COMBINING ABILITY OF QUANTITATIVE TRAITS IN SNAKE GOURD (*TRICHOSANTHES CUCUMERINA* VAR. ANGUINA)

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Abstract

The present study was carried out on snake gourd having seven diverse genotypes (TC 01, TC 05, TC 24, TC 33, TC 02, TC 46 and TC 53) used as parental lines and their 21 crosses generated from 7×7 half-diallel fashion at Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU) during March to June 2019 following RCBD with three replications. The aim of the study was to determine general combining ability (GCA) and specific combining ability (SCA) for fruit yield and its related traits including fruit quality traits. General prediction ratio (GPR) of these 14 traits was greater than 0.5 (50%), indicating predominance of additive gene effects over non-additive gene effects. The estimates of GCA for 19 quantitative traits revealed that the genotypes P_2 and P_6 were good general combiners for promoting earliness as well as most other important characters *viz.*, number of fruits/ plant, individual fruit weight and fruit yield/ plant/ hectare; P_2 and P_6 were also good for fruit length and fruit diameter, respectively whereas, P_4 was good for main vine length and number of nodes on main vine while, P_3 was superior for long fruit and 100-seed weight whereas, P_5 was good for number of seeds/ fruit and P_1 good for less fruit fly infestation including individual fruit weight and fruit length. The most promising specific combiners for fruit yield, quality and yield components were from the 13 crosses viz., $P_1 \times P_2, P_1 \times P_3, P_1 \times P_4, P_1 \times P_7, P_2 \times P_3, P_2 \times P_5, P_2 \times P_6, P_2 \times P_7, P_3 \times P_7, P_4 \times P_5, P_4 \times P_6, P_4 \times P_7$ and $P_5 \times P_7$. Out of 13 crosses only two crosses namely, $P_1 \times P_2$ and $P_2 \times P_6$ had both the good general combiner parents (high × high). These two crosses were therefore, amenable for improvement of the respective traits through pedigree selection. Remaining 11 crosses displaying high SCA effects for different traits were observed to be derived from parents having various types of GCA effects (high × medium, high × low, medium × low and low × low). The results of 13 crosses therefore, indicate the operation of additive × additive, additive × dominant and/ or dominant × dominant gene interactions for the genetic control of expression of the relative traits.

Keywords: Snake gourd, combining ability, GCA, SCA, quantitative traits, genotypes, half-diallel cross.

Introduction

Snake gourd [*Trichosanthes cucumerina* var. *anguina* (L) Haines] belonging to the family 'Cucurbitaceae', is popularly known as '*Chichinga*' in Bangladesh. It is a

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common annual creeper and an important summer vegetable, which is being cultivated all over the country. Snake gourd $(2n = 2x = 22)$ is a diploid annual climber (Devi, 2017), which is originated in India or the Indo-Malayan region in tropical Asia (Adebooye, 2008) and is widely distributed in Asian countries. Its tender fruits are consumed as edible vegetables, which have high nutritional value, because they are rich in vitamins, essential minerals, dietary fiber and other nutrients and are a wholesome, healthy addition to diets (Devi, 2017; Ojiako and Igwe, 2008). Winter vegetables are usually grown in 64.04% of the total land area under vegetable cultivation, while 35.96% areas are covered by summer vegetables and 70.83% vegetables are produced in winter and 19.17% in summer (Anon., 2021). Snake gourd is a day neutral type vegetable which usually grows well from March to October both in the field and homestead garden. As a result, it can meet the vegetable demand during early *kharif* when there exists an acute shortage of vegetables in Bangladesh. Bangladesh being the third largest vegetable production in the world stands next to India and China (Anon., 2019), and possessed about 2.83% of total cultivable area in the country and vegetable production shares about 1.60% of total global vegetable production (BBS, 2020). The current production level is over 18.0 million tons from an area of 0.90 million hectares (Anon., 2021). The per capita consumption of vegetable in Bangladesh is about 166.1 g/ day (Anon., 2011), which is lower than the recommended rate (280 g/day/person) (Ramphal and Gill, 1990) for a balanced diet. The vegetable requirement of the country is estimated to be 24.70 million tons by 2030. This target can be achieved through use of improved varieties in combination with superior crop management skills. Hence, it has become necessary to enhance the present vegetable production by developing high yielding varieties of vegetable crops including snake gourd. The varieties of snake gourd are not available in the market as per demand of the farmers in the country. However, concerted efforts towards its improvement and developing new high yielding varieties both open pollinated and hybrids are lacking. Thus, it necessities, development of high yielding, better quality varieties through efficient breeding programmes. In breeding of high yielding varieties of crop plants, the breeder often faces with the problem of selecting parents and crosses. Combining ability studies are more reliable as they provide useful information for the selection of parents in terms of performance of the hybrids and elucidate the nature and magnitude of various types of gene actions involved in the expression of quantitative traits. Combining ability analysis helps to identify superior parents to be used in breeding programs or to identify promising cross combinations for cultivar development (Acquaah, 2007). Development of superior varieties could be done by reshuffling the genes through hybridization from suitable parents. Moreover, it is also necessary to know about the nature and magnitude of gene action responsible for controlling the inheritance of various yield and quality attributes along with combining ability of the parents and their cross combinations to exploit them in further crop improvement programme (Quamruzzaman *et al.*, 2020b). General combining ability is due to additive gene

action and is fixable nature while specific combining ability is due to non-additive gene action which may be due to dominance or epistasis or both and is non-fixable. Griffing (1956b) suggested that GCA includes both additive effect as well as additive × additive interactions. The presence of additive genetic variance is the primary justification for initiating the hybrid breeding programme (Pali and Meheta, 2014). Diallel analysis provides the estimates of genetic parameters regarding combining ability as well as a rapid overall picture of the dominance relationship of the parents studied using the first filial generation (F_1) with or without reciprocals. Diallel analysis involving parents gives the additional information as presence or absence of epistasis, average degree of dominance, and distribution of dominant and recessive genes in the parents (Zongo *et al*., 2019). The heterozygous nature of snake gourd and virtually the obligatory out crossing breeding system of snake gourd opens the scope of development of open-pollinated as well as hybrid variety. Keeping the above points in view, the present investigation was undertaken to reveal the general and specific combining ability in snake gourd for the development of high yielding and better quality varieties.

Materials and Methods

The experiment was conducted at the experimental farm of the Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh during March to June 2019. The location of the site is 24.09^0N latitude and 90.26^0E longitude with an elevation of 8.2 m from sea level under agro-ecological zone (Madhupur Tract) AEZ - 28 (Anon., 1995). The field experiment was installed on a high land plot on the farm. Seven diverse genotypes were selected among 55 genotypes based on their performance for different horticultural traits, genetic diversity and heritability. The parental genotypes TC 01, TC 05, TC 24, TC 33, TC 02, TC 46 and TC 53 were symbolized as P_1, P_2, P_3, P_4, P_5, P_6 and P_7, respectively. The collection sources of genotypes are presented Table 1.

Table 1. Parental genotypes of snake gourd used in combining ability study and their sources

Sl. No.	Parents (code)	Genotypes	Sources
1.	P_1	TC 01	PGRC, BARI
2.	P_2	TC 05	PGRC, BARI
3.	P_3	TC 24	HRC, BARI
4.	P_4	TC 33	Banashree agro seed (Jumlong)
5.	P_5	TC 02	PGRC, BARI
6.	P_6	TC 46	BSMRAU
7.	P_7	TC 53	Boropara, Khagrachori

The seven parents were grown and crossed in one direction accordingly to half-diallel fashion during August to November, 2018. The parents were grown together with their F_1s during March to June, 2019. A half-diallel cross of 7×7 without reciprocals was designed. Twenty-one crosses were made from the seven parents following the formula n(n-1), where, n = 7. The crossing scheme is presented in Table 2.

Table 2. Half diallel crossing design of Griffing's second method for seven snake gourd parents

Parents	P_1	P_2	P_3	P_4	P_5	P_6	P_7
P_1							
P_2	$P_1 \times P_2$						
P_3	$P_1 \times P_3$	$P_2 \times P_3$					
P_4	$P_1 \times P_4$	$P_2 \times P_4$	$P_3 \times P_4$				
P_5	$P_1 \times P_5$	$P_2 \times P_5$	$P_3 \times P_5$	$P_4 \times P_5$			
P_6	$P_1 \times P_6$	$P_2 \times P_6$	$P_3 \times P_6$	$P_4 \times P_6$	$P_5 \times P_6$		
P_7	$P_1 \times P_7$	$P_2 \times P_7$	$P_3 \times P_7$	$P_4 \times P_7$	$P_5 \times P_7$	$P_6 \times P_7$	

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Fifteen days old seedlings each parent and F_1 were transplanted on 20 March 2019, in well-prepared pit in an experimental plot. A total of 84 (28 $\times$ 3) unit plots were made, each measuring 7.5 m $\times$ 1.5 m (11.25 m^2) accomodating 5 plants in single row of 7.5 m in length with plant and row spacing of 1.5 m and 1.5 m, respectively. Fertilizers were applied @ 5000-50-24-40-14-1.5-1.0 kg/ha of cowdung-N-P-K-S-Zn-B according to FRG (2012). The sources of N, P, K, S, Zn, and B were Urea, Triple Super Phosphate (TSP), Muriate of Potash (MoP), Gypsum, Zinc Sulphate, Boric Acid (Laboratory Grade). During the final land preparation, the entire amount of cowdung, P, S, Zn, B, and one-third of K, as well as N and the remaining part of K were applied around pit (plant) in four equal installments at 7, 21, 35 and 49 days after transplantation. Data were recorded on days to 1st male flower opening, days to 1st female flower opening, node number at 1st male flower opening, node number at 1st female flower opening, main vine length (cm), node number on main vine, number of primary branches/ plant, days to 1st fruit harvest, fruit fly infestation (%), number of fruits/ plant, fruit yield/ plant (kg), fruit yield/ hectare (ton), individual fruit weight (g), fruit length (cm), fruit diameter (cm), fruit flesh thickness (cm), number of locules/ fruit, number of seeds/ fruit, 100-seed weight (g). The data were analyzed according to Model 1 and Method 2 of Griffing (1956a) for combining ability. The Griffings analysis was designed in order to determine the performance of the parents and their relative contribution to the F_1s as measured by the general and specific combining abilities (GCA and SCA). GCA represents additive variances and SCA represents non-

additive variances. In the present case, the fixed effect model was more fitting as the parents selected were cross-pollinated lines and the population considered were the parents and F_1s. This study splited the variances into GCA and SCA effects due to genotypic variations. The ratio of combining ability variance components (predictability ratio) determine the type of gene action involved in the expression of characters and allowing inference about optimum allocation of resources in hybrid breeding. General prediction ratio (GPR) was calculated from the variances of GCA and SCA and the formula was, GRP $= \frac{2\sigma^2 GCA}{2\sigma^2 GCA + \sigma^2 SCA}$; where, $\sigma^2 GCA=$ the variances of general combining ability, $\sigma^2 SCA=$ the variances of specific combining ability (Fasahat *et al.,* 2016 and Baker, 1978). The closer the ratio to one greater the prediction of GCA effects over SCA effects.

Results and Discussion

The analysis of variance (ANOVA) exhibited substantial differences among the parents and crosses for all the characters studied (Table 3). The significant mean sum square due to general combining ability (GCA) and specific combining ability (SCA) for all the characters indicated that both additive and non-additive gene actions played dominant role in the expression of these characters. The higher magnitude of SCA variance than that of GCA variance of the one out of nineteen characters studied indicates the dominant role of non-additive gene effects for the character. Similarly, Podder *et al.* (2010) and Banik (2003) also reported highly significant variance for both general and specific combining ability for all the characters studied in snake gourd. The general prediction ratio (GPR) of 14 characters was more than 0.5 (50%), indicating that additive gene effects predominated over non-additive gene effects. Fruit diameter was non-significant for SCA but significant for GCA, implying that additive gene effects influence fruit diameter as well. Both additive and non-additive gene effects governed the attributes that were not significant due to GCA and SCA. Rukunda *et al.* (2017) and Nath *et al.* (2018) used GPR in sweat potato and mung bean crop, respectively and reported that this ratio for some characters were higher than 50% (0.5), suggesting the preponderance of additive over non-additive gene action in the expression of these traits.

General combining ability (GCA) effects

The GCA component is primarily the function of the additive genetic variance. The GCA variance with each parent plays a significant role in the choice of parents. A parent with higher positive significant GCA effects is considered as the best general combiner. The results of GCA effects for nineteen characters are presented in the Table 4. The parent P_2 showed the highest significant negative GCA effects (-3.99**) for days to 1st male flower opening. The parent P_6 (-3.51**) and P_7 (-2.06**) also showed significant negative effects (Table 4). Regarding the days to 1st male flower opening, positive values indicated late flowering and negative

Table 3. Analysis of variance and related statistics for 19 traits in snake gourd

SV	df	Characters (Mean sum square)								
		DFM[1]	DFF[2]	NOM[3]	NOF[4]	MVL[5]	NPB[6]	NMV[7]	DFH[8]	FFI[9] (%)
GCA	6	93.12**	44.64**	17.63**	12.05**	16.89**	0.21	470.40**	12.70**	7.99**
SCA	21	37.98**	25.26**	8.75**	9.37**	2.37**	0.45	68.23**	13.54**	3.33**
Error	54	1.21	1.05	2.34	3.36	0.38	0.28	18.34	1.57	0.79
σ^2_{gca}	-	-0.09	2.15	0.97	0.30	1.61	-0.03	44.68	-0.09	0.52
σ^2_{sca}	-	11.97	24.21	6.41	6.02	1.99	0.17	49.88	11.97	2.54
GPR	-	0.95	0.93	0.93	0.97	0.98	-	0.98	0.87	0.94

** Significant at 1% level, * Significant at 5% level, GPR= General prediction ratio, [1]Days to 1st male flower opening, [2]Days to 1st female flower opening, [3]Node number at 1st male flower opening, [4]Node number at 1st female flower opening, [5]Main vine length (m), [6]Number of primary branches/ plant, [7]Number of nodes on main vine, [8]Days to 1st fruit harvest, [9]Percentage of fruit fly infestation

Table 3. Continued

SV	df	Characters (Mean sum square)									
		IFW[10]	NOF[11]	YOF[12]	Y/Ha[13]	FL[14]	FD[15]	FT[16]	LN[17]	SF[18]	SW[19]
GCA	6	2217.27**	169.68**	16.17**	157.98**	163.23**	0.16**	0.003	0.179	98.30**	21.48
SCA	21	659.87**	69.37**	6.37**	62.25**	5.91**	0.04	0.003	0.115	140.65**	8.17
Error	54	72.92	9.05	0.47	4.59	2.41	0.03	0.002	0.119	27.60	9.83
σ^2_{gca}	-	173.04	11.14	1.09	10.63	17.48	0.01	0.001	0.007	-4.71	1.48
σ^2_{sca}	-	586.95	60.32	5.90	57.65	3.50	0.01	0.001	-0.004	113.04	-1.66
GPR	-	0.96	0.94	0.95	0.93	0.99	0.97	-	-	0.82	-

** Significant at 1% level, * Significant at 5% level, GPR= General prediction ratio, [10]Individual fruit weight (g), [11]Number of fruits/ plant, [12]Fruit yield/ plant (kg), [13]Fruit yield/ hectare (ton), [14]Fruit length (cm), [15]Fruit diameter (cm), [16]Fruit flesh thickness (cm), [17]Number of locules/ fruit, [18] Number of seeds/ fruit, [19]100-seed weight (g).

values indicated early flowering. Hence, the parents P_2, P_6, and P_7 were the best general combiners for earliness with regard to male flowering. Banik (2003) found negative GCA value for days to 1st male flower opening. The parent P_6 exhibited the highest significant negative GCA effects (-3.03**) followed by P_2 (-1.66**) and P7 (-1.25**), but P_3 (-0.66) was non-significant for days to 1st female flower opening (Table 4). Negative GCA value is preferred due to early flowering. Thus, the parents P_2, P_6, and P_7 performed as the best general combiners among the parents. Similarly, Banik (2003) stated one parent was found best general combiner for female flower earliness in snake gourd. Jha *et al.* (2009) reported negative GCA value for days to 1st female flower opening for earliness in pumpkin. The highest significant negative GCA effects was found in the parent P_2 (-2.09**) and P_6 (-1.90**) for node number at 1st male flower opening (Table 4). So, the parents P_2 and P_6 exhibited the best general combiners for this trait. The present findings are identical to the result of Banik (2003). The parents P_2 (-0.48), P_3 (-1.07), P_5 (-0.48), and P_6 (-1.18) showed the non-significant negative effects for node order at 1st female flower opening (Table 4). Jha *et al.* (2009) recorded both positive and negative GCA values for node number at 1st female flower opening. The findings support the present investigation for female flower earliness.

The parent P_4 estimated only significant positive GCA effect for main vine length (2.99**), while the parent P_6 (0.06) showed non-significant positive effects (Table 4). The P_4 was the best general combiner for long vine. The present investigation is in agreement with the findings of Banik (2003). The P_4 (15.03**) exhibited only significant positive GCA effects, and P_6 (2.66) showed non-significant positive effects (Table 4). The parent P_4 was the best general combiner, which contains more number of nodes on the main vine suitable for plant breeding program. Banik (2003) reported two parents as the best general combiners for more number of nodes on main vine in snake gourd. The parent P_7 (-1.41**) exhibited only significant negative GCA effects, and P_3 (-0.12), P_5 (-0.63) and P_6 (-0.93) showed non-significant negative effects for the early fruit harvest (Table 4). The parent P_7 exhibited negative GCA effects which are desirable for this character. The parent P_1 showed the highest significant negative GCA effects (-0.73**), while the parent P_5 showed the highest significant positive GCA effects (2.06**) for fruit fly infestation (Table 4). Regarding positive values indicated more infestation, and negative values indicated less infestation. Hence, the parent P_1 was the best general combiner for minimum fruit fly infestation.

The parent P_1 exhibited the maximum significant positive GCA effects (14.98**) closely followed by P_2 (13.32**) and P_6 (9.92**) for individual fruit weight (Table 4). The parents P_1, P_2 and P_6 were good general combiners for this trait. Banik (2003) found two parents as good general combiner for individual fruit

weight in snake gourd. Jha *et al.* (2009) reported significant positive GCA effects for individual fruit weight in pumpkin. The highest significant positive GCA effects were found in parent P_6 (8.07**) followed by P_2 (2.33*) for fruits/ plant (Table 4). The parents P_2 and P_6 were the best general combiners for increasing more fruits/ plant. Banik (2003) reported the two parents as good general combiners for fruits/ plant in snake gourd. Pandey *et al.* (2005) found three parents that were good general combiners for this trait in ash gourd. The parent P_6 (2.23**) exhibited the highest significant positive GCA effects for yield/ plant followed by P_2 (1.12**) (Table 4). The parent P_6 and P_2 were the best general combiners to improve the fruit bearing capacity. Podder *et al.* (2010) reported one parent as the best general combiner for fruit yield and some yield contributing charcters in snake gourd. The parent P_6 (6.96**) showed the highest significant positive GCA effects for this character followed by P_2 (3.49**) (Table 4). The parents P_6 and P_2 were the best general combiners for fruit yield/ hectare. Singh *et al.* (2013) reported one parent in bitter gourd to be a good general combiner for increasing fruit yield/ hectare.

The highest significant positive GCA effect for fruit length was found in P_1 (5.18**) followed by P_2 (4.37**) and P_3 (1.18*) (Table 4). The parents P_1, P_2, and P_3 were the best general combiners for increasing long fruit. Banik (2003) reported one parent as a good general combiner for fruit length in snake gourd. Singh *et al.* (2013) observed in bitter gourd, one parent was found to be a good general combiner for this character. The only significant positive GCA effect was found in P_6 (0.21**) while significant negative effect exhibited the parents P_1 (-0.16**) and P_5 (-0.13*) for fruit diameter (Table 4). The parent P_6 was the best general combiner to use in crossing to improve this trait. Banik (2003) reported two parents as the best general combiners for fruit diameter in snake gourd. Singh *et al.* (2013) observed in bitter gourd, one parent was found to be a good general combiner for this trait. Four parents showed non-significant positive GCA effects, and three parents showed non-significant negative effects for fruit flesh thickness (Table 4). Ahmed *et al.* (2016) reported that two parents showing significant positive GCA effects for this character in pumpkin. The highest significant negative GCA effect was found in P_6 (-4.15*) followed by P_7 (-4.08*) less seeded fruit (Table 4). So, P_6 and P_7 were the best general combiners for this trait. Likewise, Banik (2003) reported one parent was a good general combiner for less seeded type. The parent P_3 exhibited the maximum significant positive GCA effects (2.03*), while the parent P_7 (-2.65*) showed significant negative GCA effects for 100-seed weight (Table 4). Hence, the parent P_3 was a good general combiner for increasing seed weight individuals. Banik (2003) reported one parent as a good general combiner for 100-seed weight in snake gourd.

Table 4. Estimates of GCA effects of 7 parents for 19 quantitative traits in snake gourd

Parents	DFM[1]	DFF[2]	NOM[3]	NOF[4]	MVL[5]	NPB[6]	NMV[7]	DFH[8]	FFI[9] (%)
P$_1$ (TC 01)	2.79**	2.9**	1.13	1.41*	-0.73**	-0.15	-6.56**	2.18**	-0.73*
P$_2$ (TC 05)	-3.99**	-1.66**	-2.09**	-0.48	-1.07**	0.19	-2.34	0.37	-0.37
P$_3$ (TC 24)	1.27**	-0.66	0.69	-1.07	-0.64*	0.07	-2.3	-0.12	-0.46
P$_4$ (TC 33)	1.16*	1.27**	1.09	1.75*	2.99**	0.04	15.03**	0.55	-0.02
P$_5$ (TC 02)	4.34**	2.42**	0.21	-0.48	-0.36	0.15	-4.93**	-0.63	2.06**
P$_6$ (TC 46)	-3.51**	-3.03**	-1.90**	-1.18	0.06	-0.22	2.66	-0.93	-0.40
P$_7$ (TC 53)	-2.06**	-1.25**	0.87	0.04	-0.25	-0.07	-1.56	-1.41*	-0.07
SE(gi)±	0.34	0.32	0.47	0.57	0.19	0.16	1.32	0.39	0.22
SE(sij) ±	0.99	0.92	1.37	1.64	0.55	0.48	3.84	1.12	0.54

** Significant at 1% level, * Significant at 5% level, GPR= General prediction ratio, [1]Days to 1st male flower opening, [2]Days to 1st female flower opening, [3]Node number at 1st male flower opening, [4]Node number at 1st female flower opening, [5]Main vine length (m), [6]Number of primary branches/ plant, [7]Number of nodes on main vine, [8]Days to 1st fruit harvest, [9]Percentage of fruitfly infestation

Table 4. Continued

Parents	IFW[10]	NOF[11]	YOF[12]	Y/Ha[13]	FL[14]	FD[15]	FT[16]	LN[17]	SF[18]	SW[19]
P$_1$ (TC 01)	14.98**	-2.75*	0.07	0.21	5.18**	-0.16*	0.018	-0.032	2.51	-0.54
P$_2$ (TC 05)	13.32**	2.33*	1.12**	3.49**	4.37**	-0.02	-0.004	0.153	2.85	1.44
P$_3$ (TC 24)	-7.12*	1.55	-0.05	-0.16	1.18*	-0.03	-0.011	-0.106	-1.63	2.03*
P$_4$ (TC 33)	-2.42	-4.63**	-1.15**	-3.59**	-2.12**	0.12	0.007	0.227	0.77	0.31
P$_5$ (TC 02)	1.62	-2.89*	-0.47	-1.47	-2.38**	-0.13*	-0.029	-0.106	3.74*	-0.83
P$_6$ (TC 46)	9.92**	8.07**	2.23**	6.96**	0.88	0.21**	0.000	-0.143	-4.15*	0.23
P$_7$ (TC 53)	-30.31**	-1.67	-1.74**	-5.44**	-7.12**	0.01	0.018	0.005	-4.08*	-2.65*
SE(gi)±	2.64	0.93	0.21	0.66	0.48	0.05	0.013	0.107	1.30	0.78
SE(sij) ±	7.66	2.7	0.62	1.92	1.39	0.15	0.039	0.310	3.23	1.93

** Significant at 1% level, * Significant at 5% level, GPR= General prediction ratio, [10]Individual fruit weight (g), [11]Number of fruits/ plant, [12]Fruit yield/ plant (kg), [13]Fruit yield/ hectare (ton), [14]Fruit length (cm), [15]Fruit diameter (cm), [16]Fruit flesh thickness (cm), [17]Number of locules/ fruit, [18]Number of seeds/ fruit, [19]100-seed weight (g).

Specific combining ability effects (SCA)

The specific combining ability effects of twenty-one crosses for nineteen characters are given in Table 5. The highest significant negative SCA effect was observed in $P_5 \times P_7$ (-8.35**) followed by $P_1 \times P_7$ (-7.89**), $P_2 \times P_5$ (-6.43**), $P_5 \times P_6$ (-6.24**) and $P_3 \times P_5$ (-5.68**) for early male flowering (Table 5). Thus, the cross $P_5 \times P_7$ was proved to be the best specific combination for this trait. Banik (2003) reported that the cross combination $P_1 \times P_5$ had significant negative SCA effects for days to 1st male flower opening in snake gourd. The negative SCA value is preferable for this trait because it indicates the earliness. The highest significant negative SCA effect was manifested in $P_1 \times P_5$ (-7.72**) followed by $P_2 \times P_5$ (-7.17**) and $P_3 \times P_5$ (-7.17**) for early female flowering (Table 5). The cross $P_1 \times P_5$ was the best specific combination for this character. The present investigation corroborates the findings of Banik (2003) for early female flower opening. The highest significant negative SCA effect was observed in $P_1 \times P_7$ (-5.15**) followed by $P_5 \times P_6$ (-3.78**) for node number at 1st male flower opening (Table 5). Thus, the cross $P_1 \times P_7$ was the best specific combination for this trait. Banik (2003) recorded in snake gourd, the cross combination $P_1 \times P_3$ had significant negative SCA effects for node number at 1st male flower opening. The highest significant negative value of SCA effect was manifested in $P_1 \times P_4$ (-4.86**) followed by $P_1 \times P_2$ (-4.03**) for node number at 1st female flower opening (Table 5). The cross $P_1 \times P_4$ was the best specific combination for this trait. Banik (2003) revealed that the cross combination $P_2 \times P_5$ had the best significant SCA effects for this trait in snake gourd.

The cross combination $P_4 \times P_6$ (2.72**) exhibited the highest significant positive SCA effects followed by $P_1 \times P_4$ (2.08**), $P_4 \times P_5$ (1.78**) and $P_2 \times P_4$ (1.25*) for main vine length (Table 5). Thus, the cross $P_4 \times P_6$ was the best specific combination for this trait. Banik (2003) reported in snake gourd, the cross combination $P_1 \times P_5$ had the best significant SCA effects for main vine length. Singh *et al.* (2013) recorded that the best combination of bitter gourd was HABG-23 × HABG-34 for this character. The only significant positive SCA effect was found in cross combination $P_2 \times P_3$ (1.82**) for number of primary branches/ plant (Table 5). Thus, this cross was the best specific combination for this trait. The cross combination $P_3 \times P_7$ (10.39*) showed the highest significant positive SCA effects followed by $P_4 \times P_5$ (10.10*), $P_1 \times P_4$ (10.06*), $P_4 \times P_6$ (9.18*) and $P_2 \times P_3$ (8.18*) for number of nodes on main vine (Table 5). Thus, the crosses $P_3 \times P_7$, $P_4 \times P_5$, $P_1 \times P_4$, $P_4 \times P_6$, and $P_2 \times P_3$ were the good specific combiner for this trait. Banik (2003) reported in snake gourd, the cross combination $P_1 \times P_2$ was the best specific combiner to enhance number of nodes on main vine. The highest significant negative SCA effect was manifested in $P_2 \times P_5$ (-7.44**) followed by $P_3 \times P_5$ (-6.96**), $P_2 \times P_7$ (-4.00**), $P_1 \times P_5$ (-3.26**) and $P_1 \times P_6$ (-2.96*) days to 1st harvest (Table 5). So, the cross $P_2 \times P_5$ was the best specific combination for this trait. Varghese (1991) in snake gourd noticed the cross combination $P_5 \times P_3$ was the best

specific combiner for this trait. The negative SCA value is preferable for percent fruit fly infestation because it indicates minimum infestation by fruit fly. The highest significant negative SCA effect was manifested in $P_1 \times P_4$ (-2.84**) followed by $P_3 \times P_7$ (-1.73**), $P_2 \times P_7$ (-1.40*) and $P_2 \times P_6$ (-1.26*) (Table 5). Therefore, the crosses $P_1 \times P_4$ and $P_3 \times P_7$ were the best specific combinations for lower fruit fly infestation.

The highest significant positive SCA effect was manifested in $P_1 \times P_3$ (46.20**) followed by $P_3 \times P_7$ (29.83**), $P_4 \times P_5$ (27.54**) and $P_5 \times P_7$ (27.43**) for individual fruit weight (Table 5). Thus, the cross $P_1 \times P_3$ was the best specific combination for individual fruit weight. Banik (2003) reported in snake gourd, the cross combination $P_4 \times P_5$ showed the best specific combiner to increase individual fruit weight. The highest significant positive SCA effect was observed in $P_4 \times P_5$ (14.06**) followed by $P_2 \times P_6$ (12.81**), $P_2 \times P_7$ (11.55**), and $P_1 \times P_3$ (7.40*) for the number of fruits/ plant (Table 5). Hence, the cross $P_4 \times P_5$ was the best specific combination for this trait. Banik (2003) reported in snake gourd, the cross combination $P_3 \times P_6$ was the best specific combiner to enhance the number of fruits/ plant. Singh *et al.* (2013) found that the combination HABG-23 × HABG-34 exhibited the best specific combiner to increase fruits/ plant in bitter gourd. The combination $P_2 \times P_6$ (4.60**) exhibited the highest significant positive SCA effect followed by $P_4 \times P_5$ (4.39**), $P_1 \times P_3$ (4.20**), $P_2 \times P_7$ (2.26**), $P_3 \times P_7$ (2.14**) and $P_5 \times P_7$ (2.03**) for fruit yield/ plant (Table 5). Thus, the cross $P_2 \times P_6$ was considered as the best specific combination for this character. Podder *et al.* (2010) stated that the best specific combiner for fruit yield and some yield contributing characters were $P_2 \times P_3$, $P_1 \times P_2$ and $P_1 \times P_4$ in snake gourd. The cross combination $P_2 \times P_6$ (14.39**) showed the highest significant positive SCA effects followed by $P_4 \times P_5$ (13.71**), $P_1 \times P_3$ (13.12**), $P_2 \times P_7$ (7.05**), $P_3 \times P_7$ (6.70**) and $P_5 \times P_7$ (6.34**) for fruit yield/ hectare (Table 5). So, the cross $P_2 \times P_6$ was the best specific combination for this trait. Podder *et al.* (2010) examined in snake gourd, the best specific combiner for fruit yield and some yield contributing characters were $P_2 \times P_3$, $P_1 \times P_2$ and $P_1 \times P_4$.

The highest significant positive SCA effect was provided by the cross $P_1 \times P_2$ (3.32*) closely followed by $P_2 \times P_6$ (3.29*) for fruit length (Table 5). Thus, the cross $P_1 \times P_2$ was found as the best specific combination for fruit length. Banik (2003) reported in snake gourd, the cross combination $P_1 \times P_2$ was the best specific combiner for this character. Singh *et al.* (2013) found in bitter gourd, the combination HABG-23 × HABG-34 was the best specific combiner to increase fruit length. The highest significant positive SCA effect for fruit diameter was found in the cross $P_4 \times P_7$ (0.41*) followed by $P_2 \times P_5$ (0.36*) (Table 5). Hence, the cross $P_4 \times P_7$ was the best specific combination for fruit diameter. Banik (2003) reported in snake gourd, the cross combination $P_1 \times P_2$ exhibited the best specific combiner to get the widest fruit in the same crop. The only significant positive SCA effect for fruit flesh thickness was provided by the cross $P_1 \times P_7$ (0.113**)

Table 5. Estimates of SCA effects of 21 crosses for 19 quantitative traits in snake gourd

Crosses	DFM[1]	DFF[2]	NOM[3]	NOF[4]	MVL[5]	NPB[6]	NMV[7]	DFH[8]	FFI[9] (%)
$P_1 \times P_2$	2.13*	2.35*	2.81*	-4.03**	-0.89	-0.29	0.1	2.74*	0.93
$P_1 \times P_3$	8.20**	3.69**	3.37**	4.95**	-0.11	0.82	-2.93	3.22**	0.56
$P_1 \times P_4$	5.65**	2.76**	-2.04	-4.86**	2.08**	-0.47	10.06*	1.89	-2.84**
$P_1 \times P_5$	-2.87**	-7.72**	1.18	-0.97	0.11	0.42	-0.64	-3.26**	-0.67
$P_1 \times P_6$	3.65**	-0.28	4.63**	-0.94	-0.15	-0.21	-1.9	-2.96*	0.34
$P_1 \times P_7$	-7.89**	-0.39	-5.15**	-0.49	0.33	0.31	1.99	3.85**	1.14*
$P_2 \times P_3$	-0.68	0.91	-1.07	1.84	0.72	1.82**	8.18*	4.37**	0.96
$P_2 \times P_4$	-3.57**	3.31**	-2.15	3.36	1.25*	0.19	7.18	-0.96	-1.08
$P_2 \times P_5$	-6.43**	-7.17**	-2.59	-0.75	-0.39	-0.25	-4.53	-7.44**	3.10**
$P_2 \times P_6$	1.43	0.94	1.52	-0.38	-0.15	0.45	1.88	-1.15	-1.26*
$P_2 \times P_7$	1.98	-0.83	0.07	-1.27	-0.84	-0.03	-4.56	-4.00**	-1.40*
$P_3 \times P_4$	7.17**	1.98*	4.07**	-0.05	0.66	-0.36	-0.86	-0.48	-0.51
$P_3 \times P_5$	-5.68**	-7.17**	-1.37	-0.16	0.55	-0.47	3.44	-6.96**	-0.67
$P_3 \times P_6$	-3.17**	2.28*	-0.93	-0.79	-1.08	-1.12*	-4.49	0.33	0.47
$P_3 \times P_7$	1.39	3.17**	0.96	-0.01	0.74	0.75	10.39*	-0.19	-1.73**
$P_4 \times P_5$	4.43**	4.57**	3.55*	5.69**	1.78**	0.56	10.10*	4.70**	4.69**
$P_4 \times P_6$	-2.39**	-1.65	0	0.39	2.72**	0.27	9.18*	-1.33	1.06
$P_4 \times P_7$	4.83**	2.24*	3.89**	5.17**	1.07	-0.21	4.73	-1.52	0.53
$P_5 \times P_6$	-6.24**	-4.79**	-3.78*	-1.38	0.84	0.49	6.47	1.52	-0.43
$P_5 \times P_7$	-8.35**	-4.57**	-1.22	-1.6	-0.48	-0.32	-15.64	-0.33	-0.10
$P_6 \times P_7$	1.5	2.20*	-0.78	1.1	-0.17	-0.29	-0.23	-0.04	2.08**
SE(gi) ±	0.52	0.48	0.72	0.86	0.29	0.25	2.02	0.59	0.33
SE(sij) ±	1.47	1.37	2.04	2.44	0.82	0.71	5.71	1.67	0.82

** Significant at 1% level, * Significant at 5% level, GPR= General prediction ratio, [1]Days to 1st male flower opening, [2]Days to 1st female flower opening, [3]Node number at 1st male flower opening, [4]Node number at 1st female flower opening, [5]Main vine length (m), [6]Numbeer of primary branches/ plant, [7]Number of nodes on main vine, [8]Days to 1st fruit harvest, [9]Percentage of fruit fly infestation.

Table 5. Continued.

Crosses	IFW[10]	NOF[11]	YOF[12]	Y/Ha[13]	FL[14]	FD[15]	FT[16]	LN[17]	SF[18]	SW[19]
$P_1 \times P_2$	18.76*	-3.05	0.09	0.27	3.32*	0.08	0.002	0.259	-3.82	0.32
$P_1 \times P_3$	46.20**	7.40*	4.20**	13.12**	2.18	0.22	0.009	-0.148	1.66	-1.65
$P_1 \times P_4$	-36.83**	-1.75	-1.94**	-6.08**	-3.53*	-0.10	-0.009	-0.481	12.92**	-4.82*
$P_1 \times P_5$	-21.54*	-2.16	-1.57*	-4.91*	-3.60*	-0.31*	-0.072	-0.148	-1.71	-0.07
$P_1 \times P_6$	-3.83	-1.12	-0.36	-1.12	-0.53	0.05	-0.002	0.222	-4.16	1.36
$P_1 \times P_7$	-13.61	2.62	-0.14	-0.42	-3.53*	-0.11	0.113**	0.074	6.10	1.41
$P_2 \times P_3$	-11.46	3.66	0.17	0.54	-2.01	-0.11	-0.035	0.000	-13.01**	4.80*
$P_2 \times P_4$	-22.17**	-6.82*	-2.49**	-7.78**	-1.38	-0.13	-0.087*	0.333	27.25**	-1.29
$P_2 \times P_5$	9.46	4.1	1.29*	4.03*	-0.45	0.36*	0.050	0.667*	-0.05	-2.18
$P_2 \times P_6$	19.17*	12.81**	4.60**	14.39**	3.29*	0.08	-0.013	0.037	5.18	-1.57
$P_2 \times P_7$	2.05	11.55**	2.26**	7.05**	0.29	-0.15	0.035	-0.111	2.10	-0.23
$P_3 \times P_4$	16.61*	-5.38	-0.43	-1.35	-2.86	0.19	0.054	0.593	-19.27**	4.53*
$P_3 \times P_5$	4.24	3.21	0.75	2.35	0.40	0.23	0.024	-0.074	5.10	-0.02
$P_3 \times P_6$	-15.39*	-2.42	-1.43*	-4.46*	1.47	-0.35*	-0.038	-0.037	16.99**	-2.93
$P_3 \times P_7$	29.83**	3.99	2.14**	6.70**	1.81	0.03	0.043	-0.185	9.58**	-0.32
$P_4 \times P_5$	27.54**	14.06**	4.39**	13.71**	1.03	-0.02	-0.028	-0.407	19.36**	-1.75
$P_4 \times P_6$	18.24	-10.23**	-1.58*	-4.94*	1.77	0.00	0.076	-0.370	-9.08*	7.50**
$P_4 \times P_7$	16.80*	-13.49**	-1.92**	-6.00**	2.10	0.41*	-0.076	0.481	0.18	-1.01
$P_5 \times P_6$	19.20*	-1.64	0.52	1.61	0.03	-0.05	0.080	-0.037	-3.71	-1.00
$P_5 \times P_7$	27.43**	4.44	2.03**	6.34**	2.69	-0.01	-0.006	0.148	-8.45*	1.09
$P_6 \times P_7$	8.13	-2.19	-0.31	-0.96	-0.23	-0.02	-0.002	0.185	3.10	0.22
SE(gi) ±	4.03	1.42	0.32	1.01	0.73	0.08	0.020	0.163	1.99	1.19
SE(sij) ±	11.39	4.01	0.91	2.86	2.07	0.22	0.057	0.461	4.86	2.90

** Significant at 1% level, * Significant at 5% level, GPR= General prediction ratio, [10]Individual fruit weight (g), [11]Number of fruits/ plant, [12]Fruit yield/ plant (kg), [13]Fruit yield/ hectare (ton), [14]Fruit length (cm), [15]Fruit diameter (cm), [16]Fruit flesh thickness (cm), [17]Number of locules/ fruit, [18]Number of seeds/ fruit, [19]100-seed weight (g).

(Table 5) and this cross was the best specific combination for this character. Jha *et al.* (2009) examined the use of seven parents with eight characters in pumpkin, one parent however, was found to be a good combiner for fruit flesh thickness. The only significant positive SCA effect was observed in the cross $P_2 \times P_5$ (0.667*) for number of locules/ plant (Table 5), which was the best specific combination for this character. The combination $P_3 \times P_4$ (-19.27**) exhibited the highest significant negative SCA effects followed by $P_2 \times P_3$ (-13.01**), $P_4 \times P_6$ (-9.08*) and $P_5 \times P_7$ (-8.45*) for number of seeds/ fruit (Table 5). Hence, the crosses $P_3 \times P_4$ and $P_2 \times P_3$ were considered as the best specific combinations for lower number of seeds/ fruit. Banik (2003) reported in snake gourd, the cross combination $P_3 \times P_5$ showed the best specific combiner for less seeded type. The cross combination $P_4 \times P_6$ (7.50**) showed the highest significant positive SCA effects followed by $P_2 \times P_3$ (4.80*) and $P_3 \times P_4$ (4.53*) for 100-seed weight (Table 5). Hence, the cross $P_4 \times P_6$ was considered as the best specific combination to increase the seed weight. Banik (2003) reported in snake gourd, the cross combination $P_1 \times P_2$ showed the best specific combiner for increasing 100-seed weight.

SCA effects along with GCA effects and status of GCA effects of parents

The best crosses for studied 19 traits with significant SCA effects showing GCA effects and its status of parents were listed in Table 6. Combiners were mentioned as low (L), medium (M) and high (H) according to their GCA effects. The results obtained from this table indicated that, the parents involved in the best crosses of different characters were H × H, H × M, M × M, H × L, L × H, L × M, M × L, L × L types of general combiners. The results indicated that high SCA effects can occur not only in crosses with H × H combination but also in other combinations *viz.*, H × M, M × M, H × L, L × H, L × M, M × L, L × L. Kaniti (2015), Nath *et al.* (2018) and Singh *et al.* (2018) also reported similar types of results in bitter gourd, sponge gourd and mustard, respectively. The desirable cross combinations with M × M, M × L and L × L types of general combiners were obtained for specific trait which may be due to complementary (dominance x dominance) gene effects. Similar results were reported by Nath *et al.* (2018) in mungbean and Yadav *et al.* (2008) in bitter gourd. The crosses which had high significant SCA effects involving one good (high) combiner and the other medium or poor (H × M, H × L, H × M, L × H) might be due to epistasis like additive × dominance type of interactions which is considered as non-fixable genetic components, indicating possibility to obtain desirable transgressive segregants in latter generations from such crosses by using pedigree method of breeding. Nath *et al.* (2018) also reported similar type of results in pigeon pea and mungbean, respectively. Venkateswarlu and Singh (2001) suggested that high × low GCA combination could produce transgressive segregants if the additive genetic system present in the good combiner and complementary epistatic effect act in the same direction to maximize the desirable plant attributes. These crosses may be also exploited for improvement through heterosis breeding. For the characters associated with the crosses having

one of the parents with high GCA effects (H × M, H × L, H × M, L × H), population improvement with recurrent selection or reciprocal recurrent selection would appear to be highly rewarding because this type of selection utilizes both additive and non-additive genetic variation. Quamruzzaman *et al*. (2020a) suggested that recurrent and reciprocal recurrent selection procedures should be exploited for the improvement of those characters, where both additives as well as non-additive variances are present. Kaniti (2015) also reported similar type of results in bitter gourd. The desirable cross combinations involving H × H types of general combiners may be due to additive type of general combiners (additive × additive) which are heritable and fixable in nature; these types of combination may be exploited further using pedigree method of breeding for the development of pure line and this could be more profitable. Yadav *et al.* (2008); Kaniti (2015) and Singh *et al*., 2010 also reported similar types of results. Sirohi and Chaudhury (1977) in bitter gourd observed that F_1 hybrids gave good performance either of two parental lines is of high general combining ability effects for yield and its component characters. Similar results were also reported by Khan *et al*. (2017) and Kaniti (2015) in bitter gourd. The cross combinations involving L × L combiners reflected non-additive gene action which are non-fixable in nature and could be exploited only through heterosis breeding. Similar type of results was also reported by Singh *et al*. (2010). High SCA effects in the crosses involving L × L combining parents were possibly due to intra- and inter allelic interaction as reported by Quamruzzaman *et al*. (2020b) in bottle gourd. Superiority of L × L combinations may be due to interaction between favorable gene combinations of the parents as reported by Ram *et al*. (1999) in bitter gourd.

Table 6. The best crosses showing significant SCA effects along with GCA effects and status of GCA effects of parents in snake gourd for 19 traits

Characters	Crosses	SCA effects	GCA effects of parents		GCA status of parents
			Female parent	Male parent	
Main vine length (cm)	$P_4 × P_6$	2.72**	2.99**	0.06	H × M
	$P_1 × P_4$	2.08**	-0.73**	2.99**	L × H
	$P_4 × P_5$	1.78**	2.99**	-0.36	H × L
	$P_2 × P_4$	1.25*	-1.07**	2.99**	L × H
Number of nodes on main vine	$P_3 × P_7$	10.39*	-2.3	-1.56	L × L
	$P_4 × P_5$	10.10*	15.03**	-4.93**	H × L
	$P_1 x P_4$	10.06*	-6.56**	15.03**	L × H
	$P_4 × P_6$	9.18*	15.03**	2.66	H × M
Days to 1st male flower opening	$P_5 × P_7$	-8.35**	4.34**	-2.06**	L × H
	$P_1 × P_7$	-7.89**	2.79**	2.06**	L × H
	$P_2 × P_5$	-6.43**	-3.99**	4.34**	H × L
	$P_5 × P_6$	-6.24**	4.34**	-3.51**	L × H

| Characters | Crosses | SCA effects | GCA effects of parents | | GCA status of parents |
			Female parent	Male parent	
Days to 1st female flowering opening	P$_1$ × P$_5$	-7.72**	2.90**	2.42**	L × L
	P$_2$ × P$_5$	-7.17**	-1.66**	2.42**	H × L
	P$_3$ × P$_5$	-7.17**	-0.66	2.42**	M × L
	P$_5$ × P$_6$	-4.79**	2.42**	-3.03*8	L × H
Node number at 1st male flower open	P$_1$ × P$_7$	-5.15**	1.13	0.87	L × L
	P$_5$ × P$_6$	-3.78*	0.21	-1.90**	M × H
Node number at 1st female flower opeı	P$_1$ × P$_4$	-4.86**	1.41*	1.75*	L × L
	P$_1$ × P$_2$	-4.03**	1.41*	-0.48	L × M

H = Significant desirable GCA effects (+ or -); M= non-significant desirable GCA effects (+ or -); L = undesirable GCA effects (+ or -)

Table 6. Continued.

| Characters | Crosses | SCA effects | GCA effects of parents | | GCA status of parents |
			Female parent	Male parent	
Days to 1st fruit harvest	P$_2$ × P$_5$	-7.44**	0.37	-0.63	L × M
	P$_3$ × P$_5$	-6.96**	-0.12	-0.63	M × M
	P$_2$ × P$_7$	-4.00**	0.37	-1.41*	L × H
	P$_1$ × P$_5$	-3.26**	2.18**	-0.63	L × M
Individual fruit weight (g)	P$_1$ × P$_3$	46.20**	14.98**	-7.12*	H × L
	P$_3$ × P$_7$	29.83**	-7.12*	-30.31**	L × L
	P$_4$ × P$_5$	27.54**	-2.42	1.62	L × M
	P$_5$ × P$_7$	27.43**	1.62	-30.31**	M × L
Number of fruits/ plant	P$_4$ × P$_5$	14.06**	-4.63**	-2.89*8	L × L
	P$_2$ × P$_6$	12.81**	2.33*	8.07**	H × H
	P$_2$ × P$_7$	11.55**	2.33*	-1.67	H × L
	P$_1$ × P$_3$	7.40*	-2.75*	1.55	L × M
Fruit length (cm)	P$_1$ × P$_2$	3.32**	5.18**	4.37**	H × H
	P$_2$× P$_6$	3.29**	4.37**	0.88	H × M
Fruit diameter (cm)	P$_4$ × P$_7$	0.41*	0.12	0.01	M × L
	P$_2$ × P$_5$	0.36*	-0.02	-0.13*	L × L
Number of seeds/ fruit	P$_2$ × P$_4$	27.25**	2.85	0.77	M × L
	P$_4$ × P$_5$	19.36**	0.77	3.74*	L × H
	P$_3$ × P$_6$	16.99**	-1.63	-4.15*	L × L
	P$_1$ x P$_4$	12.92**	2.51	0.77	M × L

H = Significant desirable GCA effects (+ or -); M= non-significant desirable GCA effects (+ or -); L = undesirable GCA effects (+ or -).

Table 6. Continued.

Characters	Crosses	SCA effects	GCA effects of parents		GCA status of parents
			Female parent	Male parent	
100-seed weight	$P_4 \times P_6$	7.50**	0.31	0.23	L × L
	$P_2 \times P_3$	4.80**	1.44	2.03*	M × H
	$P_3 \times P_4$	4.53**	2.03*	0.31	H × L
Number of primary branches/ plant	$P_2 \times P_3$	1.82**	0.19	0.07	M × L
Fruit flesh thickness (cm)	$P_1 \times P_7$	0.113**	0.018	0.018	M × M
Number of locules/ fruit	$P_2 \times P_5$	0.667*	0.153	-0.106	M × L
Fruit yield/ plant (kg)	$P_2 \times P_6$	4.60**	1.12**	2.23**	H × H
	$P_4 \times P_5$	4.39**	-1.15	-0.47	L × L
	$P_1 \times P_3$	4.20**	0.07	-0.05	L × L
	$P_2 \times P_7$	2.26**	1.12**	-1.74**	H × L
	$P_3 \times P_7$	2.14**	-0.05	-1.74**	L × L
	$P_5 \times P_7$	2.03**	-0.47	-1.74**	L × L
Fruit yield/ hectare (tons)	$P_2 \times P_6$	14.39**	3.49**	6.96**	H × H
	$P_4 \times P_5$	13.71**	-3.59**	-1.47	L × L
	$P_1 \times P_3$	13.12**	0.21	-0.16	L × L
	$P_2 \times P_7$	7.05**	3.49**	-5.44**	H × L
	$P_3 \times P_7$	6.70**	0.16	-5.99**	L × L
Fruitfly infestation (%)	$P_1 \times P_4$	-2.84**	-0.73*	-0.02	H × M
	$P_3 \times P_7$	-1.73**	-0.46	-0.07	M × M
	$P_2 \times P_7$	-1.40*	-0.37	-0.07	M × M
	$P_2 \times P_6$	-1.26*	-0.37	-0.40	M × M

Conclusion

Combining ability studies involving 7 × 7 half-diallel crosses indicated both additive and non-additive gene action in the expression of different quantitative characters. Additive gene action was found to be predominant for most of the characters. The genotypes TC 05 (P₂) and TC 46 (P₆) were the best general combiners for promoting earliness as well as most other important characters *viz.*, number of fruits/ plant, individual fruit weight and fruit yield/ plant/ hectare. Genotypes TC 05 (P₂) and TC 46 (P₆) were also good for fruit length and fruit diameter, respectively. The genotype TC 33 (P₄) was best for main vine length

and number of nodes on main vine. The genotype TC 24 (P_3) was superior for long fruit and 100-seed weight, while the genotype TC 02 (P_5) was good for number of seeds/ fruit and TC 01 (P_1) best for less fruit fly infestation including individual fruit weight and fruit length. Significant SCA effects were displayed for early female flowering in the cross $P_1 \times P_5$; early male flowering in $P_5 \times P_7$; node number at 1st female flower opening in $P_1 \times P_2$ and $P_1 \times P_4$; node number at 1st male flower opening in $P_1 \times P_7$ and $P_5 \times P_6$; main vine length in $P_1 \times P_4$, $P_4 \times P_6$, $P_4 \times P_5$ and $P_2 \times P_4$; primary branches/ plant in $P_2 \times P_3$; fruits/ plant in $P_1 \times P_3$, $P_2 \times P_6$, $P_2 \times P_7$ and $P_4 \times P_5$; individual fruit weight in $P_2 \times P_5$, $P_3 \times P_5$, $P_2 \times P_7$ and $P_1 \times P_3$; fruit yield/ plant/ hectare in $P_1 \times P_3$, $P_2 \times P_6$, $P_4 \times P_5$, $P_2 \times P_7$ and $P_5 \times P_7$; early fruit harvest in $P_2 \times P_5$, $P_3 \times P_5$, $P_2 \times P_7$ and $P_1 \times P_3$; fruit length in $P_1 \times P_2$ and $P_2 \times P_6$; less fruit fly infestation in $P_1 \times P_4$, $P_3 \times P_7$, $P_2 \times P_7$ and $P_2 \times P_6$. So, these are the important specific combinations which may be used for the improvement of the respective characters. The desirable cross combinations involving either both or one parent with medium GCA effects and either both parents with low GCA effects may be due to complementary (dominance × dominance) gene effects. The crosses which had high significant SCA effects involving one good (high) combiner and the other medium or poor might be due to epistasis like additive × dominance type of interactions which is considered as non-fixable genetic components. The desirable cross combinations involving both parents with high GCA effects may be due to additive × additive type of interactions which are heritable and fixable in nature.

Acknowledgements

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