Studies on gene action and combining ability of cytoplasmic-genic male sterile hybrids in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract

To recognize proper parents for hybrid pigeonpea inheritance pattern of some polygenic traits was studied. The results showed that estimates of SCA variance were higher than their corresponding GCA variance for all the traits except plant height. The values of average degree of dominance were more than unity (>1) and predictability ratio was less than unity (<1) for all the traits except plant height, signifying non-additive gene action which resulted from dominance, over dominance, epistatic and various other interaction effects. Predominance of non-additive effects specifies that population is heterozygous, as such this type of genetic variance is non-fixable. Hence, heterosis breeding is effective for increasing yield potential of pigeonpea. On the basis of general combining ability, the male lines ICP 2309, NDA 2, NDA 3, NDA 96-6, NDA 98-6 and, ICP 2155 and CMS line NDACMS 1-6A were found most promising parents for yield and its major attributes. The crosses, NDACMS 1-4A x NDA GC 31, NDACMS 1-6A x NDA 5-14, NDACMS 1-6A x NDA 8-6, NDACMS 1-4A x IPA 208, NDACMS 1-3A x NDA 98-6, NDACMS 1-4A x Bahar, NDACMS 1-6A x NDA 96-1, NDACMS 1-4A x Amar had high estimates for parents and good specific combining ability effects, hence, it may be considered for hybrid breeding programme.

Key words: Pigeonpea [*Cajanus cajan* (L.) Millsp.], gene effects, combining ability, GCA and SCA variances.
Abbreviations: GCA_general combining ability, SCA_specific combining ability.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.], (2n=2x=22) member of family Fabaceae is an important pulse crop of India. Being a pulse, pigeonpea enriches soil through symbiotic nitrogen fixation and adds organic matter and other nutrients that make pigeonpea an ideal crop for sustainable agriculture (Saxena, 2008). It has been recognized as a good source of vegetarian protein particularly in south Asia where majority of the population depends on the vegetarian food. In addition the multiple uses and roles in sustainable agriculture make pulses a favorite crop of marginal farmers. Productivity of pigeonpea in comparison to cereals is very low and stagnant due to several biotic and abiotic stresses. Over time, traditional long duration types have been continually replaced by short and medium duration varieties. These varieties although improved but low yielding as compared to long duration types. Researchers emphasized genetic improvement of pigeonpea for more than five decades and a number of cultivars were developed (Singh et al., 2005). However, the progress in the genetic improvement of yield has been limited and the improved cultivars failed to enhance productivity of the crop. Therefore, use of an alternative approach such as hybrid technology is necessary to enhance the yield of pigeonpea for ensuring food and nutritional security to the country. Efficient

and economic crop improvement scheme refers to the collection of superior alleles into a single population to develop ideal genotype. Development of such genotypes would depend upon understanding of the nature and inheritance pattern of the yield and yield components. Both additive and non-additive gene effects have been reported in inheritance of important traits in pigeonpea. However, plant height, days to flowering and maturity had predominantly additive gene effects (Sharma et al. 1972; Dahiya and Barar 1977; Singh et al. 1983). The non-additive gene effects were more pronounced for grain yield, pods plant^{-1}, 100-seed weight and protein content (Dahiya and Barar 1977; Reddy et al. 1979; Sidhu and Sandhu 1981, Patel et al. 1987). Compared to other food legumes, breeding of pigeonpea is more challenging because of various crop specific traits and high sensitivity to environmental changes. Grain yield is a complex character that is integrated function of a number of component traits most of which are under polygenic control. Modification in yield must be accompanied by changes in one or more components as pointed out by Grafius (1959). Therefore, selection for yield *per se* may not be much rewarding unless other yield attributing traits are taken into consideration. The selection of a few parents having high

genetic potential is essential because analyzing and handling of very large number of crosses would be unrealistic and perhaps impossible task. Combining ability analysis is useful technique for understanding genetic worth of parents and their crosses for further exploitation in breeding programmes. Among the various methods of combining ability analyses, line x tester analysis (Kempthorne, 1957) has been widely utilized for screening of germplasm to identify valuable donor parents and promising crosses in many crops including pigeonpea (Sarode *et al.*, 2009; Kumar *et al.*, 2009; Shoba and Balan, 2010; Gupta *et al.*, 2011; Kumar *et al.*, 2012; Yerimani et al. 2013). Keeping in view the above facts, present study was undertaken to assess combining ability variances and their effects on parents and hybrid combinations.

Results

The analysis of variance (Table 1) revealed that variance due to testers was non-significant for all the characters. Variances due to lines were significant for days to 50% flowering, days to maturity, plant height, primary branches per plant, pods per plant and seed yield per plant while remaining four characters showed non-significant. The mean squires due to lines x tester interactions were found to be highly significant for all the eleven traits.

Estimates of genetic components

The GCA and SCA variances, average degree of dominance, predictability ratio, additive and dominance variances, heritability in narrow sense and genetic advance were given in Table 2. Higher magnitude of SCA than the GCA variances, more than unity (>1) values of average degree of dominance and lesser than unity (<1) predictability ratio were recorded for entire traits except plant height. Narrow sense of heritability was high (>30%) for plant height (75.04%), biological yield per plant (38.74%), pods per plant (38.54%), seed yield per plant (35.94%), days to maturity (33.11%) and harvest index (30.85%). While, secondary branches per plant (19.01%), primary branches per plant (16.08%), seeds per pod (14.52%) and 100-seed weight had moderate estimates. Pods per plant (55.96%), biological yield per plant (48.89%), plant height (39.94%) and seed yield per plant (21.51%) exhibited high genetic advance. Remaining seven characters had low genetic advance to emerge as poor indices for selection.

General combining ability (GCA) and specific combining ability (SCA)

The significant and positive general combining ability (GCA) effects for seed yield per plant were exhibited by eleven testers and one CMS line viz., ICP 2309 (17.19), NDA 2 (13.66), NDA 3 (12.61), ICP 870 (11.75), NDA 96-6 (10.00), NDA 98-6 (8.25), ICP 2155 (8.00), ICP 7353 (5.79), NDA 98-7 (5.14), NDA 7-11 (2.25) and IPA 208 (1.49) among male parents and NDACMS 1-6A (12.75) among the female lines possessed highly significant and positive GCA effects for seed yield per plant (Table 3). On the basis of specific combining ability (Table 4) twenty-six crosses emerged with positive and significant SCA effects for seed yield per plant and other yield components. Most promising combinations for seed yield per plant were NDACMS 1-4A x NDAGC 31 (39.55), NDACMS

1-6A x NDA 5-14 (34.63), NDACMS 1-6A x NDA 8-6 (31.59), NDACMS 1-4A x IPA 208 (31.57), NDACMS 1-3A x NDA 98-6 (28.72), NDACMS 1-4A x Bahar (28.48), NDACMS 1-6A x NDA 96-1 (26.340) and NDACMS 1-4A x Amar (24.73).The specific combining ability for other characters with significant and desirable SCA effects for seed yield per plant showed that the crosses NDACMS 1-3A x IPA 208 and NDACMS 1-4A x Bahar had significant and desirable specific combining ability for all the characters.

Discussion

The information regarding general combining ability of the parents is of prime importance because it helps in successful prediction of genetic potential which would give desirable individuals in subsequent segregating populations. However, specific combining ability is associated with non-additive gene effects that are non-fixable in nature thus it would be useful for commercial exploitation as hybrids. Higher magnitude of SCA than the GCA variances, more than unity (>1) values of average degree of dominance and lesser than unity (<1) predictability ratio were recorded for all the quantitative traits except plant height which indicated existence of over dominance in expression of ten characters except plant height for which partial dominance occurs. The importance of both type of gene effects with predominance of non-additive gene effects in inheritance of seed yield and yield components of pigeonpea has also been reported earlier (Jayamala and Rangaswamy, 2001; Jahagirdar, 2003; Kumar et al., 2003; Banu et al., 2006; Kumar et al., 2009; Vaghela et al., 2009; Shoba and Balan, 2010). High estimates of heritability in narrow sense recorded for plant height, biological yield per plant, pods per plant, days to maturity, days to 50% flowering, seed yield per plant and harvest index to suggest that selection would be highly effective and efficient. Primary branches per plant, secondary branches per plant, seeds per pod and 100 seed weight had moderate heritability which indicated that these traits are expected to afford logical selection indices. Pods per plant, biological yield per plant, plant height and seed yield per plant exhibited high genetic advance to emerge as ideal traits for improvement through selection owing to their high variability and transmissibility. Remaining nine characters had low genetic advance to emerge as poor indices for selection. On the basis of general combining ability the significant and positive GCA effects for seed yield per plant were exhibited by twelve parents i.e. NDA 2, NDA 3, NDA 96-6, NDA 98-6, NDA 98-7, ICP 2309, ICP 2155, ICP 870, ICP 7053, NDA 7-11 and IPA 208 among testers and NDACMS 1-6 A among CMS lines. These twelve lines may serve as valuable parents for hybridization programme or multiple crossing programme for obtaining high yielding hybrid varieties or transgressive segregants. The male sterile line NDACMS 1-6A needs special attention because it may be valuable for developing high yielding pigeonpea hybrids due to good general combiner for yield components like early flowering and maturity, tall stature, secondary branches per plant, pods per plant, seeds per pod, 100-seed weight, biological yield per plant and harvest-index. It is obvious that most of the parents showing significant positive GCA effects for seed yield per plant also exhibited positive and significant GCA effects for some of the important yield components such as 100-seed weight, harvest-index, pods per plant, biological

Table 1. Analysis of variance for combining ability following line x tester mating design for 11 quantitative characters in pigeonpea

Characters d.f.	Replication 2	Line Effect 2	Tester Effect 19	Line x Tester Effect 38	Error 118
Days to 50% flowering	4.11*	1643.54*	207.47	324.70**	1.19
Days to maturity	2.67	921.34**	128.56	151.39**	1.23
Plant height (cm)	1.29	16568.32**	731.14	499.76**	7.99
Primary branches/ plant	0.23	6.90	5.07	4.97**	0.49
Secondary branches/ plant	20.10	252.34	161.13	143.91**	14.54
Pods/ plant	56.55	57103.75**	9018.62	9162.62**	22.56
Seeds/ pod	0.04	0.16	0.30	0.21**	0.03
100-Seed Weight (g)	0.01	4.39	4.63	4.70**	0.07
Seed yield/ plant (g)	9.51	9303.02**	1173.37	1622.53**	3.71
Biological yield/ plant(g)	51.15	47801.68	2474.43	6898.23**	48.05
Harvest index (%)	1.50	783.61*	206.61	192.72**	0.87

*,** significant at 5% and 1% probability levels, respectively, d.f. = degree of freedom

Table 2. Components of genetic variance, average degree of dominance, predictability ratio and heritability in narrow sense for 11 quantitative characters in pigeonpea

Characters	GCA variance ($\sigma^2 g$)	SCA variance ($\sigma^2 s$)	Average degree of dominance	Predictability ratio	Additive variance ($\sigma^2 A$)	Dominance variance ($\sigma^2 D$)	Heritability ($h^2 n$ %)	Genetic Advance (%)
Days to 50 % Flowering	26.79	107.82	2.01	0.332	107.16	431.29	33.11	8.68
Days to Maturity	15.17	49.97	1.81	0.378	60.69	199.86	37.55	6.95
Plant Height (cm)	250.47	163.80	0.81	0.754	1001.90	655.18	75.04	39.94
Primary Branches/ Plant	0.16	1.48	3.06	0.178	0.63	5.94	16.08	0.47
Secondary Branches/ Plant	5.63	43.80	2.79	0.205	22.52	175.21	19.01	3.01
Pods/ Plant	957.55	3045.64	1.78	0.386	3830.20	12182.55	38.54	55.96
Seeds/ Pod	0.01	0.06	3.23	0.250	0.02	0.25	14.52	0.09
100 Seed Weight (g)	0.13	1.54	3.46	0.144	0.52	6.17	14.12	0.39
Seed Yield/ Plant (g)	151.70	539.31	1.89	0.360	606.79	2157.24	35.94	21.51
Biological Yield/ Plant (g)	727.04	2280.97	1.77	0.389	2908.14	9123.86	38.74	48.89
Harvest Index (%)	14.33	63.97	2.11	0.309	57.31	255.87	30.85	6.12

Table 3. Estimates of general combining ability (gca) effects of parents for 11 quantitative characters in pigeonpea.

S.No	Testers	Days to 50 % Flowering	Days to Maturity	Plant Height (cm)	Primary Branches/ Plant	Secondary Branches/ Plant	Pods/ Plant	Seeds/ Pod	100 Seed Weight (g)	Seed Yield/ Plant (g)	Biological Yield/ Plant (g)	Harvest Index (%)
1	NDA 2	-0.33	0.42	-7.61**	-0.55*	-0.58	35.54**	0.26**	-0.46**	13.66**	13.40**	5.37**
2	NDA 3	2.12**	2.64**	-0.70	0.19	2.36*	24.03**	0.06	0.47**	12.61**	9.76**	5.30**
3	NDA 3-3	1.12**	2.31**	1.09	1.59**	3.07*	-28.04**	-0.19**	0.49**	-8.17**	-27.59**	-2.09**
4	NDA 5-14	6.56**	4.98**	3.83**	0.96**	3.86**	-44.82**	-0.19**	0.89**	-14.79**	-0.74	-7.96**
5	NDA 8-6	3.67**	1.64**	-9.74**	-0.43	-2.19	-41.13**	-0.28**	0.55**	-16.28**	-37.70	-6.53**
6	NDA 96-1	-1.99**	-5.24**	-10.82**	-0.08	-4.19**	-19.63**	-0.01	-0.86**	-10.56**	11.07**	-4.29**
7	NDA 96-6	0.89*	-0.02	1.11	-0.60*	2.25	18.33**	0.28**	0.13	10.00**	6.59**	4.53**
8	NDA 98-6	-4.66**	-1.13**	-4.49**	1.33**	3.88**	22.05**	0.07	-0.89**	8.25**	-5.07*	2.38**
9	NDA 98-7	-2.77**	-2.91**	-14.26**	-0.48*	0.11	10.52**	0.09	0.11	5.14**	-8.55**	4.24**
10	NDA 7-11	3.56**	2.98**	1.21	-0.58*	-6.35**	-4.92**	0.02	-0.11	2.25**	-19.56**	3.80**
11	NDA 7-15	0.01	2.76**	-1.42	-1.01**	-5.30**	-52.37**	-0.14*	-0.25**	-19.96**	-13.67**	-5.53**
12	NDA GC 31	4.67**	5.42**	-17.00**	-0.53*	-8.30**	-22.85**	-0.28**	0.58**	-17.12**	8.51**	-8.53**
13	NDA GC 1010	3.78**	1.98**	8.82**	-0.47*	5.48**	-10.53**	-0.26**	-0.05	-6.37**	14.08**	-2.98**
14	ICP 2309	-2.99**	-5.36**	8.54**	0.06	7.57**	63.52**	0.10*	-1.03**	17.19**	25.17**	5.05**
15	ICP 2155	1.12**	-2.13**	8.25**	-0.29	-4.98**	19.36**	0.22**	-0.31**	8.00**	6.49*	3.56**
16	ICP 870	-3.44**	-4.24**	15.16**	-0.72**	-0.47	46.28**	0.25**	-1.19**	11.75**	18.87**	3.28**
17	ICP 7353	8.23**	5.53**	15.66**	0.35	-0.66	25.36**	0.10*	-0.69**	5.79**	0.77	3.28**
18	IPA 208	0.34	0.20	2.34*	0.12	0.19	-2.08	0.10*	0.37**	1.49*	-21.05**	2.43**
19	Bahar	-11.55**	-7.58**	-4.51**	-0.19	0.12	-14.34	-0.11*	0.73**	-1.72**	8.98**	-2.75**
20	Amar	-8.33**	-2.24**	4.51**	1.31**	4.15**	-24.28	-0.11*	1.53**	-1.15	10.24**	-2.54**
	SE(gi) testers	0.370	0.407	0.965	0.239	1.179	1.609	0.052	0.087	0.715	2.480	0.301
	SE(gi-gj)	0.523	0.574	1.365	0.377	1.668	2.390	0.073	0.123	1.011	3.501	0.526
	Lines											
1	NDACMS 1-3A	-0.08	0.33	-13.13**	-0.07	-2.35**	-29.59**	0.00	-0.31**	-12.13**	-9.59**	-4.12**
2	NDACMS 1-4A	5.27**	3.74**	-5.55**	0.37**	1.44**	-2.37**	-0.05*	0.18**	-0.62*	-22.18**	1.51**
3	NDACMS 1-6A	-5.19**	-4.07**	18.68**	-0.30**	0.91*	31.97**	0.05*	0.13**	12.75**	31.77**	2.61**
	SE(gi)	0.143	0.157	0.373	0.092	0.457	0.655	0.020	0.034	0.277	0.960	0.117
	SE(gi-gj)	0.203	0.223	0.529	0.131	0.646	0.923	0.028	0.048	0.392	1.358	0.165

*,** significant at 5% and 1% probability levels, respectively, SE(gi) = standard error due to lines, SE(gi-gj)= standard error due to testers

Table 4. Estimates of specific combining ability (sca) effects of parents for 11 quantitative characters in pigeonpea.

S. No.	Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/ plant	Seeds/ Pod	100 Seed Weight (g)	Seed Yield/ Plant (g)	Biological Yield/ Plant (g)	Harvest Index (%)
1	NDACMS1-3A X NDA 2	1.41*	-2.11**	5.95**	0.27	7.59**	50.54**	0.17	-0.57**	19.78**	26.76**	5.21**
2	NDACMS1-3A X NDA 3	4.63**	0.67	5.57**	0.28	8.25**	32.58**	0.12	0.99**	18.86**	17.54**	6.02**
3	NDACMS1-3A X NDA 3-3	3.97**	2.01**	2.22	2.34**	1.32	39.92**	0.62**	-0.71**	18.49**	14.26**	8.86**
4	NDACMS1-3A X NDA 5-14	-6.81**	-3.99**	-11.06**	0.26	-3.18	-28.35**	-0.37**	-0.45**	-11.93**	36.00**	-6.10**
5	NDACMS1-3A X NDA 8-6	-5.92**	-1.66*	-0.69	-0.40	1.94	-5.90*	-0.32**	0.32*	-8.74**	-1.37	-4.11**
6	NDACMS1-3A X NDA 96-1	-2.92**	-0.44	25.54**	1.55**	2.54	7.19*	-0.34**	-1.40**	-11.02**	68.67**	-8.79**
7	NDACMS1-3A X NDA 96-6	-4.48**	-5.33**	0.81	-0.42	0.59	-3.77	0.08	1.47**	10.91**	3.59	4.30**
8	NDACMS1-3A X NDA 98-6	-16.59**	-10.55**	-0.68	3.03**	10.02**	67.60**	0.25**	0.68**	28.72**	56.12**	8.25**
9	NDACMS1-3A X NDA 98-7	-3.48**	-2.11**	6.18**	-0.48	10.33**	37.46**	0.11	-0.49**	12.77**	1.39	5.56**
10	NDACMS1-3A X NDA 7-11	-7.14**	-3.66**	1.52	0.45	0.83	-5.39	0.01	-2.21**	-4.52*	-19.93**	-0.54
11	NDACMS1-3A X NDA 7-15	-0.92	1.56*	-2.68	0.42	2.59	33.79**	0.02	-0.13	16.71**	-32.91**	9.17**
12	NDACMS1-3A X NDAGC 31	-5.59**	-1.44*	9.62**	0.56	1.78	31.17**	-0.10	0.77**	-8.19**	2.78	-4.29**
13	NDACMS1-3A X NDAGC 1010	0.30	3.01**	-2.40	-1.13**	-3.01	-62.71**	-0.19*	0.65**	-19.67**	32.52**	-11.04**
14	NDACMS1-3A X ICP 2309	-3.26**	-2.66**	-12.32**	-1.04*	-6.72**	-42.06**	0.08	0.73**	-7.01**	-28.22**	0.31
15	NDACMS1-3A X ICP 2155	15.97**	11.78**	-12.03**	-1.64**	-6.55**	11.16**	0.18*	0.93**	11.80**	13.35**	3.54**
16	NDACMS1-3A X ICP 870	20.19**	11.89**	-8.98**	-0.26	-7.48**	-22.29**	-0.10	-0.02	-10.03**	-42.35**	0.15
17	NDACMS1-3A X ICP 7353	11.19**	3.45**	-3.15	-0.67	-6.09**	22.71**	0.08	0.46**	10.27**	1.86	4.24**
18	NDACMS1-3A X IPA 208	11.08**	5.45**	-19.29**	-0.96*	-5.73**	-47.60**	0.10	-0.57**	-18.22**	-60.37**	-3.30**
19	NDACMS1-3A X BAHAR	-5.37**	-2.77**	15.56**	-0.54	-3.24	-73.68**	-0.21*	0.13	-24.93**	-43.72**	-9.07
20	NDACMS1-3A X AMAR	-6.26**	-3.11**	0.31	-1.62**	-5.78**	-42.38**	-0.19*	-0.58**	-24.05**	-45.98**	-8.38**
21	NDACMS1-4A X NDA 2	-2.94**	0.48	-9.85**	-0.72	-7.95**	-11.92**	0.02	-0.41**	-8.96**	-17.25**	-0.70
22	NDACMS1-4A X NDA 3	-4.38**	-2.74**	-17.13**	0.07	-3.00	3.96	0.09	-1.60**	-7.97**	-7.30**	-1.60**
23	NDACMS1-4A X NDA 3-3	-2.38**	-0.41	-13.60**	-2.03**	-4.26*	-63.31**	-0.47**	-1.10**	-30.15**	-39.50**	-12.76**
24	NDACMS1-4A X NDA 5-14	1.17	1.26	1.34	-0.95*	-5.86**	-49.46**	0.23*	-0.68**	-22.69**	-77.69**	-5.17**
25	NDACMS1-4A X NDA 8-6	15.06**	8.26**	6.56**	0.52	0.85	-64.80**	0.25**	-1.26**	-22.85**	-56.41**	-6.34**
26	NDACMS1-4A X NDA 96-1	16.73**	13.14**	-12.91**	-1.23**	-4.05*	-50.60**	0.24**	0.07	-15.32**	-91.62**	1.91**
27	NDACMS1-4A X NDA 96-6	8.84**	7.26**	4.07*	0.77	-7.10**	-14.72**	0.02	1.06**	-0.54	11.42**	-0.67
28	NDACMS1-4A X NDA 98-6	12.06**	6.70**	1.38	-2.18**	-7.00**	-109.34**	-0.32**	-1.70**	-44.14**	-68.88**	-14.57**
29	NDACMS1-4A X NDA 98-7	3.84**	-0.52	-1.90	-0.39	-6.59**	-32.60**	-0.21*	2.00**	-5.67**	2.35	-1.99**
30	NDACMS1-4A X NDA 7-11	11.17**	7.59**	-12.55**	-0.44	0.76	-12.99**	0.21*	0.88**	-4.27**	-0.85	-0.14
31	NDACMS1-4A X NDA 7-15	3.73**	3.48**	-13.86**	-0.49	-6.95**	48.23**	-0.28**	0.68**	12.56**	-5.64	5.82**
32	NDACMS1-4A X NDAGC 31	1.39*	-1.52*	-2.97	-1.27**	-3.58	50.42**	0.38**	0.70**	39.55**	37.97**	14.42**
33	NDACMS1-4A X NDAGC 1010	-0.05	-2.08**	-5.68**	0.63	1.22	16.22**	-0.20*	0.18	1.34	-36.25**	5.16**
34	NDACMS1-4A X ICP 2309	-1.61*	-0.08	4.53**	0.47	3.81	34.52**	0.00	-0.18	9.14**	33.47**	0.88
35	NDACMS1-4A X ICP 2155	-15.05**	-6.63**	20.20**	2.33**	9.51**	23.66**	0.04	-0.50**	6.85**	37.13**	-0.55
36	NDACMS1-4A X ICP 870	-22.83**	-14.86**	9.89**	-0.19	1.80	15.50**	0.15	-0.45**	4.02**	28.28**	-0.29
37	NDACMS1-4A X ICP 7353	-3.49**	0.03	4.66**	1.07*	10.84**	17.19**	-0.08	-0.23	4.32**	31.16**	-0.93

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38	NDACMS1-4A X IPA 208	-11.94**	-9.63**	14.82**	1.36**	10.57**	64.47**	0.02	1.53**	31.57**	87.53**	5.17**
39	NDACMS1-4A X BAHAR	-7.72**	-8.52**	5.18**	0.32	9.53**	78.48**	0.04	0.28	28.48**	72.65**	6.24**
40	NDACMS1-4A X AMAR	-1.61*	-1.19	17.82**	2.37**	7.45**	57.10**	-0.11	0.74**	24.73**	59.44**	6.11**
41	NDACMS1-6A X NDA 2	1.53*	1.63*	3.90*	0.45	0.37	-38.62**	-0.20*	0.98**	-10.82**	-9.51**	-4.51**
42	NDACMS1-6A X NDA 3	-0.25	2.07**	11.57**	-0.35	-5.25*	-36.53**	-0.21*	0.61**	-10.89**	-10.24**	-4.42**
43	NDACMS1-6A X NDA 3-3	-1.58*	-1.59*	11.38**	-0.32	2.94	23.39**	-0.15	1.81**	11.66**	25.24**	3.90**
44	NDACMS1-6A X NDA 5-14	5.64**	2.74**	9.72**	0.70	9.04**	77.81**	0.13	1.13**	34.63**	41.69**	11.28**
45	NDACMS1-6A X NDA 8-6	-9.14**	-6.59**	-5.87**	-0.12	-2.79	70.70**	0.08	0.94**	31.59**	57.79**	10.44**
46	NDACMS1-6A X NDA 96-1	-13.81**	-12.71**	-12.64**	-0.32	1.51	43.41**	0.10	1.34**	26.34**	22.95**	6.88**
47	NDACMS1-6A X NDA 96-6	-4.36**	-1.93**	-4.88**	-0.34	6.50**	18.49**	-0.10	-2.53**	-10.36**	-15.01**	-3.63**
48	NDACMS1-6A X NDA 98-6	4.53**	3.85**	-0.70	-0.85*	-3.02	41.74**	0.08	1.02**	15.42**	12.76**	6.32**
49	NDACMS1-6A X NDA 98-7	-0.36	2.63**	-4.28*	0.87*	-3.74	-4.86	0.10	-1.51**	-7.09**	-3.74	-3.57**
50	NDACMS1-6A X NDA 7-11	-4.03**	-3.93**	11.03**	-0.01	-1.59	18.38**	-0.22*	1.33**	8.79**	20.78**	0.68
51	NDACMS1-6A X NDA 7-15	-2.81**	-5.04**	16.54**	0.08	4.36*	-82.02**	0.27**	-0.55**	-29.27**	38.56**	-14.99**
52	NDACMS1-6A X NDAGC 31	4.19**	2.96**	-6.65**	0.71	1.79	-81.59**	-0.27**	-1.47**	-31.36**	-40.75**	-10.13**
53	NDACMS1-6A X NDAGC 1010	-0.25	-0.93	8.07**	0.50	1.79	46.49**	0.39**	-0.83**	18.33**	3.73	5.88**
54	NDACMS1-6A X ICP 2309	4.86**	2.74**	7.78**	0.57	2.91	7.54*	-0.07	-0.55**	-2.13	-5.25	-1.19*
55	NDACMS1-6A X ICP 2155	-0.92	-5.15**	-8.16**	-0.69	-2.96	-34.82**	-0.22*	-0.42**	-18.65**	-50.48**	-2.99**
56	NDACMS1-6A X ICP 870	2.64**	2.96**	-0.91	0.46	5.68**	6.78*	-0.05	0.47**	6.00**	14.07**	0.14
57	NDACMS1-6A X ICP 7353	-7.69**	-3.48**	-1.51	-0.41	-4.75*	-39.90**	0.00	-0.23	-14.59**	-33.02**	-3.31**
58	NDACMS1-6A X IPA 208	0.86	4.18**	4.47**	-0.41	-4.84*	-16.87**	-0.12	-0.96**	-13.35**	-27.17**	-1.87**
59	NDACMS1-6A X BAHAR	13.08**	11.29**	-20.74**	0.23	-6.29**	-4.80	0.17	-0.42**	-3.55	-28.93**	2.83**
60	NDACMS1-6A X AMAR	7.86**	4.29**	-18.13**	-0.75	-1.67	-14.73**	0.30**	-0.16	-0.68	-13.46**	2.27**
	SE(Sij)	0.906	0.995	2.364	0.585	2.888	4.140	0.126	0.213	1.752	6.074	0.737
	SE(Sij-Ski)	0.405	0.445	1.057	0.261	1.292	1.852	0.057	0.095	0.783	2.716	0.330

*,** significant at 5% and 1% probability levels, respectively

yield per plant and plant height. This indicates that the significant GCA effects for seed yield in positive direction resulted from similar GCA effects of some other yield components suggesting that the combining ability for seed yield was influenced by the combining ability of its components. Therefore, simultaneous improvement in important yield components and other associated traits along with seed yield may be better approach for raising yield potential in pigeonpea. Similar findings were also reported by Jahagirdar, (2003), Banu et al., (2006), Kumar et al., (2009), Vaghela et al., (2009), Shoba and Balan, (2010). The specific combining ability which are supposed to be manifestation of non-additive components of genetic variance, are highly valuable for discrimination of crosses for their genetic worth as breeding materials. The sixty crosses studied here only two crosses had significant and desirable SCA effects for all the characters. Several crosses exhibited significant and desirable SCA effects for one or more characters but none of them emerged as good specific combination for more than nine characters. The critical examination of results would reveal that the crosses exhibiting high order significant and desirable SCA effects for different characters involved parents having all types of combinations of GCA effects such as high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), average × low (A × L) and low × low (L × L). Pandey and Singh, 2002) have also observed involvement of high x high (H x H) and low x high (L x H) general combiner parent in manifestation of high order significant and desirable SCA effects for seed yield per plant and its components. The foregoing observation clearly indicated that there was no particular relationship between positive and significant SCA effects of crosses with GCA effects of their parents for the characters under study and also supported by previous workers in pigeonpea (Khorgade et al., 2000; Pandey and Singh, 2002; Jahagirdar, 2003; Sekhar et al., 2004; Banu et al., 2006; Baskaran and Muthiah, 2007; Sarode et al., 2009; Kumar et al., 2009; Shoba and Balan, 2010; Gupta et al., 2011; Kumar et al., 2012; Yarimani et al., 2013).

Materials and Methods

Plant material and experimental detail

Three cytoplasmic-genic male sterile lines (NDACMS 1-3A, NDACMS 1-4A and NDACMS 1-6A) were crossed with twenty elite genotypes of pigeonpea during 2011-12. Thus, a total of 60 F_1's were produced and evaluated along with their parents and check variety NDA 2 during next growing season 2012-13 at Genetics and Plant Breeding Research Farm, Narendra Deva University of Agriculture & Technology, Faizabad. The experiment was laid out in a randomized complete block design with three replications.The seeds of each entry were sown on 27th July, 2012 in separate plots in single row plots of 4 m length with intra-row and inter-row spacing of 25 cm and 75 cm, respectively. The recommended agronomic practices were done timely to raise good crop stand.

Data collection

The data were recorded on five randomly selected competitive plants in each genotype for eleven characters *viz.,* days to 50%

flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height (cm), pods per plant, seeds per pod, 100-seed weight, seed yield per plant (g), biological yield per plant (g) and harvest index (%).

Statistical analysis

The experimental data were compiled by taking mean values over randomly selected plants in each plot and subjected to statistical analysis. The analysis of variance for the design of the experiment was carried out following Panse and Sukhatme (1967). Narrow sense heritability was computed using Falconer's methods (Falconer and Mackay, 1996) and it was classified according to Robinson (1966). Genetic advance was estimated adopting the method suggested by Johnson et al. (1955). Estimates of combining ability were computed according to Kempthorne, (1957) and average degree of dominance by Kempthorne and Curnow, (1961).

Conclusions

Commencing the experimental findings it is evident that both additive and non-additive gene effects were important with predominance of non-additive gene effects in inheritance of seed yield and its components. On the basis of general combining ability the most promising parents identified were ICP 2309, NDA 2, NDA 3, NDA 96-6, NDA 98-6 and, ICP 2155 and NDACMS 1-6A among CMS lines. Twenty-six crosses showed significant and desirable SCA effects for seed yield and its major components. Among them best cross combinations *viz.,* NDACMS 1-4A x NDA GC 31, NDACMS 1-6A x NDA 5-14, NDACMS 1-6A x NDA 8-6, NDACMS 1-4A x IPA 208, NDACMS 1-3A x NDA 98-6, NDACMS 1-4A x Bahar, NDACMS 1-6A x NDA 96-1, NDACMS 1-4A x Amar which had high estimates for parents and good SCA effects may be considered for hybrid breeding programme.

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