

## Original Research Article

### Genetic Architecture of Watermelon (*Citrullus lanatus* L.)

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#### ABSTRACT

The present experiment was carried out with ten watermelon entries collected from all over India in *Rabi* 2018-19 in Randomized Block Design (RBD). Wide range of variability was present in the different entries of watermelon under study. The range of GCV and PCV was 6.74% to 34.27% and 8.45% to 36.74%, respectively for yield and quality traits. The estimates of phenotypic, genotypic and environmental variances revealed that phenotypic variances were higher in magnitude over the respective genotypic variances for all the characters under study which indicates that there is influence of genetic and environment on the expression of traits. PCV and GCV were high for rind thickness and 100 seed weight. The broad sense heritability ranged from 66.92% - 96.40%. The genetic advance and genetic advance as per cent of mean (GAM) were ranged from 0.12% - 10.32% and 9.18% - 68.37%, respectively. Heritability along with genetic advance is more useful for selection than the heritability alone. High heritability along with low genetic advance were observed in total fruit yield per vine, 100 seed weight, days to first male flowering, days to first male flowering days to maturity and fruit length which showed non-additive gene action and these traits was used for further crop improvement.

#### Keywords

Variability,  
Heritability,  
Genetic advance  
and GAM

#### Introduction

The watermelon (*Citrullus lanatus* L.) belongs to the Cucurbitaceae family with diploid chromosome number ( $2n=2x=22$ ). It is native to Africa (Whitaker and Davis, 1962; Shimotsuma, 1963) and important food crop in many African countries. Watermelon has a centre of diversity in the southern part of the continent which could also be the area of origination (Rubatzky 2001; Dane and

Lang, 2004). It was introduced to Brazil in two phases, the first during the slave trade and the second when bred cultivars were introduced from breeding programs in the United States and Japan (Romao *et al.*, 2008). It is cross-pollinated crop and has a wide genetic diversity (Gama *et al.*, 2013). This annual species grows as a vine with a climbing or sprawling growth habit, large green leaves with three to five deep lobes, medium-sized monoecious and often

bee-pollinated flowers with short pedicels, medium to large fruit with smooth skin and flesh with a high water content and oval to oblong seeds of a white, grey, red or brown colour (Shimotsuma, 1963; Rubatzky, 2001; Dane and Lang, 2004). In Africa, watermelon cultivation is prevalent in drought-prone, semi-arid areas with an annual rainfall below 650 mm. In these areas, watermelon is grown as a staple food (edible seeds), a dessert (edible flesh), and for animal feed. The fruit can be eaten fresh or cooked. The rind can be pickled or candied, while the seeds are baked or roasted for consumption. Cultivation is based on seed-propagated landraces and farmer varieties that have been integrated with the indigenous knowledge, agricultural practices, food habits and cultural dynamics of the rural communities. Traditionally grown sweet watermelons and cow-melons can be white, yellow, orange or red-fleshed and have different fruit shapes and seed coat patterns including colour variation of both fruit rinds and seeds. An important step in cultivar development is studying the genetic variability found in genetic resources. The use of genetic resources to create new varieties is important for obtaining higher yields and for the technological transformations required for modernization of agribusiness. It is a dynamic process, but requires continuous enrichment and characterization of the materials maintained in germplasm collections (Valls, 2007). The genotypic and phenotypic coefficients of variation (GCV & PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the traits and the extent to which improvement is possible after selection. So, the present investigation was carried out for estimation of magnitude and extent of genetic variability, heritability and gene action in watermelon.

## Materials and Methods

The present investigation was carried out at the Experimental farm of Department of Agronomy, College of Agriculture, Dapoli during *Rabi* 2018-19. The experimental trial was included 10 diverse entries (Table 1) laid out in Randomized Block design replicated thrice. Row to row and plant to plant spacing were maintained at 150 and 50 cm, respectively. All the agronomic package of practices was followed to grow a healthy crop in each replication. Randomly five plants were selected and tagged for observation in each entry. Observations were recorded on fifteen characters *viz.*, days to first female flowering, days to first male flowering, number of primary branches per vine, number of marketable fruits per vine, fruit weight (g), fruit diameter (cm), fruit length (cm), Rind Thickness (cm), 100 seed weight (g), days to maturity, TSS (<sup>o</sup> Brix), total fruit yield per vine, fruit colour, fruit shape and colour of flesh. The recorded data were analyzed as suggested by Panse and Sukhatme (1985) for analysis of variance. The genotypic and phenotypic coefficient of variance was calculated as per the formula suggested by Burton and De Vane (1952) and Johnson *et al.*, (1955) for heritability and genetic advance.

## Results and Discussion

The mean sum of square was highly significant for all traits except number of marketable fruit per vine, rind thickness and TSS, indicating the presence of wide variability in the genotypes (Table 2). Mean performance of twelve qualitative and quantitative traits of watermelon was studied and presented in Table 3. Days to first female flowering was recorded maximum in Namtan (42.67 days) and minimum in NS 295 (32.67 days), respectively while days to first male flowering registered considerable variability,

which ranged from 34.67 days (NS 295) to 44.67 days (Augusta), respectively. Days to maturity was ranged from (79.33 days - 89.33 days), the minimum and maximum days required for maturity was recorded in genotypes Madhubala (79.33 days) and GS 286 (89.33 days), respectively. Maximum number of primary branches per vine was recorded in Sugarbaby (7.33) and minimum (3.33) in both the genotypes NBH Benazir and Nelson, respectively. Average number of marketable fruits per vine showed wide range (1.33-2.67). Maximum total number of marketable fruits per vine was recorded in Sugarbaby (2.67) and minimum (1.33) in both the genotypes Akira and NBH Benazir, respectively. Fruit weight at edible stage showed a wide range (1.77g - 6.20g), the minimum and maximum fruit weight at edible stage was recorded in genotypes Namtan (1.77g) and Madhubala (6.20g), respectively while fruit diameter at edible stage showed a wide range (16.33 cm - 23.33 cm), the maximum and minimum fruit weight at edible stage was recorded in genotypes Madhubala (23.33 cm) and Namtan (16.33 cm), respectively. The genotype NBH Benazir exhibited maximum length of edible fruit (34.00 cm) while it was minimum in Namtan (17.67 cm) whereas, minimum and maximum rind thickness of edible fruit was recorded in Akira (0.97 cm) and Sugarbaby (1.23 cm), respectively. The 100 seed weight was ranged from 1.47g (Akira) to 7.97g (Madhubala). Maximum TSS of fruit at edible stage was recorded in Madhubala (13.10<sup>0</sup> Brix) whereas, minimum in Nelson (10.13<sup>0</sup> Brix), respectively. The present set of genotypes possessed an average of total fruit yield per vine which was ranged from (4.33 kg - 12.00 kg), the maximum total fruit yield per vine was recorded in genotypes Sugarbaby (12.00 kg) followed by Madhubala (11.33 kg), Goody Ball (10.33 kg) and Augusta (10.00 kg). Results are in accordance with findings of Joshi *et al.*,

(1981), Mariappan and Pappiah (1990) in cucumber and Gama *et al.*, (2013) in watermelon (Fig. 1).

On the basis of visual observations (Table 4), among all, four entries *viz.*, Augusta, Goody Ball, Nelson and Sugarbaby showed dark green colour of the fruit with round/spherical in shape. Regarding to the colour of flesh, these genotypes observed granular crispy with crimson red flesh. Among all, three genotypes *viz.*, NS 295, Madhubala and NBH Benazir showed light green colour with dull green stripes on the fruit. Fruits of these genotypes were observed round/spherical in shape and granular crispy with deep pinkish flesh colour. Amongst all, two entries *viz.*, Akira and Namtan showed dark green colour of the fruit with oblong in shape. Regarding to the colour of flesh, these genotypes observed granular crispy with crimson red flesh. Remaining genotype *viz.*, GS 286 showed light green colour with dull green stripes on the fruit. Fruits of this genotype were observed round/spherical in shape and granular crispy with deep pinkish flesh colour. Similar results also reported by Scott (1931), Weetman (1935), Weetman (1937) and Solmaz and Sari (2009) in watermelon.

In general, the phenotypic variance and phenotypic coefficients of variation were higher than the respective genotypic variance and genotypic coefficients of variation for all the traits (Table 5 and 6) indicating a considerable influence of environment on their expression. In the present investigation, genotypes were found to possess a high to moderate phenotypic variation for various characters as revealed by PCV. Phenotypic coefficient of variation varied from 8.45% (rind thickness) to 36.74% (fruit weight). The PCV expressed in form of percentage (Table 6) were comparatively high for rind thickness (36.74%) followed by 100 seed weight (34.94%), number of primary branches per

vine (32.78%), number of marketable fruit per vine (31.54%) and TSS (31.13%). As the estimates of phenotypic variability cannot differentiate between the effects of genetic and environmental effects, so the study of genetic variability is effective in partitioning out the real genetical differences. Similar results also reported by Joshi *et al.*, (1981), Mariappan and Pappiah (1990) in cucumber and Gama *et al.*, (2013) in watermelon. Higher the GCV, more the chances of improvement in that characters. In the present investigation, genotypic coefficient of variation (Table 6) ranged from 6.74% (rind thickness) to 34.27% (fruit weight). GCV were comparatively high for rind thickness (34.27%) followed by 100 seed weight (34.01%), number of primary branches per vine (30.75%), TSS (27.26%) and number of marketable fruit per vine (25.80%). The GCV was less than the corresponding PCV, indicating the role in the expression of the traits under observation. Similar findings supported by Joshi *et al.*, (1981), Mariappan and Pappiah (1990) in cucumber, Yadav *et al.*, (2012) in cucumber and Gama *et al.*, (2013) in watermelon.

The difference between GCV and PCV were more in case of number of marketable fruit per vine, total yield per vine, fruit weight, fruit diameter and number of primary branches per vine. The large difference between GCV and PCV indicated that environmental affects to a large extent the traits. The character having high GCV possessed better potential for further gain and improvement (Burton and De Vane, 1952).

Burton and De Vane (1952) suggested that GCV together with heritability estimate would give the best option expected for selection. Heritability (Table 6) estimated were high > 90% for days to first male flowering (96.40), days to first female flowering (95.93), 100 seed weight (94.99),

fruit length (93.52), days to maturity (93.27) and total fruit yield per vine (91.02). High heritability for the characters controlled by polygene might be to plant breeder for making effective selection.

Moderate heritability (70-80%) are found for numbers primary branches per vine (88.03), fruit weight (87.02) and total soluble solids (76.67) suggested that the environmental effects constitute a major portion of the total phenotypic variation and hence direct selection for these traits will be less effective.

Similar findings supported by Joshi *et al.*, (1981), Mariappan and Pappiah (1990) in cucumber, Yadav *et al.*, (2012) in cucumber and Gama *et al.*, (2013) in watermelon. Johnson *et al.*, (1955) reported that the heritability estimates along with genetic advance (Table 6) is more useful than the resultant effect for selecting the best genotype(s) as it suggests the presence of non-additive gene action. Lowest genetic advance was recorded for rind thickness (0.12) followed by total marketable fruits per vine (0.96).

The information on heritability alone may be misleading when used in combination with genetic advance, the utility of heritability estimates increases. Similar results were also reported by Joshi *et al.*, (1981), Mariappan and Pappiah (1990) in cucumber, Saroj *et al.*, (2004) in watermelon and Gama *et al.*, (2013) in watermelon. In the present study, low genetic advance coupled with high heritability was observed for total fruit yield per vine, 100 seed weight, days to first male flowering, days to first male flowering days to maturity and fruit length. It indicated that non-additive gene action was more important for these traits. Therefore, improvement in these traits would be more efficiently done by heterosis breeding method in the present materials.

**Table.1** List of genotypes/varieties and their sources

Sr. No.	Genotypes/Varieties	Source/Origin
1.	<b>Augusta</b>	Syngenta India Limited
2.	<b>NS 295</b>	Namdhari Seeds Private Limited
3.	<b>Goody Ball</b>	Welcome Crop Science Private Limited
4.	<b>GS 286</b>	UPL Limited
5.	<b>Akira</b>	Namdeo Umaji Agritech Private Limited
6.	<b>Madhubala</b>	Local selection
7.	<b>Namtan</b>	Chiatai India Private Limited
8.	<b>NBH Benazir</b>	Noble Seeds Private Limited
9.	<b>Nelson</b>	Namdeo Umaji Agritech Private Limited
10.	<b>Sugarbaby</b>	Syngenta India Limited

**Table.2** Analysis of variance for quantitative and qualitative traits in watermelon

Sr. No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	<b>Days to First Female Flowering</b>	0.23	40.61**	0.57
2.	<b>Days to First Male Flowering</b>	0.93	39.81**	0.49
3.	<b>No. of Primary Branches Per Vine</b>	1.73	7.51**	0.33
4.	<b>No. of Marketable Fruits Per Vine</b>	1.90	1.13	0.16
5.	<b>Fruit Weight (kg)</b>	0.09	5.41**	0.26
6.	<b>Fruit Diameter (cm)</b>	4.23	17.26**	2.32
7.	<b>Fruit Length (cm)</b>	1.71	82.29**	1.86
8.	<b>Rind Thickness (mm)</b>	0.001	0.019	0.003
9.	<b>Seed Index (g)</b>	0.15	10.34**	0.18
10.	<b>Days to Maturity</b>	0.10	46.80**	1.10
11.	<b>Total Yield Per Vine (kg)</b>	1.73	20.03**	1.84
12.	<b>Total Soluble Solid</b>	0.18	3.21	0.10
	<b>DF</b>	2	11	22

**Table.3** Mean Performance of twelve quantitative and qualitative traits in watermelon

Sr. No.	Characters Genotypes	DFFF	DFMF	NPBV	NMFV	FW (g)	FD (cm)	FL (cm)	RT (cm)	SI (g)	DM	TSS (° Brix)	TFYV (kg)
1.	<b>Augusta</b>	42.33	44.67	6.67	2.33	2.77	20.30	18.97	1.17	5.10	84.67	11.17	10.00
2.	<b>NS 295</b>	32.67	34.67	6.00	2.33	4.40	20.77	26.67	1.07	7.70	79.67	10.47	9.67
3.	<b>Goody Ball</b>	40.33	41.33	6.00	1.67	4.17	22.33	22.77	1.13	5.53	86.33	11.53	10.33
4.	<b>GS 286</b>	35.33	36.67	3.33	2.33	3.20	21.53	18.97	1.10	5.37	89.33	10.43	8.33
5.	<b>Akira</b>	37.33	39.33	4.33	1.33	2.23	16.37	21.00	0.97	1.47	87.00	11.27	4.67
6.	<b>Madhubala</b>	33.33	35.33	6.33	2.67	6.20	23.33	30.00	1.03	7.97	79.33	13.10	11.33
7.	<b>Namtan</b>	42.67	44.33	3.67	2.33	1.77	16.33	17.67	1.17	4.17	90.67	10.27	4.33
8.	<b>NBH Benazir</b>	34.67	36.33	3.33	1.33	5.07	21.33	34.00	1.03	6.70	80.33	11.27	9.67
9.	<b>Nelson</b>	35.33	37.33	3.33	2.33	4.23	22.00	22.00	1.17	5.17	85.33	10.13	10.00
10.	<b>Sugarbaby</b>	34.33	36.33	7.33	3.33	4.20	21.90	23.07	1.23	4.87	83.33	12.87	12.00
	<b>General mean</b>	36.83	38.63	5.03	2.20	3.82	20.62	23.51	1.11	5.40	84.60	11.25	9.03
	<b>Range</b>	32.67-42.67	34.67-44.67	3.33-7.33	1.33-3.33	1.77-6.20	16.33-23.33	17.67-34.00	0.97-1.23	1.47-7.97	79.33-89.33	10.13-13.10	4.33-12.00
	<b>S.E.</b>	0.61	0.57	0.47	0.33	0.41	1.24	1.11	0.05	0.35	0.86	1.11	0.26
	<b>C.D. @ 5 Per cent</b>	1.29	1.20	0.98	0.68	0.87	2.61	2.34	0.10	0.72	1.80	2.33	0.55

**Note:-** DFFF: Days to First Female Flowering, DFMF: Days to First Male Flowering, NPBV: Number of Primary Branches per Vine, NMFV: Number of Marketable Fruits per Vine, FW: Fruit Weight, FD: Fruit Diameter, FL: Fruit Length, RT: Rind Thickness, SI: Seed Index (100 seed weight), DM: Days to Maturity, TSS: Total Soluble Solid and TFYV: Total Fruit Yield per Vine.



**Table.4** Visual observations in watermelon

<b>Sr. No.</b>	<b>Characters Genotypes</b>	<b>Fruit colour</b>	<b>Fruit shape</b>	<b>Colour of flesh</b>
1.	<b>Augusta</b>	Dark green	Round/Spherical	Crimson red and granular crispy
2.	<b>NS 295</b>	Light green with dull green stripes	Oblong	Deep pinkish and granular crispy
3.	<b>Goody Ball</b>	Dark green	Round/Spherical	Crimson red and granular crispy
4.	<b>GS 286</b>	Light green with dull green stripes	Round/Spherical	Deep pinkish and granular crispy
5.	<b>Akira</b>	Dark green	Oblong	Crimson red and granular crispy
6.	<b>Madhubala</b>	Light green with dull green stripes	Oblong	Deep pinkish and granular crispy
7.	<b>Namtan</b>	Dark green	Oblong	Crimson red and granular crispy
8.	<b>NBH Benazir</b>	Light green with dull green stripes	Oblong	Deep pinkish and granular crispy
9.	<b>Nelson</b>	Dark green	Round/Spherical	Crimson red and granular crispy
10.	<b>Sugarbaby</b>	Dark green	Round/Spherical	Crimson red and granular crispy

**Table.5** Components of variation for quantitative and qualitative traits in watermelon

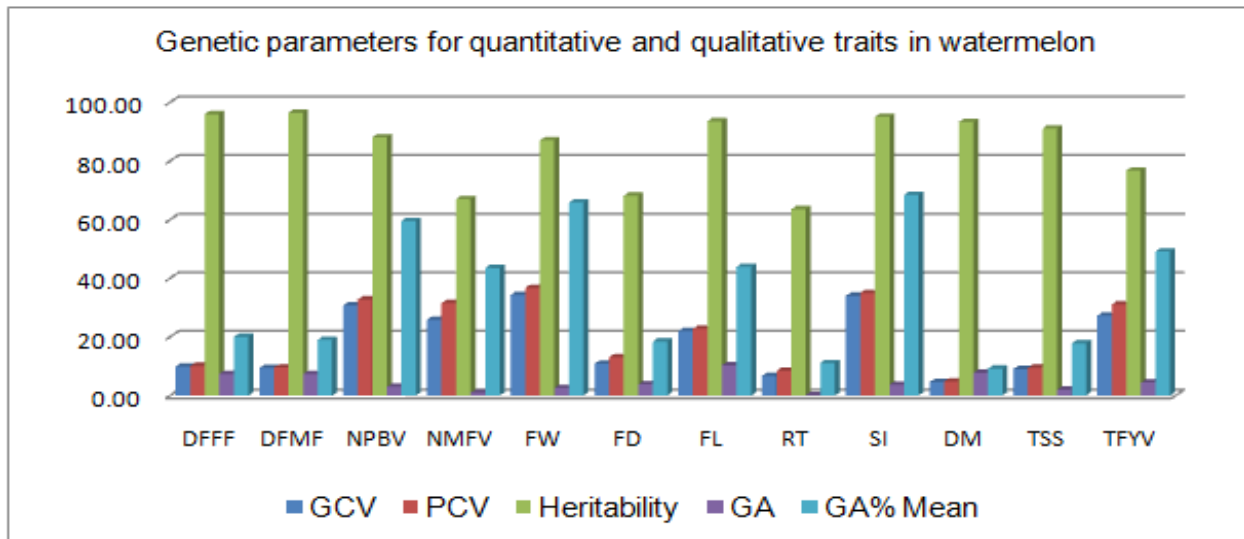
<b>Sr. No.</b>	<b>Characters</b>	<b>Genotypic Variance</b>	<b>Phenotypic Variance</b>	<b>Environmental Variance</b>
1.	<b>Days to First Female Flowering</b>	13.35	13.91	0.57
2.	<b>Days to First Male Flowering</b>	13.11	13.60	0.49
3.	<b>No. of Primary Branches Per Vine</b>	2.40	2.72	0.33
4.	<b>No. of Marketable Fruits Per Vine</b>	0.32	0.48	0.16
5.	<b>Fruit Weight (kg)</b>	1.72	1.97	0.26
6.	<b>Fruit Diameter (cm)</b>	4.98	7.30	2.32
7.	<b>Fruit Length (cm)</b>	26.81	28.67	1.86
8.	<b>Rind Thickness (mm)</b>	0.006	0.009	0.003
9.	<b>Seed Index (g)</b>	3.39	3.56	0.18
10.	<b>Days to Maturity</b>	15.23	16.33	1.10
11.	<b>Total Yield Per Vine (kg)</b>	6.06	7.91	1.84
12.	<b>Total Soluble Solid</b>	1.03	1.14	0.10

**Table.6** Estimates of genetic parameters for quantitative and qualitative traits in watermelon

Sr. No.	Characters	GCV (%)	PCV (%)	Heritability (BS) (%)	Genetic Advance	Genetic Advance Per cent Mean
1.	<b>Days to First Female Flowering</b>	9.92	10.13	95.93	7.37	20.01
2.	<b>Days to First Male Flowering</b>	9.37	9.54	96.40	7.32	18.95
3.	<b>No. of Primary Branches Per Vine</b>	30.75	32.78	88.03	2.99	59.44
4.	<b>No. of Marketable Fruits Per Vine</b>	25.80	31.54	66.92	0.96	43.48
5.	<b>Fruit Weight (kg)</b>	34.27	36.74	87.02	2.52	65.85
6.	<b>Fruit Diameter (cm)</b>	10.82	13.10	68.18	3.80	18.41
7.	<b>Fruit Length (cm)</b>	22.02	22.78	93.52	10.32	43.88
8.	<b>Rind Thickness (mm)</b>	6.74	8.45	63.56	0.12	11.06
9.	<b>Seed Index (g)</b>	34.05	34.94	94.99	3.69	68.37
10.	<b>Days to Maturity</b>	4.61	4.78	93.27	7.76	9.18
11.	<b>Total Yield Per Vine (kg)</b>	9.04	9.48	91.02	2.00	17.77
12.	<b>Total Soluble Solid</b>	27.26	31.13	76.67	4.44	49.17

**Note:** GCV-Genotypic coefficient of variation, PCV-Phenotypic coefficient of variation and BS- Broad Sense

**Fig.1** Graphical representation of genetic parameters for quantitative and qualitative traits in watermelon





Depending upon the variability, heritability and genetic advance estimates, it could be predicted that improvement by heterosis breeding was possible in watermelon for traits like total fruit yield per vine, 100 seed weight, days to first male flowering, days to first male flowering days to maturity and fruit length.

The yield is controlled by both GCV and PCV also to use appropriate selection procedure for improvement of the characters in general and yield in particular since high heritability with low genetic advance was indicated the influence of non-additive gene action. The heritability provides the information on the magnitude of inheritance of quantitative characters, but it does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful for selection than the heritability alone. This study helps in the selection of genetically superior parents for their exploitation in hybridization programmes.

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