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Combining ability studies in snap melon (*Cucumis melo* var. momordica)

S Praneetha and R Muthuselvi

Abstract
Combining ability analysis was computed for thirty four traits in thirty six hybrid combinations (including parents) in snap melon. *GCA* and *SCA* variances were significant for all the characters. The parent P_6 was found to be the best combiner for number of fruits per plant, fruit yield per plant, flavonoid and calcium content. The parent P_2 ranked 1st for fruit length, fruit girth, fruit weight, total carotene, fibre and alkaloid content. The parent P_5 recorded positive and significant general combining ability effects for days to 1st female flower appearance. The hybrid P_2xP_4 exhibited positive and significant *sca* effects for the trait fruit length, fruit girth, fruit weight and fruit yield per plant.

Keywords: Snap melon, general combining ability, specific combining ability

Introduction
Snap melon (*Cucumis melo* var. *momordica*) is one of the important group of Cucurbitaceous crop worldwide and play an important role in international trade. India is being one of the secondary centre of origin of *Cucumis melo* var. *momordica* which comprises nearly 40 species (Whitaker and Davis 1962) [7] and is still remains as an under exploited crop in India. This is a potent crop, the fruits are rich in many nutrients and possess numerous nutraceutical and pharmaceutical properties. It is cultivated in various parts of the world including India and Pakistan. It is very popular in arid and semi-arid regions. In North India snap melon is commonly called as 'Phoot' which means "To split". The large scale cultivation of 'Phoot' is confined to the states of UP, Rajasthan, Haryana, Punjab and Bihar in India. In Kerala it is called as Kanivellari (fruit cucumber) or Pottuvellari (split/crack cucumber) and cultivated in Thrissur, Ernakulam and Malappuram districts of the state. In Tamil Nadu, it is grown in Ramanathapuram, Madurai, Virudhunagar, Tirunelveli, Villupuram, Karur and Pudukkottai districts.

Combining ability analysis is one of the powerful tools available which give the estimates of combining ability effects and aids in selecting desirable parents and crosses for further exploitation. Sprague and Tatum (1942) [5] suggested that GCA could be considered as the average performance of the strain in a series of crosses and might be due to additive gene effects. The specific combining ability is the deviation from the performance predicted on the basis of general combining ability and its effects are due to non-additive gene action (Allard 1960) [1].

Materials and Methods
The present investigation was carried out at the College Orchard, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore during 2016-19 to study the genetic architecture for yield, nutritional and quality traits in snap melon (*Cucumis melo* var. *momordica*). Twenty three genotypes of snap melon (*Cucumis melo* var. *momordica*) were used for evaluation and screening. The details of the germplasm used in the study are described in Table 1.

Table 1: Details of snap melon genotypes used in the study

Treatments/Genotypes	Name of the genotypes/varieties	Source
G_1	Virudhunagar local	Virudhunagar District
G_2	Tanjore local	Tanjore District
G_3	Amaravathi local	Sivagangai District
G_4	Vilavayal local	Pudukkottai District
G_5	Sathyamangalam local	Erode District
G_6	Kariapatti local	Virudhunagar District
G_7	Thirumangalam short	Madurai District.
G_8	Pattukottai local	Tanjore District
G_9	Kalacherry local	Cuddalore District
G_{10}	Kodikulam local	Virudhunagar District
G_{11}	Vizhupuram local	Vizhupuram Dt.
G_{12}	Ranne bannur	Haveri District, Karnataka
G_{13}	Gujarat local	Gujarat
G_{14}	Namanasamuthiram local	Pudukkottai District
G_{15}	Watrap local	Virudhunagar District
G_{16}	Thirumangalam long	Madurai District
G_{17}	Kothayapatti local	Pudukkottai District
G_{18}	Melur local	Pudukkottai District
G_{19}	PAU	Punjab Agricultural University, Punjab.
G_{20}	Kodungallur local	Mala Block, Kerala
G_{21}	Pusa Shandar	IARI, New Delhi
G_{22}	Thambipatti local	Virudhunagar District
G_{23}	Kulasekaranatham local	Tuticorin District

These all genotypes were raised in the field and the following observations were recorded *viz.*, vine length, number of primary branches per plant, internodal length, stem girth, node at which 1st male flower appearance, node at which 1st female flower appearance, days to 1st male flower appearance, days to 1st female flower appearance, number of male flowers per plant, number of female flowers per plant, days to 1st harvest, length of the fruits, girth of the fruits, weight of the fruits, flesh thickness, number of fruits per plant, fruit yield per plant and quality parameters like TSS, acidity, TSS acid ratio, ascorbic acid, reducing sugar and non-reducing sugar, total carotene content, moisture content, protein content, fibre, carbohydrate, alkaloid, flavonoid, phenolics, calcium and iron content. All the genotypes were evaluated and crossed with full diallel mating design with 36 hybrid combinations including parents.

Results and Discussion

ANOVA for combining ability and heterosis for yield reflects significant differences among the crosses for all the characters.

Table 2: Analysis of variance for combining ability in snap melon

Characters	Mean squares of			GCA/SCA
	gca	*Sca*	Reciprocal	
Vine length (m)	0.34**	0.10**	0.13**	3.40
Number of primary branches	1.14**	1.15**	0.77**	0.99
Internodal length (cm)	0.83**	1.75**	0.59**	0.47
Stem girth (cm)	0.06**	0.41**	0.29**	0.14
Node at which 1st male flower appearance	0.71**	0.66**	0.33**	1.07
Node at which 1st female flower appearance	0.35**	0.37**	0.35**	0.94
Days to 1st male flower appearance	1.28**	3.12**	1.72**	0.41
Days to 1st female flower appearance	0.24**	3.54**	1.28**	0.06
Number of male flowers per plant	38.96**	43.31**	82.60**	0.89
Number of female flowers per plant	10.75**	33.13**	10.56**	0.32
Days to 1st harvest	1.40**	11.65**	4.08**	0.12
Length of the fruit (cm)	40.93**	95.21**	72.73**	0.42
Girth of the fruit (cm)	13.24**	16.97**	19.46**	0.78
Weight of the fruit (kg)	0.51**	0.59**	0.66**	0.86
Peduncle length (cm)	0.33**	0.23**	0.24**	1.43
Flesh thickness (cm)	0.14**	0.93**	0.23**	0.15
Number of fruits per plant	0.21**	1.31**	2.43**	0.16
Yield/plant (kg)	5.90**	10.08**	9.38**	0.58
TSS (ºBrix)	0.88**	0.73**	0.42**	1.20
Titratable acidity (%)	0.007**	0.009**	0.008**	0.77
TSS/Acid ratio (%)	5.48**	5.37**	5.51**	1.02
Ascorbic acid (mg $100g^{-1}$)	0.53**	1.64**	2.57**	0.32
Reducing sugar (%)	0.21**	0.13**	0.19**	1.61
Non reducing sugar (%)	0.69**	0.24**	0.52**	2.87
Total carotene (mg $100g^{-1}$)	0.004**	0.011**	0.002**	0.36

Protein (g 100g^{-1})	68.51**	21.08**	56.06**	3.25
Fibre (g 100g^{-1})	0.004**	0.003**	0.006**	1.33
Carbohydrate content (g 100g^{-1})	0.002**	0.010**	0.003**	0.20
Alkaloid content (mg 100g^{-1})	5.02**	7.18**	1.12**	0.69
Flavonoid content (mg 100g^{-1})	0.14**	0.89**	0.16**	0.15
Phenol content (mg 100g^{-1})	126.65**	42.93**	32.12**	2.95
Calcium (mg 100g^{-1})	0.006**	0.005**	0.005**	1.20
Iron (mg 100g^{-1})	0.003**	0.013**	0.004**	0.23

**-Significant at 1%.

Results and Discussion

Morphological traits

Among the parents, P_1 and P_4 were found to be best general combiners for number of primary branches, stem girth and vine length. The hybrid P_5 was found to be best for the characters *viz*., node at which first male flower appearance, node at which first female flower appearance, days to first female flower appearance, internodal length, peduncle length, flesh thickness and vine length which indicated dominance x dominance, additive x dominance and dominance x additive types of gene interaction. The hybrid *viz.,* $P_1 \times P_3$ was found to be good specific combiner for number of primary branches, node at which first male flower appearance, node at which first female flower appearance and stem girth. Also the hybrid P_1xP_4 was found to be good specific combiner for the traits *viz*., days to first female flower appearance, peduncle length and vine length which indicated dominance x dominance, additive x dominance and dominance x additive types of gene interaction. This was in accordance with the results of (Allard 1960) [1], Manikandan *et al*., 2017 [3] in ash gourd. Hence, these hybrids can be forwarded by cyclic types of mating through recurrent selection.

Flowering traits

Among the parents, P_1, P_2, P_3, P_4 and P_6were found to be the best general combiners for days to first female flower. The significant *gca* value was recorded in the parent P_2 and P_6 which may combine better with other parents for days to first male flower appearance and nodes to first female flower and the hybrids *viz.,* $P_2 \times P_6$ and $P_4 \times P_6$ were found to be good specific combiners which indicated dominance x dominance, additive x dominance and dominance x additive types of gene interaction. This result confirmed the findings of Pandey *et al.* (2005) [4] in ash gourd and Tamilselvi (2010) in pumpkin.

Harvesting trait: The parent P_4 recorded negative significant *gca* value for the trait days to first harvest. The hybrid $P_1 \times P_6$ was found to be a good specific combiner which indicated dominance x dominance, type of gene interaction.

Yield traits

The estimates of *gca* for average, fruit length, fruit girth, fruit weight and number of fruits per plant and yield per plant showed that P_2 and P_6 was the best general combiner and when it used in crossing, it increase these parameters. This resulted in increase of, fruit length, fruit girth, fruit weight, number of fruits per plant and yield per plant.

The following hybrids P_2x P_6, P_2x P_3 and P_2x P_4 recorded best specific combining ability when P_3 and P_6 were used as the male parent. It may be due to expression of dominant alleles. The parents P_4 were negatively significant gca effects were noticed for the trait yield per plant, fruit length, fruit girth, fruit weight, number of fruits per plant and yield though one or both the parents involved in the cross were poor combiners indicating the role of complementary gene action this results are in agreement with that of (Bahari *et al*., 2012) [2] in watermelon.

Quality traits

The parents P_3 and P_5 were the best general combiners for total soluble solids, acidity, TSS acid ratio, ascorbic acid, reducing sugar, non-reducing sugar, protein, carbohydrate, alkaloid, flavonoid, phenolics, calcium and iron content. The parents *viz*., P_1, P_2 and P_4 were best general combiners for the traits total carotene and fibre content. The evaluation of genotypes based on *per se*, combining ability, heterosis, correlation and path analysis in first season and second season revealed the excellent performance of the parents Amaravathi local (P_1), Kothayapatti local (P_2), Thambipatti local (P_3), Kariaptti local (P_4), Gujarat local (P_5) and Thirumangalam long (P_6). The hybrids P_4xP_2, P_4xP_6, P_2xP_6 and P_3xP_2 were found to be a good specific combiner for growth, yield and quality traits which indicated dominance x dominance type of gene interaction. Regarding the evaluation of hybrids, the only hybrid, which ranked top for most of the economic traits, was P_4xP_6. The other promising hybrids were P_4xP_2 and P_3xP_2. These identified parents and hybrids can be recommended for exploitation of their high yield, nutraceutical and pharmaceutical values.

Table 3: Estimates of *gca* (diagonal values), *sca* (above the diagonal) and *rca* effects (below the diagonal) for important yield and quality characters in snap melon

Parents /Hybrids	**Number of female flowers per plant**						**Weight of the fruit**						**Number of fruits per plant**					
	P_1	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**
P_1	-0.96**	-0.14	-1.22**	3.74**	0.00	1.53**	0.01	-0.50**	-0.17**	-0.02	-0.12**	0.45**	-0.22**	-0.21*	0.59**	0.04	0.13	-0.49**
P_2	4.26**	0.85**	3.16**	3.58**	0.56	2.23**	-0.40**	0.15**	0.85**	0.48**	0.56**	-0.21**	-0.25*	0.06	1.44**	0.19	0.15	0.29**
P_3	-1.30**	1.77**	-0.43**	0.84**	2.14**	1.37**	-0.42**	0.81**	0.06**	-0.46**	-0.10**	0.63**	-1.20**	0.13	0.11*	-0.21	-0.34	-0.06
P_4	-0.56	0.82**	2.66**	0.74**	0.07	0.46	0.17**	0.80**	-0.11**	-0.17**	-0.05**	0.47**	-0.63**	1.40**	0.45**	0.02	-0.27	1.29
P_5	3.56**	2.07**	0.50	-1.40**	-1.12**	4.05**	-0.25**	-0.00	-0.10**	0.81**	-0.30**	-0.24**	-0.07	-1.25**	1.80**	-1.29**	-0.10*	0.64
P_6	-1.78**	-2.98**	-2.49**	-3.16**	-0.84*	0.92**	-0.06*	-1.23**	-0.11**	-0.98**	0.32**	0.26**	-1.34**	-1.60**	-1.50**	-0.96**	0.40**	0.13**
	SE (g_i) = 0.12		SE (s_{ij}) =0.29		SE (r_{ij}) =0.34		SE (g_i) = 8.41		SE (s_{ij}) =1.91		SE (r_{ij}) =2.25		SE (g_i) = 4.51		SE (s_{ij}) =0.10		SE (r_{ij}) =0.12	
*- Significance at 5% level **- significance at 1% level							*- Significance at 5% level **- significance at 1% level						*- Significance at 5% level **- significance at 1% level					
Parents /Hybrids	**Yield per plant**						**Total Carotene**						**Carbohydrate**					
	P_1	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**
P_1	0.18**	-1.83**	0.03	-0.93**	-0.02	1.96**	0.01**	-0.00	0.03**	-0.01*	0.04**	-0.02**	0.01**	-0.04**	0.01	-0.06**	0.01**	-0.00
P_2	-0.24	0.03	2.40**	2.17**	2.46**	0.12	0.02**	0.01**	0.07**	0.09**	-0.02*	0.08**	0.02**	-0.03**	-0.04**	-0.07**	-0.05**	0.01**

P_3	-1.57**	2.22**	-0.01	-0.90**	-0.40**	2.66**	0.08**	-0.01	-0.01**	0.01*	0.00	0.03**	0.03**	-0.05**	-0.01**	0.02**	-0.05**	-0.01
P_4	-1.00**	3.85**	0.27*	-1.16**	-0.18	1.80**	0.00	0.01	0.06**	0.02**	0.02*	0.01*	0.01	-0.03**	-0.03**	0.01**	0.06**	-0.12**
P_5	-1.57**	0.98**	2.79**	2.38**	-0.08	-1.15**	-0.03**	-0.01	0.04**	-0.02**	-0.03**	0.04**	0.04**	0.00	-0.02**	0.02**	0.01**	0.01
P_6	0.10	-4.43**	-0.06	-3.15**	0.82**	1.04**	-0.04**	0.02*	0.01	-0.05**	-0.05**	-0.00	0.01	0.09**	-0.09**	0.04**	0.00	-0.00
	SE (g_i) = 4.69		SE (s_{ij}) =0.10		SE (r_{ij}) =0.12		SE (g_i) =2.72		SE (s_{ij}) =6.21		SE (s_{ij}) =7.30		SE (g_i) = 2.19		SE (s_{ij}) =4.99		SE (r_{ij}) =5.88	
*- Significance at 5% level **- significance at 1% level							*- Significance at 5% level **- significance at 1% level						*- Significance at 5% level **- significance at 1% level					

Table 3: Contd…

Parents/Hybrids	Fibre						Alkaloid						Flavonoid					
	P_1	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**
P_1	0.02**	0.04**	0.04**	-0.02**	-0.00	-0.05**	0.70**	0.34	0.38*	0.04	0.01	1.50**	-0.06*	-0.25**	0.55**	0.50**	0.89**	-0.43**
P_2	-0.01*	0.01**	-0.06**	0.01	0.02**	0.05**	0.05	0.70**	-0.32	1.63**	0.76**	1.62**	0.12	0.04	0.39**	0.33**	0.50**	0.42**
P_3	0.03**	0.10**	-0.02**	0.02**	-0.01*	-0.01**	0.48*	-0.41	0.24**	0.91**	1.32**	-0.96**	0.10	0.30**	0.09**	-0.19**	0.16*	-0.01
P_4	-0.03**	0.06**	0.04**	0.02**	0.02**	-0.02**	-1.24**	0.56**	0.99**	-0.31**	1.97**	0.65**	0.35**	0.04	0.16	-0.06*	-0.11	0.50**
P_5	0.00	-0.08**	0.03**	-0.02**	-0.01**	-0.05**	-0.16	0.69**	-1.50**	-0.22	-0.86**	0.04	-0.11	0.30**	0.30**	-0.52**	-0.15**	0.12
P_6	0.06**	-0.08**	0.00	-0.11**	0.03**	-0.02**	-1.28**	-0.70**	-0.10	-0.39	-0.36	-0.46**	-0.15	-0.29**	-0.44**	-0.41**	-0.27**	0.15**
	SE (g_i) = 1.45		SE (s_{ij}) =3.31		SE (r_{ij}) =3.90		SE (g_i) = 7.78		SE (s_{ij}) =0.177		SE (r_{ij}) =0.208		SE (g_i) = 3.04		SE (s_{ij}) =6.94		SE (r_{ij}) =8.16	
*- Significance at 5 per cent level **- significance at 1 per cent level							*- Significance at 5 per cent level **- significance at 1 per cent level						*- Significance at 5 per cent level **- significance at 1 per cent level					
Parents/Hybrids	**Phenolics**						**Calcium**						**Iron**					
	P_1	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P6**
P_1	-2.06**	3.32**	0.02	2.67**	2.49**	-2.60**	0.04**	0.00	0.02**	-0.01	0.03**	0.04**	-0.01**	0.04**	0.06**	-0.07**	0.00	0.02**
P_2	0.63	5.40**	2.83**	4.95**	-0.53**	0.53	-0.01	-0.02**	0.02**	0.04**	0.03**	0.07**	0.02*	0.01**	0.01	0.11**	-0.01	0.02**
P_3	-0.06	0.11	2.56**	-3.81**	-0.38	-0.52	-0.03**	0.10**	0.01**	0.02*	0.00	0.02**	-0.04**	0.05**	0.03**	0.04**	-0.04**	0.03**
P_4	1.12	0.28	-2.63**	-1.27**	7.33**	0.50	0.04**	0.06**	0.00	-0.01**	-0.00	0.01	0.05**	0.02*	-0.08**	-0.01**	0.05**	0.10**
P_5	-4.13**	-4.23**	-1.49	-2.48**	-1.86**	-3.21**	-0.02	-0.01	0.07**	-0.04**	0.03**	-0.01	0.09**	-0.01	-0.03**	-0.02*	-0.01*	-0.01
P_6	4.00**	-7.59**	-4.97**	-6.78**	-6.69**	-2.78**	-0.02**	-0.09**	-0.08**	-0.04**	-0.03**	0.01**	-0.04**	0.00	0.04**	-0.04**	0.08**	-0.01**
	SE (g_i) = 0.33		SE (s_{ij}) =0.77		SE (r_{ij}) =0.90		SE (g_i) = 2.83		SE (s_{ij}) =6.47		SE (r_{ij}) =7.61		SE (g_i) = 3.34		SE (s_{ij}) =7.62		SE (r_{ij}) =8.97	
*- Significance at 5 per cent level **- significance at 1 per cent level							*- Significance at 5 per cent level **- significance at 1 per cent level						*- Significance at 5 per cent level **- significance at 1 per cent level					

Conclusion

The parent P_6 was found to be the best combiner for number of fruits per plant, fruit yield per plant, flavonoid and calcium content. The parent P_2 ranked 1st for fruit length, fruit girth, fruit weight, total carotene, fibre and alkaloid content. The parent P_5 recorded positive and significant general combining ability effects for days to 1st female flower appearance. The hybrid P_2xP_4 exhibited positive and significant *sca* effects for the trait fruit length, fruit girth, fruit weight and fruit yield per plant.

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