

Combining ability study for yield and its component traits through diallele mating design in upland cotton (*Gossypium hirsutum* L.)

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ABSTRACT : The analysis of variance for combining ability revealed that, the variance due to SCA variances were higher than GCA variances for all the characters except for days to 50 per cent flowering and 2.5 per cent span length indicating the predominance of non additive gene action. The estimates of *gca* effects revealed that the parents NDLH 1938, RAH 1004 and L 770 were found best general combiners for yield and its component traits in desired direction. The crosses, NDLH 1938 × L 604, L 770× RAH 1004 and SURABHI× HYPS 152 recorded high *per se* performance (309.2, 276.65 and 257.19 g) and significant positive *sca* effects (80.99, 72.25 and 51.92) for seed cotton yield/plant, respectively. These hybrids were also recorded high *per se* performance and significant positive *sca* effects for bolls/plant, boll weight, lint yield/plant.

Key words: Combining ability, non additive, upland cotton

Cotton (*Gossypium*spp.) popularly called "King of Fibre" is the most important renewable natural fibre crop. In India, cotton is being grown over an area of 126.55 lakh ha with an annual production of 400 lakh bales with a productivity of 537 kg/ha (Anonymous, 2014). Hybridisation is the most potent technique for breaking yield barriers and evolving genotypes with higher yield potential. The first step in a successful breeding programme is to select appropriate parents. Selection of appropriate parents based on the knowledge of gene action and combining ability helps in identifying the best combiners for hybridisation. There are several techniques for the evaluation of the genetic makeup of genotypes and diallel analysis is the one which is commonly being used. Combining ability analysis helps in identifying the parents with high general combining ability (GCA) and parental combinations with high specific combining ability (SCA) effects. The present experiment was carried out with an objective of finding out the combining ability of parents for seed cotton yield and yield attributes.

The present investigation was carried out

by crossing 10 parents *viz.*, NDLH 1938, L 788, L 770, NA 1325, L604, SURABHI, RAH 1004, HYPS 152, MCU 5 and G COT 16 in diallel fashion without reciprocals and 45 intra specific cross combinations were generated and the evaluation of hybrids along with parents was done at Regional Agricultural Research Station, Lam Farm, Guntur during *kharif*, 2013-2014. Each entry was represented by following 120 x 60 cm spacing with 3 rows for each entry with a row length of 6m. Recommended doses of fertilizers 120 N, 60 P 2O5 and 40 K 2O kg/ha were applied in split doses. Observations were recorded on 5 randomly selected plants from each genotype/replication for the characters *viz.*, plant height (cm), monopodia/plant, sympodia/plant, bolls/plant, boll weight (g), chlorophyll content (mg/g fresh weight), seed index (g), lint index (g), seed cotton yield/plant (g) and lint yield/plant (g). The data on days to 50 flowering, ginning outturn (%), 2.5 per cent span length (mm), micronaire value (10-6 g/inch), bundle strength (g/tex), uniformity ratio and elongation (%) were recorded on plot basis. The fibre quality parameters were studied at Central Institute for

Research on Cotton Technology (CIRCOT), RARS, Lam, Guntur, Andhra Pradesh by using HVT Expert 1201 high volume fibretester instrument. The data was statistically analysed.

The analysis of variance for combining ability recorded significant differences for most of the characters. The differences among the parents and hybrids was significant for all the characters except for monopodia/plant, sympodia/plant and chlorophyll content for parents and monopodia/plant for hybrids. Where as the differences among the parents vs hybrids were significant for the characters days to 50 per cent flowering, plant height, sympodia/plant, boll weight, lint index, ginning outturn, micronaire value, uniformity ratio and seed cotton yield/plant. The analysis of variance for combining ability revealed that, the variance due to SCA variances were higher than GCA variances for all the characters except for days to 50 per cent flowering and 2.5 per cent span length indicating the predominance of non additive gene action for all characters and additive gene action for days to 50 per cent flowering and 2.5 per cent span length.

General combining ability effects of parents and specific combining ability effects of crosses were estimated and presented in Tables 1 to 2, respectively. The estimate of GCA and SCA variances in pooled analysis is presented in Table 3.

The *gca* effects from the analysis revealed that none of the parent recorded significant *gca* effects for all the characters studied. Among the parents NDLH 1938 showed significant positive *gca* effects for plant height, bolls/plant, boll weight, seed index, lint index, micronaire value, uniformity ratio, elongation, seed cotton yield/plant and lint yield/plant. It can be extensively used as parent in the breeding programme. The parent RAH 1004 showed significant positive *gca* effects for plant height, monopodia/plant, bolls/plant, lint index, ginning outturn, micronaire value, uniformity ratio and elongation. The

parent L 770 showed significant positive *gca* effects for days to 50 per cent flowering, seed index, lint index, ginning outturn, 2.5 per cent span length and lint yield/plant. The results regarding significant GCA effects are in conformity with those of Tuteja and Banga (2013) and Deosarkar *et al.*, (2014).

The hybrids shown the highest significant positive *sca* effects for various characters are L 770 × L 604 (13.39) for plant height, L 770 × HYPS 152 (0.46) for monopodia/plant, L 770 × RAH 1004 (1.77) for sympodia/plant, NDLH 1938 × L 604 (6.84) for bolls/plant, L 604 × HYPS 152 (1.14) for boll weight, RAH 1004 × MCU 5 (0.13) for chlorophyll content, L 788 × SURABHI (3.04) for seed index, L 788 × SURABHI (1.29) for lint index, L 788 × HYPS 152 (4.48) for ginning outturn, L 770 × RAH 1004 (2.49) for 2.5 per cent span length, RAH 1004 × MCU 5 (0.66) for micronaire value, NA 1325 × SURABHI (1.72) for bundle strength, L 788 × HYPS 152 (3.48) for uniformity ratio, L 788 × RAH 1004 (0.22) for elongation, NDLH 1938 × L 604 (80.99) for seed cotton yield/plant and L 770 × RAH 1004 (27.33) for lint yield/plant. The crosses between high × low or low × high general combiners resulted in superior cross combinations due to complementary gene action which has arisen out of both additive and non additive gene action. These crosses may likely throw superior transgressive segregants. These components may be exploited by adopting breeding procedures like cyclic hybridization, biparental mating and diallel selective mating system. The best specific crosses identified from the above study were NDLH 1938 × L 604 (80.99) followed by the crosses L 770 × RAH 1004 (72.25) and SURABHI × HYPS 152 (51.92) for seed cotton yield/plant.

The hybrid NDLH 1938 × L 604 also showed significant *sca* effects for days to 50 per cent flowering (-2.23), plant height (10.63), bolls/plant (6.84) boll weight (1.00), bundle strength, (1.57) and lint yield/plant (23.97) in the desired direction. This hybrid recorded the highest seed

Table 2 contd...

L 770 × HYPS 152	-1.87**	-3.26	0.46**	-0.89	1.91	-0.35*	-0.09	1.33**	0.58**	-0.21	-0.01	-0.09	-0.18	-0.63**	-2.00**	-0.64	-0.36**	-0.01	-5.19	-4.67
L 770 × MCU 5	-0.9	-3.97	0.05	-0.37	0.12	-0.08	-0.10*	-0.15	1.80**	-0.20**	-0.01	-0.64	-0.18	-2.20**	-0.19*	-0.14	-0.19*	-0.14	-2.06	-7.14*
L 770 × G COT 16	-0.12	8.10*	-0.01	-0.29	-3.08**	0.98**	0.05	-0.61**	1.23**	-0.61	0.03	1.64**	0.03	1.64**	-0.61	0.46**	-0.61	0.14	20.37	8.45*
NA 1325 × L 604	0.38	-5.39	0.05	-0.09	-8.24**	0.54**	-0.04	0.42**	0.16	-0.23	0.07	0.16*	0.07	1.23*	-0.26	1.23*	-0.26	-0.01	-23.51	-9.26**
NA 1325 × SURABHI	-0.46	-1.83	0.1	-0.7	-0.27	-0.37*	0	0.18	-0.39*	-0.39*	0.85	-0.27**	0.85	-2.00**	-0.26	-0.26	0.11	-13.33	-9.30**	
NA 1325 × RAH 1004	-0.73	5.15	-0.27	-0.19	3.33**	0.07	0.03	0.37*	0.2	0.07	0.56	-0.60**	-0.82*	-0.45	-0.19	-0.19	0.11	-17.81	5.43	
NA 1325 × HYPS 152	-0.93	5.56	0.21	1.14*	3.15**	-0.03	-0.02	1.11**	0.46**	-0.36	1.18*	-0.15	0.01	-1.13*	-0.06	14.98	-0.06	14.98	3.5	
NA 1325 × MCU 5	-0.29	-1.49	0.01	-0.58	2.06*	-0.40*	-0.08	-0.75**	-0.48*	-0.17	0.94	-0.04	-0.53	-0.35	-0.02	27.55*	-0.02	27.55*	7.98*	
NA 1325 × G COT 16	0.15	-2.87	-0.09	-0.06	4.89**	0.09	0	-0.2	0.04	0.82	0.49	0.27**	-0.42	1.54**	0.14	30.32*	11.26*	30.32*	11.26*	
L 604 × SURABHI	-0.04	-7.97*	-0.13	-0.27	0.37	-0.14	-0.04	-0.35*	0.02	0.68	-0.32	-0.26*	0.61	1.75**	-0.01	-0.31	0.62	-0.31	0.62	
L 604 × RAH 1004	-0.65	2.28	-0.56	-0.37	-0.22	0	-1.18**	-0.31*	1.51**	-0.60**	-1.60**	-0.22**	1.03	-1.60**	-0.24*	-0.24*	-0.24*	-11.27	-0.6	
L 604 × HYPS 152	0.82	-6.37	0.02	-1.26*	0.58	1.14**	0.08	-1.26**	0	0.25	-0.09	1.13*	0.17	0.22*	-0.22*	4.750**	-14.42**	-14.42**	-14.42**	
L 604 × MCU 5	-0.54	-12.36**	-0.16	-0.81	-2.67*	0.42*	-0.05	-0.52**	0.05	0.12*	0.61	0.39**	-0.74	-0.74	-0.05	-0.11	1.93	3.86	3.86	
L 604 × G COT 16	-0.1	-2.88	0.08	-0.04	3.59**	-0.04	-0.67**	-0.01	0.55**	0.48**	0.81	0.05	0.35**	-0.3	-0.09	0.09	-10.08	-1.1	-10.08	-10.08
SURABHI × RAH 1004	-0.15	-8.84*	-0.15	-0.37	-1.39	-0.44*	0.05	-1.27**	-0.46**	-0.46	0.02	-1.40**	0.93	-0.16	-1.40**	-0.93	-0.16	-24.28	-6.21	
SURABHI × HYPS 152	-0.68	-1.89	-0.1	1.30*	3.36**	0.79**	0.03	-1.07*	-0.26	1.35*	0.5	-0.64**	0.77*	-1.25*	-0.05	51.92**	21.21**	21.21**	21.21**	
SURABHI × MCU 5	0.29	2.46	-0.17	0.32	-0.86	0.33	0.11*	-0.61*	-0.31*	-0.83	0.12	-1.97**	-1.23*	0	0.12	9.79	3.25	3.25	3.25	
SURABHI × G COT 16	0.4	4.21	0	-0.4	-1.96	-0.38*	0.01	-0.06	0.07	0.32	1.26*	-0.84**	-1.14**	0.17	0.22*	-0.22*	-0.22*	-0.22*	-0.22*	-8.21*
RAH 1004 × HYPS 152	-0.62	-3.64	-0.1	-0.33	-0.15	-0.29	-0.04	-0.40**	-0.19	0.46	-1.09*	-0.47**	-0.57	-0.57	-0.57	-12.48	-3.57	-12.48	-12.48	
RAH 1004 × MCU 5	-0.98*	-0.22	0.02	0.42	2.46*	0.13	-0.13*	-0.60**	-0.89**	-2.58**	-0.67	-0.66**	0.09	0.18*	0.16	6.1	6.1	6.1	6.1	
RAH 1004 × G COT 16	-0.79	-0.87	0.79	0.16	0.8	-1.85	0.14	0.02	-0.55**	-0.78**	-2.26*	-1.65**	-0.97*	0.35**	-0.35**	0.1	-2.44	-4.97	-2.44	-4.97
HYPS 152 × MCU 5	0.49	1.53	0.11	-0.05	1.08	-0.26	-0.02	1.06**	0.2	-1.49*	0.19	-1.49*	-0.01	-1.77**	-2.48**	-0.15	-4.35	-3.98	-4.35	-3.98
HYPS 152 × G COT 16	-1.40**	-6.33	0.05	-0.97	-0.95	-0.88**	-0.04	0.44**	-0.07	-1.45*	-1.45*	-1.46**	-0.02	-0.09	-0.94	-0.1	-38.42**	-14.69**	-14.69**	-14.69**
MCU 5 × G COT 16	-0.76	-8.71*	0.23	-1.18*	0.16	0.08	-0.07	0.39*	0.53**	1.49*	0.83	-0.21*	0.53	-0.84	-0.09	-0.05	4.55	4.8	4.55	4.8
S E (Sij)	0.47	3.429	0.143	0.52	0.165	0.165	0.048	0.146	0.132	0.1559	0.537	0.076	0.378	0.551	0.083	12.887	3.335	12.887	12.887	12.887

**Significant at 1% level *Significant at 5% level

Table 3. Estimates of gca and sea variances for yield and yield components in cotton at RARS, Lam Farm during kharif, 2013-2014

Source	Location	Days to flowering	50 per cent height (cm)	Mono-podial/ plant	Sym-podial/ plant	Boll/ plant	Chlorophyll content (mg/g fresh weight)	Seed index (%)	Ginning index (%)	Outturn (%)	2.5 per cent span length (mm)	Microfibre length (10-6 g/inch)	Bundle strength (g/tex)	Fibre fineness (g/ tex)	Elongation ratio (%)	Fibre uniformity (%)	Cotton yield/ plant (g)	Seed cotton yield/ plant (g)	Lint yield/ plant (g)
s2GCA	RARS, Lam Farm	3.92	14.12	0.00	0.12	1.01	0.02	0.00	0.45	0.09	1.28	1.41	0.04	0.45	0.60	0.01	50.81	15.68	
s2SCA	RARS, Lam Farm	1.66	34.00	0.01	0.63	8.10	0.28	0.00	1.40	0.31	2.59	1.29	0.14	0.92	2.56	0.01	674.52	88.03	
s2GCA/s2	SCA RARS, Lam Farm	2.36	0.42	0.15	0.13	0.09	0.13	0.32	0.31	0.49	1.09	0.30	0.49	0.24	0.55	0.08	0.18		

cotton yield/plant (309.2g). The high seed cotton yield combination (high x low or high x average) might be attributed due to interaction between positive alleles in the good combiner. The cross L 770×RAH 1004 showed significant positive sca effects also for sympodia/plant (1.77), bolls/plant (5.76) and lint yield/plant (27.33). The hybrid NDLH 1938 × L 770 showed significant positive sca effects for the important fibre quality characters i.e. 2.5 per cent span length (1.97), bundle strength (1.68) and uniformity ratio (1.84). Similar results were earlier reported by Senthil Kumar *et al.*, (2013) and Rajamani *et al.*, (2014). It was observed that the cross combinations involving high x high general combiners produce crosses with significant sca effect indicating the role of additive and additive x additive genetic component of variance which could be easily improved through simple selection procedures. From the results on the combining ability, it can be concluded that the choice of the parents for crossing programme should be based not only on the *per se* performance and gca effects but also on sca effects of the cross combinations. Parents with good individual performance and good gca effects may not nick well, on the other hand parents with poor gca effect may nick well in combination due to complementary gene action. Hence, in breeding programme low gca parents can also be added.

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