



GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR GROWTH AND YIELD ATTRIBUTES IN WATERMELON (CITRULLUS LANATUS THUNB)

Sheidu, A¹*. Silifatu A. A¹., and Igyuve T.M² ¹Nasarawa State University Keffi, Nigeria ²Ahmadu Bello University Zaria, Nigeria

Corresponding Email: sheiduabdullaziz8@gmail.com

A B S T R A C T

Field investigation was carried out to study the genetic variability, heritability and genetic advance of watermelon genotypes. The result of the studied showed significant differences among the nine genotypes for all the nine characters studied. Genetic analysis indicated maximum phenotypic and genotypic coefficient of variation among the studied traits. The results indicates high phenotypic variation for vine length (week 4, 6 and 8), number of leaves (week 6 and 8), number of tendrils (week 6 and 8), number of male flower, and fruit burst however, moderate values was observed for vine length (week 6 and 8) while high genotypic coefficient of variation was observed for number of leaves (week 6), number of branches (week 4 and 6), number of tendrils (week 4), number of male flower, number of female flower, fruit burst, while moderate values were recorded for vine length (week 4,6 and 8), number of leaves (week 4 and 8), number of branches (week 8), number of tendrils (week 6 and 8). High heritability was observed for vine length at (6 weeks), vine length at (8 weeks), number of branches at (6 weeks), and number of tendrils at (8 weeks). High genetic advance was recorded for vine length at (6 weeks), vine length at (8 weeks), and number of leaves at (6 weeks). Coefficient of correlation showed positive and highly significant association for most of the studied traits. These traits can be modified based on the variability observed and can be exploited in watermelon breeding programs for improvement of other traits.

KEYWORDS

Genetic advance, Heritability, GCV, PCV and Watermelon

This work is licensed under Creative Commons Attribution 4.0 License.

INTRODUCTION

The family Cucurbitaceae has different species, and the only cultivated species of this genus is watermelon (*Citrulluslanatus* var. Lanatus) with the chromosome number of 2n = 2x = 22 (Bisognin, 2002)^[1]. Watermelon originates from the South African region and watermelon is currently being cultivated worldwide as a fruit crop. China has taken the first place with 62,803,768 tons (60.40% production) and Iran (4,113,711 tons), Turkey (4,031,174 tons), India (2,520,000 tons), and Brazil (2,240,796 tons) are in the next places (FAOSTAT, 2018)^[3]. It is a tender warm season vegetable crop which can be grown in all part of Nigeria. But mainly produced in the Northern part of Nigeria. Watermelon is widely cultivated and most consumed cucubit in the world (Huh et al., $.2008)^{[9]}$. According to (Goreta et al., 2005)^[7]. The crop account for about 6.8% of world area devoted to vegetable production. Different species and varieties of watermelon are very similar at the beginning of growth but show great variation in fruit shape and other traits (NorelahiSoghaniet al., 2018)^[8]. One of the most important steps in cultivar development is understanding the genetic variability found in genetic resources. It is a dynamic process that required continues enrichment and characterization of the materials maintained in germplasm collections (Valls 2007)^[22]. The information on the nature and the magnitude of variability existing in the genetic material is of great relevance to a plant breeder to design an effective breeding program. Therefore, this study is geared towards understanding the level of phenotypic and genotypic coefficient of variation, heritability, genetic advance and correlation among the studied traits in water melon.

MATERIALS AND METHOD

The experiment was carry out during the dry season and early wet season of 2022 at the research and development farm of Nasarawa State University, Shabu-Lafia Campus with latitude 08°33N and 08°33E,162m above Sea level.

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three

replications. Two row of 1m per plot was used with a spacing of 1m inter and 1m intra row, three seed of water melon was sown and later thin to two plant per stand, and a total of 9 plots and 9 varieties will be used for the experiment respectively.Planting materials were source from Lafia L.G.A. Nasarawa state.Each plot was demarcated 1m allay-way, uniform bed size of 10x15m (150m²) was prepared manually, in each bed, and 30x30x30cm (spots) were dug for depth, width and length respectively. 5kg of organic manure was incorporated in each spot (hole) and water was applied two weeks before planting.

Data on the following parameters were taken at 4, 6, and 8 weeks after planting; number of leaves per plant, number of branch per tagged plant, vine length (cm), number of tendrils, number of male flower, number of female flower.

Weeding was done at 2, 4, 6 and 8WAS manually using hoe to keep the experimental plots weed free. Pest and disease of plant was control with insecticide, fungicide and bactericide base on infestation. Fruit harvest was done at physiological maturity of plant.

Data collected were subjected to analysis of variance (ANOVA) using SAS software, mean was separated using Duncan's new multiple range test (DNMRT) significant different at 5% level of probability. PCV and GCV, heritability, genetic advance and correlation were also analyzed using the SAS software. The heritability percentage was categorized as low, moderate and high as suggested by Robinson *et al.* (1949)^[17], (0-30%): Low, (30-60%): Moderate and (60% and above): High,

respectively. The Genetic advance as percent of mean was categorized as (0-10%): Low, (10-20%): Moderate and (Above 20%): High low, moderate and high (Johnson *et al.*, 1955)^[12].

Results and Discussions

The mean square of analysis of variance of nine watermelon traits is presented in Table 1. Results on variety indicated a highly significant difference for all traits evaluated except for Vine length at 4 weeks after planting and days to first flowering which were not significantly different indicating a considerable variability among the genotypes studied. Jagtap and Bhuktar $(2021)^{[13]}$, Damor*et al.* $(2016)^{[4]}$, and Sultan *et al.* $(2018)^{[20]}$ reported similar findings.

Mean performance of nine watermelon varieties for agronomic character is presented in Table 2. Result revealed wide range of variation among the nine watermelon varieties evaluated. SIL 03 had the highest vine length at 4 weeks (42.83) while kaolack had the least length (26.65), logone had the highest length at 6 and 8 weeks (187.67 and 216.83) while kaolack had the least length at 6 and 8 weeks (113.50 and 127.97) respectively, in the same trend the variety logone sustained highest number of branches at 6 (11.67) at 8 weeks (17.83), number of tendrils at 4 weeks (9.67), at 6 weeks (94.33), at 8 weeks (92.17), number of male flowers (21.50), number of female flowers (14.17), yield (21.33), fruit weight (3.73) and number of fruit burst (9.00), conversely the following varieties had least and lowest kayack for number of leaves at 4 weeks (7.67), number of branches at 6 weeks (5.17) at 8 weeks (9.17), number of tendrils at 4 weeks (3.00), number of tendrils at 8 weeks (49.50), number of male flowers (2.83), and yield (14.33). AMI 02 had the highest number of branches at 4 weeks (5.33), least number of tendrils of 6 weeks (43.17), the variety SAM 02 had the number of days to first flowering (30.67) while Faransa was earliest for days to first flowering (29.33).

The estimates of variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variance (GCV), heritability (broad sense) and genetic advance are presented in Table 3. Result revealed a wide range of genotypic and phenotypic variation for vine length (cm) at 4 weeks (17.61 and 91.57), vine length (cm) at 6 weeks (463.98 and 725.94), vine length (cm) at 8 weeks (619.17 and 1009.34), Number of leaves at 4 weeks (3.22 and 11.43), Number of leaves at 6 weeks (335.12 and 700.4), Number of leaves at 8 weeks (152.28 and 592.95), Number of branches at 4 weeks (0.81 and 2.20), Number of branches at 6 weeks (3.21 and 4.45), Number of branches at 8 weeks (5.13 and 13.81), Number of Tendrils at 4 Weeks (1.65 and 10.69), Number of Tendrils at 6 Weeks (98.37 and 503.15), Number of Tendrils at 8 Weeks (117.89 and 187.46), days to first flowering (-0.08 and 0.74), Number of male flower (11.41 and 21.33), Number of female flower (7.10 and 17.83), yield (2.22 and 10.76), fruit weight (0.02 and 0.07), Number of fruit burst (11.41 and 21.33). The PCV for the different characters evaluated ranged from 2.85 (Days to first flowering) to 107.07 (Number of fruit burst), similarly, GCV and ECV had a range of 0.93% and 3% (Days to first flowering) to 71.15% and 80.01% (Number of fruit burst) respectively. The transgressive variation of the phenotypic and genotypic indicates the influence of environment in the studied traits. This result is in accordance with the findings of Jagtap and Bhuktar (2021)^[11], Rashid et al., (2020)^[15], Sultan et al., (2018)^[20] and Husna et al., (2011)^[10].

The results indicates high phenotypic variation for vine length (week 4, 6 and 8) (91.57, 725.94, 1009.34 respectively), number of leaves (week 6 and 8) (33.00, 31.17 respectively), number of tendrils week 6 and 8(35.88, 19.96 respectively), number of male flower (28.93), and fruit burst (107.07) meanwhile, moderate values was observed for vine length (week 6 and 8) (17.08 and 17.33 respectively) while high genotypic coefficient variation was observed for number of leaves week 6

(22.82), number of branches week 4 and 6 (33.36 and 22.98 respectively), number of tendrils week4 (20.03), number of male flower (21.16), number of female flower (32.16), fruit burst (71.15), while moderate values was recorded for vine length week 4,6 and 8 (11.69, 13.65 and 13.57 respectively), number of leaves week 4,8 (15.79, 15.80 respectively), number of branches week 8 (18.38), number of tendrils week 6 and 8 (15.86 and 15.83 respectively). This result is similar to the findings of Jagtap and Bhuktar (2021)^[11], Sultan et al., (2018)^[20], Joydip et al., (2015)^[13], Tomar et al., (2008)^[21]. Traits indicating moderate to high coefficient of variation suggested that viable improvement can be achieved through selection. A wide range of Phenotypic and genotypic estimates further indicates that this character can respond to selection for better improvement. Those characters who shows low phenotypic and genotypic variation may barely be improved through selection. This is in accordance with the findings of Jagtap and Bhuktar $(2021)^{[11]}$, Husna et al., $(2011)^{[10]}$ and Pandit et al., $(2009)^{[14]}$. Low heritability Was observed for vine length at 4 weeks (19%), Number of leaves at 4 weeks (28%), number of leaves at 8 weeks (26%), number of tendrils at 4 Weeks (15%), number of tendrils at 6 Weeks (20%), days to first flowering (-11%) and yield (21%), fruit weight (27%) and number of fruit burst (19%). The result suggest that these traits are more control more by the environment. Moderate heritability was observed for number of leaves at 4 weeks (37%), number of branches at 8 weeks (37%), number of male flowers (54%), and number of female flowers (40%), suggesting a slight environmental effect on the characters. High heritability was observed for vine length at 6 weeks (64%), vine length at 8 weeks (61%), number of branches at 6 weeks (72%), and number of tendrils at 8 weeks (63%). This indicates that the characters are influenced more by gene action than the environmental effect. Thus, these characters can be reliable transmitted to the progeny. Similar result was reported by (Rashid et al., 2020^[15]; Sharma et al., 2010^[18]; Vishwa, 2018^[23]; Collins, 2007^[2]; Ren, 2012^[16]; Xia, 2018^[24], Dane, 2004^[5]& 2007^[6]). Result on genetic advance revealed that low advance was observed for vine length at 4 weeks (3.79), number of leaves at 4 weeks (1.96), number of branches at 4 weeks (1.13), number of branches at 6 weeks (3.13), number of branches at 8 weeks (2.84), number of tendrils at 4 weeks (1.04), number of tendrils at 6 weeks (9.03), days to first flowering (-0.19), number of male flower (5.09), number of female flower (3.46), yield (1.4), fruit weight (0.14), number of fruit burst (2.89) suggesting that these traits are highly controlled by environmental effect and selection based on the traits may be ineffective. Moderate genetic advance was recorded for number of leaves at 8 weeks (12.88), and number of tendrils at 8 weeks (17.75) suggesting slight influence of the environment on these traits. High genetic advance was recorded for vine length at 6 weeks (35.47), vine length at 8 weeks (40.15), and number of leaves at 6 weeks (26.09) suggesting that these traits are influenced by additive gene action. This result is in accordance with the findings of Sriramamurthy $(2000)^{[19]}$.

Conclusions

The result of the studied showed significant differences among the nine genotypes for all the nine characters. Genetic analysis indicated maximum phenotypic and genotypic coefficient of variation among the studied traits. The results indicates high phenotypic variation for vine length (week 4, 6 and 8), number of leaves (week 6 and 8), number of tendrils (week 6 and 8), number of male flower, and fruit burst however, moderate values was observed for vine length (week 6 and 8) while high genotypic coefficient of variation was observed for number of leaves (week 6), number of branches (week 4 and 6), number of tendrils (week 4), number of male flower, number of female flower, fruit burst, while moderate values were recorded for vine length (week 4, 6 and 8), number of leaves (week 4 and 8), number of branches (week 8), number of tendrils (week 6 and 8), number of leaves (week 4 and 8), number of branches (week 8), number of tendrils (week 6 and 8), number of leaves (week 4 and 8), number of branches (week 8), number of tendrils (week 6 and 8), number of leaves (week 4 and 8), number of branches (week 8), number of tendrils (week 6 and 8), number of leaves (week 4 and 8), number of branches (week 8), number of tendrils (week 6 and 8). High heritability was observed for vine length at (6 weeks), vine length at (8 weeks), number of branches at (6 weeks), and number of tendrils at (8 weeks). High genetic advance were recorded for vine length at (6 weeks),

vine length at (8 weeks), and number of leaves at (6 weeks). Coefficient of correlation showed positive and highly significant association for most of the studied traits. Therefore, breeders can take can take advantage of the variability existing between the genotypes in developing superior watermelon varieties.

Table 1. Mean squares from the ANOVA for agronomic Traits of Watermelon varieties evaluated in 2022 growing season.																			
SOV	Df	VL4wk	VL6wk	VL8wk	NL4wk	NL6wk	NL8wk	NB4wk	NB6wk	NB8wk	TenD4wk	TenD6wk	TenD_8wk	DFF	No. MF	No.FF	YLD	FrtWt	FrtBrst
Rep	2	688.65	502.58	974.15	62.29	96.73	1438.69	2.4	0.4	50.69	45.36	1669.59	1084.23	69.58	167.23	149.27	178.37	0.22	12.7
Variety	8	126.79ns	1653.9**	2247.68**	17.87**	1370.64**	897.5**	3.83**	10.87**	24.07**	14.00**	699.88**	423.23**	0.58ns	44.16**	32.03**	15.20*	0.10*	18.95*
Error	16	73.96	261.96	390.17	8.2	365.28	440.67	1.39	1.24	8.68	9.04	404.78	69.58	0.82	9.92	10.73	8.54	0.05	5.62
*, **, ***: $p \le 0.05$, 0.01, and 0.001, SOV = Source of Variation, Df= Degree of freedom, VL4wk= Vine Length at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6, VL8wk= Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, VL6wk= Vine Length at Weeks 6,																			
NL6wk= Number of Leave at 6 Weeks, NL8wk= Number Of Leave at 8 Weeks, NB4wk= Number of Branches at 4 Weeks, NB6wk= Number of Branches at 6 Weeks, NB8wk= Number of Branches at 8 Weeks,																			
TenD4wk	= Num	nber of Tendr	rils at 4 Week	s, TenD6wk=	Number of T	endrils at 6 We	eks, TenD8	wk= Numbe	er of Tendril	s at 8 Weeks	s, DFF = Days t	to First Floweri	ing, No. MF= N	lumber of I	Male Flower	, No. FF= N	lumber of I	Female Flor	wer,
YLD=Yie	ld, Frt	Wt= Fruit W	eight, FrtBrs	st= Number of	Fruit Burst.														

	Table 2. Component of variance, coefficient of variation, heritability in broad sense and genetic advance																	
Traits	VL_4	VL_6	VL_8	NL_4	NL_6	NL_8	NB_4	NB_6	NB_8	NTenD_	NTenD_	NTenD_	DFF	No.	No.F	YLD	FrtW	FrtB
	wk	wk	wk	wk	wk	wk	wk	wk	wk	4wk	6wk	8wk		MF	F		t	rst
GM	35.9	157.78	183.34	11.37	80.2	78.11	2.7	7.8	12.33	6.42	62.52	68.59	30.22	15.96	8.17	16.96	3.35	2.96
SEm	4.97	9.34	11.4	1.65	11.03	12.12	0.68	0.64	1.7	1.74	11.62	4.82	0.52	1.82	1.89	1.69	0.13	1.37
CD 5%	14.89	28.01*	34.19*	4.96N	33.08*	36.34	2.04*	1.93*	5.10*	5.20NS	34.82NS	14.44*	1.57	5.45*	5.67*			4.10*
	NS			S		NS							NS			5.06N	0.38N	
CD 1%	20.51	38.6*	/7 11*	6 83N	15 58	50.06	2.81N	2 66*	7.02N	7 17NS	17 98NS	10 80*	2 16	7 51*	7.81	5 6 97N	0.53N	5 65
CD 170	20.51 NS	50.0	4/.11	S	45.56 NS	NS	2.011V S	2.00	7.021 S	7.17105	47.70145	17.07	2.10 NS	7.51	NS	S.	S.551	NS
$FV(\delta^2 a)$	73.96	261.96	390.17	82	365.28	440.67	1 39	1 24	8 68	9.04	404 78	69 58	0.82	9.92	10.73	8 54	0.05	5.62
$CV(\delta^2 a)$	17.61	201.90 463.98	610 17	3.22	335.12	152.28	0.81	3.24	5.13	1.65	98 37	117.80	-0.02	11 /1	7 10	2.54	0.03	J.02 A AA
GV(O y)	01.57	725.04	1000.2	11 /2	700.4	502.20	2.20	J.21 4 45	12.91	10.60	502.15	117.07	-0.00	21.41	17.92	10.76	0.02	10.06
$PV(0^{-}P)$	91.57	123.94	1009.5 4	11.45	/00.4	392.93	2.20	4.43	15.61	10.09	505.15	187.40	0.74	21.55	17.65	10.76	0.07	10.00
ECV(%)	23.95	10.26	10.77	25.19	23.83	26.87	43.57	14.29	23.9	46.81	32.18	12.16	3.00	19.73	40.07	17.22	6.59	80.01
GCV(%)	11.69	13.65	13.57	15.79	22.82	15.8	33.36	22.98	18.38	20.03	15.86	15.83	0.93	21.16	32.6	8.79	3.95	71.15
PCV(%)	26.65	17.08	17.33	29.73	33.00	31.17	54.88	27.06	30.15	50.92	35.88	19.96	2.85	28.93	51.66	19.34	7.68	107.0
																		7
h^2b	19	64	61	28	48	26	37	72	37	15	20	63	-11	54	40	21	27	19
GA	3.79	35.47	40.15	1.96	26.09	12.88	1.13	3.13	2.84	1.04	9.03	17.74	-0.19	5.09	3.46	1.4	0.14	2.89
GA(%)	10.56	22.48	21.9	17.27	32.52	16.49	41.78	40.19	23.08	16.23	14.45	25.86	-0.62	31.89	42.38	8.23	4.19	97.4

PCV: Phenotypic coefficient of variation; **GCV**: Genotypic coefficient of variation, **PV** ($\delta^2 p$): Phenotypic variance,

 $GV(\delta^2 g)$: Genotypic variance, GA: Genetic advance, GA (%): Percentage genetic advance; h2b; Heritability in broad sense.

VL4wk=Vine Length at 4 Weeks, VL6wk=Vine Length at Weeks 6, VL8wk=Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks,

NL6wk= Number of Leave at 6 Weeks, NL8wk= Number of Leave at 8 Weeks, NB4wk= Number of Branches at 4 Weeks, NB6wk= Number of Branches at 6 Weeks, NB8wk= Number of

Branches at 8 Weeks,

TenD4wk= Number of Tendrils at 4 Weeks, TenD6wk= Number of Tendrils at 6 Weeks, TenD8wk= Number of Tendrils at 8 Weeks, DFF= Days to First Flowering, No. MF= Number of Male Flower, No. FF= Number of Female Flower,

YLD=Yield, FrtWt= Fruit Weight, FrtBrst= Number of Fruit Burst.

	Table 3. mean performance of Nine (9) Water melon varieties																	
Variety	VL4w	VL6w	VL8w	NL4w	NL6w	NL8w	NB4w	NB6w	NB8w	TenD4wk	TenD6wk	TenD_8wk	DFF	No. MF	No.F	YLD	FrtW	FrtBrs
	k	k	k	k	k	k	k	k	k						F		t	t
KAYACK	27.47	143.33	160.3	7.67	69.83	70.33	1.50	5.17	9.17	3.00	51.50	49.50	30.0	9.50	2.83	14.3	3.35	2.67
FARANSA	39.47	175.83	107 3	10.67	76.00	76.67	2 50	8 33	10.67	8 13	58 33	77 33	0 29.3	15 17	7 57	3 163	3.03	0.00
TAKANSA	37.47	175.05	177.5	10.07	70.00	70.07	2.50	0.55	10.07	0.15	50.55	11.55	3	13.17	1.51	3	5.05	0.00
SIL 02	41.03	156.17	186.98	11.17	70.33	71.00	2.33	7.83	11.27	7.67	64.50	61.00	30.0	16.00	7.33	17.3	3.4	3.00
													0			3		
SAM 02	28.83	140.5	171.25	12.33	68.00	70.17	2.33	8.33	12.00	5.33	54.33	65.67	30.6 7	17.50	12	15.0	3.22	2.33
LOGONE	42.22	187 67	216.83	15.67	130.67	119.67	2.83	11.67	17.83	9.67	94 33	92.17	7 30.6	21.50	14 17	21.3	3 73	9.00
LOGOILE	42.22	107.07	210.05	15.07	150.07	119.07	2.05	11.07	17.05	9.07	74.55	2.17	7	21.50	14.17	3	5.75	9.00
KAOLACK	26.65	113.50	127.97	8.50	62.83	61.67	1.67	6.00	10.83	3.83	53.33	64.50	30.3	13.83	6.5	15.3	3.33	3.00
													3			3		
BIN 02	37.78	175.00	203.62	13.67	85.83	82.50	2.50	8.17	14.17	7.00	74.83	74.00	30.6	19.50	7.17	18.6	3.33	1.67
SH 02	42.92	150.92	100.12	11.02	(5.00	(5.92	2.22	6.17	0.92	7 (7	74.92	64.17	7	11.02	7 17	7	2.20	1.22
SIL 03	42.85	150.85	180.15	11.85	65.00	05.85	3.33	0.17	9.85	/.0/	/4.85	04.17	30.3 3	11.85	/.1/	15.0 7	3.39	1.55
AMI 02	36.85	156.17	205.68	10.83	93.33	85.17	5.33	8.50	15.17	5.5	43.17	69.00	30.0	18.83	8.83	, 18.6	3.41	3.67
													0			7		
CV	23.95	10.26	10.77	25.19	23.83	26.87	43.57	14.29	23.9	46.81	32.18	12.16	3.00	19.73	40.07	17.2	6.59	80.01
																2		
CM	25.0	157 79	192.24	11.27	80.2	79.11	27	7 0	10.22	6.42	62.52	69.50	20.2	15.06	9 17	16.0	2.25	2.06
UM	55.9	137.78	103.34	11.57	60.2	/0.11	2.1	/.0	12.33	0.42	02.32	08.39	50.2 2	13.90	0.1/	10.9 6	5.55	2.90

VL4wk=Vine Length at 4 Weeks, VL6wk=Vine Length at Weeks 6, VL8wk=Vine Length at Weeks 8, NL4wk= Number of Leave at 4 Weeks, NL6wk= Number of Leave at 6 Weeks, NL8wk= Number of Leave at 4 Weeks, NL8wk= Number of Branches at 4 Weeks, NB8wk= Number of Branches at 6 Weeks, NB8wk= Number of Branches at 8 Weeks, TenD6wk= Number of Branches at 8 Weeks, TenD6wk= Number of Branches at 8 Weeks, TenD6wk= Number of Tendrils at 8 Weeks, DFF= Days to First Flowering, No. MF= Number of Male Flower, No. FF= Number of Female Flower, YLD=Yield, FrtWt= Fruit Weight, FrtBrst= Number of Fruit Burst.

References

[1] Bisognin D. A. (2002). Origin and evolution of cultivated cucurbits. Ciência Rural, vol. 32, no. 4, pp. 715–723.

[2] Collins J. K. (2007). Watermelon consumption increases plasma arginine concentrations in adults. Nutrition 23, 261-266

[3] FAOSTAT, (2018). Statistical databases, In Food and Agriculture Organization of the United Nations.

[4] Damor A. S., Patil J. N., Parmer H. K., and Vyas N. D. (2016) Studies on genetic variability, heritability and genetic advance for yield and quality traits in bottle gourd [*Lageneria seceraria* (Molina) Stand I.] genotypes. Int. J. Sci. Envi. Tech, 5(4):2301-2307.

[5] Dane F., Lang P., and Bakhtiyarova R (2004). Comparative analysis of chloroplast DNA variability in wild and cultivated Citrullus species. Theor Appl Genet 108: 958-966

[6] Dane F. and Liu J. (2007). Diversity and origin of cultivated and citron type watermelon (*Citrullus lanatus*). Genetic Resources and Crop Evolution September, Volume 54, Issue 6, pp 1255-1265
[7] Goreta S., Perica S., Dumicic G., Bucan L. and Zanic K. (2005). Growth and yield of watermelon

on polyethylene mulch with different spacing and nitrogen rates. American J. Hort. Sci. 40(2): 366-369

[8] NorelahiSoghani Z., Rahimi M., Nasab M. A. and Maleki M. (2018). "Grouping and genetic diversity of different watermelon ecotypes based on agro-morphological traits and ISSR marker," Iheringia, Série Botânica, vol. 73, no. 1, pp. 53–59.

[9] Huh, Y. C., Solmaz I. and sari N. (2008). Morphological characterization of Korean and Turkish watermelon germplasm. Cucurbitaceae, proceedings of the IXth EUCARPIA meeting on genetics and breeding of Cucurbitaceae (Pitrat M.). INRA, Avignon (France). May 21-24.

[10] Husna A., Mahmud F., Islam M. R., Mahmud M. A. A. and Ratna M. (2011). Genetic variability correlation and path coefficient in Bottle gourd [*Lagenaria siceraria* (Molina) Standl.]. Advance in Biological Res. 5(6):323-327.

[11] Jagtap B. R. and Bhuktar A. (2021). Variability study in watermelon (*Citrullus lanatus*).
International Journal of Botany Studies ISSN: 2455-541X Volume 6, Issue 6, Page No. 788-791.
[12] Johnson H. W., Robinson H. F. and Comstock R. E. (1955) Estimates of genetic and environmental variability in soybean. *Agronomy J.* 47:314-318.

[13] Joydip M., Mangala T., and Vinod K. D. (2015). Studies on genetic variability and trait interrelationship in bottle gourd (Lageneria seceraria L.). Hort. Res. Spect. 4(1): 34-38

[14] Pandit M. K., Mahato B., and Sakar A. (2009). Genetic variability heritability and genetic advance for some fruit characters and yield in bottle gourd [*Lagenaria siceraira* (Molina.) Standl.]. Acta Hort. 809: 221223.

[15] Rashid M., Wani K. P., Hussain K., Dar Singh, Khalil Z. A., and Ali P.K. (2020). Studies on genetic variability, heritability and genetic advance in bottle gourd [*Lagenaria siceraria* (Molina) Stand I.] genotypes. Internat. J. Chemical Studies, 8(3):455-458.

[16] Ren, Y. (2012). A high resolution genetic map anchoring scaffolds of the sequenced watermelon genome. PLoS ONE 7, e29453.

[17] Robinson H. F., Comstock R. E., Harvey P. H. (1949). Estimation of heritability and degree of dominance in corn. *J. Agronomy*, 4:353-359.

[18] Sharma N., Sharma N. K., Malik Y. S. (2010) Estimation of genetic variation in bottle gourd. Haryana J. Hort. Sci. 39(3-4):313-315. 15

[19] Sriramamurthy, N. (2000). Genetic variability and correlation studies in cucumber (*Cucumissativas* L.). M. Sc., (Ag.) Thesis, Annamalai University, Annamalai Nagar.

[20] Sultan S., Rahman M. S., Ferdous J., Ahamed F. and Chowdhury A. K. (2018) Studies on genetic variability and inter-relationship in bottle gourd [*Lagenariasiceraria*(Mol.) Standl]. Int. J. Agril. Res. Innov. & Tech. 8(1):14-17.

[21] Tomar R. S., Kulkarni G. U. and Kakade D. K. (2008). Genetic analysis in muskmelon (*Cucumismelo* L.). J. Hort. Sci. 3(2): 112-118.

[22] Valls JFM. (2007). Caracterização de RecursosGenéticosVegetais. In:

RecursosGenéticosVegetais (Nass LL, ed.). EmbrapaRecursosGenéticos e Biotecnologia, Brasília, 282-305.

[23] VishwaNathVerma. (2018). Elemental analysis of Citrulluscolocynthis (L.) using atomic absorption spectrometer. World Scientific News 95 (2018) 64-74

[24] Xia L., Yawo M., Nevame A., Gilbert N. C., Mamadou G., Zhijun D., Luhua T., Xuelai Z., Gang S., Longting S., Wenhu L. (2018) Identification of high-efficiency SSR markers for assessing watermelon genetic purity. Journal of Genetics, 97 (5), 1295-1306