Received: 25 Sep 2019 | Revised: 29 Jun 2020 | Accepted: 30 Jun 2020

Electronic Journal of Plant Breeding

Research Article

Combining ability study for yield and quality traits in cucumber (*Cucumis sativus* L.)

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Abstract
Seven cucumber (*Cucumissativus* L.) genotypes (3 lines and 4 testers) were crossed in a line × tester mating design. The resultant 12 hybrids and their parents were evaluated using Randomised Block Design with two replications during Kharif 2018. Sufficient genetic variability was observed for all the characters under study. In this study, the parents L2 (Koradacherry local), T2 (Orathanadu local) and T3 (Aipatti local) exhibited high positive GCA (General Combining Ability) effects for yield related traits and high negative GCA effects for earliness characters. The parent T2 identified in this study may be used in multiple crossing programme to isolate high yielding varieties. Among the hybrid combinations, L2xT3, L1xT2 and L3xT4 expressed the maximum positive significant SCA (Specific Combining Ability) effects for yield and yield associated characters. In the above cross combinations one parent was a good combiner and the other was an average/poor combiner; hence the hybrids can be exploited for transgressive selection.

Key words
Combining ability, *Cucumis sativus*, Line x Tester, GCA, SCA

INTRODUCTION

Cucumber, an ideal summer vegetable crop is chiefly grown as an edible tender fruits. The cucumber fruits with high water content are preferred to be eaten raw in salads, desserts and also as pickled or cooked vegetable. Higher yield is one of the main objectives of crop improvement in cucumber. The success of any breeding procedure is determined by an useful gene combination organized in the form of high combining inbred and heterosis in their crosses. The genetic improvement of yield and its contributing characters are largely depends on the study of general combining ability (GCA) of the parents and specific combining ability (SCA) of the hybrids. GCA in respect to characters is the manifestation of additive gene action for the selection of parents, while SCA in respect to a particular character is the capitalization of non additive gene action in the hybrids (Singh *et al.* 2011). It is an established fact that the dominance is a component of non-additive genetic variance and it helps in the selection of superior parents and crosses for further exploitation of heterosis. In this study, genotypes with good marketable fruit yield and quality traits were subjected to Line x Tester mating design in order to understand the combining ability of seven best cucumber genotypes from Tamilnadu for the exploitation of heterosis.

MATERIALS AND METHODS

Seven Cucumber genotypes (**Table 1)** (3 lines and 4 testers) were inter-mated in Line x Tester mating design. The crosses among lines and testers were attempted during the year 2018 and all the parents along with their 12 F_1 progenies were grown during June, 2018 at Krishi Vigyan Kendra, Needamangalam, Tiruvarur district of Tamil Nadu. The experiment was laid out in randomized block design with two replications. The experimental area represents Cauvery delta region of Tamil Nadu and can be located in 10.77° North latitude and 79.41° East longitude.

The soil was sandy clay loam with neutral pH in the wet land agro eco system. During evaluation of F1 generation along with parents, all the 19 genotypes were sown in 8m x 3m sized beds consisting of pits size 1'x1'x1' and 10 plants were maintained for each replication. Standard agronomic practices and plant protection measures were carried out for good crop development. The observations were recorded for fourteen yield and quality attributing traits of cucumber *viz.,*Vine length, Days to first male flower anthesis, Days to first female flower anthesis, the number of primary branches per vine, Days to first harvest, Fruit length, Fruit weight, Flesh thickness, Fruit Diameter, the number of fruits per vine, Marketable fruit yield per vine, Total soluble solids content, Ascorbic acid content and Total chlorophyll content. Data recorded for plant traits were analyzed according to Analysis of variance (ANOVA) technique as outlined by Steel and Torrie (1980). Combining ability analysis was done by using the line x tester method (Kempthorne, 1957).

Table 1. List of cucumber genotypes used in this study

S.No.	Genotype	Source
	Lines	
1	L1 – Amaravathi local	Thanjavur, Tamilnadu
2	L2- Koradacherry local	Tiruvarur, Tamilnadu
3	L3- Vennamuthupatti local	Pudhukottai, Tamilnadu
	Testers	
1	T1- Kattur local	Thanjavur, Tamilnadu
2	T2-Orathanadu local	Thanjavur, Tamilnadu
3	T3-Aipatti local	Pudhukottai, Tamilnadu
4	T4-Periyakollapatti local	Virudhunagar, Tamilnadu

RESULTS AND DISCUSSION

The analysis of variances of the line x testers for all the characters are presented in **Table 2,** depict the variances due to genotype, parents and crosses and were found significant for all the characters. The variances due to female parents (Lines) were found highly significant to all the characters except flesh thickness. The variances due to male parents (Testers) were significant for fourteen characters taken for the study. Line vs Testers and cross vs parents were also found significant for nine out of fourteen characters studied. Mean performance of the parents and hybrids are presented in **Table 3**. Among the various fourteen traits of cucumber under study, the character total marketable fruit yield per vine exhibited a range from 1.50 (T1) to 2.70 kg (L1) in parents and from 1.85 to 3.84 kg per vine in hybrids. Similar trend was noticed for most of the traits, that the hybrids exhibited better performance than parents.

Table 2. Analysis of variance for line x tester analysis including parents in cucumber

	Df	VL	DFMFA	DFFFA	NPB	DFH	FL	FW	FT	FD	NFP	MFY	TSS	AA	TC
Replication	1	25.12	1.85	0.009	0.47	1.53	3.28	108.02	0.006	0.14	0.52	0.0004	0.007	0.003	0.001
Genotype	18	379.37**	19.79**	52.13**	2.30**	58.61**	28.87**	1283.23**	0.14**	2.11**	7.83**	0.85**	0.69**	0.99**	0.08**
Parent	6	211.48**	24.42**	59.58**	2.88**	45.79**	26.84**	927.26**	0.11**	1.02**	3.94**	0.41**	0.58**	1.13**	0.07**
Line	2	195.02**	33.56**	112.38**	5.04**	81.71**	12.14**	837.44**	0.04	1.28**	4.70**	0.46**	0.53**	1.85**	0.11**
Tester	3	135.16**	25.84**	39.50**	1.96**	36.85**	43.42**	1293.59**	0.16**	1.19**	2.75**	0.45**	0.16**	0.17**	0.01**
Line Vs Tester	1	473.35**	1.90	14.23	1.33*	0.76	6.48*	7.89	0.08*	0.02	6.01**	0.20**	1.92**	2.57**	0.19**
Hybrid	11	360.52**	19.05**	52.06**	2.18**	69.45**	32.31**	1446.33**	0.16**	1.22**	9.06**	0.98**	0.66**	0.89**	0.09**
Hybrid Vs Parent	1	1594.04**	0.02	8.29	0.01	16.35	3.27	1624.95**	0.07*	18.36**	17.60**	2.02**	1.77**	1.24**	0.04**
Error	18	6.16	0.48	3.69	0.29	2.30	1.18	105.24	0.01	0.06	0.38	0.02	0.02	0.03	0.0004

Df = Degrees of freedom

Where, VL=Vine length, DFMFA=Days to first male flower anthesis, DFFFA=Days to first female flower anthesis, NPB=Number of primary branches per vine, DFH=Days to first harvest, FL=Fruit length, FW=Fruit weight, FT=Flesh thickness, FD=Fruit Diameter, NFP=Number of fruits per vine, MFY =Marketable fruit yield per vine, TSS=Total soluble solids, AA =Ascorbic acid, TC=Total chlorophyll content.

https://doi.org/10.37992/2020.1102.106

Table 3. Mean Performance of Parents and Hybrids for 14 characters in Cucumber

	VL	DFMFA	DFFFA	NPB	DFH	FL	FW	FT	FD	NFP	MFY	TSS	AA	TC
LINES(Female)														
L1	184.40	29.70	33.20	6.91	44.80	16.46	228.80	2.21	5.16	12.75	2.70	2.38	4.36	1.92
L2	170.50	34.50	41.65	8.82	50.20	21.20	202.50	2.04	4.07	11.75	2.27	3.04	5.66	2.40
L3	189.60	37.85	48.15	5.66	57.53	17.66	188.50	1.91	3.60	9.74	1.74	2.01	6.23	2.14
TESTERS(Male)														
T1	173.00	39.10	47.20	6.04	48.66	12.95	178.06	1.50	4.05	8.95	1.50	3.13	6.13	2.28
T2	171.00	34.70	38.20	6.78	45.70	22.70	217.55	2.10	4.58	10.95	2.23	3.29	6.65	2.49
T3	158.00	30.30	40.35	7.75	51.32	19.07	237.60	2.13	4.95	11.24	2.54	3.59	6.38	2.41
T4	177.00	34.95	46.40	5.45	55.82	13.55	199.26	1.84	3.17	9.21	1.71	2.90	5.97	2.37
HYBRID														
L1T1	211.15	36.85	45.05	6.50	54.78	17.76	207.90	1.45	5.06	12.25	2.45	3.18	6.16	2.06
L1T2	185.65	28.40	32.20	9.16	42.95	21.89	246.52	2.37	6.10	15.50	3.60	4.02	7.04	2.57
L1T3	179.75	34.85	42.15	5.87	52.77	12.55	188.50	1.73	5.54	11.36	2.04	3.48	5.72	2.24
L1T4	164.45	38.05	46.90	6.97	59.16	16.60	221.80	2.08	4.66	10.32	2.21	2.75	6.82	1.97
L2T1	192.95	33.85	43.15	5.92	54.66	14.72	196.88	2.00	5.41	9.76	1.85	3.00	6.08	2.28
L2T2	200.85	30.65	33.75	7.12	41.28	23.51	263.80	2.54	6.85	14.90	3.84	4.12	7.10	2.58
L2T3	203.40	32.15	36.80	8.26	48.51	25.23	240.26	2.27	7.10	15.35	3.62	3.94	6.88	2.63
L2T4	182.85	37.70	48.00	6.05	60.26	20.66	205.84	1.88	4.82	10.10	1.94	2.51	5.84	2.34
L3T1	189.05	38.65	42.70	7.37	53.32	14.42	173.43	2.10	5.21	12.91	2.10	3.82	4.82	2.47
L3T2	186.45	35.00	45.55	6.10	56.71	17.30	236.12	1.97	6.32	10.10	2.26	3.00	6.73	2.53
L3T3	169.50	34.10	40.00	6.72	50.09	14.36	227.20	2.08	5.78	11.42	2.48	3.79	6.32	2.18
L3T4	192.50	33.65	38.10	5.77	48.73	20.15	244.03	2.22	5.14	10.85	2.53	2.65	5.95	2.43
S.E. (d)±	2.48	0.69	1.92	0.54	1.51	1.08	10.25	0.11	0.24	0.61	0.15	0.16	0.18	0.02
C.D. (0.05)	5.21	1.46	4.03	1.13	3.19	2.28	21.54	0.24	0.52	1.29	0.33	0.34	0.38	0.04

Where,
VL=Vine length, DFMFA=Days to first male flower anthesis, DFFFA=Days to first female flower anthesis, NPB=Number of primary branches per vine, DFH=Days to first harvest, FL=Fruit length, FW=Fruit weight, FT=Flesh thickness, FD=Fruit Diameter, NFP=Number of fruits per vine, MFY =Marketable fruit yield per vine, TSS=Total soluble solids, AA =Ascorbic acid, TC=Total chlorophyll content.

Estimates of GCA effects (**Table 4**) of earliness (days to first male flower anthesis, days to first female flower anthesis and days to first harvest) found to be non-significant for most of the lines. Line L2 alone expressed a negative significance of GCA for days to first male flower anthesis and testers, T2 and T3 were found to be the best combiners due to negatively significant GCA effects for earliness. Parents with negative GCA effects for earliness were reported by various researchers (Munshi *et al*. 2006, Yadav *et al*. 2007, Dogra and Kanwar, 2011, Kumar *et al*. 2011) in cucumber. The estimates of GCA effects revealed that none of the parents exhibited good GCA for all the characters together. It was also reported by Airina *et al.* 2017 in Cucumber. In the present study, among the seven parents, L2 and T2 were positively significant towards total marketable fruit yield per vine and found to be good combiners. For other traits, parent L2 expressed a maximum positive significance to vine length, fruit length, flesh thickness, fruit diameter, ascorbic acid content and total chlorophyll content followed by L1 which was positively significant only to ascorbic acid content among the lines. For fruit weight, days to first harvest, the number of primary branches per vine and total soluble solids content (TSS), all the three lines expressed non-significant effect and were designated to be average combiners. Testers T2 expressed a positive significance for ten out of fourteen traits followed by T3 which expressed a positive significance for three characters. Significant positive GCA effect for characters positively associated to fruit yield were found in T1 and L2 for vine length, T2 for the number of primary branches per vine, L2 and T2 for fruit length, T2 for fruit weight, T2 and L2 for flesh thickness, T2,T3 and L2 for fruit diameter, T2 and T3 for number of fruits per vine, T2 and L2 for fruit yield, T2 and T3 for TSS, T2, L2 and L1 for ascorbic acid content and T2 and L2 for total chlorophyll content. Among the parents, T2, L2, T3 and L1 were found to be good combiners. These parents were superior for most of the characters. An inter mating population involving all possible crosses among themselves subjected to bi-parental mating in early generation will be expected to offer the maximum promise in breeding for yield, quality and earliness. Similar results were reported by Nehe *et al*. (2007) in cucumber and Niyaria and Bhalala (2001) in ridge gourd. Also it was observed that the high general combining ability effects observed were primarily due to additive and additive x additive gene effects (Griffing, 1956). Similar results were reported by Musmade and Kale (1986a) in cucumber, Maurya *et al*. 1993 in bottle gourd, Shaha *et al*., (1999) in ridge gourd and Gill and Kumar (1988) in watermelon.

Table 4. Estimate of general combining ability (GCA) effects of parents for different characters of cucumber

	VL	DFMFA	DFFFA	NPB	DFH	FL	FW	FT	FD	NFP	MFY	TSS	AA	TC
LINES														
L1	-2.96*	0.05	0.38	0.31	0.48	-1.06*	-4.84	-0.15**	-0.33**	0.29	-0.00	0.00	0.15*	-0.15**
L2	6.80**	-0.90**	-0.77	0.02	-0.75	2.77**	5.67	0.12*	0.38**	0.46	0.24**	0.04	0.19*	0.10**
L3	-3.84**	0.86**	0.39	-0.33	0.28	-1.70**	-0.83	0.03	-0.05	-0.75**	-0.23**	-0.04	-0.33**	0.05*
TESTERS														
T1	9.50**	1.96**	2.44**	-0.22	2.32**	-2.63**	-28.29**	-0.21**	-0.44**	-0.43	-0.44**	-0.02	-0.60**	-0.08**
T2	2.77	-3.14**	-4.03**	0.64*	-4.95**	2.64**	27.79**	0.24**	0.76**	1.43**	0.66**	0.35**	0.67**	0.20**
T3	-4.00**	-0.79*	-1.55	0.13	-1.48*	-0.88	-2.37	-0.03	0.48**	0.64*	0.13	0.38**	0.02	-0.01
T4	-8.28**	1.97**	3.14**	-0.56*	4.11**	0.88	2.87	0.00	-0.79**	-1.65**	-0.35**	-0.72**	-0.09	-0.11**
SE (Lines)	1.09	0.23	0.66	0.18	0.47	0.43	3.28	0.04	0.10	0.23	0.05	0.06	0.06	0.02
SE (Testers)	1.26	0.27	0.77	0.21	0.55	0.50	3.78	0.05	0.11	0.26	0.06	0.07	0.07	0.02

* =Significant at 5% level of significance   ** =Significant at 1% level of significance

Where,

VL=Vine length, DFMFA=Days to first male flower anthesis, DFFFA=Days to first female flower anthesis, NPB=Number of primary branches per vine, DFH=Days to first harvest, FL=Fruit length, FW=Fruit weight, FT=Flesh thickness, FD=Fruit Diameter, NFP=Number of fruits per vine, MFY =Marketable fruit yield per vine, TSS=Total soluble solids, AA =Ascorbic acid, TC=Total chlorophyll content.

The SCA effects of hybrids have been attributed to the combination of positive favorable genes from different parents or might be due to the presence of linkage in repulsion phase. Hence, the selection of hybrids based on SCA effects would excel in their heterotic effect. In the present study, out of the twelve hybrid combinations, five hybrids exhibited higher magnitude of significant positive SCA effects for marketable fruit yield per vine were L2xT3 (good x average), L3xT4 (poor x poor), L2xT2 (good x good), L1xT2 (average x good) and L1xT1 (average x poor). In the cross L2 x T2, both the parents were good combiners and governed by an additive gene action which is fixable and heritable in nature. Therefore, following pedigree method or any other selection procedure, true breeding good progenies can be identified from the segregating population in succeeding generations. In the cross L2 x T3, only one parent was a good combiner. Higher fruit yield in these cross can be exploited by heterosis breeding. The estimation of SCA revealed that L2xT3, L1xT2, L3xT4 were found to exhibit maximum positively significant SCA for yield and yield component traits (**Table 5**).The highest positive significant SCA effects were observed in L1xT1 (16.40) and L3xT4 (16.40) for vine length, L1xT2 (1.39) for number of primary branches per vine, L2xT3 (5.08) for fruit length, L3xT4 (20.97) for fruit weight, L1xT2 (0.22) and L3xT1 (0.22) for flesh thickness, L2xT3 (0.58) for fruit diameter, L2xT3 (2.18) for number of fruits per vine, L3xT1 (0.53) for TSS, L1xT4 (0.47) for ascorbic acid content, L2xT3 (0.18) for total chlorophyll content.

The cross L2xT3 exhibited a maximum positive significant SCA effect to yield associated traits among the twelve hybrid combinations and the same cross combination contributed a maximum positive significant effect for fruit yield per vine (0.67) also. Similar findings for identification of superior parental lines, tester and hybrids with GCA and SCA effects were reported for fruit yield traits by Golabadi *et al*. (2015), Kumar *et al*. (2013), Musmade and Kale (1986b) and Tasdighi and Baker (1981). Negatively significant cross combinations were found in L3xT4 (poor x poor), L1xT2 (average x good) and L2xT1 (good x poor) for days to first male flower anthesis, L3xT4 (average x poor) and L1xT2 (average x good) for days to first female flower anthesis and L3xT4 (average x poor), L2xT2 (average x good) and L1xT2 (average x good) for days to first harvest. SCA effect of these crosses indicated inclusion of at least one good combining parent in superior hybrids. However, few crosses involved both parents with poor combining abilities. This suggested the non compulsion of the involvement of parents in the SCA effect of any cross combination or on the GCA effects. The superiority of SCA effects might be attributed to complementary type of gene action or involvement of non allelic interaction of fixable and non fixable genetic variance. (Patel and Desai, 2008 and Purohit, 2007). The higher SCA effect was observed in the cross between poor x poor general combiners might be due to the non-additive gene effects and could be exploited through hybridization, which is possible in the crop due to the monoecious nature of the flowers. The cross involving poor x good general combiners can produce good transgressive segregants in later generations. Crosses between average × poor combiners might be used for the exploitation of heterosis in the F_1 generation. The crosses involving parents with good × good combiners revealed the additive × additive type of gene action. It was also reported by Ramesh Kumar *et al*. (2018) in Cucumber.

Table 5. Estimate of specific combining ability (SCA) effects of hybrids for different characters of cucumber

Crosses	VL	DFMFA	DFFFA	NPB	DFH	FL	FW	FT	FD	NFP	MFY	TSS	AA	TC
L1xT1-5	16.40**	0.35	1.04	-0.41	0.05	3.19**	20.01*	-0.25*	0.16	0.32	0.32*	-0.15	0.33*	-0.06**
L1xT2-7	-2.37	-3.00**	-5.35**	1.39**	-4.51**	2.05*	2.55	0.22*	0.00	1.71**	0.37*	0.30*	-0.07	0.16**
L1xT3	-1.50	1.10*	2.12	-1.39**	1.83	-3.77**	-25.31**	-0.15	-0.27	-1.64**	-0.67**	-0.26	-0.73**	0.03
L1xT4-1	-12.52**	1.54**	2.19	0.40	2.63*	-1.48	2.76	0.17	0.11	-0.39	-0.01	0.11	0.47**	-0.13**
L2xT1-1	-11.57**	-1.70**	0.29	-0.69	1.16	-3.69**	-1.53	0.03	-0.19	-2.34**	-0.52**	-0.38*	0.21	-0.09**
L2xT2-2	3.07	0.20	-2.65	-0.36	-4.94**	-0.16	9.31	0.13	0.05	0.94	0.37**	0.37*	-0.04	-0.08**
L2xT3-9	12.38**	-0.65	-2.08	1.29**	-1.19	5.08**	15.94*	0.13	0.58*	2.18**	0.67**	0.16	0.38*	0.18**
L2xT4-	-3.88	2.14**	4.44**	-0.24	4.97**	-1.24	-23.72**	-0.30**	-0.44	-0.79	-0.53**	-0.16	-0.55**	-0.01
L3xT1-4	-4.83*	1.34*	-1.32	1.10*	-1.21	0.49	-18.48*	0.22*	0.03	2.02**	0.20	0.53**	-0.54**	0.15**
L3xT2-	-0.70	2.79**	7.99**	-1.03*	9.45**	-1.90	-11.86	-0.36**	-0.05	-2.65**	-0.74**	-0.68**	0.11	-0.08**
L3xT3-1	-10.88**	-0.46	-0.04	0.10	-0.64	-1.31	9.38	0.02	-0.30	-0.54	-0.00	0.10	0.34*	-0.21**
L3xT4-6	16.40**	-3.67**	-6.63**	-0.16	-7.60**	2.72**	20.97**	0.12	0.32	1.17*	0.54**	0.05	0.08	0.14**
SE (Hybrids)	2.18	0.47	1.33	0.37	0.95	0.87	6.56	0.08	0.20	0.46	0.11	0.12	0.12	0.01

* =Significant at 5% level of significance ** =Significant at 1% level of significance

Where,

VL=Vine length, DFMFA=Days to first male flower anthesis, DFFFA=Days to first female flower anthesis, NPB=Number of primary branches per vine, DFH=Days to first harvest, FL=Fruit length, FW=Fruit weight, FT=Flesh thickness, FD=Fruit Diameter, NFP=Number of fruits per vine, MFY =Marketable fruit yield per vine, TSS=Total soluble solids, AA =Ascorbic acid, TC=Total chlorophyll content.

In the present study, the parents L2 (Koradacherry local), T2 (Orathanadu local) and T3 (Aipatti local) exhibited high positive GCA effects for yield related traits and high negative GCA effects for earliness characters. It was noticed that these parents were good genetic combiners and showed significant values for most of the traits. This suggested that the use of these genotypes as one of the parents would produce good hybrid combinations. The parent T2 identified in this study can be used in a multiple crossing programme for isolating high yielding varieties. Among the hybrid combinations, L2xT3 followed by L1xT2 and L3xT4 expressed maximum positive significant SCA effects for yield and yield associated characters. The same findings were found that these three hybrid combinations were with negative significant SCA effects for earliness like days to first male flower anthesis, days to first female flower anthesis and days to first harvest. Therefore, these crosses can be exploited to isolate transgressive segregants or single plant selection that could be effective in advanced segregating generations.

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