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Heterosis and combining ability in bitter gourd (*Momordica charantia* L.)

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Abstract: Ten parents of bitter gourd viz., Solan Hara, Pusa Do-Mousmi, BG-14, Green Long, MDU-1, IC-85605, IC-45346, IC-68272-1, IC-68237 and Solan Collection and their forty five crosses (using half diallelic system) along with check viz., Jhalri, US-6214 and US-6203 were evaluated in field trials in two locations Udaipur and Chittaurgarh in two different seasons which consists four environments. Economical heterobeltiosis for yield per vine (kg) were recorded in IC 85605 x IC 45346 (38.94%) and MDU 1 x IC 85605 (34.98%) over the environments. Good general combiners for various economic traits IC-68237 for number of primary branches per vine (0.09), fruit length (0.52), fruit diameter (0.17) & number of fruits per vine (0.22) over the pooled environments. SCA (Specific Combining Ability) for economic traits were observed in Solan Collection x IC 68237 (1.24) for number of fruits per vine, IC 68237 x MDU-1 for fruit length (1.82) and fruit weight (7.81). These results indicate that both additive and non-additive gene effects are involved in the inheritance of the studied traits. The additive gene action was more important than the non-additive ones in the genetics of most studied traits.

Keywords: Parents, Heterosis, GCA, SCA, Yield, *Momordica charantia*

Introduction

It is a large genus with many species of annual and perennial climbers of which *Momordica charantia* L. is widely cultivated. A native of old world tropics, bitter gourd (also known as bitter melon, balsam pear or bitter cucumber) was long ago fanned out into rest of new world. Wild *Momordica charantia* var. *abbreviata*, a native of Asia may be the progenitor of domesticated ones. Heterosis is an useful parameter in introducing new high yielding hybrid varieties. On the basis of high GCA (General Combining Ability) estimates, good combiner parental inbred lines can be selected to be involved in hybrid combinations to detect the best hybrids, through the comparison among SCA values. A high SCA of particular combination means that the parents of this hybrid can produce a superior hybrid. When the additive gene action represents the main component of the total genetic variation, a maximum progress would be expected in selection programs. On the other hand, the presence of a relatively high non-additive gene action as reflected with the estimates of SCA indicates that production of F1 hybrids should be considered. With these points in consideration, heterosis and combining ability studies are important, which give us valuable information pertaining to the improvement or exploiting heterosis for commercial purposes. Though many reports on combining

ability and heterosis breeding are available in bitter gourd [1,2] information on identification of better parents for F1 production is lacking. Therefore this experiment was conducted to draw the results about heterosis and combining ability for different yield contributing and quality traits.

Materials and Methods

Present study were carried out at the Horticulture Farm, Department of Horticulture, Rajasthan College of Agriculture, Udaipur and Farmer field of Chittaurgarh district during kharif and zaid season, 2012-2013 and 2013-14 to find out the suitable germplasm and their cross combinations for the growers of the regions. Crossing were made among ten parents of bitter gourd viz., Parents and their crosses were evaluated in field trials in two locations: Solan Hara (P1), Pusa Do-Mousmi (P2), BG-14 (P3), Green Long (P4), MDU-1 (P5), IC-85605 (P6), IC-45346 (P7), IC-68272-1 (P8), IC-68237 (P9) and Solan Collection (P10) using partial diallel mating system to produce 45 F1 crosses. Parents, their crosses and check viz., Jhalri, US-6214 and US-6203 were evaluated in field trials in two locations at Udaipur and Chittaurgarh in two different seasons which consists four environments. The experiment was laid out in Randomized Block Design with three replications. Randomization of lines was done with the help of random number table as advocated by [3]

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and observed data were subjected to combining ability analysis according to [4].

Results

ANOVA Tables 1-4 indicated that highly significant

mean sum of square due to genotypes for all the characters in each individual environment as well as pooled over the environments revealed significant differences among the genotypes for majority of the characters except node number at which first

Table 1: Mean square for different characters.

SN	Characters	Env	Source					
			Rep	Genotype	Parent	F1	P vs F1	Error
			[2]	[54]	[9]	[44]	[1]	[108]
1	Days to anthesis of first male flower	1	8.12	19.54**	13.17**	17.73**	156.61**	3.18
		2	1.50	18.93**	13.80**	17.97**	107.48**	5.04
		3	20.10**	19.50**	13.17**	19.12**	93.16**	3.21
		4	3.75	19.61**	14.63**	19.78**	56.88**	3.77
2	Days to anthesis of first female flower	1	22.26**	29.54**	27.99**	28.48**	90.34**	2.70
		2	13.99*	23.62**	14.60**	25.74**	11.52	4.12
		3	21.35**	30.78**	27.99**	30.14**	84.18**	2.41
		4	10.30	26.06**	21.32**	26.00**	71.25**	3.92
3	Node number at which I female flower appeared	1	0.87	2.62	3.41	2.50	0.46	2.69
		2	0.04	2.42	1.71	2.60	0.68	2.89
		3	2.08	2.64	3.41	2.53	0.57	2.58
		4	0.19	2.31	2.58	2.22	3.93	2.74
4	Number of male flowers per vine	1	34.66	536.08**	9.93	155.06**	22036.40**	11.53
		2	171.35	615.60**	18.90	340.72**	18080.67**	133.26
		3	11.39	521.72**	48.26**	199.18**	18974.76**	8.31
		4	21.57	721.24**	16.80	508.48**	16422.98**	61.13
5	Number of female flowers per vine	1	14.44**	3.44	2.96	3.38	10.43	2.84
		2	127.44**	2.64	1.72	2.78	4.61	2.70
		3	5.82	5.82**	3.63	3.22*	140.08**	2.14
		4	8.66	12.58**	1.76	15.07**	0.16	5.38
6	Number of primary branches	1	0.04	0.57**	0.18	0.29**	16.29**	0.13
		2	0.65	0.37	0.31	0.38	0.32	0.82
		3	0.32	0.92**	0.40	0.46*	25.83**	0.30
		4	1.06	0.39	0.31	0.42	0.15	0.78
7	Number of fruits per vine	1	7.85	1.96	0.92	2.17	2.43	3.24
		2	182.31**	1.95	0.89	2.17	1.94	3.14
		3	1.02	6.04**	5.47**	1.37	216.57**	1.47
		4	1.32	15.36**	4.00	17.68**	15.28*	3.19
8	Fruit length (cm)	1	17.04*	7.97*	1.99	5.05	190.41**	4.88
		2	2.62	11.74**	8.70**	10.80**	80.51**	2.57
		3	3.01	8.93**	10.05**	2.75**	270.55**	1.30
		4	2.84	9.25**	0.98	7.90**	143.13**	2.48
9	Fruit weight (g)	1	86.62*	618.67**	730.45**	609.78**	4.15	20.19
		2	28.44	602.33**	756.77**	583.98**	19.88	16.93
		3	27.29	529.52**	781.11**	486.33**	165.45**	19.03
		4	17.39	568.04**	909.04**	509.84**	59.68	15.81
10	Fruit diameter (cm)	1	0.14	0.64**	0.08	0.49**	12.20**	0.12
		2	0.40*	0.57**	0.62**	0.50**	3.39**	0.11
		3	0.10	0.45**	0.08	0.21**	14.15**	0.12
		4	0.24	0.66**	0.76**	0.60**	2.34**	0.11
11	Specific gravity (g/cc)	1	0.00	0.00**	0.00**	0.00**	0.01**	0.00
		2	0.00	0.00**	0.00**	0.00**	0.00	0.00
		3	0.00	0.00**	0.00**	0.00**	0.00	0.00
		4	0.00	0.00**	0.00**	0.00**	0.01**	0.00
12	Number of seeds per fruit	1	0.78	55.86**	52.18**	51.78**	268.50**	2.39
		2	3.81	55.50**	29.27**	51.94**	448.39**	2.29
		3	11.58**	58.13**	52.18**	54.49**	272.12**	1.84
		4	6.48	55.07**	48.52**	50.74**	304.51**	2.21
13	Yield per vine (kg)	1	0.07	0.27**	0.29**	0.27**	0.01	0.03
		2	1.25**	0.28**	0.33**	0.27**	0.00	0.03
		3	0.02	0.28**	0.31**	0.25**	1.10**	0.02

SN	Characters	Env	Source					
			Rep	Genotype	Parent	F1	P vs F1	Error
			[2]	[54]	[9]	[44]	[1]	[108]
14	Vine length (cm)	4	0.01	0.26**	0.39**	0.24**	0.02	0.02
		1	2428.87*	5358.28**	6930.91**	5129.32**	1278.99	589.98
		2	1065.04	5681.12**	6029.35**	5704.42**	1521.84*	358.47
		3	307.66	6337.30**	3498.98*	6767.46**	12955.29**	1510.08
15	Days to maturity	4	42.02	1157.70**	223.44**	516.11**	37795.97**	19.27
		1	4.09	94.29**	107.22**	79.49**	629.19**	3.99
		2	13.68	83.38**	113.96**	67.49**	506.91**	7.57
		3	29.19**	90.96**	88.16**	77.86**	692.38**	3.66
16	Total soluble solids (%)	4	31.75*	88.67**	91.24**	74.73**	678.92**	6.89
		1	0.03	0.32**	0.47**	0.28**	0.67**	0.01
		2	0.01	0.28**	0.36**	0.27**	0.42**	0.01
		3	0.02	0.31**	0.35**	0.29**	0.86**	0.01
17	Ascorbic acid (mg/100 g)	4	0.03	0.31**	0.45**	0.27**	0.69**	0.01
		1	3.35*	41.91**	22.69**	22.52**	1068.00**	0.94
		2	2.92*	39.05**	26.39**	22.37**	886.91**	0.95
		3	4.26*	29.11**	25.56**	23.39**	312.89**	1.25
		4	3.35*	41.91**	22.69**	22.52**	1068.00**	0.94

*,** Significant at 5 and 1 percent respectively (Model I)

Table 2: Mean square over the environments for different characters.

SN	Characters	Source										Bartlet		
		Env	Rep/ Env	Genotype	Parents	F1	P vs F1	GxE	PxE	F1xE	PvsF1xE	Error		
		[3]	[8]	[54]	[9]	[44]	[1]	[162]	[27]	[132]	[3]	[432]	[3]	
1	Days to anthesis of first male flower	8.76	8.37*	33.96**	15.59**	29.36**	401.50**	14.54**	13.06**	15.08**	4.21	3.80	7.84*	
2	Days to anthesis of first female flower	10.40*	16.97**	26.62**	18.42**	25.70**	140.73**	27.80**	24.49**	28.22**	38.85**	3.29	11.48**	
3	Node number at which I female flower appeared	0.07	0.80	2.21	0.59	2.48	4.49	2.59	3.50	2.46	0.38	2.73	0.35	
4	Number of male flowers per vine	270.64**	59.74	1803.64**	30.04	496.08**	75298.68**	197.00**	21.28	235.78**	72.04	53.56	254.39**	
5	Number of female flowers per vine	5.17	39.09**	8.78**	5.43	7.90**	77.58**	5.23**	1.55	5.52**	25.90**	3.26	27.28**	
6	Number of primary branches	303.26**	0.52	1.05**	0.85	0.54	25.37**	0.40	0.12	0.33	5.74**	0.51	104.04**	
7	Number of fruits per vine	27.45**	48.13**	5.26**	3.23	4.72**	47.35**	6.68**	2.69	6.22**	62.96**	2.76	21.17**	
8	Fruit length (cm)	663.08**	6.38*	19.96**	4.05	8.78**	654.95**	5.98**	5.89**	5.91**	9.88*	2.81	46.23**	
9	Fruit weight (g)	1722.72**	39.94*	2095.30**	2717.63**	2014.86**	33.83	74.42**	153.25**	58.36**	71.78**	17.99	1.98	
10	Fruit diameter (cm)	137.80**	0.22	1.32**	0.64**	0.85**	28.22**	0.33**	0.30**	0.32**	1.29**	0.11	0.70	
11	Specific gravity (g/cc)	0.02**	0.00	0.01**	0.01**	0.01**	0.01**	0.00**	0.00**	0.00**	0.00**	0.00	4.59	
12	Number of seeds per fruit	0.12	5.66**	117.78**	62.89**	102.63**	1278.33**	35.59**	39.76**	35.43**	5.06	2.19	2.10	
13	Yield per vine (kg)	1.46**	0.34**	0.89**	1.05**	0.87**	0.25**	0.06**	0.09**	0.05**	0.29**	0.03	16.49**	
14	Vine length (cm)	561649.90**	960.90	11126.28**	7983.28**	11884.88**	6034.52**	2469.38**	2899.80**	2077.48**	15839.19**	619.45	342.88**	
15	Days to maturity	28.81**	19.68**	153.82**	75.44**	116.57**	2498.38**	67.83**	108.38**	61.01**	3.01	5.53	22.02**	
16	Total soluble solids (%)	0.31**	0.02	0.92**	1.58**	0.74**	2.60**	0.10**	0.02	0.12**	0.01	0.01	0.67	
17	Ascorbic acid (mg/100 g)	89.33**	3.47**	124.59**	49.84**	70.38**	3182.68**	9.13**	15.83**	6.81**	51.04**	1.02	3.52	

Table 3: Five best hybrids identified on the basis of heterobeltiosis for total yield and its contributing traits on pooled basis.

Hybrids	Heterobeltiosis (%)
P ₆ xP ₇	43.85
P ₅ xP ₆	41.38
P ₁ xP ₈	22.18
P ₆ xP ₉	24.72
P ₉ xP ₁₀	51.53

Table 4: General and specific combiners for the various traits of bitter gour gourd.

S.N	Characters	General Combiners			Specific Combiner		
		Good	Average	Poor	Good	Average	Poor
1	Days to anthesis of first male flower	Solan Hara	BG-14, IC-45346	IC-68272-1	SCxIC-85605	-	IC-85605x SH
2	Days to anthesis of first female flower	MDU-1, GL	IC-68237, IC-68272-1, and Pusa Do Mausmi	SH and BG-14	IC-45346 x Green Long	IC-85605 x BG-14, MDU-1 x BG-14	IC-85605 x MDU-1, Solan Collection x Green Long and IC-45346 x MDU-1
3	Node at which first female flower appeared	Solan Hara, BG-14, Green Long	-	-	Solan Collection x IC 68272-1	Solan Collection x MDU-1, IC 68237x IC 45346	-
4	Number of male flower per vine	Solan Hara	-	-	PDM x SH	IC 85605 x Solan Hara, BG-14 x PDM	-
5	Number of female flower per vine	Solan Collection	MDU-1, IC-68237	-	IC45346 x IC 85605, MDU-1x PDM	Solan Collection x IC 45346, IC 68237x IC 68272-1	-
6	Number of primary branches	IC-68237	-	-	MDU -1 x Solan Hara, SL x IC 68237	-	-
7	Number of fruits per vine	IC-68237	MDU-1 & Solan Collection	-	Solan Collection x IC 68237	Solan Collection x IC 68272-1	-
8	Fruit length (cm)	IC-68237	Solan Collection	-	IC 68237 x MDU-1	Green Long x BG 14, BG 14 x PDM	-
9	Fruit weight (g)	Solan Hara and PDM	BG 14, Green Long, IC 68272-1	-	IC 68237 x MDU-1	Green Long x BG 14, BG 14 x PDM	-
10	Fruit diameter (cm)	IC-68237	BG-14, IC-68272-1	-	IC-85605xMDU-1	SCxSH, SCxPDM, IC-68272-1xMDU-1	-
11	Specific gravity	MDU-1	IC-85605	-	GLxPDM, IC-68237xIC-68272-1	-	-
12	Number of seeds per fruit	PDM	-	-	IC-68237xPDM,IC-45346xSH	SCxGL	-
13	Yield per vine (kg)	SH, PDM	-	-	MDU-1xBG-14, SCxIC-68237	-	-
14	Vine length (cm)	BG-14	PDM	-	IC-45346xBG-14	IC-68237xBG-14	-
15	Days to maturity	IC45346	IC-68272-1	-	IC-68272-1xGL, MDU-1xBG-14	IC-68272-1xMDU-1	-
16	Total soluble solids (%)	IC-68237, SC	-	-	IC-68272-1xGL, SCxIC-45346	MDU-1 xPDM, SC x BG-14	-
17	Ascorbic acid (mg/100 g)	IC-68272-1, IC-68237, SC	-	-	PDMxSH	BG-14 x SH	-

female flower appeared. In pooled analysis over four environments, Genotype x Environment (G x E) considered as source of variation i.e. mean square values due to G x E interaction were significant for all the characters except node number at which first female flower appeared and number of primary branches which indicated that the genotypes under study responded differently to the environments. The parents significantly differed among themselves for majority of the characters across and over the environments except node number at which first female flower appeared, number of male flower per

vine, number of female flower per vine, number of fruits, fruit length and number of primary branches.

The hybrids also significantly differed among themselves for all the characters in each individual environment as well as pooled over the environments except node number at which first female flower appeared. The comparisons of mean sum of squares due to parents vs hybrids were significant for sixteen characters viz. days to anthesis of first male flower, days to anthesis of first female flower, number of male flower per vine, number of female flower per

vine, number of primary branches, number of fruits per vine, fruit length (cm), fruit weight (g), fruit diameter (cm), specific gravity (g/cc), number of seeds per fruit, yield per vine (kg), vine length (cm), days to maturity, total soluble solids (%) and ascorbic acid (mg/100 g) in all the four environments and pooled over the environments while, characters node number at which first female flower appeared mean square values due to parents vs hybrids were significant.

Heterosis

Heterosis for growth parameters is an indication of heterosis for yield and yield associated traits. Significant and higher magnitude of heterosis over mid parent and better parent was reported in majority of the traits. For improving yield potential of varieties and hybrids, selection of potential type of parents is very important. This can only be done by testing the genetic worth of the parents, because many times the high yielding parents may not mix well to give desirable segregates. The phenomenon of heterosis has provided the most important genetic tool for improving yield potential of crop plant.

Among 45 crosses significant per cent negative heterobeltiosis on days to anthesis of first male flower in pooled only three hybrids which showed were P6xP10 (-0.19), P3xP7 (-1.67) and P7xP8 (-1.48) per cent over environments. Economic heterosis (%) for days to anthesis of first male flower was observed in some of the hybrids viz.- P1xP9 (-2.31), P1xP10 (-3.08), P2xP3 (-1.54), P4xP5 (-0.77), P4xP6 (-3.85), P7xP8 (-3.08) and P7xP9 (-2.31) in environment 1 which had significant economic heterosis for the character and also highlight that these hybrids are superior over check in E1. Out of 45 hybrids significant per cent heterobeltiosis for female earliness was observed in P3xP5 (-0.15), P3xP6 (-1.90), P3xP7 (-1.14) and P4xP7 (-4.58) per cent over pooled environments. Hybrid P1xP7 (-4.20%) exhibited negative significant economic heterosis for days to anthesis of first female flower over the environment. Similar finding was reported by [5] for earliness for days to first male and female opening in bitter gourd.

Among 45 hybrids significant per cent hetero-beltiosis in desired direction on node number at which first female flower appeared was recorded in few hybrids which showed hetero-beltiosis were P3xP6 (-0.56), P2xP3 (-2.96) and P2xP4 (-2.94) per cent over environments as well as better parents on pooled basis. Economic heterosis (%) were observed in P1xP3, P1xP4, P3xP4, P4xP6, P5xP10 and P7xP9 (-6.25). A similar finding was reported by [6].

Pooled data on heterosis (%) on fruit length (cm) was reported in P6xP10 (24.72), P5xP9 (23.58), P7xP10 (21.92), P9xP10 (21.04) and P6xP9 (19.61), on fruit weight (g) P6xP7 (38.94), P5xP6 (34.98) and P7xP7 (12.62). Significant economic heterosis on fruit weight was observed in a hybrid P1xP8 (3.66). Heterobeltiosis (%) on fruit diameter (cm) reported in P2xP10 (20.00) and P1xP10 (18.12). In environment E3 crosses depict economic heterosis that were P3xP8 (81.89) and P2xP4 (80.37). Negative significant per cent hetero-beltiosis for number of seeds per fruit were recorded in a hybrid viz., P2xP9 (-4.08) in E1. In E2 hybrids showed significantly maximum heterosis over better parent were P4xP6 (-17.54) and P2xP7 (-10.53), whereas, in E3 P3xP4 (-22.97), P4xP10 (-19.67), P4xP5 (-17.39) and P3xP5 (-11.59). However, in E4 P5xP7 (-26.09) and P5xP6 (-17.39), whereas, in pooled hybrids were P4xP6 (-3.67) and P5xP7 (0.83). Significant per cent heterobeltiosis on yield (kg) per vine recorded upto 62.92 per cent for yield per vine (kg) in in E3 environments and in hybrids were P6xP7 (43.85) and P5xP6 (41.38) on pooled basis. These results are in agreement with the findings of [7] where the results indicated that the yield per vine was a potential character for heterosis breeding in bitter gourd. They observed 98% better parent heterosis for yield per plant.

In the majority of the crosses for fruit diameter, the role of additive and additive×additive was more pronounced which suggests that this character can be fixed in the progeny by proper selection methods revealed by [8,9] also support to the results Bahera T K [10] also reported heterosis in bittergourd for yield/vine ranges from 27.3 to 86.1% over better parent.

Eleven hybrids showed significant positive economic heterosis (%) on total soluble solids over the environments (pooled basis). Out of them maximum significant economic heterosis possessing hybrids were P7xP10 (7.76%), P7xP9 (6.94%) and P8xP9 (6.94%) over best check for TSS in individual as well as over the environments. The highest estimates of positive significant heterobeltiosis on ascorbic acid (mg/100 g) was exhibited by hybrid P1xP3 (12.71%) in E1, and P1xP2 (12.55%) in E2, P1xP2 (13.39%) in E3, P1xP3 (12.55%) in E4 and P1xP2 (10.84%) on pooled basis (29.29%).

Combining ability

The concept of combining ability in terms of genetic variation was first given by [11] using single crosses in maize. Combining ability analysis is one of the powerful tools available which give the estimates of combining ability effect and

aids in selecting desirable parents and crosses for further exploitation, either to exploit for heterosis or to combine favourable fixable genes. This analysis provides information on i) the nature and amount of genetic parameters and ii) general and specific combining ability of parents and crosses, respectively. The term combining ability is defined as the relative ability of a genotype to transmit its desirable trait to its progenies. General Combining Ability (GCA) may be defined as the average performance of a line (or population) in a series of crosses while Specific Combining Ability (SCA) is the deviation of the crosses from the performance predicted on the basis of general combining ability of the parent involved. The former is a measure of

additive genetic factors while the latter is due to non additive genetic factors [4,11] suggested that GCA included both additive effects as well as additive X additive interaction. The high yielding lines may not be necessarily being able to transmit their superiority to their hybrids. (Tables 5-13)

Earliness is desirable, hence, parents and crosses with significant and negative GCA and SCA effects were considered as good general combiner and specific combiner, respectively. Among ten pistillate parents, viz. Solan Hara {E1 (-0.72), E2 (-1.08), E3 (-0.51), E4 (-0.53) and PEVs (-0.71)} and IC-85605 exhibited significant and negative GCA effect across and over the environments. The cross Solan

Table 5: GCA and SCA effects for days to anthesis of first male flower and days to anthesis of first female flower.

SN	Genotype	Days to anthesis of first male flower					Days to anthesis of first female flower				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	-0.72*	-1.08**	-0.51	-0.53	-0.71*	0.07	0.97**	-0.30	1.62**	0.59**
2	P2	0.78**	0.36	-0.48	-0.78*	-0.03	0.29	0.72*	0.01	0.56	0.39**
3	P3	0.14	0.06	0.02	-0.25	-0.01	-0.07	0.80*	1.09**	-1.72**	0.02
4	P4	-0.22	0.36	-0.18	-0.17	-0.05	1.21**	-1.56**	-0.83**	-0.55	-0.43*
5	P5	-0.33	0.33	-0.07	1.08**	0.25	-0.52*	-0.23	-1.72**	0.64*	-0.45*
6	P6	0.03	-1.14**	0.21	-1.14**	-0.51*	0.01	-2.28**	-0.24	0.37	-0.54*
7	P7	0.17	0.67	-0.23	0.42	0.25	0.29	0.24	0.09	-1.94**	-0.33*
8	P8	0.56	0.28	-0.04	0.11	0.23	-0.16	0.30	1.78**	0.39	0.58**
9	P9	-0.22	0.06	0.41	0.64*	0.22	-0.07	0.86**	1.17**	-0.30	0.41**
10	P10	-0.17	0.11	0.88**	0.61*	0.36*	-1.04**	0.19	-1.05**	0.92**	-0.25
11	P2 x P1	2.28*	3.51**	-1.87	-2.24*	0.42	-1.19	0.31	-4.15**	-0.84	-1.47**
12	P3 x P1	1.25	0.48	-2.03*	-3.10**	-0.85	3.50**	0.23	0.76	2.11*	1.65**
13	P4 x P1	1.28	-2.49*	-2.84**	-1.52	-1.39**	1.22	1.26	3.35**	2.27*	2.02**
14	P5 x P1	0.06	3.20**	2.05*	1.90	1.80**	2.95**	-3.08**	6.23**	0.08	1.55**
15	P6 x P1	3.36**	2.01	3.11**	4.45**	3.23**	1.09	-0.69	-0.90	0.36	-0.04
16	P7 x P1	2.89**	-4.13**	3.88**	-0.43	0.55	-2.19*	2.45*	-1.57	1.33	0.00
17	P8 x P1	1.17	2.93*	0.02	-2.80**	0.33	-1.41	0.39	-0.27	-4.01**	-1.32**
18	P9 x P1	-3.06**	-1.18	2.24*	2.34*	0.09	4.17**	-0.83	1.68*	-2.98**	0.51
19	P10 x P1	-3.44**	-0.91	0.44	-0.30	-1.05*	3.14**	-2.83*	3.90**	1.47	1.42**
20	P3 x P2	-4.58**	-0.63	1.61	-3.52**	-1.78**	1.28	0.14	2.46**	3.16**	1.76**
21	P4 x P2	1.44	1.40	3.47**	3.07**	2.34**	-2.66**	1.84	0.04	1.33	0.14
22	P5 x P2	1.22	0.09	-1.64	3.48**	0.79	3.06**	-1.49	-4.74**	-1.87	-1.26*
23	P6 x P2	2.53**	-2.77*	2.74**	4.04**	1.64**	2.20*	0.23	-1.88*	1.74	0.57
24	P7 x P2	0.72	1.76	-1.81	-0.85	-0.04	-1.08	-0.30	2.12*	1.72	0.61
25	P8 x P2	1.33	1.48	-0.01	0.12	0.73	0.36	-0.02	1.43	1.38	0.79
26	P9 x P2	1.78	0.04	2.22*	1.59	1.41**	-0.72	1.76	2.71**	-0.92	0.71
27	P10 x P2	-2.28*	2.32	-4.26**	-1.05	-1.32*	-1.08	1.76	2.26**	-4.14**	-0.30
28	P4 x P3	1.75	-0.30	-1.70	2.54*	0.57	-2.97**	2.42*	3.29**	0.94	0.92
29	P5 x P3	1.86	2.40*	-2.81**	1.29	0.68	-3.25**	-3.24**	1.18	-2.92**	-2.06**
30	P6 x P3	-2.50**	-3.13*	2.58**	-0.49	-0.89	-6.11**	-5.52**	3.37**	-4.98**	-3.31**
31	P7 x P3	-0.64	-3.60**	-3.98**	-0.05	-2.07**	-4.72**	-0.05	0.37	-1.01	-1.35**
32	P8 x P3	1.97*	2.79*	-2.84**	2.93**	1.21*	-1.28	1.89	0.68	-0.34	0.24
33	P9 x P3	2.75**	2.68*	2.72**	2.40*	2.64**	3.64**	-0.66	-3.71**	5.36**	1.16*
34	P10 x P3	2.69**	2.62*	2.24*	2.76**	2.58**	2.61**	2.01	-4.49**	2.13*	0.57
35	P5 x P4	-2.78**	-0.57	0.38	-3.80**	-1.69**	2.81**	-0.22	-3.57**	3.24**	0.57
36	P6 x P4	-4.47**	4.57**	-1.89*	-2.91**	-1.18*	0.28	-1.16	-0.38	1.52	0.07
37	P7 x P4	2.39*	0.43	2.55**	2.54*	1.98**	-1.00	-5.36**	-3.04**	-4.17**	-3.39**
38	P8 x P4	1.33	-1.52	-0.98	0.18	-0.25	2.45**	-3.08**	-2.40**	-2.17*	-1.30**
39	P9 x P4	2.78**	-1.30	2.58**	2.32*	1.59**	0.03	-0.97	-2.13*	2.86**	-0.05
40	P10 x P4	2.06*	1.65	2.11*	0.01	1.46**	3.67**	-1.63	4.43**	2.63*	2.27**
41	P6 x P5	2.64**	1.26	2.99**	2.18*	2.27**	3.67**	2.51*	2.51**	2.66*	2.84**
42	P7 x P5	0.17	-0.88	2.44*	1.29	0.75	2.39**	2.64*	1.18	2.63*	2.21**
43	P8 x P5	2.11*	-2.49*	3.91**	-4.74**	-0.30	-1.50	-1.08	2.48**	-0.03	-0.03

SN	Genotype	Days to anthesis of first male flower					Days to anthesis of first female flower				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
44	P9 x P5	0.22	2.73*	1.80	-0.93	0.96	-5.91**	1.70	3.43**	-1.34	-0.53
45	P10 x P5	1.83	2.68*	-1.67	1.43	1.07*	-1.28	4.03**	-4.68**	0.77	-0.29
46	P7 x P6	2.14*	2.59*	3.16**	2.84**	2.68**	1.20	5.37**	-4.29**	-1.42	0.21
47	P8 x P6	2.08*	-1.02	-1.03	-0.85	-0.20	2.64**	3.64**	-1.99*	1.58	1.47**
48	P9 x P6	1.86	-2.80*	-3.48**	-3.38**	-1.95**	0.56	-2.24*	1.62	0.27	0.05
49	P10 x P6	-2.19*	-2.85*	-1.62	-3.35**	-2.50**	5.53**	-5.24**	5.85**	-0.28	1.46**
50	P8 x P7	-5.06**	2.18	-3.59**	-1.41	-1.97**	1.36	0.45	-0.32	2.88**	1.09*
51	P9 x P7	-3.94**	-1.60	-2.03*	2.07*	-1.38**	4.95**	-0.44	3.29**	-4.76**	0.76
52	P10 x P7	-1.33	1.68	1.49	-1.91	-0.02	3.25**	-0.44	1.51	-2.31*	0.50
53	P9 x P8	2.33*	1.45	2.77**	1.70	2.07**	-0.28	0.84	-0.40	1.91	0.52
54	P10 x P8	-1.72	2.40*	1.97*	1.07	0.93	-3.30**	-3.83**	0.82	2.36*	-0.99*
55	P10 x P9	2.39*	-2.05	0.52	1.54	0.60	-6.39**	0.95	-2.90**	3.72**	-1.16*
Standard error											
	Gi	0.28	0.35	0.28	0.31	0.15	0.26	0.32	0.25	0.31	0.14
	Gi-Gj	0.42	0.53	0.42	0.46	0.23	0.39	0.48	0.37	0.47	0.21
	Sii	0.85	1.07	0.85	0.93	0.46	0.78	0.97	0.74	0.94	0.43
	Sij	0.95	1.19	0.95	1.03	0.52	0.87	1.08	0.83	1.05	0.48
	Sij-ik	1.39	1.76	1.40	1.52	0.76	1.28	1.59	1.21	1.55	0.71
	Sij-Skl	1.33	1.67	1.34	1.45	0.73	1.22	1.51	1.16	1.48	0.68

*, ** Significant at 5% and 1% respectively.

Table 6: GCA and SCA effects for node number at which female flower appeared and number of male flowers per vine.

SN	Genotype	Node number at which I female flower appeared					Number of male flowers per vine				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	-0.40	-0.01	-0.33	-0.06	-0.20	-3.47**	-4.98**	-7.33**	-4.26**	-5.01*
2	P2	-0.04	-0.06	0.17	0.31	0.09	-2.17**	-3.37	-1.99**	-3.34**	-2.72*
3	P3	0.16	0.24	-0.47	-0.25	-0.08	0.86	-2.48	-0.69	-0.23	-0.63
4	P4	-0.29	-0.01	0.20	-0.28	-0.09	-0.56	1.83	-2.05**	1.55	0.19
5	P5	0.49	0.02	-0.19	0.28	0.15	2.75**	3.97*	0.92*	2.41	2.51**
6	P6	-0.18	-0.45	0.42	0.00	-0.05	0.31	4.63*	-0.55	5.94**	2.58**
7	P7	0.02	0.05	0.17	-0.33	-0.02	0.97	3.69*	1.84**	1.22	1.93**
8	P8	-0.09	-0.03	0.12	0.17	0.04	1.06	-1.31	3.23**	-1.59	0.35
9	P9	0.41	-0.23	0.03	0.25	0.12	1.00	-2.06	4.03**	-0.12	0.71
10	P10	-0.07	0.47	-0.13	-0.08	0.05	-0.75	0.08	2.59**	-1.59	0.08
11	P2 x P1	-0.24	0.36	-0.20	-0.64	-0.18	13.12**	-18.66**	-11.46**	-10.84*	-6.96**
12	P3 x P1	-1.10	0.39	0.77	0.24	0.08	5.43**	3.78	-1.43	6.39	3.54
13	P4 x P1	-0.66	0.64	0.44	0.61	0.26	-5.15**	15.48*	-3.74*	8.28*	3.72
14	P5 x P1	-0.43	-0.39	0.83	0.05	0.01	8.21**	13.01*	-1.38	-12.59**	1.81
15	P6 x P1	1.57	0.09	-0.45	0.66	0.47	-14.35**	9.67	-2.24	8.89*	0.49
16	P7 x P1	-0.63	0.59	-0.20	-1.01	-0.31	3.32	7.28	3.71*	5.28	4.90*
17	P8 x P1	0.15	-1.66	0.85	0.16	-0.12	12.90**	4.95	9.65**	-4.25	5.81**
18	P9 x P1	-0.35	0.86	-0.06	-0.59	-0.03	12.62**	-0.30	12.18**	10.28*	8.69**
19	P10 x P1	0.79	-0.16	-0.56	-0.92	-0.22	-2.29	-7.77	16.29**	16.41**	5.66**
20	P3 x P2	0.20	-0.55	-1.06	-0.45	-0.47	-1.54	-10.83	14.57**	-17.20**	-3.75
21	P4 x P2	0.32	-1.64	-1.06	0.91	-0.37	7.54**	-0.47	-0.07	-17.64**	-2.66
22	P5 x P2	-0.46	0.67	0.66	0.02	0.22	10.23**	9.06	-6.04**	12.16**	6.35**
23	P6 x P2	-0.80	1.14	-0.95	0.97	0.09	11.35**	9.73	6.10**	9.97*	9.28**
24	P7 x P2	1.01	0.97	0.96	-0.37	0.65	13.68**	12.01	4.71**	16.03**	11.60**
25	P8 x P2	0.45	1.39	-1.31	0.47	0.25	-5.40**	15.67*	11.65**	17.50**	9.85**
26	P9 x P2	-0.71	-1.08	1.44	1.05	0.17	-11.68**	19.42**	11.85**	19.03**	9.65**
27	P10 x P2	0.76	-0.78	0.27	0.05	0.08	6.40**	-3.38	4.29**	-0.17	1.78
28	P4 x P3	-1.21	0.06	0.24	0.47	-0.11	13.18**	4.64	0.96	4.25	5.76**
29	P5 x P3	0.68	0.70	-0.37	-1.09	-0.02	5.87**	3.51	0.65	4.39	3.60
30	P6 x P3	1.01	-0.83	-1.31	-1.14	-0.57	8.32**	11.17	6.12**	9.19*	8.70**
31	P7 x P3	-0.18	-0.33	0.60	0.86	0.24	8.65**	13.12*	8.07**	16.25**	11.52**
32	P8 x P3	-0.41	1.09	-0.01	-0.31	0.09	4.57*	9.12	12.01**	8.72*	8.60**
33	P9 x P3	0.76	-0.39	1.74*	1.27	0.85	9.96**	3.20	3.54*	0.58	4.32*
34	P10 x P3	-0.43	-0.41	0.24	-0.06	-0.17	-3.29	3.73	7.65**	4.72	3.20
35	P5 x P4	0.12	-1.39	-0.04	-0.06	-0.34	-2.38	-0.47	14.01**	2.94	3.53
36	P6 x P4	-0.88	-0.91	0.69	-0.78	-0.47	12.40**	3.20	1.15	3.75	5.13**

37	P7 x P4	-0.74	0.25	0.94	1.55	0.50	5.40**	9.81	3.76*	14.14**	8.28**
38	P8 x P4	0.37	0.34	-1.67	0.38	-0.15	6.98**	6.81	6.37**	8.94*	7.28**
39	P9 x P4	0.20	1.53	0.41	-0.37	0.44	11.71**	13.56*	8.57**	13.47**	11.83**
40	P10 x P4	2.01*	-0.83	-0.42	-1.03	-0.07	2.46	6.09	13.01**	9.61*	7.79**
41	P6 x P5	0.68	1.06	0.74	0.99	0.87	8.76**	3.39	10.18**	5.22	6.89**
42	P7 x P5	-0.85	0.22	-1.01	0.99	-0.16	4.43*	3.34	9.12**	8.94*	6.46**
43	P8 x P5	0.93	-2.03*	-0.95	-0.51	-0.64	4.35*	8.34	6.40**	11.75**	7.71**
44	P9 x P5	-0.24	0.84	0.13	0.08	0.20	6.73**	13.09*	4.26**	14.28**	9.59**
45	P10 x P5	-1.77*	1.14	1.96*	1.41	0.69	7.82**	5.95	6.71**	10.75*	7.81**
46	P7 x P6	1.82*	-0.30	0.38	-0.39	0.38	6.87**	-3.33	11.93**	5.41	5.22**
47	P8 x P6	-0.41	0.11	0.77	-0.56	-0.02	1.79	7.67	5.21**	2.22	4.22*
48	P9 x P6	-0.57	-0.03	-0.15	-0.98	-0.43	3.18	6.09	0.07	0.08	2.35
49	P10 x P6	-0.43	-0.05	-1.31	0.02	-0.44	12.60**	7.62	2.85	11.22**	8.57**
50	P8 x P7	0.07	-1.39	0.69	-1.23	-0.47	10.46**	5.62	-0.85	15.61**	7.71**
51	P9 x P7	-1.77*	0.14	-0.56	0.02	-0.54	3.18	2.70	-1.65	7.14	2.84
52	P10 x P7	0.04	0.78	-0.40	1.69	0.53	1.60	10.23	10.12**	-37.72**	-3.94*
53	P9 x P8	1.01	0.22	-0.84	-0.48	-0.02	5.76**	-30.63**	4.29**	-30.72**	-12.83**
54	P10 x P8	0.15	1.20	1.66	1.52	1.13*	11.85**	7.89	2.40	10.75*	8.22**
55	P10 x P9	1.32	-0.28	-1.26	-0.23	-0.11	7.57**	7.98	1.93	8.28*	6.44**
Standard error											
	Gi	0.26	0.27	0.25	0.26	0.13	0.54	1.83	0.46	1.24	0.58
	Gi-Gj	0.39	0.40	0.38	0.39	0.19	0.80	2.72	0.68	1.84	0.86
	Sii	0.78	0.81	0.77	0.79	0.39	1.62	5.50	1.37	3.73	1.74
	Sij	0.87	0.90	0.86	0.88	0.44	1.81	6.14	1.53	4.16	1.95
	Sij-ik	1.28	1.33	1.26	1.29	0.65	2.65	9.02	2.25	6.11	2.86
	Sij-Skl	1.22	1.27	1.20	1.23	0.62	2.53	8.60	2.15	5.83	2.73

*, **, Significant at 5% and 1% respectively.

Table 7: GCA and SCA effects for number of female flowers per vine and number of primary branches.

SN	Genotype	Number of female flowers per vine					Number of primary branches				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	-0.21	-0.28	-0.52*	-1.21**	-0.56*	0.10	-0.13	-0.05	-0.16	-0.06
2	P2	-0.13	-0.70**	-0.27	-0.04	-0.28*	-0.02	0.15	0.03	0.07	0.06
3	P3	0.32	0.38	0.45	-1.26**	-0.03	0.06	-0.02	0.20*	0.12	0.09
4	P4	-0.38	-0.39	0.01	0.35	-0.10	-0.00	-0.04	0.06	-0.02	-0.00
5	P5	0.07	0.36	0.45	0.57	0.36*	-0.12*	-0.16	-0.19*	-0.10	-0.14*
6	P6	0.12	0.19	0.31	-0.37	0.06	0.00	0.01	-0.02	-0.04	-0.01
7	P7	0.12	-0.14	-0.47*	-0.01	-0.13	0.01	0.01	-0.08	-0.07	-0.03
8	P8	0.15	-0.14	-0.22	0.41	0.05	-0.08	-0.02	-0.08	0.07	-0.03
9	P9	-0.10	0.16	0.28	0.57	0.23	0.07	0.09	0.09	0.12	0.09
10	P10	0.04	0.58*	-0.02	0.99**	0.40**	-0.02	0.09	0.03	0.01	0.03
11	P2 x P1	-0.86	-1.20	1.41	1.11	0.11	0.28	0.38	0.48	0.53	0.42*
12	P3 x P1	0.69	1.38	0.02	1.00	0.77	0.33	-0.45	0.64*	-0.53	-0.00
13	P4 x P1	0.39	-1.18	-1.20	0.06	-0.48	0.26	-0.09	0.12	-0.06	0.06
14	P5 x P1	-1.39	-0.93	0.35	-0.17	-0.53	0.57**	0.69	0.70*	0.69	0.66**
15	P6 x P1	0.89	0.57	-0.18	-5.56**	-1.07*	-0.35	0.19	-0.80**	0.30	-0.16
16	P7 x P1	0.56	0.24	0.60	-1.25	0.04	0.07	-0.14	-0.08	-0.00	-0.04
17	P8 x P1	1.86*	-0.09	0.35	1.67	0.95	-0.14	-0.12	-0.08	-0.14	-0.12
18	P9 x P1	-0.22	-0.07	1.85*	0.17	0.43	0.41*	0.11	0.09	0.14	0.19
19	P10 x P1	-0.36	0.52	0.82	-2.25	-0.32	0.40*	0.11	0.48	-0.42	0.14
20	P3 x P2	0.28	0.13	0.77	1.50	0.67	0.25	0.27	0.23	0.25	0.25
21	P4 x P2	-0.03	0.91	-0.12	-0.11	0.16	0.45*	0.30	0.37	-0.61	0.13
22	P5 x P2	2.53**	0.49	2.10**	2.00	1.78**	-0.00	-0.59	0.28	0.47	0.04
23	P6 x P2	0.47	0.66	-0.09	0.28	0.33	-0.22	0.24	-0.22	-0.59	-0.19
24	P7 x P2	1.14	1.32	0.02	-0.75	0.43	0.30	0.24	0.51	0.44	0.37
25	P8 x P2	0.78	-0.34	-0.90	0.17	-0.07	-0.07	-0.39	-0.16	0.30	-0.08
26	P9 x P2	-0.64	-0.32	-0.07	-1.33	-0.59	0.21	-0.51	0.34	-0.42	-0.09
27	P10 x P2	-2.44**	-1.40	0.57	-0.75	-1.01*	0.33	0.49	0.06	-0.31	0.14
28	P4 x P3	0.19	-0.18	0.16	-0.56	-0.10	0.20	0.13	0.20	0.66	0.30
29	P5 x P3	0.75	0.74	2.05**	-1.44	0.52	-0.28	0.24	-0.22	0.08	-0.04
30	P6 x P3	0.03	-0.76	0.18	-0.50	-0.26	0.43*	0.08	0.28	0.03	0.20
31	P7 x P3	-0.31	-0.09	0.30	-0.19	-0.07	0.18	-0.26	0.01	0.05	-0.00

32	P8 x P3	-0.33	-0.43	2.05**	-1.61	-0.08	0.41*	0.11	0.67*	-0.09	0.28
33	P9 x P3	-0.75	0.93	-0.45	-2.11	-0.60	0.09	-0.01	0.17	-0.14	0.03
34	P10 x P3	-0.22	0.85	-0.48	-1.53	-0.35	-0.09	-0.34	-0.11	-0.03	-0.14
35	P5 x P4	0.11	0.85	0.82	0.28	0.52	0.35	-0.73	0.59*	-0.11	0.02
36	P6 x P4	-1.28	-0.65	1.30	0.22	-0.10	-0.34	-0.23	-0.24	0.50	-0.08
37	P7 x P4	0.06	0.35	0.41	2.19	0.75	0.01	0.77	0.14	-0.14	0.20
38	P8 x P4	0.03	0.02	0.49	-3.22*	-0.67	0.27	0.13	0.14	0.05	0.15
39	P9 x P4	1.61	0.38	-0.01	0.61	0.65	-0.08	0.36	-0.02	0.33	0.15
40	P10 x P4	-1.53	-0.37	1.63*	0.19	-0.02	0.48*	-0.31	0.70*	-0.22	0.16
41	P6 x P5	0.94	-0.07	-0.15	3.00*	0.93	0.17	0.22	0.34	-0.42	0.08
42	P7 x P5	-1.06	-0.73	-0.37	-1.36	-0.88	0.20	-0.12	0.39	-0.72	-0.06
43	P8 x P5	-0.42	-1.40	0.05	-1.11	-0.72	-0.38	0.24	-0.27	0.14	-0.07
44	P9 x P5	-0.17	0.63	1.55*	1.39	0.85	0.53**	0.13	0.56	0.08	0.33
45	P10 x P5	0.03	1.55	-1.15	-0.69	-0.07	-0.08	0.47	-0.05	0.53	0.22
46	P7 x P6	2.56**	0.77	2.43**	1.58	1.84**	0.31	-0.62	0.56	-0.45	-0.05
47	P8 x P6	-1.14	0.10	1.18	0.17	0.08	0.07	0.08	-0.11	0.08	0.03
48	P9 x P6	1.11	-0.20	-0.32	-1.67	-0.27	-0.02	-0.03	0.06	0.03	0.01
49	P10 x P6	0.64	0.05	-1.01	0.58	0.06	0.51**	-0.03	0.45	0.14	0.26
50	P8 x P7	-0.14	-0.57	0.63	-1.19	-0.32	-0.01	0.08	-0.05	0.11	0.03
51	P9 x P7	0.44	0.13	0.46	-0.03	0.25	0.27	-0.37	0.45	-0.28	0.02
52	P10 x P7	0.97	-0.29	1.77*	3.89**	1.59**	-0.54**	0.30	-0.49	0.50	-0.06
53	P9 x P8	-1.25	0.80	1.21	3.22*	0.99*	-0.21	-0.34	-0.22	-0.42	-0.29
54	P10 x P8	0.28	-0.29	-0.48	1.81	0.33	0.55**	-0.01	0.84**	0.03	0.35
55	P10 x P9	0.53	0.74	-0.98	2.97*	0.81	0.57**	0.22	0.67*	0.30	0.44*
Standard error											
	Gi	0.27	0.26	0.23	0.37	0.14	0.06	0.14	0.09	0.14	0.06
	Gi-Gj	0.40	0.39	0.34	0.55	0.21	0.09	0.21	0.13	0.21	0.08
	Sü	0.80	0.78	0.70	1.11	0.43	0.17	0.43	0.26	0.42	0.17
	Sij	0.90	0.87	0.78	1.23	0.48	0.19	0.48	0.29	0.47	0.19
	Sij-ik	1.32	1.28	1.14	1.81	0.71	0.28	0.71	0.43	0.69	0.28
	Sij-Skl	1.26	1.22	1.09	1.73	0.67	0.27	0.67	0.41	0.66	0.27

*, **, Significant at 5% and 1% respectively.

Table 8: GCA and SCA effects for number of fruits per vine and fruit length (cm).

SN	Genotype	Number of fruits per vine					Fruit length				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	-0.04	-0.10	-0.22	-0.68*	-0.26*	-0.12	-1.41**	-0.68**	-0.66**	-0.72*
2	P2	-0.23	-0.35	0.00	-0.43	-0.25	0.21	-0.41	-0.38*	-0.79**	-0.34*
3	P3	0.18	0.40	0.25	-0.82**	0.00	-0.15	-0.83**	0.37*	-0.04	-0.16
4	P4	-0.23	-0.24	0.17	-0.34	-0.16	-0.57	0.95**	0.66**	-0.27	0.19
5	P5	0.35	0.34	0.25	0.35	0.32*	-0.29	-0.91**	0.56**	0.26	-0.09
6	P6	0.04	0.04	0.03	-0.26	-0.04	0.38	0.03	-0.27	-0.35	-0.05
7	P7	-0.26	-0.27	-0.22	0.16	-0.15	-0.51	0.70**	-0.37*	0.43	0.06
8	P8	-0.04	-0.04	-0.64**	0.57*	-0.04	-0.01	0.64*	-0.42*	0.40	0.15
9	P9	0.10	0.09	0.36	0.32	0.22	0.66	0.34	0.54**	0.54*	0.52**
10	P10	0.13	0.12	0.03	1.13**	0.35**	0.41	0.89**	-0.01	0.48	0.44**
11	P2 x P1	-1.29	-1.11	0.19	0.52	-0.42	-0.10	-0.63	1.94**	1.67*	0.72
12	P3 x P1	0.96	0.80	-0.06	-0.76	0.24	2.26	1.79*	1.39*	0.59	1.51**
13	P4 x P1	-0.62	-0.56	-0.31	0.43	-0.26	2.01	0.35	1.94**	-1.85*	0.61
14	P5 x P1	-0.87	-0.81	0.94	1.07	0.08	1.40	-0.79	0.86	1.29	0.69
15	P6 x P1	1.10	1.16	0.16	-5.65**	-0.80	1.40	-1.07	0.40	-0.77	-0.01
16	P7 x P1	-0.59	-0.53	0.08	1.93*	0.22	-0.05	-0.74	1.03	-0.21	0.01
17	P8 x P1	-0.48	-0.42	1.83**	4.18**	1.28**	-0.55	0.32	1.18	-0.52	0.11
18	P9 x P1	0.71	0.78	0.83	-0.23	0.52	-0.21	-0.38	0.56	1.34	0.33
19	P10 x P1	0.69	0.75	0.83	-3.04**	-0.19	0.04	-1.60	1.10	-0.60	-0.27
20	P3 x P2	-0.51	-0.61	0.39	0.66	-0.02	0.59	-1.21	0.86	-1.94*	-0.42
21	P4 x P2	-0.42	-0.31	0.80	0.52	0.15	0.34	2.01*	-0.13	1.95*	1.05*
22	P5 x P2	-0.34	-0.22	-0.28	-0.84	-0.42	0.07	0.87	-1.60**	-0.24	-0.23
23	P6 x P2	0.63	0.75	0.94	0.10	0.61	1.07	1.93*	-0.50	-1.63	0.22
24	P7 x P2	-0.06	0.05	1.19	0.35	0.38	1.62	1.26	-0.80	0.92	0.75

25	P8 x P2	1.71	1.83	-0.39	-0.07	0.77	0.79	-1.68	-0.75	-0.38	-0.51
26	P9 x P2	0.24	0.36	0.28	-0.48	0.10	0.79	-1.71*	1.56*	-1.19	-0.14
27	P10 x P2	-1.12	-1.00	0.94	-0.62	-0.45	-0.96	-1.60	1.27*	2.54**	0.31
28	P4 x P3	0.16	-0.06	-0.11	0.24	0.06	1.37	0.10	-0.54	3.20**	1.03*
29	P5 x P3	1.24	1.03	0.80	-0.79	0.57	1.09	1.29	0.49	1.01	0.97*
30	P6 x P3	0.88	0.66	-0.64	-0.18	0.18	-1.24	-1.65	0.69	0.95	-0.31
31	P7 x P3	0.52	0.30	0.94	-0.26	0.38	-1.02	1.01	0.75	-0.49	0.06
32	P8 x P3	0.30	0.08	2.03**	-2.68**	-0.07	-2.52*	-0.27	1.14	0.20	-0.36
33	P9 x P3	-1.17	-1.39	1.03	-1.76	-0.83	2.15	-0.63	-0.65	0.73	0.40
34	P10 x P3	0.13	-0.09	0.69	-1.90*	-0.29	0.73	2.48**	-0.57	-0.88	0.44
35	P5 x P4	0.66	0.66	0.55	1.41	0.82	-1.49	3.18**	-0.77	-1.10	-0.05
36	P6 x P4	-1.70	-1.70	0.44	-0.65	-0.90*	0.84	1.57	0.90	-1.16	0.54
37	P7 x P4	0.60	0.61	0.69	-0.73	0.29	2.07	-0.77	0.69	1.06	0.76
38	P8 x P4	0.71	0.72	0.78	-4.15**	-0.48	-0.43	-1.38	1.38*	1.09	0.16
39	P9 x P4	0.91	0.91	0.11	0.10	0.51	-0.77	0.26	0.36	-2.05*	-0.55
40	P10 x P4	-0.79	-0.78	1.11	-1.37	-0.46	-0.85	0.71	0.77	1.34	0.49
41	P6 x P5	-0.62	-0.61	0.69	4.32**	0.95*	2.23	-0.57	1.03	2.31**	1.25**
42	P7 x P5	0.02	0.03	0.94	-0.76	0.06	-1.55	-1.24	1.66**	1.54	0.10
43	P8 x P5	-0.87	-0.86	1.03	-2.18*	-0.72	1.62	0.82	2.01**	-0.44	1.00*
44	P9 x P5	-0.34	-0.34	0.69	-1.59	-0.39	0.95	3.79**	0.45	2.09*	1.82**
45	P10 x P5	0.96	0.97	-0.31	-2.07*	-0.11	0.54	-0.77	1.30*	-1.85*	-0.20
46	P7 x P6	0.66	0.66	0.16	-1.15	0.08	-0.21	-0.52	0.06	-0.19	-0.21
47	P8 x P6	0.44	0.44	1.58*	-1.23	0.31	0.29	-0.46	0.11	-0.16	-0.06
48	P9 x P6	0.63	0.64	0.58	-0.98	0.22	1.29	1.18	0.85	1.04	1.09*
49	P10 x P6	-0.06	-0.06	0.91	0.88	0.42	-0.13	2.62**	1.80**	3.09**	1.85**
50	P8 x P7	-0.59	-0.59	1.83**	-1.65	-0.25	1.18	1.21	0.37	1.06	0.95*
51	P9 x P7	0.60	0.61	0.83	-1.07	0.24	0.51	1.18	0.78	1.26	0.93*
52	P10 x P7	-0.42	-0.42	0.50	4.46**	1.03*	2.09	0.96	0.29	1.65	1.25**
53	P9 x P8	-0.95	-0.95	-0.09	3.85**	0.47	1.34	1.90*	-0.24	1.29	1.07*
54	P10 x P8	0.02	0.03	-0.42	2.71**	0.58	0.93	1.01	1.51*	1.01	1.11*
55	P10 x P9	0.88	0.89	-1.42*	4.63**	1.24**	1.26	0.65	0.26	1.20	0.84
Standard error											
	Gi	0.28	0.28	0.19	0.28	0.13	0.35	0.25	0.18	0.25	0.13
	Gi-Gj	0.42	0.42	0.29	0.42	0.20	0.52	0.38	0.27	0.37	0.20
	Sii	0.86	0.84	0.58	0.85	0.40	1.05	0.76	0.54	0.75	0.40
	Sij	0.96	0.94	0.64	0.95	0.44	1.17	0.85	0.61	0.84	0.45
	Sij-ik	1.41	1.38	0.95	1.40	0.65	1.73	1.25	0.89	1.23	0.65
	Sij-Skl	1.34	1.32	0.90	1.33	0.62	1.65	1.19	0.85	1.17	0.62

*, ** Significant at 5% and 1% respectively.

Table 9: GCA and SCA effects for fruit weight (g) and fruit diameter (cm).

SN	Genotype	Fruit weight (g)					Fruit diameter (cm)				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	9.69**	8.82**	6.84**	8.51**	8.46**	0.01	-0.22**	-0.03	-0.20**	-0.11*
2	P2	7.16**	6.21**	7.54**	8.06**	7.24**	-0.11*	-0.05	0.05	0.01	-0.03
3	P3	3.83**	2.90**	3.23**	4.76**	3.68**	0.10	0.14**	0.06	0.07	0.09**
4	P4	2.38**	2.15**	2.73**	0.45	1.93**	-0.27**	-0.06	-0.11*	-0.03	-0.12*
5	P5	-4.51**	-3.85**	-6.24**	-3.38**	-4.49*	0.01	-0.15**	-0.03	-0.36**	-0.13*
6	P6	-4.23**	-4.32**	-3.91**	-2.99**	-3.86*	-0.01	-0.04	-0.05	0.05	-0.01
7	P7	-7.89**	-7.77**	-5.74**	-3.55**	-6.24*	0.04	0.13*	-0.00	-0.04	0.03
8	P8	0.41	0.90	1.21	4.09**	1.65**	0.06	0.10	0.02	0.07	0.06*
9	P9	1.63*	3.15**	1.59*	-1.24	1.28**	0.10	0.11*	0.06	0.40**	0.17**
10	P10	-8.48**	-8.18**	-7.27**	-14.69**	-9.65*	0.08	0.06	0.03	0.03	0.05
11	P2 x P1	-10.95**	-15.92**	-5.16*	-4.41*	-9.11**	0.54**	-0.71**	0.38*	0.40*	0.15
12	P3 x P1	7.05**	2.39	-6.52**	-7.44**	-1.13	0.33	0.27	0.36	-0.82**	0.03
13	P4 x P1	-8.17**	-8.20**	-6.69**	-2.80	-6.46**	0.20	-0.80**	0.03	0.44*	-0.03
14	P5 x P1	16.39**	19.80**	-5.38*	-5.96**	6.21**	0.18	0.82**	0.22	-0.50**	0.18*
15	P6 x P1	4.44	4.94*	6.29**	1.98	4.41**	-0.29	0.25	-0.26	0.62**	0.08
16	P7 x P1	3.44	1.39	5.12*	1.20	2.79*	0.06	-0.19	0.09	-0.52**	-0.14
17	P8 x P1	15.80**	15.72**	18.51**	12.56**	15.65**	-0.07	0.51**	-0.03	0.14	0.14

18	P9 x P1	9.58**	8.80**	11.79**	12.56**	10.68**	0.19	0.60**	0.23	0.35	0.34**
19	P10 x P1	-5.97*	-2.53	-6.35**	4.01	-2.71*	0.15	0.68**	0.19	0.68**	0.42**
20	P3 x P2	-5.75*	-9.00**	-1.55	-5.66**	-5.49**	0.45*	0.36*	0.28	0.34	0.36**
21	P4 x P2	9.69**	12.41**	5.29*	3.31	7.68**	-1.52**	0.09	0.55**	-0.76**	-0.41**
22	P5 x P2	2.91	3.75	6.92**	4.15	4.43**	-0.09	-0.42*	-0.26	-0.23	-0.25**
23	P6 x P2	2.97	7.55**	2.92	0.76	3.55**	-0.14	-0.03	-0.30	-0.15	-0.15
24	P7 x P2	-2.36	-0.34	-2.91	-1.69	-1.82	0.51**	0.23	0.35	0.38*	0.37**
25	P8 x P2	-5.00*	-2.67	-4.85*	-4.99*	-4.38**	0.49**	0.30	0.32	0.30	0.35**
26	P9 x P2	7.78**	10.08**	5.09*	6.01**	7.24**	-0.32	0.39*	-0.49**	0.08	-0.08
27	P10 x P2	7.55**	9.41**	2.62	11.79**	7.84**	0.34	0.57**	0.18	0.58**	0.42**
28	P4 x P3	-7.97**	-7.95**	-6.41**	2.29	-5.01**	0.24	-0.10	0.08	-0.02	0.05
29	P5 x P3	18.58**	16.72**	17.56**	14.12**	16.75**	-0.17	-0.14	-0.14	0.17	-0.07
30	P6 x P3	12.97**	11.19**	14.90**	8.40**	11.86**	0.31	0.15	0.35	0.16	0.24**
31	P7 x P3	0.64	1.30	-2.27	-3.05	-0.84	0.16	0.31	0.20	0.59**	0.32**
32	P8 x P3	1.33	0.64	-1.55	3.98	1.10	0.44*	0.14	0.48*	0.28	0.34**
33	P9 x P3	-13.22**	-11.61**	-14.60**	-18.69**	-14.53**	0.00	0.24	0.04	0.05	0.08
34	P10 x P3	-15.45**	-15.61**	-14.41**	-12.58**	-14.51**	-0.24	-0.39*	-0.20	-0.25	-0.27**
35	P5 x P4	6.03*	4.14	9.06**	11.42**	7.66**	0.13	-0.01	-0.04	0.21	0.07
36	P6 x P4	6.08*	3.94	6.73**	11.37**	7.03**	0.79**	-0.05	0.62**	0.19	0.39**
37	P7 x P4	-1.59	-2.28	-0.44	0.92	-0.84	0.14	0.38*	-0.03	-0.72**	-0.06
38	P8 x P4	-5.89*	-3.95	-9.38**	-8.71**	-6.98**	-0.35	-0.29	-0.52**	-0.16	-0.33**
39	P9 x P4	0.89	0.14	1.23	7.62**	2.47*	0.27	0.00	0.11	0.12	0.12
40	P10 x P4	-14.00**	-15.86**	-13.58**	-4.60*	-12.01**	0.67**	-0.16	0.50**	0.48**	0.37**
41	P6 x P5	8.64**	6.61**	11.04**	12.87**	9.79**	0.34	0.58**	0.37*	0.72**	0.50**
42	P7 x P5	-0.36	1.39	-2.46	-4.24*	-1.42	0.25	0.47**	0.29	0.28	0.32**
43	P8 x P5	-7.67**	-5.61*	-10.08**	-13.55**	-9.23**	0.36	0.50**	0.40*	0.37*	0.41**
44	P9 x P5	5.78*	3.14	9.54**	12.79**	7.81**	0.29	-0.54**	0.33	-0.26	-0.05
45	P10 x P5	-26.78**	-26.20**	-18.27**	-10.10**	-20.34**	0.08	-0.23	0.12	0.04	0.00
46	P7 x P6	11.69**	13.19**	11.20**	12.70**	12.20**	0.14	0.09	0.18	0.20	0.15
47	P8 x P6	5.72*	6.19**	8.59**	6.40**	6.72**	-0.11	-0.47**	-0.08	-0.51**	-0.29**
48	P9 x P6	-24.17**	-24.06**	-21.80**	-15.60**	-21.41**	0.04	0.32	0.08	-0.04	0.10
49	P10 x P6	-6.39**	-7.72**	-7.27**	-4.49*	-6.47**	0.27	-0.37*	0.31	-0.40*	-0.05
50	P8 x P7	10.05**	6.97**	9.42**	5.29*	7.93**	0.20	-0.38*	0.24	-0.15	-0.02
51	P9 x P7	2.16	1.72	0.04	6.29**	2.55*	0.26	0.24	0.30	0.16	0.24**
52	P10 x P7	-4.39	-3.28	-5.77*	0.06	-3.34**	-0.18	-0.34*	-0.14	-0.11	-0.19*
53	P9 x P8	-21.81**	-27.61**	-25.58**	-28.35**	-25.84**	0.07	0.04	0.11	-0.19	0.01
54	P10 x P8	-13.36**	-9.61**	-9.38**	-2.58	-8.73**	0.20	0.02	0.24	0.11	0.14
55	P10 x P9	19.75**	19.14**	17.56**	-2.58	13.47**	0.13	0.11	0.16	-0.11	0.07
Standard error											
	Gi	0.71	0.65	0.69	0.63	0.34	0.05	0.05	0.05	0.05	0.03
	Gi-Gj	1.06	0.97	1.03	0.94	0.50	0.08	0.08	0.08	0.08	0.04
	Sii	2.14	1.96	2.08	1.90	1.01	0.17	0.16	0.17	0.16	0.08
	Sij	2.39	2.19	2.32	2.11	1.13	0.18	0.17	0.18	0.18	0.09
	Sij-ik	3.51	3.22	3.41	3.11	1.66	0.27	0.25	0.27	0.26	0.13
	Sij-Skl	3.35	3.07	3.25	2.96	1.58	0.26	0.24	0.26	0.25	0.13

*, ** Significant at 5% and 1% respectively.

Table 10: GCA and SCA effects for specific gravity (g/cc) and number of seeds per fruit.

SN	Genotype	Specific gravity (g/cc)					Number of seeds per fruit				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	0.00	0.00	-0.00	0.00	0.00	1.24**	1.37**	1.81**	1.77**	1.55**
2	P2	-0.00	0.00	0.01	-0.00	0.00	-1.78**	-0.77**	-2.36**	-1.62**	-1.63*
3	P3	-0.01*	0.00	0.00	-0.01*	-0.00	-1.42**	0.78**	1.01**	-1.65**	-0.32*
4	P4	-0.00	-0.01**	-0.00	-0.00	-0.01*	-2.26**	-1.24**	-1.58**	-0.40	-1.37*
5	P5	0.01**	0.02**	0.01**	0.01**	0.01**	-0.23	-1.72**	-0.38	-0.23	-0.64*
6	P6	0.01**	0.01*	0.00	0.01**	0.01**	1.99**	0.92**	-1.86**	1.18**	0.56**
7	P7	-0.00	0.00	-0.02**	-0.00	-0.00*	1.77**	0.31	0.39	1.10**	0.89**
8	P8	-0.01*	-0.01**	-0.01	-0.01*	-0.01*	0.99**	-1.08**	0.59**	-0.40	0.03
9	P9	-0.00	-0.00	-0.01*	-0.00	-0.00*	-0.48	0.28	1.39**	-0.21	0.25*
10	P10	-0.01*	-0.01**	0.01**	-0.01*	-0.00	0.16	1.14**	0.98**	0.46	0.69**
11	P2 x P1	0.04**	0.04**	0.04**	0.04**	0.04**	-2.13*	-2.89**	2.85**	-2.46**	-1.16**

12	P3 x P1	0.03**	0.05**	0.03**	0.03**	0.04**	0.51	0.22	3.49**	2.23**	1.61**
13	P4 x P1	0.03**	0.04**	0.03**	0.03**	0.04**	4.34**	6.25**	6.74**	4.98**	5.58**
14	P5 x P1	0.02*	0.01	-0.03**	0.02*	0.00	5.31**	7.39**	-0.79	5.48**	4.35**
15	P6 x P1	-0.03**	-0.03**	-0.05**	-0.03**	-0.03**	-2.58**	-1.59	-0.31	-2.27**	-1.69**
16	P7 x P1	-0.05**	-0.05**	-0.01	-0.05**	-0.04**	-3.36**	-1.97*	-0.90	-3.18**	-2.35**
17	P8 x P1	-0.02	-0.02	0.00	-0.02	-0.01**	-0.91	1.08	1.91**	-0.02	0.52
18	P9 x P1	-0.01	-0.00	0.01	-0.01	-0.00	3.56**	2.72**	3.10**	2.79**	3.04**
19	P10 x P1	0.00	0.00	-0.01	0.00	-0.00	4.92**	0.86	0.52	4.12**	2.61**
20	P3 x P2	0.01	0.00	0.02*	0.01	0.01*	6.53**	6.36**	1.66*	6.62**	5.29**
21	P4 x P2	0.02*	0.04**	0.03**	0.02*	0.03**	2.70**	8.72**	1.24	2.37**	3.76**
22	P5 x P2	0.02*	0.01	0.02	0.02*	0.02**	8.67**	-2.47**	-2.29**	8.21**	3.03**
23	P6 x P2	0.02**	0.03**	0.01	0.02**	0.02**	0.78	-5.45**	-1.48*	1.46	-1.17**
24	P7 x P2	0.03**	0.01	-0.01	0.03**	0.02**	-0.66	-5.17**	2.27**	0.54	-0.76
25	P8 x P2	-0.01	-0.01	-0.02	-0.01	-0.01*	-2.22**	-1.78*	1.41	-1.63*	-1.05**
26	P9 x P2	-0.04**	-0.01	-0.01	-0.04**	-0.03**	-4.74**	0.86	-0.40	-5.15**	-2.36**
27	P10 x P2	0.01	0.00	0.00	0.01	0.00	-3.38**	6.00**	-3.31**	-3.82**	-1.13**
28	P4 x P3	0.01	0.04**	0.03**	0.01	0.02**	-1.66*	0.83	-3.12**	-3.60**	-1.89**
29	P5 x P3	0.04**	0.01	-0.00	0.04**	0.02**	-3.69**	4.30**	-2.98**	2.23**	-0.03
30	P6 x P3	-0.02*	0.00	0.03**	-0.02*	-0.00	-6.24**	-4.34**	-1.84*	0.15	-3.07**
31	P7 x P3	0.04**	0.03**	-0.02*	0.04**	0.02**	-4.02**	5.28**	1.91**	-0.43	0.68
32	P8 x P3	-0.01	-0.03*	-0.03**	-0.01	-0.02**	1.76*	2.33**	-1.29	0.73	0.88*
33	P9 x P3	-0.04**	-0.03**	-0.01	-0.04**	-0.03**	5.56**	-0.03	3.91**	-2.79**	1.66**
34	P10 x P3	0.00	-0.01	-0.02	0.00	-0.01	7.59**	-1.89*	-1.67*	-2.46**	0.39
35	P5 x P4	-0.02**	-0.01	-0.03**	-0.02**	-0.02**	2.81**	-0.67	-1.73*	-1.68*	-0.32
36	P6 x P4	0.00	-0.02	-0.05**	0.00	-0.02**	3.59**	-6.64**	-2.26**	-3.43**	-2.19**
37	P7 x P4	-0.00	-0.04**	-0.02	-0.00	-0.02**	-2.19**	-4.03**	-4.17**	2.65**	-1.94**
38	P8 x P4	0.02*	-0.01	-0.07**	0.02*	-0.01*	-1.08	-3.31**	-4.37**	1.15	-1.90**
39	P9 x P4	-0.01	-0.06**	-0.01	-0.01	-0.02**	-2.61**	1.33	-4.84**	6.96**	0.21
40	P10 x P4	-0.03**	0.00	-0.01	-0.03**	-0.02**	-3.58**	-0.20	-5.76**	0.29	-2.31**
41	P6 x P5	-0.04**	-0.02	0.02*	-0.04**	-0.02**	-1.44	-0.17	-0.79	-4.60**	-1.75**
42	P7 x P5	-0.07**	0.01	0.01	-0.07**	-0.03**	-1.88*	-3.22**	-0.70	-6.52**	-3.08**
43	P8 x P5	-0.01	-0.00	0.00	-0.01	-0.01	-2.11*	-0.84	0.77	-4.68**	-1.71**
44	P9 x P5	0.01	-0.01	0.01	0.01	0.00	-3.97**	-0.86	5.63**	-4.54**	-0.94*
45	P10 x P5	0.04**	0.00	-0.01	0.04**	0.02**	4.73**	2.94**	0.71	4.46**	3.21**
46	P7 x P6	0.01	0.01	0.01	0.01	0.01	2.23**	5.14**	0.44	3.40**	2.80**
47	P8 x P6	0.01	-0.00	0.00	0.01	0.01	2.67**	7.19**	2.24**	0.57	3.17**
48	P9 x P6	0.01	0.00	-0.00	0.01	0.01	4.48**	4.50**	-1.23	-1.96*	1.45**
49	P10 x P6	0.02*	-0.00	0.01	0.02*	0.01**	3.84**	4.30**	7.19**	-0.63	3.68**
50	P8 x P7	0.01	0.03**	0.01	0.01	0.02**	3.56**	-0.86	4.66**	-2.35**	1.25**
51	P9 x P7	0.01	-0.00	0.00	0.01	0.01	5.03**	-0.22	5.19**	5.46**	3.86**
52	P10 x P7	0.01	-0.01	0.00	0.01	0.00	-3.61**	-0.42	4.27**	4.12**	1.09**
53	P9 x P8	0.04**	0.02	0.03*	0.04**	0.03**	0.48	-0.17	4.66**	7.62**	3.15**
54	P10 x P8	0.02*	0.03**	-0.02	0.02*	0.01**	-2.16**	1.30	4.41**	6.29**	2.46**
55	P10 x P9	-0.00	0.01	0.03*	-0.00	0.01	1.64*	4.28**	2.27**	2.10**	2.57**
Standard error											
	Gi	0.00	0.00	0.00	0.00	0.00	0.24	0.24	0.21	0.24	0.12
	Gi-Gj	0.00	0.00	0.00	0.00	0.00	0.36	0.36	0.32	0.35	0.17
	Sii	0.01	0.01	0.01	0.01	0.00	0.74	0.72	0.65	0.71	0.35
	Sij	0.01	0.01	0.01	0.01	0.00	0.82	0.81	0.72	0.79	0.39
	Sij-ik	0.01	0.01	0.01	0.01	0.01	1.21	1.18	1.06	1.16	0.58
	Sij-Skl	0.01	0.01	0.01	0.01	0.01	1.15	1.13	1.01	1.11	0.55

*, ** Significant at 5% and 1% respectively.

Table 11: GCA and SCA effects for yield (kg) per vine and vine length (cm).

SN	Genotype	Yield per vine (kg)					Vine length (cm)				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	0.19**	0.17**	0.19**	0.12**	0.17**	11.54**	11.74**	0.49	-5.01**	4.69*
2	P2	0.12**	0.10**	0.13**	0.13**	0.12**	14.57**	22.38**	13.47*	-6.98**	10.86**
3	P3	0.09**	0.10**	0.10**	0.04	0.08**	29.16**	25.19**	49.88**	0.82	26.26**
4	P4	0.03	0.02	0.05*	-0.01	0.02	-22.43**	-16.48**	-12.92*	0.02	-12.95*
5	P5	-0.07*	-0.05	-0.06**	-0.03	-0.05*	-7.79*	-14.26**	-17.76**	0.02	-9.95*

6	P6	-0.08**	-0.08**	-0.09**	-0.09**	-0.08*	-5.01	-3.20	3.63	-1.84**	-1.61
7	P7	-0.18**	-0.18**	-0.14**	-0.06*	-0.14*	-4.43	-7.51*	-6.26	0.68	-4.38*
8	P8	0.01	0.01	-0.05*	0.13**	0.02	-9.82*	-10.56**	-8.48	5.16**	-5.92*
9	P9	0.04	0.07*	0.04*	-0.01	0.04**	3.93	-0.70	-18.76**	5.41**	-2.53
10	P10	-0.16**	-0.16**	-0.17**	-0.22**	-0.18*	-9.73*	-6.62*	-3.31	1.74*	-4.48*
11	P2 x P1	-0.34**	-0.41**	-0.16*	-0.05	-0.24**	-2.19	-23.10*	5.67	-16.41**	-9.01
12	P3 x P1	0.23*	0.13	0.20**	-0.23**	0.08	-88.11**	-91.58**	-48.08*	-8.22**	-58.99**
13	P4 x P1	-0.22*	-0.22*	-0.23**	-0.03	-0.17**	-29.52*	-26.58**	-66.28**	17.59**	-26.20**
14	P5 x P1	0.25*	0.34**	0.48**	-0.05	0.26**	37.84**	39.87**	13.56	25.92**	29.30**
15	P6 x P1	0.18	0.20*	0.06	-0.43**	0.00	16.73	20.81*	0.50	12.78**	12.71
16	P7 x P1	0.00	-0.02	0.02	0.18*	0.05	-19.86	-13.55	-1.61	15.26**	-4.94
17	P8 x P1	0.26**	0.27**	0.47**	0.67**	0.42**	-6.13	12.84	30.95	16.45**	13.53*
18	P9 x P1	0.26**	0.25**	0.25**	0.22**	0.25**	-5.22	1.65	-61.11**	18.20**	-11.62
19	P10 x P1	-0.06	0.01	-0.13	-0.13	-0.08	23.45	26.56**	51.11*	-13.47**	21.91**
20	P3 x P2	-0.17	-0.23*	-0.01	-0.07	-0.12**	30.87*	29.79**	73.28**	-1.58	33.09**
21	P4 x P2	0.14	0.21*	0.20**	0.10	0.16**	14.12	13.79	-5.91	4.89*	6.72
22	P5 x P2	0.03	0.06	0.07	0.01	0.04	30.14*	23.90*	49.25*	-4.77*	24.63**
23	P6 x P2	0.12	0.24*	0.15*	0.03	0.13**	-11.63	-2.83	-46.14*	1.42	-14.79*
24	P7 x P2	-0.05	-0.01	0.04	0.00	-0.00	25.78*	6.48	-29.91	4.23	1.64
25	P8 x P2	0.05	0.10	-0.11	-0.10	-0.01	-23.49	-12.80	11.64	15.42**	-2.31
26	P9 x P2	0.18	0.24*	0.15*	0.09	0.17**	-7.91	4.67	-19.08	17.84**	-1.12
27	P10 x P2	0.06	0.11	0.16*	0.21*	0.13**	4.76	4.26	-15.53	7.17**	0.16
28	P4 x P3	-0.14	-0.17	-0.15*	0.05	-0.10*	7.53	3.65	-45.00*	13.42**	-5.10
29	P5 x P3	0.51**	0.46**	0.36**	0.18*	0.38**	-19.77	-8.91	-44.83*	22.76**	-12.69
30	P6 x P3	0.34**	0.29**	0.22**	0.15	0.25**	48.12**	39.04**	16.45	25.62**	32.30**
31	P7 x P3	0.05	0.04	0.00	-0.08	0.00	77.20**	68.01**	40.67	16.09**	50.49**
32	P8 x P3	0.05	0.01	0.13	-0.17*	0.00	23.92	39.40**	10.22	14.62**	22.04**
33	P9 x P3	-0.36**	-0.36**	-0.24**	-0.45**	-0.35**	64.17**	69.54**	55.84**	0.03	47.39**
34	P10 x P3	-0.31**	-0.34**	-0.26**	-0.34**	-0.31**	34.84**	23.12*	27.06	8.70**	23.43**
35	P5 x P4	0.18	0.15	0.19**	0.34**	0.21**	45.48**	54.42**	52.31*	-1.44	37.69**
36	P6 x P4	-0.03	-0.06	0.18**	0.18*	0.07	47.37**	61.04**	21.25	-7.91**	30.44**
37	P7 x P4	0.02	-0.00	0.06	-0.03	0.01	-51.55**	-61.99**	-58.53**	-15.11**	-46.79**
38	P8 x P4	-0.06	-0.02	-0.10	-0.47**	-0.16**	6.51	10.06	-10.30	13.42**	4.92
39	P9 x P4	0.10	0.08	0.05	0.17*	0.10*	18.76	18.20	-1.36	20.51**	14.03*
40	P10 x P4	-0.32**	-0.36**	-0.18*	-0.17*	-0.26**	8.42	10.12	-1.80	17.51**	8.56
41	P6 x P5	0.12	0.08	0.23**	0.62**	0.26**	-35.27**	-45.52**	-32.91	1.09	-28.15**
42	P7 x P5	-0.01	0.03	-0.05	-0.13	-0.04	-6.52	13.79	-5.36	6.89**	2.20
43	P8 x P5	-0.20*	-0.18	-0.17*	-0.41**	-0.24**	13.20	18.17	0.86	16.42**	12.16
44	P9 x P5	0.09	0.04	0.21**	0.14	0.12**	-28.55*	-83.02**	16.81	7.17**	-21.90**
45	P10 x P5	-0.51**	-0.51**	-0.43**	-0.32**	-0.44**	-11.55	-0.44	15.36	6.84**	2.55
46	P7 x P6	0.28**	0.31**	0.23**	0.17*	0.25**	22.70	22.06*	-1.08	0.76	11.11
47	P8 x P6	0.15	0.16	0.32**	0.03	0.17**	16.42	5.79	15.47	-1.38	9.07
48	P9 x P6	-0.46**	-0.46**	-0.40**	-0.34**	-0.41**	8.67	4.26	28.42	1.03	10.60
49	P10 x P6	-0.14	-0.16	-0.07	-0.03	-0.10*	5.67	5.17	-18.03	22.03**	3.71
50	P8 x P7	0.14	0.09	0.36**	-0.03	0.14**	-29.83*	-46.24**	-28.97	5.09*	-24.99**
51	P9 x P7	0.09	0.08	0.07	0.06	0.08	-38.91**	-18.10	-20.69	9.84**	-16.97*
52	P10 x P7	-0.11	-0.09	-0.07	0.26**	-0.00	0.09	5.48	-16.80	14.51**	0.82
53	P9 x P8	-0.50**	-0.63**	-0.49**	-0.37**	-0.50**	-57.19**	-50.71**	-56.80**	-12.63**	-44.34**
54	P10 x P8	-0.26**	-0.20*	-0.17*	0.12	-0.13**	-31.86*	-36.13**	-37.58	-14.63**	-30.05**
55	P10 x P9	0.48**	0.49**	0.25**	0.22**	0.36**	-68.61**	-69.99**	-50.97*	17.12**	-43.11**
Standard error											
	Gi	0.03	0.03	0.02	0.02	0.01	3.84	2.99	6.14	0.69	1.97
	Gi-Gj	0.04	0.04	0.03	0.04	0.02	5.73	4.46	9.16	1.03	2.93
	Sii	0.09	0.09	0.06	0.07	0.04	11.58	9.03	18.53	2.09	5.93
	Sij	0.10	0.10	0.07	0.08	0.04	12.92	10.07	20.67	2.33	6.62
	Sij-ik	0.14	0.14	0.10	0.12	0.06	18.99	14.80	30.38	3.43	9.73
	Sij-Skl	0.14	0.14	0.10	0.11	0.06	18.10	14.11	28.96	3.27	9.28

*, ** Significant at 5% and 1% respectively.

Table 12: GCA and SCA effects for days to maturity and total soluble solids (%).

SN	Genotype	Days to maturity					Total soluble solids				
		E1	E2	E3	E4	Pool	E1	E2	E3	E4	Pool
1	P1	-1.97**	1.01*	-1.88**	0.39	-0.61*	0.06**	0.06**	0.06**	0.05*	0.06**
2	P2	-2.08**	-1.46**	2.67**	0.92*	0.01	0.05**	0.03	-0.00	0.05*	0.03**
3	P3	0.48	0.98*	0.37	-1.41**	0.10	-0.23**	-0.23**	-0.22**	-0.22**	-0.22*
4	P4	0.06	1.37**	1.45**	2.95**	1.46**	-0.05**	0.00	-0.00	-0.05**	-0.03*
5	P5	0.28	0.26	-0.80**	-0.08	-0.08	-0.09**	-0.13**	-0.13**	-0.11**	-0.12*
6	P6	2.59**	-0.49	1.26**	-0.63	0.68**	-0.00	0.03	0.04*	0.00	0.02*
7	P7	0.34	-1.82**	-1.30**	-1.19**	-0.99*	-0.06**	0.01	0.02	-0.05**	-0.02*
8	P8	1.84**	-1.52**	-1.30**	-1.97**	-0.74*	-0.07**	-0.01	0.02	-0.06**	-0.03*
9	P9	-0.61	0.84	-0.74*	-0.66	-0.29	0.17**	0.22**	0.23**	0.18**	0.20**
10	P10	-0.94**	0.82	0.28	1.67**	0.46*	0.22**	0.01	-0.02	0.22**	0.11**
11	P2 x P1	3.87**	1.43	-0.93	3.11*	1.87**	0.10	-0.01	0.07	0.12	0.07*
12	P3 x P1	3.31**	4.32**	6.04**	4.78**	4.61**	0.24**	-0.13*	-0.28**	0.25**	0.02
13	P4 x P1	9.06**	2.27	4.29**	-1.25	3.59**	-0.50**	-0.29**	-0.38**	-0.49**	-0.42**
14	P5 x P1	7.17**	-2.62	4.87**	7.11**	4.13**	-0.21**	-0.29**	-0.26**	-0.36**	-0.28**
15	P6 x P1	-1.13	-9.87**	8.15**	-10.33**	-3.30**	-0.43**	-0.34**	-0.31**	-0.42**	-0.38**
16	P7 x P1	-6.88**	-8.21**	-7.30**	-7.44**	-7.46**	-0.26**	0.21**	0.24**	-0.25**	-0.01
17	P8 x P1	-8.05**	7.15**	-4.96**	-7.00**	-3.21**	0.28**	0.20**	0.17**	0.29**	0.24**
18	P9 x P1	-7.94**	2.13	-5.85**	-0.30	-2.99**	0.01	0.17**	0.16*	0.02	0.09**
19	P10 x P1	10.40**	-0.51	1.12	3.36*	3.59**	0.16**	-0.16**	-0.13*	0.18**	0.01
20	P3 x P2	3.76**	2.13	2.48*	7.59**	3.99**	0.09	-0.08	-0.07	0.08	0.01
21	P4 x P2	6.51**	3.07*	3.07**	-2.11	2.63**	-0.29**	0.16*	0.18**	-0.29**	-0.06
22	P5 x P2	1.62	2.18	-0.02	-4.08**	-0.07	0.22**	0.36**	0.37**	0.24**	0.30**
23	P6 x P2	7.65**	4.60**	-5.07**	6.81**	3.49**	0.20**	-0.01	0.01	0.19**	0.10**
24	P7 x P2	-0.10	-3.07*	2.82**	6.03**	1.42*	0.06	-0.59**	-0.58**	0.05	-0.27**
25	P8 x P2	-9.27**	-7.37**	5.82**	1.47	-2.34**	-0.54**	0.23**	0.23**	-0.54**	-0.15**
26	P9 x P2	-4.49**	-2.07	3.93**	1.17	-0.37	0.03	0.07	0.09	0.02	0.05
27	P10 x P2	0.51	7.96**	-2.43*	-3.16*	0.72	0.04	-0.34**	-0.73**	0.04	-0.25**
28	P4 x P3	-3.71**	-6.37**	-0.30	0.22	-2.54**	-0.03	-0.08	-0.10	-0.04	-0.06*
29	P5 x P3	5.73**	4.40**	-0.05	3.25*	3.34**	0.00	0.32**	0.29**	0.01	0.15**
30	P6 x P3	4.76**	6.49**	0.23	-0.53	2.74**	0.18**	-0.12	-0.14*	0.16*	0.02
31	P7 x P3	4.67**	1.82	-1.55	-3.64*	0.33	-0.03	-0.26**	-0.29**	-0.05	-0.16**
32	P8 x P3	1.84	6.85**	-5.21**	-3.86**	-0.10	-0.19**	-0.37**	-0.17**	-0.21**	-0.23**
33	P9 x P3	2.62*	3.15*	-6.77**	-0.50	-0.37	-0.56**	0.23**	0.21**	-0.43**	-0.14**
34	P10 x P3	-2.05	-2.15	-3.13**	2.17	-1.29*	0.22**	0.37**	0.39**	0.21**	0.30**
35	P5 x P4	-7.52**	-0.98	1.87	1.22	-1.35*	0.29**	-0.01	-0.02	0.31**	0.14**
36	P6 x P4	-3.83**	-2.23	1.48	-0.55	-1.28*	-0.10	-0.15*	-0.16*	-0.11	-0.13**
37	P7 x P4	3.76**	1.43	1.70	6.00**	3.22**	-0.01	0.40**	0.39**	-0.02	0.19**
38	P8 x P4	5.26**	-3.21*	7.70**	5.45**	3.80**	0.53**	0.26**	0.23**	0.52**	0.39**
39	P9 x P4	6.37**	3.43*	5.82**	-5.53**	2.52**	0.13*	-0.27**	-0.28**	0.12	-0.08*
40	P10 x P4	1.37	4.79**	-4.88**	3.47*	1.19	-0.23**	-0.08	-0.04	-0.22**	-0.14**
41	P6 x P5	-1.38	1.21	-2.93**	-1.19	-1.07	0.03	0.12*	0.10	0.03	0.07*
42	P7 x P5	-1.13	4.88**	-5.05**	-8.30**	-2.40**	0.17**	-0.33**	-0.35**	0.17**	-0.08**
43	P8 x P5	-0.30	-2.10	-7.38**	-3.53*	-3.32**	-0.29**	-0.10	-0.14*	-0.28**	-0.20**
44	P9 x P5	-1.52	-8.12**	-0.27	4.17**	-1.44*	-0.33**	-0.50**	-0.52**	-0.32**	-0.42**
45	P10 x P5	-6.52**	2.90*	8.70**	0.17	1.31*	-0.55**	-0.43**	-0.40**	-0.53**	-0.48**
46	P7 x P6	4.23**	5.96**	-1.43	6.59**	3.84**	-0.49**	0.07	0.05	-0.38**	-0.19**
47	P8 x P6	0.06	2.65	1.57	7.03**	2.83**	0.19**	0.06	0.02	0.17**	0.11**
48	P9 x P6	-0.49	3.96**	-1.99	2.72	1.05	-0.08	-0.24**	-0.25**	-0.10	-0.17**
49	P10 x P6	3.51**	3.99**	-0.02	4.06**	2.88**	-0.20**	0.01	0.03	-0.21**	-0.09**
50	P8 x P7	4.98**	9.65**	7.12**	8.25**	7.50**	0.18**	0.28**	0.24**	0.16*	0.21**
51	P9 x P7	4.76**	-1.37	9.23**	8.95**	5.39**	0.17**	0.21**	0.20**	0.15*	0.18**
52	P10 x P7	2.09	1.65	6.20**	-2.05	1.97**	0.29**	0.33**	0.35**	0.28**	0.31**
53	P9 x P8	-2.74*	-1.68	3.57**	4.06**	0.80	0.25**	0.17**	0.14*	0.23**	0.20**
54	P10 x P8	0.59	1.35	5.54**	-1.28	1.55*	0.23**	0.08	0.09	0.22**	0.16**
55	P10 x P9	0.04	-8.68**	7.65**	0.42	-0.14	-0.31**	-0.18**	-0.16*	-0.32**	-0.24**
	Standard error										
	Gi	0.32	0.44	0.30	0.42	0.19	0.02	0.02	0.02	0.02	0.01
	Gi-Gj	0.47	0.65	0.45	0.62	0.28	0.03	0.03	0.03	0.03	0.01
	Sii	0.95	1.31	0.91	1.25	0.56	0.05	0.05	0.05	0.06	0.03
	Sij	1.06	1.46	1.02	1.40	0.63	0.06	0.06	0.06	0.06	0.03
	Sij-ik	1.56	2.15	1.49	2.05	0.92	0.09	0.09	0.09	0.09	0.05
	Sij-Skl	1.49	2.05	1.43	1.96	0.88	0.09	0.08	0.09	0.09	0.04

*, ** Significant at 5% and 1% respectively.

Table 13: GCA and SCA effects for ascorbic acid (mg/100 g).

SN	Genotype	Ascorbic acid (mg/100 g)				
		E1	E2	E3	E4	Pool
1	P1	-2.10**	-2.19**	-1.82**	-2.10**	-2.05*
2	P2	-1.68**	-1.49**	-1.46**	-1.68**	-1.58*
3	P3	0.07	-0.33*	0.54**	0.07	0.09
4	P4	-0.21	-0.83**	-0.79**	-0.21	-0.51*
5	P5	-0.77**	0.70**	-0.18	-0.77**	-0.25*
6	P6	1.29**	-0.11	-0.29	1.29**	0.55**
7	P7	-0.24	0.87**	-0.04	-0.24	0.09
8	P8	1.48**	0.92**	1.57**	1.48**	1.37**
9	P9	1.18**	0.84**	1.54**	1.18**	1.18**
10	P10	0.98**	1.62**	0.91**	0.98**	1.12**
11	P2 x P1	2.89**	6.27**	8.02**	2.89**	5.01**
12	P3 x P1	4.80**	2.77**	3.35**	4.80**	3.93**
13	P4 x P1	2.75**	-0.40	2.35**	2.75**	1.86**
14	P5 x P1	-0.36	-2.60**	-1.93**	-0.36	-1.31**
15	P6 x P1	-3.09**	-0.79	-2.48**	-3.09**	-2.36**
16	P7 x P1	-0.56	4.57**	-1.73**	-0.56	0.43
17	P8 x P1	4.05**	-1.82**	2.99**	4.05**	2.32**
18	P9 x P1	-1.97**	-1.73**	-3.32**	-1.97**	-2.25**
19	P10 x P1	-1.78**	0.49	-2.68**	-1.78**	-1.44**
20	P3 x P2	1.72**	-3.60**	0.32	1.72**	0.04
21	P4 x P2	-3.34**	-0.76	-3.68**	-3.34**	-2.78**
22	P5 x P2	-0.45	1.71**	-1.95**	-0.45	-0.28
23	P6 x P2	1.50**	3.18**	2.16**	1.50**	2.08**
24	P7 x P2	3.69**	-0.46	2.57**	3.69**	2.37**
25	P8 x P2	-0.70	2.49**	-1.70**	-0.70	-0.15
26	P9 x P2	2.61**	0.24	1.32*	2.61**	1.69**
27	P10 x P2	0.47	-0.21	-0.37	0.47	0.09
28	P4 x P3	0.25	-0.93	-0.34	0.25	-0.19
29	P5 x P3	-1.20*	0.21	-2.95**	-1.20*	-1.28**
30	P6 x P3	-0.59	3.68**	-0.18	-0.59	0.58*
31	P7 x P3	3.61**	1.71**	2.24**	3.61**	2.79**
32	P8 x P3	0.89	2.65**	-0.37	0.89	1.01**
33	P9 x P3	2.19**	3.40**	0.66	2.19**	2.11**
34	P10 x P3	3.05**	0.29	1.96**	3.05**	2.09**
35	P5 x P4	2.75**	-1.62**	2.05**	2.75**	1.48**
36	P6 x P4	-2.64**	2.18**	-1.18	-2.64**	-1.07**
37	P7 x P4	1.89**	2.54**	1.57**	1.89**	1.97**
38	P8 x P4	1.50**	4.15**	1.30*	1.50**	2.11**
39	P9 x P4	3.47**	4.24**	2.99**	3.47**	3.54**
40	P10 x P4	3.66**	2.13**	3.63**	3.66**	3.27**
41	P6 x P5	2.58**	-2.01**	2.88**	2.58**	1.51**
42	P7 x P5	-0.22	2.02**	-1.70**	-0.22	-0.03
43	P8 x P5	3.05**	0.29	1.68**	3.05**	2.02**
44	P9 x P5	1.69**	2.04**	0.05	1.69**	1.37**
45	P10 x P5	3.55**	2.27**	2.35**	3.55**	2.93**
46	P7 x P6	3.72**	3.49**	4.41**	3.72**	3.83**
47	P8 x P6	1.66**	1.77**	2.46**	1.66**	1.89**
48	P9 x P6	0.30	2.18**	0.82	0.30	0.90**
49	P10 x P6	0.83	2.07**	1.80**	0.83	1.38**
50	P8 x P7	2.53**	1.79**	1.55*	2.53**	2.10**
51	P9 x P7	2.83**	-3.79**	1.57**	2.83**	0.86**
52	P10 x P7	-2.64**	1.77**	-3.45**	-2.64**	-1.74**
53	P9 x P8	1.78**	1.49**	0.63	1.78**	1.42**
54	P10 x P8	0.97	-0.29	0.27	0.97	0.48
55	P10 x P9	0.28	0.13	-0.70	0.28	-0.01
	Standard error					
	Gi	0.15	0.15	0.18	0.15	0.08
	Gi-Gj	0.23	0.23	0.26	0.23	0.12
	Sii	0.46	0.46	0.53	0.46	0.24
	Sij	0.52	0.52	0.60	0.52	0.27
	Sij-ik	0.76	0.76	0.88	0.76	0.39
	Sij-Skl	0.72	0.72	0.83	0.72	0.38

*, ** Significant at 5% and 1% respectively.

Collection x IC-85605 exhibited significant and negative SCA effect in each individual environment and pooled over the environments for days to anthesis of first male flower. Whereas, crosses BG-14 x Pusa Do Mausmi in E1 (-4.58), E4 (-3.52) and PEVs (-1.78) and IC-45346 x BG-14 in E2 (-3.60), E3 (-3.98) and PEVs (-2.07) exhibited significant and negative SCA effect in either of two environments and PEVs; hence, these were considered as good specific combiners.

Earliness in days to anthesis of first female flower is a desirable trait; hence, parents and crosses with significant and negative GCA and SCA effect were considered as good general combiner and specific combiner, respectively. Out of ten female parents, only parent MDU-1 {E1 (-0.52), E2 (-0.23), E3 (-1.72) and PEVs (-0.45)} and Green Long {E2 (-1.56), E3 (-0.83), E4 (-0.55) and PEVs (-0.43)} showed significant and negative GCA effect in at least three environments and pooled. Among of 45 crosses, 12 in E1, 10 in E2, 14 in E3, 10 in E4 and 12 in PEVs registered significant and negative estimates of SCA effect. The cross IC-45346 x Green Long exhibited significant and negative SCA effect in each individual environment and pooled over the environments, and the estimates were E1 (-1.00), E2 (-5.36), E3 (-3.04), E4 (-4.17) and PEVs (-3.39); hence, these were considered as good specific combiners. The negative estimates of GCA for days to first female flowering and indicate that these can be utilized in hybridization programmes for developing earliness in bitter gourd it being monoecious with earliness as an important trait [12,13] found similar results in snakegourd and bittergourd, respectively [14,15] also recorded similar genetic structure in bitter gourd.

In present findings parent Solan Hara (P1) showed significant GCA effects in all the environments, which indicated good general combiner for less number of male flowers per plant. The cross Pusa Do Mausmi x Solan Hara exhibited significant and negative SCA effect in each individual environment and pooled over the environments. Whereas, crosses IC 85605 x Solan Hara, BG-14 x PDM, Green Long x Solan Hara and IC 68237x IC 68272-1 showed significant and negative SCA affect either in of two environments and PEVs; hence, these were considered as good specific combiners in two environments. Results pertaining to number of female flower per vine on general combining effects revealed that, parent Solan Collection (P10) showed significant GCA effects in all the environments, which indicated good general combiner for more number of female flowers per plant. SCA effect indicated that the cross IC45346 x IC 85605 (1.84)

and MDU-1x PDM (1.78) exhibited significant and positive SCA effect in each individual environment and pooled over the environments. Whereas, crosses Solan Collection x IC 45346 (1.59) and IC 68237x IC 68272-1 (0.99) showed significant and positive SCA affect either in of two environments and PEVs; hence, these were considered as good specific combiners in two environments. Thus, the above combinations were the best specific combinations to improve the respective characters in bitter gourd found similar results in snake gourd and bitter gourd, respectively.

Out of these, parent IC 68237 (P1) showed significant GCA effects in all the environments, which indicated good general combiner for more number of primary branches per plant. SCA effect indicated that the cross MDU -1 x Solan Hara (0.66) and Solan Collection x IC 68237 (0.40) exhibited significant and positive SCA effect in each individual environment and pooled over the environments. Whereas, crosses IC 85605 x BG 14 and Green Long x PDM showed significant and positive SCA affect either in of two environments and PEVs; hence, these were considered as good specific combiners in two environments.

GCA pertaining to the number of fruit per vine revealed that out of ten parents GCA was significant for parents, MDU-1, IC-68237 & Solan Collection in the entire environment as well as pooled over the environment in desired direction. Out of these, parent IC 68237 (P9) showed significant GCA effects in all the environments, which indicated good general combiner among the parents used in study programme for more number of fruits per vine. SCA on number of fruits per vine indicated that cross Solan Collection x IC 68237 (1.24) exhibited significant and positive SCA effect in each individual environment and pooled over the environments and considered best specific combiner among all the crosses made. High GCA and SCA values of parents and crosses of bitter gourd for these characters have also been reported by [7].

Fruit length directly contributes in the production of bitter gourd. GCA pertaining to the fruit length depicted that out of ten parents significant and positive GCA observed for parents, IC-68237 & Solan Collection in the entire environment as well as pooled over the environment in desired direction, which indicated best general combiner among the parents under studied for more fruits length. Specific Combining Ability (SCA) on fruits length indicated that cross IC 68237 x MDU-1 (1.82) exhibited significant and positive SCA effect in each individual environment and pooled over the environments and considered best specific combiner among all

the crosses made [6,16-18] in Cucumis have also reported significant positive and negative GCA and SCA effects for this trait.

For fruit weight significant and positive GCA observed for parent, Solan Hara, PDM, BG 14, Green Long, IC 68272-1 and IC-68237 in the entire environment as well as pooled over the environment in desired direction. Out of these, parent Solan Hara and PDM showed significant GCA effects in all the environments, which indicated best general combiner among the parents under studied for more fruits weight. Specific Combining Ability (SCA) on fruits weight indicated that cross IC 68237 x MDU-1 (1.82) exhibited significant and positive SCA effect in each individual environment and pooled over the environments and considered best specific combiner among all the crosses made. The positive significant estimates of GCA effects for fruit diameter (cm) varied from 0.06 (P8) to 0.17 (P9) on pooled basis. The inbred lines P9 exhibited significant positive GCA effects in E2, E4 environment as well as on pooled basis. Out of 45 hybrids, sixteen hybrids expressed positive significant SCA effects on pooled basis, with range varied from 0.18 (P5xP1) to 0.50 (P6 x P5). The maximum estimates of positive SCA effects was exhibited by hybrids P6xP4 (0.79) in E1, P5xP1 (0.82) in E2, P6xP4 (0.62) in E3 and P6xP5 (0.72) in E4, (Table 4). For fruit weight significant GCA and SCA effects were also reported by [6,16-19] in Cucumis.

For number of seeds per fruit inbred line P6, P7 and exhibited positive significant GCA effects in majority of the environment as well as on pooled basis. The highest magnitude of positive significant SCA effects was expressed by hybrids P5xP2 (8.67) in E1, P4xP2 (8.72) in E2, P10xP6 (7.19) in E3, P5xP2 (8.21) in E4 and P3xP2 (5.29) on pooled basis for number of seeds per fruit. Similar results of significant GCA and SCA effects were also reported by [17] for number of seeds per fruit in bitter gourd.

The inbred line P1 and P2 exhibited positive significant GCA effects in all the environments as well as over the environment for yield per vine. The estimates of significant positive SCA effects was observed in seventeen hybrids on pooled basis with range varied from 0.12 (P9xP5) to 0.42 (P8xP1). The maximum estimates of positive significant SCA effects was exhibited by hybrid P5xP3 (0.51) in E1, P5xP3 (0.46) in E2, P8 xP1 (0.47) in E3 and P8xP1 (0.67) in E4 environment. These results are in accordance to the [2] who reported non additive type of gene action for yield and yield related traits in their material. However, [14] found that both

additive and non additive gene actions involved in the expression of yield and yield related characters. The differences in the results might have due to the differences in the genetic material studied. The significant GCA and SCA effects for this trait were also reported by [16,17].

Inbred line P2 exhibited significant positive GCA effects in majority of environments as well as pooled analysis for vine length. The significant positive SCA effects was observed hybrid P7 x P3 on pooled basis [6,16,17] were also reported significant GCA and SCA effects for vine length in bitter gourd.

Earliness is a desirable direction for days to maturity. The parental line P8 expressed significant GCA effects in negative direction in majority of environments as well as pooled basis. Eleven hybrids exhibiting negative significant SCA effects on pooled basis with the range of negative significant SCA effects varied from -7.46 (P7 x P1) to -1.28 (P6 x P4). This study reveals that the high SCA effects in these crosses was mainly through additive gene effects. Therefore, the best option for improvement is the identification of transgressive segregants based on SCA effects which may lead to isolation of promising lines of high total yield in bitter gourd. These results are in conformity with those of [20].

Five inbred lines viz., P1, P2, P6, P9 and P10 exhibited positive significant GCA effects in all the environments as well as on pooled basis for TSS. Positive significant SCA effects on pooled basis was recorded in 17 hybrids with range varied from 0.07 (P2 x P1) to 0.39 (P8 x P4). The estimates of positive significant GCA effects varied from 0.55 (P6) to 1.37 (P8) on pooled basis. Five inbred lines viz., P6, P8, P9 and P10 exhibited positive significant GCA effects in all the environments as well as on pooled basis for ascorbic acid content. Estimates of SCA effects revealed that 28 hybrids exhibited positive significant SCA effects on pooled basis with range varied from 0.90 (P9 x P4) to 5.01 (P2 x P1).

High general combining ability effects observed for different characters may be helpful in identifying sorting out outstanding parents with favourable alleles for different components of yield. Therefore, high general combining ability of the parents seems to be a reliable criterion for prediction of specific combining ability. Similar findings in cucumber were reported by [21,22] for yield and its components and for fruit texture by [23].

Out of these, parent IC 68237 (P1) showed significant GCA effects in all the environments, which indicated good general combiner for more number of primary branches per plant. SCA effect

indicated that the cross MDU -1 x Solan Hara (0.66) and Solan Collection x IC 68237 (0.40) exhibited significant and positive SCA effect in each individual environment and pooled over the environments. Whereas, crosses IC 85605 x BG 14 and Green Long x PDM showed significant and positive SCA affect either in of two environments and PEVs; hence, these were considered as good specific combiners in two environments.

GCA pertaining to the number of fruit per vine revealed that out of ten parents GCA was significant for parents, MDU-1, IC-68237 & Solan Collection in the entire environment as well as pooled over the environment in desired direction. Out of these, parent IC 68237 (P9) showed significant GCA effects in all the environments, which indicated good general combiner among the parents used in study programme for more number of fruits per vine. SCA on number of fruits per vine indicated that cross Solan Collection x IC 68237 (1.24) exhibited significant and positive SCA effect in each individual environment and pooled over the environments and considered best specific combiner among all the crosses made. High GCA and SCA values of parents and crosses of bitter gourd for these characters have also been reported by [7].

Fruit length directly contributes in the production of bitter gourd. GCA pertaining to the fruit length depicted that out of ten parents significant and positive GCA observed for parents, IC-68237 & Solan Collection in the entire environment as well as pooled over the environment in desired direction, which indicated best general combiner among the parents under studied for more fruits length. Specific Combining Ability (SCA) on fruits length indicated that cross IC 68237 x MDU-1 (1.82) exhibited significant and positive SCA effect in each individual environment and pooled over the environments and considered best specific combiner among all the crosses made [6,16-18] in Cucumis have also reported significant positive and negative GCA and SCA effects for this trait.

For fruit weight significant and positive GCA observed for parent, Solan Hara, PDM, BG 14, Green Long, IC 68272-1 and IC-68237 in all the environment as well as pooled over the environment in desired direction. Out of these, parent Solan Hara and PDM showed significant GCA effects in all the environments, which indicated best general combiner among the parents under studied for more fruits weight. Specific Combining Ability (SCA) on fruits weight indicated that cross IC 68237 x MDU-1 (1.82) exhibited significant and positive SCA effect in each individual environment and pooled over the environments and considered best specific combiner

among all the crosses made. The positive significant estimates of GCA effects for fruit diameter (cm) varied from 0.06 (P8) to 0.17 (P9) on pooled basis. The inbred lines P9 exhibited significant positive GCA effects in E2, E4 environment as well as on pooled basis. Out of 45 hybrids, sixteen hybrids expressed positive significant SCA effects on pooled basis, with range varied from 0.18 (P5xP1) to 0.50 (P6 x P5). The maximum estimates of positive SCA effects was exhibited by hybrids P6xP4 (0.79) in E1, P5xP1 (0.82) in E2, P6xP4 (0.62) in E3 and P6xP5 (0.72) in E4, (Table 4). For fruit weight significant GCA and SCA effects were also reported by [6,16-18].

For number of seeds per fruit inbred line P6, P7 and exhibited positive significant GCA effects in majority of the environment as well as on pooled basis. The highest magnitude of positive significant SCA effects was expressed by hybrids P5xP2 (8.67) in E1, P4xP2 (8.72) in E2, P10xP6 (7.19) in E3, P5xP2 (8.21) in E4 and P3xP2 (5.29) on pooled basis for number of seeds per fruit. Similar results of significant GCA and SCA effects were also reported by [17] for number of seeds per fruit in bitter gourd.

The inbred line P1 and P2 exhibited positive significant GCA effects in all the environments as well as over the environment for yield per vine. The estimates of significant positive SCA effects was observed in seventeen hybrids on pooled basis with range varied from 0.12 (P9 x P5) to 0.42 (P8 x P1). The maximum estimates of positive significant SCA effects was exhibited by hybrid P5 x P3 (0.51) in E1, P5 x P3 (0.46) in E2, P8 x P1 (0.47) in E3 and P8 x P1 (0.67) in E4 environment. These results are in accordance to the [24] who reported non additive type of gene action for yield and yield related traits in their material. However [14] found that both additive and non additive gene actions involved in the expression of yield and yield related characters. The differences in the results might have due to the differences in the genetic material studied [25,26] also reported SCA effects on yield and yield related characters.

Inbred line P2 exhibited significant positive GCA effects in majority of environments as well as pooled analysis for vine length. The significant positive SCA effects was observed hybrid P7 x P3 on pooled basis. [6,16,17,27] were also reported significant GCA and SCA effects for vine length in bitter gourd.

Earliness is a desirable direction for days to maturity. The parental line P8 expressed significant GCA effects in negative direction in majority of

environments as well as pooled basis. Eleven hybrids exhibiting negative significant SCA effects on pooled basis with the range of negative significant SCA effects varied from -7.46 (P7 x P1) to -1.28 (P6 x P4). This study reveals that the high SCA effects in these crosses was mainly through additive gene effects. Therefore, the best option for improvement is the identification of transgressive segregants based on SCA effects which may lead to isolation of promising lines of high total yield in bitter gourd. These results are in conformity with those of [19].

Five inbred lines viz., P1, P2, P6, P9 and P10 exhibited positive significant GCA effects in all the environments as well as on pooled basis for TSS. Positive significant SCA effects on pooled basis was recorded in 17 hybrids with range varied from 0.07 (P2 x P1) to 0.39 (P8 x P4). The estimates of positive significant GCA effects varied from 0.55 (P6) to 1.37 (P8) on pooled basis. Five inbred lines viz., P6, P8, P9 and P10 exhibited positive significant GCA effects in all the environments as well as on pooled basis for ascorbic acid content. Estimates of SCA effects revealed that 28 hybrids exhibited positive significant SCA effects on pooled basis with range varied from 0.90 (P9 x P4) to 5.01 (P2 x P1).

The results assumed that a good combiner for any economic character need not be a good combiner for all other characters [28]. High general combining ability effects observed for different characters may be helpful in identifying sorting out outstanding parents with favourable alleles for different components of yield. Therefore, high general combining ability of the parents seems to be a reliable criterion for prediction of specific combining ability [29]. Similar findings in cucumber were reported by [20, 21] for yield and its components.

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