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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND YIELD COMPONENTS IN WATERMELON (*CITRULLUS LANATUS* THUMB.)

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Abstract

Watermelon (*Citrullus lanatus* Thumb.) is one of the most popular cucurbitaceous fruit vegetable crops grown in different parts of India. The genetic variability that exist in the available genotypes has got a significant role to play in the crop improvement programmes. A number of local genotypes differing in size and shape of fruits are grown in different regions and this result in assembling these genotypes to assess the variability in order to exercise selection or to involve them in hybridization programmes. Further, for an effective selection programme, an understanding of the direction and magnitude of association of various quantitative traits are essential. The present investigation was carried out using thirty genotypes of watermelon from diversified origin to elicit information on the quantum of genetic variability, heritability and genetic advance in watermelon in the Department of Horticulture, Faculty of Agriculture, Annamalai University, Annamalai Nagar. Variability studies showed significant differences among the thirty genotypes for all the thirteen characters. Yield per plant was maximum in CL 4 genotype collected from Atchirupakkam in Villupuram district. The characters *viz.*, number of vines per plant, sex ratio, days to first female flowers, node number of first female flower, days to fruit maturity and number of fruits per plant were recorded the maximum in the same genotype. Genetic analysis indicated maximum phenotypic and genotypic coefficient of variation for single fruit weight and 100 seed weight. The characters *viz*., fruits diameter, flesh thickness, number of fruits per plant and yield per plant, recorded highest estimate of PCV and moderate estimation of GCV. The characters *viz*., number of seeds per fruits, flesh thickness, number of primary branches and fruit diameter recorded moderate estimate of PCV and GCV. Lower estimation of GCV was observed for sex ratio, fruit length, number of male and female flowers. High heritability (broad sense) was observed for 100 seed weight, number of seeds per fruit, single fruit weight, vine length, fruit diameter, fruit length, flesh thickness, number of male flowers,sex ratio, yield per plant, number of primary branches per plant, number of female flowers and number of fruits per plant. Based on mean performance, CL 4 followed by CL 22 and CL 10 were selected as the best genotypes in watermelon for the costal ecosystem, by virtue of their higher yield combined with desirable component characters.

Key words : Genotypes, watermelon, yield components

Introduction

Watermelon (*Citrullus lanatus* Thumb.) is one of the most popular and widely grown cucurbitaceous fruit vegetable crops in tropical and sub tropical countries of the world. It's global consumption is greater than that of any other cucurbits (Goreta *et al*., 2005). In desert areas the juicy flesh serves as substitute for drinking water. The flesh which is soft and spongy is reddish or pink or yellow or yellowish white in colour. It is an important vegetable crop grown in coastal ecosystem during Adipattam (June - July) and Thaipattam (January - February) seasons. The fruit size various in size from that of an apple to about 50 cm in diameter. Hence, screening of germplasm is essential to select the best genotype for commercial exploitation. In any crop improvement programme. assessment of variability in the germplasm is a preliminary step which will help in the selection of types showing high variability and for the desirable characters that contribute to yield. Yield, being a complex character is influenced by different component

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characters and an understanding of the magnitude and direction of association between yield and its component traits will help in fixing the selection criteria for selection of better genotypes.

Materials and Methods

The study was conducted at the experimental field of the orchard, Department of Horticulture, Faculty of Agriculture, Annamalai University, Tamil Nadu. The experiment was carried out in a Randomized Block Design with 30 genotypes collected from diverse sources in three replications. Among the 30 genotypes CL1 (Coimbatore), CL2 (Dharmapuri), CL3(Hosur), CL4(Atchirupakkam), CL5 (Soonameadu), CL6 (Karur), CL7 (Sangarankovil), CL8 (Chidambaram), CL9 (Thirunelveli), CL10 (Thiruvanamalai), CL11 (Nagarkovil), CL12 and CL13 (Bangalore), CL14 (Nagapattinam), CL15 (Pondicherry), CL16 (Panruty), CL17 (Virudhachalam), CL18 (Karagudi),CL19 (Bangalore), CL20 (Ganamedu),CL21 (Theni), CL22 (Devakottai), (Pudukotti),CL24 (Vathalakundu), CL25(Kovilpatti), CL26 (Trichy), CL27 (Villupuram), CL28(Thanjavur), CL29 (Virudhunagar), CL 30 (Thindivanam). The main field was prepared in to plots of uniform size and the seeds were sown at spacing of 2.5×1.0 m, respectively. The required intercultural operation and plant protection measures were carried out as per the requirement of the crop. Observations were recorded on various characters and subjected to statistical analysis. The differences exhibited by the various genotypes for various characters studied were tested for significance by using analysis of variance technique (Snedecor and Cochran, 1967). Heritability was worked out according to the method suggested by Lush (1940) and genetic advance for each character was computed according to the model given by Johnson *et al.* (1955).

Results and Discussion

The general analysis of variance showed significant differences among the thirty genotypes of watermelon for all the thirteen characters studied (Table 1).

Evaluation of genotypes based on higher yield per plant, CL 4 (11.60 kg), followed by CL 22 (10.62 kg) and CL 10 (9.85 kg) as the top three ranking genotypes (Table 2).It's evident that the increased yield characters would have contributed higher yield in the best genotype (CL 4). The lowest yield characters and yield was recorded in CL 2 and the reason could be due to minimum vine length, fruit length, fruit diameter, flesh thickness, fruit size index, number of seeds per fruit and 100 seed weight and similar finding was reported by Mohamed *et al.* (2011) in snakemelon. Hence, from the results obtained based on the mean performance the genotype CL 4 appeared to be promising donor for yield and other yield attributing economic traits.

The attainment of maximum fruit yield is one of the important objectives in most watermelon breeding programmes. The range of mean value revealed sufficient variation for all the traits under study, the maximum range of variability was observed for average fruit weight (1.59 to 9.58), followed by vine length (2.21 to 4.42 m) and days to fruit maturity (46.00 to 61.00) indicating the presence of height variability

Table 1 : General analysis of variance for various characters of watermelon genotypes.

Source	Df	Mean sum of squares (MSS)												
		Vine length (m)	Number of primary branches per plant	Number of male flower	Number of female flower	Sex ratio	Number of fruit per plant	Fruit length (cm)	Fruit diameter (cm)	Single fruit weight (kg)	Flesh thickness (cm)	Number of seeds per fruit	100 seed weight (g)	Yield per plant (kg)
Replication	2	0.31	0.03	6.03	0.23	0.47	0.21	8.24	2.67	0.06	3.13	83.43	0.24	1.30
Genotype	29	1.15*	1.09*	701.57**	4.56**	7.11**	3.69**	96.99**	35.07**	9.14**	33.78**	19161.38**	18.78**	9.92**
Error	58	0.95	0.01	40.17	1.23	0.70	0.67	1.94	0.48	0.09	0.72	207.64	0.16	1.42

for these characters and thus offering greater scope for selecting desirable lines. On the basis of mean performance, CL 4, CL 22 and CL 10 were found to be promising with respect to fruit yield. From these results, it is evident that there was sufficient variation in the material under study. These findings are in agreement with those of earlier researchers (Torkadi *et al*., 2007).

Selection is the fundamental process in the development of superior varieties and it depends on the variability available in the crop. Genetic variability is the basic need for a plant breeder to initiate any breeding programme. A wide range was observed for days to first female flower in (38.33 to 62.33) and fruit maturity (46.00 to 61.00) which determines earliness of a variety. Fruit length, fruit girth, fruit diameter, flesh thickness, fruit size index, single fruit weight and yield per plant are the major yield contributing characters and wide variances were observed for these traits. Greater variability ensures better changes of producing new desirable forms. In the present study, the variation that existed among the genotypes was estimated as coefficient of variation. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed for thirteen characters in thirty genotypes of watermelon.

The PCV for different characters ranged from 15.51% (number of female flower) to 41.07% (single fruit weight). The GCV ranged from 10.68% (number of female flower) to 40.41% (single fruit weight). Higher GCV observed in the present study for number of fruits per plant also confirm the presence of fixable variation among the genotypes which can be exploited. High amount of fixable variation in watermelon has been reported by Lalta Prasad *et al*. (1998). In the present study, high estimates for both PCV and GCV were registered for the traits *viz*., single fruit weight (41.07 and 40.41% respectively) and number of fruits per plant (36.82 and 33.37%, respectively), which suggest greater phenotypic and genotypic variability among the accession and responsiveness of the attributes for making further improvement by selection. In watermelon, high estimates for both PCV and GCV were obtained for single fruit weight.

The magnitudes of heritability were quite high for all the characters except for days taken to first picking and number of branches per plant. High value of heritability suggests the major role of genetic constitution in the expression of the character and such traits are considered to be dependable from breeding point of view. In the present study, moderate estimates of PCV and GCV were registered for the traits *viz*., number of seeds per fruit and flesh thickness. These findings are in conformity with reports Rukam *et al*. (2008) in muskmelon, whereas moderate and low estimate of PCV and GCV was registered for sex ratio.

Low estimates of PCV and GCV were registered for the traits *viz.,* vine length, number of male flower, number of female flower, sex ratio, fruit length, fruit diameter, which indicated that these traits were less affected by environment. Indiresh (1982) reported similar results in bitter gourd. This suggests that these characters may be less influenced by environment which is in agreement with the findings of Tomer *et al*. (2008) in muskmelon. In the present study, almost all the characters exhibited high heritability value which ranged from 97.51 to 37.19 per cent . The characters included 100 seed weight, number of seed per fruit, single fruit weight, vine length, fruit diameter, fruit length, flesh thickness, number of male flower, sex ratio and yield per plant. High heritability values obtained for most of the traits in the present study suggest that these traits may generally be governed by additive gene action and hence the phenotype would provide a fairly reliable measure of the genotype which provides scope for selection based on the phenotypic performance.

Genetic advance as per cent of mean indicates the expected genetic progress for a particular trait under a suitable selection system. Higher values of genetic advance as per cent of mean were recorded for single fruit weight, 100 seed weight, number of seeds per fruit, flesh thickness, yield per fruit, fruit diameter, vine length, fruit length, number of male flowers, number of fruits per plant, sex ratio, number of primary branches, number of female flower and these characters are governed by additive gene effects. It may also be concluded that selection on the basis of these characters will be more useful for the improvement of this crop. These findings are in line with those of Sriramamurthy (2000) in cucumber. In the present study, moderate genetic advance as per cent of mean was recorded for vine length and number of fruits per plant which indicated that the expression of these characters were governed by non-additive gene action and could be exploited for heterosis breeding.

A high heritability coupled with high genetic advance as per cent of mean provides the most effective criteria for selection. High heritability along with genetic advance as per cent of mean could be helpful in assessing the nature of gene action. In the present study, the characters *viz*., 100 seed weight, pulp thickness, single fruit weight, fruit diameter, fruit length, fruit girth, days to fruit maturity, sex ratio, number of female flowers, number of male flowers and days to first female flower showed higher

Table 2 : Mean performance of watermelon genotypes on yield parameters.

Genotypes	Fruit length (cm)	Fruit girth (cm)	Fruit diameter (cm)	Number of seeds per fruit	100 seed weight (g)	Number of fruits per plant	Single fruit weight (kg)	Yield per plant (kg)
CL 1	33.17	41.63	15.17	252.67	6.23	2.66	2.96	7.87
CL 2	20.17	37.33	10.10	115.00	5.24	2.33	1.59	3.70
CL 3	32.17	57.53	19.17	270.33	6.43	1.67	4.79	7.99
CL 4	33.63	66.67	20.17	189.67	5.21	5.00	5.48	27.40
CL 5	31.63	57.13	17.83	256.00	7.24	2.67	3.50	9.34
CL 6	35.63	52.00	16.13	315.00	6.30	1.67	4.57	7.63
CL 7	28.03	45.37	13.80	312.33	4.25	3.00	2.98	8.94
CL 8	32.00	41.73	13.00	236.00	10.87	4.00	2.38	9.52
CL 9	32.17	47.67	15.33	225.33	5.20	2.33	2.42	5.63
CL 10	45.47	75.33	23.17	319.33	5.37	1.67	9.58	15.99
CL 11	33.47	52.23	16.33	414.33	4.93	2.66	3.64	9.68
CL 12	26.67	41.60	15.63	151.67	5.57	3.00	2.62	7.89
CL 13	34.33	56.30	17.47	311.67	12.63	2.67	4.58	12.22
CL 14	37.30	54.87	16.17	319.33	6.40	2.33	4.76	11.09
CL 15	41.53	66.03	21.10	253.33	11.90	2.00	6.54	13.08
CL 16	27.13	48.50	15.20	371.66	9.87	2.33	3.63	8.65
CL 17	35.33	47.30	14.33	186.33	11.73	2.67	5.50	14.68
CL 18	36.33	48.77	15.10	278.33	10.57	3.67	3.70	13.57
CL 19	35.13	66.50	20.23	363.33	8.37	2.67	5.55	9.87
CL 20	37.20	68.33	21.23	374.00	12.61	2.00	4.77	9.54
CL 21	29.27	34.77	10.27	367.67	7.24	3.00	2.57	7.71
CL 22	52.00	75.30	21.67	282.67	6.50	2.67	8.60	22.96
CL 23	32.17	54.40	17.17	225.67	5.63	3.33	3.58	11.92
CL 24	33.57	65.37	20.20	417.67	7.20	3.33	4.74	15.78
CL 25	37.57	57.07	18.10	325.00	6.53	3.00	4.50	13.50
CL 26	32.43	44.40	13.63	316.67	7.07	2.00	3.28	6.56
CL 27	34.63	70.23	22.03	301.33	4.30	2.67	5.45	12.12
CL 28	32.23	50.80	14.63	422.67	9.53	1.67	4.72	7.88
CL 29	34.40	49.50	16.00	252.67	7.20	2.00	3.72	7.44
CL 30	31.97	40.40	12.27	155.33	6.30	2.33	2.55	5.94
Grand mean	33.95	53.83	16.75	286.10	7.46	2.63	4.31	12.58
Range	20.17 to 52.00	34.77 to 75.33	10.10 to 23.17	115.00 to 422.67	4.25 to 12.63	1.67 to 5.00	1.59 to 9.58	3.70 to 27.40
CV%	4.10	2.19	4.15	5.04	5.40	14.23	7.37	14.23
CD (P=0.05)	2.25	1.91	1.12	23.55	0.65	1.32	0.51	1.32

Table 3 : Estimation of PCV, GCV, heritability and genetic advance as per cent of mean for various characters in watermelon.

S. no.	Characters	PCV (%)	GCV (%)	Heritability (%)	GA (%) of mean
1	Vine length(m)	18.40	18.09	96.61	36.63
2	Number of primary branches per plant	22.52	17.45	60.08	27.87
3	Number of male flower	17.53	16.12	84.59	30.55
4	Number of female flower	15.51	10.68	47.39	15.14
5	Sex ratio	18.05	15.65	75.13	27.94
6	Number of fruits per plant	36.82	22.46	37.19	28.21
7	Fruit length (cm)	17.08	16.57	94.21	33.14
8	Fruit diameter (cm)	20.68	20.26	95.96	40.89
9	Single fruit weight (kg)	41.07	40.41	96.78	81.89
10	Flesh thickness (cm)	24.45	23.69	93.86	47.28
11	Number of seeds per fruit	28.23	27.78	96.82	56.31
12	100 seed weight (g)	33.79	33.37	97.51	67.88
13	Yield per plant	30.53	24.72	65.58	41.24

estimates of heritability and genetic advance as per cent of mean which may be ascribed to the predominance of additive gene action and simple selection, therefore could be effective for improvement of these traits. However, moderate to high heritability with moderate genetic advance as per cent of mean was exhibited by the other characters *viz.,* vine length and number of fruits per plant which indicated that expression of these characters were governed by both additive and non-additive gene action. Therefore, fruit yield may be improved by selecting genotypes having higher fruit weight, fruit length, fruit diameter number of fruits per plant, flesh thickness and total soluble solids.

Conclusion

Hence from the present experiment it can be concluded that variability studies showed significant differences among the thirty genotypes for all the thirteen characters. Yield and yield parameters per plant was maximum in CL 4 genotype collected from Atchirupakkam in Villupuram district. Genetic analysis indicated maximum phenotypic and genotypic coefficient of variation for single fruit weight and 100 seed weight. High heritability coupled with high genetic advance as per cent of mean was observed for yield characters. Based on mean performance, CL 4 followed by CL 22 and CL 10 were selected as the best genotypes in watermelon for the costal ecosystem, by virtue of their higher yield combined with desirable component characters.

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