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## Diallel analysis numerical approach for growth, yield and quality traits of pumpkin (*Cucurbita moschata* Duch. Ex. Poir)

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#### Abstract

Diallel analysis study was conducted at Department of Horticulture, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai during 2016 according to Hayman on growth, yield and quality traits of pumpkin. Six genotypes of pumpkin viz. P1: Acc.No. MDU CM23-Thirumangalam local, Madurai district, P2: Acc.No. MDU CM28-Oddanchatram local, Dindugul district, P3: Acc.No. MDU CM29-Harur local, Dharmapuri district, P4: Acc.No. MDU CM12-Department of Horticulture, AC &RI Madurai, P5: Acc.No. MDU CM1-Attur local, Salem district, P6: Acc.No. MDU CM31-Rajapalayam local, Virudhunagar district were used to study the gene action underlying the inheritance of various quantitative and qualitative traits. The six parents and their 30 F1 hybrids were sown in the field in randomized block design with two replications. The various growth, yield and quality traits were recorded. The vine length, number of primary branches, sex ratio, days to first harvest, number of fruits per vine, flesh thickness, number of seeds per fruit, total soluble solids, beta carotene and dry matter content of fruits had both additive and dominance gene action. The days to first male flower, days to first female flower, node to first male flower, node to first female flower, moisture content indicated the presence of dominance gene action. The average fruit weights, fruit length, fruit diameter, yield per plant traits were influenced by additive gene action. The recessive alleles were more pronounced in vine length, days to first male flower, number of fruits per vine, average fruit weight, fruit length, fruit diameter, total soluble solids and dry matter content. The dominant alleles were more pronounced in number of primary branches, days to first female flower, node to first male flower, sex ratio, days to first harvest, flesh thickness, number of seeds per fruit, yield per plant, beta carotene and moisture content traits. The traits vine length, days to first female flowers, node to first male flower, sex ratio, number of fruits per vine, fruit diameter, flesh thickness, number of seeds per fruit, total soluble solids, beta carotene and moisture content were controlled by single block of genes as they had  $K_D/K_R$  ratio more than one. The traits number of primary branches, days to first male flower, average fruit weight, fruit length, yield per vine, and dry matter content were controlled by more than group of gene as they recorded  $K_D/K_R$  ratio less than one.

**Keywords:** Pumpkin, *Cucurbita moschata*, genetic analysis, diallel analysis, numerical approach

#### 1. Introduction

Pumpkin (*Cucurbita moschata* Duch. ex. Poir) is an economically important cucurbitaceous vegetable having diploid chromosome number of  $2n=40$ . It is grown throughout the tropics of India and it occupies a prominent position due to its high productivity, nutritive values, good storability, better transport quality and extensive cultivation in sub tropical and tropical regions of the globe. It is used both immature and mature stages as vegetable and consumed as processed products. In India, pumpkin occupies an area of 11,060 hectares with an annual production of 2.77 lakh tonnes accounting to an average productivity of 25.10 tonnes per hectare during 2014. In Tamil Nadu, pumpkin occupies an area of 1,530 hectares with an annual production of about 37,340 tonnes and an average productivity of 24.41 tonnes per hectare during 2014 (Saxena and Chander, 2015) [14]. Pumpkin has received little attention in crop improvement, as compared to other cucurbitaceous vegetables. Being a cross-pollinated crop, development of varieties or hybrids is possible through heterosis breeding. A precise knowledge of combining ability and gene action responsible for inheritance of yield and yield components is essential for successful crop improvement programme. Comparatively little attention had been made for the improvement of this crop. Plant breeding programme aims at improving the existing types and creating a new type which will be better than the existing commercial cultivars. For such crop improvement programme, variability is the pre-requisite.

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If there is adequate variability, it is conveniently exploited by breeders. Otherwise, variability is induced by employing several breeding techniques of which hybridization continues to be the primary tool for plant breeder. Among the several biometrical methods available to study the complex nature of yield and the influence of environment on its expression, diallel analysis was preferred as it has proved to be a successful tool in plant breeding (Diojode and Sulladmath, 1986 and Sirohi, 1994) [4, 17]. Complete exploitation of genetic variation enables to produce not only heterotic F<sub>1</sub> hybrids but also recombinants with desirable attributes. Considering these points, the present study was carried out to understand the gene action underlying the inheritance of various qualitative and quantitative characters so as to fix the appropriate breeding technique.

## 2. Material and Methods

A field experiment was conducted at the College Orchard, Department of Horticulture, Agricultural College and Research Institute, Madurai, during 2016-17. The research area located at 09°58' 30.5" N latitude, 078°12' 27.4 E longitude and at an altitude of 158 m above the mean sea level. The climate at the experimental location is generally warm. The district receives an average annual rainfall of 620.5 mm. Six genotypes of pumpkin were used as parents for crossing programme in all possible combinations adopting full diallel mating design. The details on parents used in the study are P1: Acc.No. MDUCM23-Thirumangalam local, Madurai district, P2: Acc.No. MDUCM28-Oddanchatram local, Dindugul district, P3: Acc.No. MDUCM29-Harur local, Dharmapuri district, P4: Acc.No. MDUCM12-Department of Horticulture, AC &RI Madurai, P5: Acc.No. MDUCM1-Attur local, Salem district, P6: Acc.No. MDUCM31-Rajapalayam local, Virudhunagar district. All the 30 F<sub>1</sub> hybrids along with their parents and standard check hybrid were raised in Randomized Block Design (RBD) with three replications during December 2016 to evaluate the hybrids. A spacing of 2 x 2 m was adopted. Recommended cultural practices and plant protection measures were followed to all the plants. Five plants were tagged in each hybrid and parents in each

replications and biometrical observations were recorded from the tagged plants. Observations were recorded on various biometrical and biochemical characters in all the parents and hybrids of pumpkin. The mean values were analyzed for genetic studies and the gene action was determined by using Hayman (1958) [6] and Jinks (1956) [8] methods. The genetic components estimated are, D= Component of variation due to additive effect of the gene, F= Covariance of additive and non-additive effects, H<sub>1</sub> = Component of variation due to dominance effect of the gene. H<sub>2</sub>=Proportion of dominance variance due to positive and negative effect of the genes, h<sup>2</sup>= Net dominance effects expressed as the algebraic sum overall loci in heterozygous phase, E = Environmental component obtained from Me of the analysis of variance table, P=Number of parents, The significance of above mentioned parameters was tested by t test at (n - 2) degree of freedom using the standard errors of respective genetic parameters. The ratios of genetic components are (H<sub>1</sub>/D)<sup>1/2</sup> = Mean degree of dominance overall loci, H<sub>2</sub>/4H<sub>1</sub> = Proportion of genes with positive and negative effects in the parents, K<sub>D</sub> / K<sub>R</sub> = Proportion of dominant and recessive genes in the parents (K<sub>D</sub> / K<sub>R</sub>), Heritability in the narrow sense and broad sense (H) and genetic advance (GA).

## 3. Results and Discussion

The gene action responsible for the inheritance of the characters was studied through diallel technique. The estimates of genetic parameters viz., D (Components of variation due to additive effect of the genes), F (Covariance of additive and non-additive effects), H<sub>1</sub> (Components of variation due to dominance effects of the genes), H<sub>2</sub> (Proportion of dominance variance due to positive and negative effects of the genes) and h<sup>2</sup> (Net dominance effects expressed as the algebraic sum overall loci in heterozygous phase) are furnished in Table 1. The ratios were computed from the actual values of the components of variation and are presented in Table 2. Heritability (both narrow and broad sense) and genetic advance as percentage of mean for different traits were estimated.

**Table 1:** Estimates of genetic parameters of pumpkin - F<sub>1</sub>

Characters	D±SE(D)	F±SE(D)	H <sub>1</sub> ±SE(H <sub>1</sub> )	H <sub>2</sub> ±SE(H <sub>2</sub> )	H <sup>2</sup> ±SE(h <sup>2</sup> )	E±SE(E)
Vine length	3.36 ±0.32**	8.51 ±0.77**	13.25±0.80**	9.60±0.72**	3.22 ±0.48**	6.00 ±0.12
Number of primary branches	0.45±0.19*	1.16±0.46*	2.80 ±0.48**	2.20±0.43**	0.28 ±0.29	0.59 ±0.07
Days to first male flowering	1.96 ±0.11**	0.17 ±0.27	0.35±0.28	0.15±0.25	0.29 ±0.17	0.62 ±0.04
Days to first female flowering	1.53±0.43**	1.68 ±1.05	3.59 ±1.09**	2.09 ±0.97**	0.36 ±0.66	0.37 ±0.16
Nodes to first male flower	0.40 ±0.21	0.40 ±0.50	1.57±0.52**	1.14 ±0.47**	0.13 ±0.31	0.26 ±0.08
Nodes to first female flower	0.39 ±0.71	0.65 ±1.74	2.26±1.81	2.82 ±1.62	0.75 ±1.09	1.37 ±0.27
Sex ratio	6.56 ±0.50**	0.46 ±1.23	2.39 ±1.28	2.10 ±1.14	1.48 ±0.77**	0.36 ±0.19
Days to first harvest	7.91 ±0.79**	4.75 ±1.94**	2.25 ±2.02	1.68 ±1.80	0.63±1.21	1.19 ±0.30
Number of fruits per vine	0.07 ±0.01**	0.05 ±0.03	0.11 ±0.03**	0.10 ±0.03**	0.01 ±0.02	0.01 ±0.01
Average fruit weight	6.59 ±0.27**	0.72 ±0.66	0.82 ±0.68	0.48 ±0.61	0.51 ±0.41	0.92 ±0.10
Fruit length	25.10 ±1.66**	8.40 ±4.04*	8.70 ±4.20*	7.77 ±3.75*	3.24 ±2.53	0.27 ±0.63
Fruit diameter	64.12 ±0.82**	2.64 ±1.99	3.42 ±2.07	2.89±1.85	0.21±1.24	0.99 ±0.31
flesh thickness	0.14 ±0.01**	0.06 ±0.03	0.08 ±0.03*	0.07 ±0.02**	0.03 ±0.02	0.01 ±0.00
Number of seeds per fruit	1553.48 ±54.55**	675.05 ±133.28**	408.82 ±138.49**	312.63 ±123.72*	113.50 ±83.27	26.27 ±20.62
Fruit yield per plant	8.26 ±1.00**	0.91 ±2.45	3.79 ±2.55	3.45 ±2.28	0.02 ±1.53	0.02 ±0.38
Total soluble solids	0.86±0.09**	0.29 ±0.24	0.74 ±0.25**	0.58 ±0.22*	0.70 ±0.15**	0.02 ±0.037
Beta carotene	0.0062±0.0013**	0.007±0.003	0.01±0.003**	0.0064±0.003	0.0006 ±0.002	0.0006±0.005
Moisture content	0.32 ±0.24	0.38 ±0.58	1.69 ±0.60**	0.58 ±0.54	0.42 ±0.36	0.85 ±0.09
Dry matter content	0.003±0.001**	0.004 ±0.003	0.01±0.003**	0.009 ±0.003**	0.01±0.002**	0.001 ±0.01

\* Significant at 5 per cent level

\*\* Significant at 1 per cent level

**Table 2:** Ratio of genetic parameters of pumpkin - F<sub>1</sub>

Characters	(H <sub>2550</sub> /D) <sup>1/2</sup>	H <sub>2</sub> /4H <sub>1</sub>	K <sub>D</sub> /K <sub>R</sub>	h <sup>2</sup> /H <sub>2</sub>	Heritability (NS)(%)	Heritability (BS)(%)	GA as percentage of mean
Vine length(m)	1.98	0.18	0.22	0.33	-0.07	97.34	36.66
Number of primary branches	2.50	0.20	3.15	0.12	-0.04	25.12	21.10
Days to first male flower	-0.42	0.11	0.81	1.93	1.28	56.34	2.46
Days to first female flowering	1.53	0.15	2.12	0.17	0.23	78.00	3.02
Nodes to first male flower	1.98	0.18	1.68	0.11	0.24	56.21	16.11
Nodes to first Female flower	2.40	0.31	0.49	0.26	0.83	36.54	3.28
Sex ratio	0.60	0.22	1.12	0.70	0.76	91.34	10.04
Days to first harvest	0.53	0.19	3.57	0.37	0.27	66.21	1.51
Number of fruits per vine	1.28	0.22	0.53	0.10	1.74	85.38	99.48
Average fruit weight(kg)	-0.35	0.15	0.73	1.06	1.32	69.41	34.83
Fruit length(cm)	0.58	0.22	0.55	0.41	1.60	98.13	8.60
Fruit diameter(cm)	0.23	0.21	0.84	0.07	1.06	96.34	3.36
Flesh thickness(cm)	0.74	0.22	1.83	0.42	0.36	80.45	61.23
Number of seeds per fruit	0.51	0.19	2.47	0.36	0.39	96.27	0.58
Fruit yield per plant(kg)	0.68	0.23	1.18	5.79	0.69	99.10	38.04
Total soluble solids(TSS)	0.93	0.20	0.69	0.12	1.29	96.21	24.75
Beta carotene(mg/100g)	1.33	0.15	2.58	0.00	0.17	71.32	180.56
Moisture content (percent)	2.32	0.09	1.71	0.72	0.50	42.12	0.89
Dry matter content(percent)	2.05	0.18	0.50	1.11	1.54	92.62	246.12

### 3.1 Vine length

The genetic parameters for vine length *viz.*, D, F, H<sub>1</sub>, H<sub>2</sub> and h<sup>2</sup> were significant suggesting both additive and dominance gene action. The mean degrees of dominance (H<sub>1</sub>/D)<sup>1/2</sup> was greater than one (1.98) suggested the over dominance nature. The ratio of H<sub>2</sub>/4H<sub>1</sub> was 0.18. The ratio K<sub>D</sub>/K<sub>R</sub> was less than one and the recessive alleles were more pronounced. The ratio h<sub>2</sub>/H<sub>2</sub> (0.33) was less than one and this trait was controlled by single gene inheritance. The narrow sense heritability (-0.07 per cent) was low and broad sense heritability (97.34 per cent) was high. The genetic advance as percentage of mean (36.66) was high. It indicates the preponderance of non additive gene action when compared to additive. The present result is in accordance with Rana *et al.* (2016), Dhatt and Singh (2008) [3] in pumpkin.

### 3.2 Number of primary branches

The genetic parameters *viz.*, D, F, H<sub>1</sub> and H<sub>2</sub> were significant for number of primary branches suggesting both additive and dominance gene action. The mean degrees of dominance (H<sub>1</sub>/D)<sup>1/2</sup> was more than one (2.50) suggested the over dominance nature. Both positive and negative genes were asymmetrically distributed. The ratio of H<sub>2</sub>/4H<sub>1</sub> was 0.20. The ratio K<sub>D</sub>/K<sub>R</sub> was more than one shows that dominance alleles were more pronounced. The ratio h<sup>2</sup>/H<sub>2</sub> (1.93) was greater than one and this trait may be controlled by more than one group of gene inheritance. The narrow sense heritability (-0.04 per cent) was low and the broad sense heritability (25.12 per cent) was low. The genetic advance as percentage of mean (21.10) was high. Low heritability and high genetic advance indicates the non- additive gene action. Present result is in accordance with Srinivasan (2003) [19] in pumpkin.

### 3.3 Days to first male flower

The genetic parameter D was significant for days to first male flower. The mean degrees of dominance (H<sub>1</sub>/D)<sup>1/2</sup> was less than one (-0.42) expressed partial dominance. The ratio of H<sub>2</sub>/4H<sub>1</sub> was (0.11). The ratio K<sub>D</sub>/K<sub>R</sub> was less than one (0.81) indicates that recessive alleles were more pronounced as the K<sub>D</sub>/K<sub>R</sub> ratio was less than one. The ratio h<sup>2</sup>/H<sub>2</sub> (1.93) was more than one and it may due to more than one group of genes involvement than unity. The narrow sense heritability (1.28 per cent) was moderate while the broad sense heritability was high (56.34). The genetic advance as

percentage of mean (2.46) was high. It indicates the non-additive gene action compared to additive. Muthulakshmi and Pappiah (1995) [10] and Punitha (2000) [11] observed high heritability and genetic advance.

### 3.4 Days to first female flower

The genetic parameters *viz.*, D and H<sub>1</sub> were significant for days to first female flower suggesting dominance gene action. The mean degrees of dominance (H<sub>1</sub>/D)<sup>1/2</sup> was more than one (1.53) and due to the expression over dominance. The ratio of H<sub>2</sub>/4H<sub>1</sub> (0.15) was less than one. The ratio K<sub>D</sub>/K<sub>R</sub> was more than one (2.12) and it shows the pronounced expression of dominant alleles. The ratio h<sup>2</sup>/H<sub>2</sub> (0.17) was less than one and this trait may control by single block of gene. The narrow sense heritability (0.23 per cent) was low and broad sense heritability (78.00) was high. The genetic advance as percentage of mean (3.02) was low. It indicates the non-additive gene action compared to additive. Gopalakrishnan *et al.* (1980) [5] in pumpkin observed high heritability and low genetic advance as percentage of mean and this result was contrary with the finding of Sahithya (2001) [12].

### 3.5 Nodes to first male flower

The genetic parameters H<sub>1</sub> and H<sub>2</sub> were significant for nodes to first male flower, suggesting dominance gene action. The mean degrees of dominance (H<sub>1</sub>/D)<sup>1/2</sup> was more than one (1.98) and it may due expression of over dominance. The ratio of H<sub>2</sub>/4H<sub>1</sub> was (0.18). The ratio K<sub>D</sub>/K<sub>R</sub> was more than one (1.68) and the trait pronounced by dominant alleles. The ratio h<sup>2</sup>/H<sub>2</sub> (0.11) was less to one and this trait may be controlled by single block of gene. The narrow sense heritability (0.24 per cent) was low while the broad sense heritability (56.21 per cent) was high. The genetic advance as percentage of mean (16.11) was moderate indicates the non-additive gene action on this trait.

### 3.6 Sex ratio

The genetic parameters *viz.*, D, H<sup>2</sup> were significant showed the presence of both additive and dominance gene action for sex ratio. The mean degrees of dominance (H<sub>1</sub>/D)<sup>1/2</sup> was less than one (0.60) and it is the expression of partial dominance. The ratio of H<sub>2</sub>/4H<sub>1</sub> was (0.22). The ratio K<sub>D</sub>/K<sub>R</sub> was more than one (1.22). The ratio h<sup>2</sup>/H<sub>2</sub> (0.70) was less than one and this trait was controlled by single block of gene. The narrow

sense heritability (0.76 per cent) was low while the broad sense heritability (91.34 per cent) was high. The genetic advance as percentage of mean (10.04) was moderate. Indicate the non-additive gene action compared to additive gene action. But additive gene action for sex ratio was reported by Solanki and Seth (1980) and Muthulakshmi and Pappiah (1995) [10].

### 3.7 Days to first harvest

The genetic parameters *viz.*, D and F were significant suggesting both additive and dominance gene action for days to harvest. The mean degrees of dominance  $(H_1/D)^{1/2}$  was less than one (0.53) suggested the partial dominance nature. The ratio of  $H_2/4H_1$  was (0.19). The ratio  $K_D/K_R$  was more than one (3.57) and the dominance alleles may be more pronounced. The ratio  $h^2/H_2$  (0.37) was less than one. The narrow sense heritability (0.27 per cent) was low while the broad sense heritability (66.21 per cent) was high. The genetic advance as percentage of mean (1.51) was low. It indicated the non-additive gene action. Similar result was observed by Samadia (2011) [13] in ridge gourd and Hazara *et al.* (2007) [7] in pumpkin.

### 3.8. Number of fruits per vine

The genetic parameters *viz.*, D,  $H_1$  and  $H_2$  were significant suggesting both additive and dominance gene action for number of fruits per vine. The mean degrees of dominance  $(H_1/D)^{1/2}$  (1.28) was more than one suggested the over dominance nature. The ratio of  $H_2/4H_1$  was (0.22). The ratio  $K_D/K_R$  (0.53) was less than one so recessive alleles may be more pronounced. The ratio  $h^2/H_2$  (0.10) was less than one and this trait was controlled by single block of gene. The narrow sense heritability (1.74 per cent) was low while the broad sense heritability (85.38 per cent) was very high. The genetic advance as percentage of mean (99.48) was very high. Indicate the non-additive gene action. The present result is in accordance with Choudhary *et al.* (1985) [1], Vijay (1987) [22] Muthulakshmi and Pappiah in musk melon (1995) and Punitha (2000) [11] in cucumber. Additive and over dominance effect for this character was reported by Sirohi (1994) [17].

### 3.9 Average fruit weight

The components of variance D alone showed significance indicating the presence of additive gene action for average fruit weight. The mean degrees of dominance  $(H_1/D)^{1/2}$  was less than one (-0.35) suggest the partial dominance nature. The ratio of  $H_2/4H_1$  was (0.15). The ratio  $K_D/K_R$  was less than one (0.73) and recessive alleles may be more pronounced. The ratio  $h^2/H_2$  (1.06) was more than one and this trait was controlled by more than one group of gene. The narrow sense heritability (1.32 per cent) was low while the broad sense heritability (69.41 per cent) was high. The genetic advance as percentage of mean (34.83) was moderate. It indicate the non-additive gene action. This was in accordance with the result of Devadas (1993) in bitter gourd.

### 3.10 Fruit length

The genetic parameters D,  $H_1$ ,  $H_2$  and  $h^2$  showed significance indicating the presence of additive gene action for fruit length. The mean degrees of dominance  $(H_1/D)^{1/2}$  was less than one (0.58) suggested the partial dominance nature. The ratio of  $H_2/4H_1$  was (0.22). Both positive and negative genes were asymmetrically distributed. Recessive alleles were more pronounced as the  $K_D/K_R$  ratio was less than one (0.55). This trait was controlled by more than one group of genes as the

ratio  $h^2/H_2$  (0.41) was less than one. The narrow sense heritability (1.60 per cent) was low while the broad sense heritability (98.13 per cent) was very high. The genetic advance as percentage of mean (8.60) was low and indicates the non-additive gene action. Similar results were reported by Vidya (2001) in cucumber.

### 3.11 Fruit diameter

The significance of D variance alone showed significance indicating the presence of additive gene action for fruit diameter. The mean degrees of dominance  $(H_1/D)^{1/2}$  was less than one (0.23) suggested the partial dominance nature. Both positive and negative genes were asymmetrically distributed. Recessive alleles were more pronounced as the  $K_D/K_R$  ratio was less than one (0.84). The ratio of  $H_2/4H_1$  was (0.21). The ratio  $K_D/K_R$  was less than one (0.84). The ratio  $h^2/H_2$  (0.07) was less than one and this trait was controlled by single block of gene. The narrow sense heritability (1.06 per cent) was low while the broad sense heritability (96.34 per cent) was high. The genetic advance as percentage of mean (3.36) was low and indicate the non-additive gene action. Present result is in accordance with Dhatt and Singh (2008) [3] in pumpkin.

### 3.12 Flesh thickness

The genetic parameters *viz.*, D,  $H_1$  and  $H_2$  were significant suggesting both additive and dominance gene action for flesh thickness. The mean degrees of dominance  $(H_1/D)^{1/2}$  was less than one (0.74) suggested the partial dominance nature. The ratio of  $H_2/4H_1$  was (0.22). Both positive and negative genes were asymmetrically distributed. Dominant alleles were more pronounced as the  $K_D/K_R$  ratio was more than one (1.83). The ratio  $h^2/H_2$  (0.42) was less than one and this trait was controlled by single block of gene. The narrow sense heritability (0.36 per cent) was low while the broad sense heritability (80.45 per cent) was high. The genetic advance as percentage of mean (61.23) was high. It indicates the non-additive gene action. Similar results were reported by Vidya (2001) in cucumber. This finding was on the contrary to the reports of Muthulakshmi and Pappiah (1995) [10] in cucumber and Swamy *et al.* (1985) in muskmelon.

### 3.13 Number of seeds per fruit

The genetic parameters *viz.*, D, F,  $H_1$  and  $H_2$  were significant suggesting both additive and dominance gene action for number of seeds per fruit. The mean degrees of dominance  $(H_1/D)^{1/2}$  was less than one (0.51) suggested the partial dominance nature. The ratio of  $H_2/4H_1$  was (0.19). Both positive and negative genes were asymmetrically distributed. Dominant alleles were more pronounced as the  $K_D/K_R$  ratio was more than one (2.47). The ratio  $h^2/H_2$  (0.36) was less than one and this trait was controlled by single block of gene. The narrow sense heritability (0.39 per cent) was low while the broad sense heritability (96.27 per cent) was high. The genetic advance as percentage of mean (0.58) was low. It indicates the non-additive gene action. Similar results were reported by Vidya (2001) in cucumber.

### 3.14 Fruit yield per vine

The significance of variance D alone showed significance indicating the presence of additive gene action for yield per vine. The mean degrees of dominance  $(H_1/D)^{1/2}$  was less than one (0.68) suggested the partial dominance nature. The ratio of  $H_2/4H_1$  was (0.23). Both positive and negative genes were asymmetrically distributed. Dominant alleles were more pronounced as the  $K_D/K_R$  ratio was more than one (1.18). The

ratio  $h^2/H_2$  (5.79) was more than one hence; this trait was controlled by more group of gene. The narrow sense heritability (0.69 per cent) was low while the broad sense heritability (99.10 per cent) was high. The genetic advance as percentage of mean (38.04) was high. It indicates the non-additive gene action. This is in agreement with results of Shivanand *et al.* (2015) in ridge gourd and Hazara *et al.* (2007)<sup>[7]</sup> in pumpkin.

### 3.15 Total soluble solids

The components of variance D, H,  $H_1$ ,  $H_2$  and  $h^2$  were significant suggesting both additive and dominance gene action for total soluble solids. The mean degrees of dominance  $(H_1/D)^{1/2}$  (0.93) was less than one suggested the partial dominance nature. The ratio of  $H_2/4H_1$  was (0.20). Both positive and negative genes were asymmetrically distributed. Recessive alleles were more pronounced as the  $K_D/K_R$  ratio was less than one (0.69). The ratio  $h^2/H_2$  (0.12) was less than one and the trait was controlled by single group of gene. The narrow sense heritability (1.29 per cent) was low while the broad sense heritability (96.21 per cent) was high. The genetic advance as percentage of mean (24.75) was high. It indicates the non-additive gene action. This present result is in contrary with Mariappan and Pappiah (1991)<sup>[9]</sup> in cucumber and Vidya (2001)<sup>[21]</sup> in cucumber.

### 3.16 Beta carotene

The genetic parameters D,  $H_1$ ,  $H_2$  and  $h^2$  were significant suggesting both additive and dominance gene action for beta carotene. The mean degrees of dominance  $(H_1/D)^{1/2}$  was more than one (1.33) suggested the over dominance nature. The ratio of  $H_2/4H_1$  was (0.15). Both positive and negative genes were asymmetrically distributed. Dominant alleles were more pronounced as the  $K_D/K_R$  ratio was more than one (2.58). The ratio  $h^2/H_2$  was equal to zero and this trait was controlled by single block of gene. The narrow sense heritability (0.17 per cent) was low while the broad sense heritability (71.32 per cent) was high. The genetic advance as percentage of mean (180.56) was very high. It indicates the non-additive gene action. This was in consonance with the findings of Srinivasan (2003)<sup>[19]</sup> in pumpkin.

### 3.17 Moisture content

The component of variance  $H_1$  alone was significant suggesting dominance gene action for moisture content. The mean degrees of dominance  $(H_1/D)^{1/2}$  was more than one (2.32) suggested the over dominance nature. The ratio of  $H_2/4H_1$  was (0.09). Both positive and negative genes were asymmetrically distributed. Dominant alleles were more pronounced as the  $K_D/K_R$  ratio was more than one (1.71). The ratio  $h^2/H_2$  (0.72) was less than one and this trait was controlled by single block of gene. The narrow sense heritability (0.50 per cent) was low while the broad sense heritability (42.12 per cent) was high. The genetic advance as percentage of mean (0.89) was very low. It indicates the non-additive gene action. Similar results were observed by Dhatt and Singh (2008)<sup>[3]</sup> in pumpkin.

### 3.18 Dry matter content

The genetic parameters *viz.*, D,  $H_1$ ,  $H_2$  and  $h^2$  were significant suggesting both additive and dominance gene action for dry matter content. The mean degrees of dominance  $(H_1/D)^{1/2}$  was more than one (2.05) suggested the over dominance nature. The ratio of  $H_2/4H_1$  was (0.18). Both positive and negative genes were asymmetrically distributed. Recessive alleles were

more pronounced as the  $K_D/K_R$  ratio was less than one (0.50). The ratio  $h^2/H_2$  (1.11) was more than one and this trait was controlled by more than one group of gene. The narrow sense heritability (1.54 per cent) was low while the broad sense heritability (92.62 per cent) was high. The genetic advance as percentage of mean (246.12) was very high. It indicates the non-additive gene action. Similar results were reported by Singh *et al.* (2014) in bitter gourd.

## 4. Conclusion

The genetic analysis showed that there was dominance action for days to first male flower, days to first female flower, node to first male flower and moisture content. The additive gene action exhibited for fruit length, fruit diameter, fruit yield. The combination of dominant and additive gene action was ascertained for vine length, number of primary branches, sex ratio, days to first harvest, number of fruit per vine, flesh thickness and number of seeds per fruit.

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