055	0.065	0.051	0.185	0.284	0.087	0.095	0.881
	**	**										*							*			**
																						1.000

*, ** represent significance at 5% and 1%, respectively.

(G%: Germination percentage; CS: Cotyledon Size; LBL: Leaf blade length; LBW: Leaf blade width; LBR: Leaf blade ratio; PL: Petiole length; IL: Internode length; VL: Vine length; NPB: No. of primary branches; NSB: No. Of secondary branches; EFSF: Days to emergence of 1st staminate flower; EFPF: Days to emergence of 1st pistillate flower; DTFM: Days taken to fruit maturity; BP: Blooming Period; FL: Fruit length; FD: Fruit diameter; FW: Fruit weight; F/V: No. of fruits per vine; PT: Pericarp thickness; TSS: Total soluble solids of fruit flesh; SN: Seediness; SL: Seed length; SW: Seed width)

Conclusion

As the sufficient genetic variability was found in the studied watermelon genotypes accompanied with desirable heritability and genetic advance. Phenotypic and genotypic coefficients of variation were recorded high for important traits. High heritability coupled with high genetic advance as percent of mean was also observed for most of the morphological characters. Number of fruits per vine had significant genotypic and phenotypic positive correlation with the traits leaf blade length, internode length, number of primary branches and number of secondary branches. Fruit weight recorded significant positive association with the traits vine length, number of primary branches, number of secondary branches, days to fruit maturity, fruit length, fruit diameter, seediness and Pericarp thickness. Thus, the genetic variability and correlation among important traits suggested importance of selection and emphasis should be given on above mentioned traits.

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