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COMBINING ABILITY STUDIES FOR SEED YIELD AND ITS COMPONENT TRAITS IN PIGEONPEA (*CAJANUS CAJAN* L. MILLSPAUGH)

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ABSTRACT

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is a perennial legume vital to subsistence agriculture in semi-arid tropics, providing food, fodder and soil enrichment. The present study was undertaken in order to access combining ability using a line × tester mating scheme comprising four cytoplasmic male sterile (CMS) lines and ten fertility restorer lines. The experimental set included 40 hybrids, their 14 respective parents and a standard check (GTH 1), evaluated during the *kharif* 2024 within a randomized block design with three replications at Sardarkrushinagar. The magnitude of general combining ability variance was lower than specific combining ability variance for all traits except plant height, which indicated importance of non-additive gene effects in the inheritance of these traits. None of the parent was good general combiner for all the characters. Among parents, CMS GT 1615 A, CMS GT 307 A, SKNP 1715 and NAM 314 were good general combiners for seed yield and its contributing traits. Notably, hybrid combinations surpassed parental lines in seed yield and related parameters. Among the crosses, CMS GT 1615 A × SKNP 1715 was found promising followed by CMS GT 307 A × WRGE 133 and CMS GT 1615 A × NAM 314. Combining ability analysis revealed that both additive and non-additive gene actions played a role though non-additive effects were predominant in most of the traits. Crosses with high specific combining ability (SCA) suggest strong potential for future hybrid development. Thus these cross combinations could be utilized in breeding programme for further amelioration of seed yield in pigeonpea.
***Keywords* :** Combining ability, Gene action, Line x tester and Pigeonpea.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], commonly referred to as Arhar or Tur, stands as a crucial pulse crop in India ranking second only to chickpea in terms of cultivation area and total production. It is a short-lived perennial plant belonging to the *leguminaceae* family and the *papilionaceae* subfamily. Unlike other legumes, pigeonpea is considered an "often cross-pollinated crop," with natural out-crossing rates ranging from 25% to 70% depending on the location (Saxena *et al.*, 1990). Renowned for its rich nutritional profile, pigeonpea serves as a vital source of vegetarian protein, carbohydrates, essential vitamins, and minerals, making it a dietary staple for millions, particularly across South Asia. Despite its ecological and dietary importance, India's per capita pulse intake remains below the World Health Organization's recommended levels, highlighting the urgent need to boost pigeonpea productivity. Although pigeonpea is mainly self-fertilizing, its tendency toward cross-pollination enables the exploitation of heterosis. Initial hybridization efforts employed Genetic Male Sterility (GMS) systems, culminating in the release of the first commercial hybrid ICPH 8 in 1991 (Saxena *et al.*, 1992). However, challenges associated with large-scale seed production using GMS systems led to the adoption of more reliable Cytoplasmic-Genetic Male Sterility (CGMS) systems, developed using wild relatives such as *C. scarabaeoides* and *C. cajanifolius*. Hybrid breeding through CGMS offers a viable and sustainable path to address stagnating yields. Given the polygenic inheritance patterns of complex traits like seed yield and pods per plant deciphering the contributions of additive and non-additive gene actions is essential. Breeding strategies such as diallel, test crosses, biparental mating, line × tester analysis and multiple crosses are commonly employed to assess genetic potential. Among these, line × tester analysis is particularly effective in evaluating general and specific combining abilities, thereby facilitating the identification of elite parental lines and superior heterotic hybrids. Therefore the present investigation was undertaken with an objective to assess the nature of gene action involved and combining ability of parental genotypes for various traits for evolving productive hybrids in pigeonpea.

Materials and Methods

The parental materials for the study was obtained from the Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The experimental material consisting of four cytoplasmic male sterile lines, *viz*., CMS GT 301 A, CMS GT 307 A, CMS GT 1609 A and CMS GT 1615 A and ten diverse testers *i.e*., ICPL 19018, IPA 15-6, WRGE 133, BRG 20-506, BRG 20-511, GT 107, GT 108, NAM 314, SKNP 1701 and SKNP 1715 crossed in a line × tester mating design. The resultant 40 hybrid combinations was tested during *kharif* 2024 along with 14 parents and one check GTH 1 (hybrid) in randomized block design with three replications. The each genotype were grown in a single row of 2.0 meter length with row to row spacing of 60 cm and plant to plant spacing of 20 cm. The guard rows were provided on all the sides of each block. All recommended agronomical and plant protection measures were followed to raise healthy crop. Data were recorded on five randomly selected plants from each net plot of parents and F_1s in all the three replications. Mean value on per plant basis were recorded for various characters *viz*., plant height (cm), number of branch per plant, number of pod per plant, pod length (cm), number of seed per pod, test weight (g), seed yield per plant (g), harvest index (%) and crude protein content (%), while for days to flowering and days to maturity observations were recorded on plot basis. The data analysis of variance for different character were studied using method suggested by Panse and Sukhatme (1978). The combining ability analysis was carried out according to the method given by Kempthorne (1957).

Results and Discussion

An analysis of variance for combining ability was conducted to partition the total genetic variance into general combining ability representing additive genetic effects and specific combining ability, which reflects non-additive genetic interactions. The results summarized in Table 1, showed that the mean sum of squares due to lines was statistically significant for all traits with the exception of pod length, number of seed per pod, test weight and harvest index. Similarly, the mean sum of squares for testers was significant across all traits except for plant height, pod length and crude protein content. Notably, the interaction between females and males showed significant variation for all traits except pod length and number of seed per pod highlighting the meaningful contribution of hybrids to SCA variance. The ratio of σ^2_{gca} / σ^2_{sca} exceeding one for plant height indicated that additive genetic variance plays a dominant role in the inheritance of this trait. While, the ratio of σ^2_{gca} / σ^2_{sca} being less than one was observed in other characters which indicated non additive genetic variance (Table 1). These results are in agreement with earlier studies by Khorgade *et al.* (2000), Singh and Srivastava (2001), Kumar *et al.* (2001) and Patil *et al.* (2016) which also highlighted the significance of additive gene action in determining plant height. Non-additive gene action for the number of pod per plant and number of seed per pod has also been observed aligning with the findings of Reddy *et al.* (2004), Banu *et al.* (2006), Baskaran and Muthiah (2007) and Patel *et al.* (2020). For pod length, non-additive genetic control was identified by Singh and Srivastava (2001), Baskaran and Muthiah (2007) and Soni and Patel (2016). The dominance of non-additive gene action highlights the importance of preserving heterozygosity within the breeding population. This significant contribution of non-additive genetic variance reinforces the value of heterosis breeding as a promising and effective approach for enhancing desirable traits in pigeonpea.

Nature and magnitude of combining ability effects helps in identifying superior parents and their utilization in further breeding programme. General combining ability effects of male and female parents for various eleven traits shown in Table 2. Among the lines, CMS GT 1615 A emerged as a good general combiner for key traits such as days to flowering, days to maturity, number of branch per plant, number of pod per plant and seed yield per plant. Similarly, CMS GT 1609 A demonstrated good GCA for days to maturity. CMS GT 307 A was identified as a good general combiner for characters like number of pod per plant and seed yield per plant. CMS GT 301 A also showed favorable GCA for plant height. Among the testers, SKNP 1715 was a good combiner for days to maturity, number of pod per plant, test weight, seed yield per plant and harvest index. Also, NAM 314 and GT 107 stood out as good general combiners for seed yield and associated traits. Therefore the parents CMS GT 1615 A, CMS GT 307 A, SKNP 1715 and NAM 314 can be considered as a good source of favourable genes for increasing seed yield along with other yield attributes. Thus, it would be worthwhile to use these parental lines in hybridization programme.

The estimate of specific combining ability effects were presented in Table 3 revealed that eight cross combinations exhibited significant and positive sca effects for seed yield per plant. Among the 40 cross combination, CMS GT 1615 A × SKNP 1715, CMS GT 307 A × WRGE 133 and CMS GT 1609 A × BRG 20-511 were found significant positive for seed yield per plant. These hybrids also depicted positive sca effects for number of pod per plant as well as harvest index. The similar results were also found by Jahagirdar (2003), Pandey (2004), Banu *et al.* (2006), Rizwana *et al.* (2006) and Baskaran and Muthiah (2007). The cross combinations, CMS GT 307 A × SKNP 1715, CMS GT 1615 A × GT 108 and CMS GT 1609 A × BRG 20-511 for days to flowering; CMS GT 1615 A × IPA 15-6, CMS GT 1609 A × GT 108 and CMS GT 307 A × BRG 20-506 for days to maturity and CMS GT 301 A × SKNP 1701, CMS GT 307 A × BRG 20-506 and CMS GT 307 A × GT 108 for plant height exhibited significant negative sca effects. The results aligned with the findings of Khorgade *et al.* (2000), Kumar *et al.* (2001) and Patel and Tikka (2014). While, crosses, CMS GT 1615 A × SKNP 1715, CMS GT 307 A × ICPL 19018 and CMS GT 307 A × IPA 15-6 for number of branch per plant; CMS GT 1615 A × SKNP 1715, CMS GT307 A × WRGE 133 and CMS GT 1609 A × BRG 20-511 for number of pod per plant; CMS GT 307 A × NAM 314 and CMS GT 1609 A × GT 108 for pod length; CMS GT 1615 A × BRG 20-506 for number of seed per pod; CMS GT 1615 A × SKNP 1715, CMS GT 307 A × GT 107 and CMS GT 307 A × SKNP 1715 for test weight; CMS GT 1609 A × BRG 20-511, CMS GT 301 A × SKNP 1701 and CMS GT 307 A × WRGE 133 for harvest index and CMS GT 301 A × ICPL 19018 and CMS GT 301 A × BRG 20-506 for crude protein content were found significant positive sca effects (Table 3). Significant positive sca effects for different traits have also been reported by Gupta *et al.* (2011), Ceyhan *et al.* (2014), Chaudhary *et al.* (2016) and Soni and Patel (2016).

Conclusion

From the foregoing discussion, it may be concluded that the parents *viz.*, CMS GT 1615 A, CMS GT 307 A, SKNP 1715 and NAM 314 were found promising general combiner for various traits. The crosses CMS GT 1615 A × SKNP 1715, CMS GT 307 A× WRGE 133, CMS GT 1615 A × NAM 314, CMS GT 307 A × NAM 314 and CMS GT 1609 A × BRG 20-511 were found to be most promising for seed yield and other desirable traits. Hence, these crosses are recommended for further testing in multilocation trials in order to develop high yielding hybrids in pigeonpea. It is also clear that high magnitude of non-additive type of gene action for seed yield per plant and most of its important components traits observed in the present study favours hybrid breeding programmec.

Table 1: Analysis of variance for combining ability and estimates of components of variance for eleven characters in pigeonpea

Source of variation	d.f	Days to flowering	Days to maturity	Plant height	Number of branch per plant	Number of pod per plant	Pod length	Number of seed per pod	Test weight	Seed yield per plant	Harvest index	Crude protein content
Replications	2	11.03	1.23	147.53	0.01	284.65	0.15	0.03	0.24	13.31	0.77	0.46
Females	3	136.98**	133.62**	1458.10**	6.79**	10016.99**	0.06	0.03	0.65	130.30**	7.77*	5.57*
Males	9	92.37**	235.33**	102.98	3.65**	5825.037**	0.30	0.16*	1.14**	114.90**	13.94**	1.34
Females × Males	27	41.17**	140.02**	174.34*	3.90**	5254.89**	0.27	0.09	0.84**	126.61**	13.50**	2.78*
Error	78	14.56	15.86	101.86	1.02	123.45	0.17	0.06	0.26	8.52	2.30	1.47
Components of Variance												
σ^2 Females		3.19*	-0.21	42.79**	0.10	158.74	-0.01	-0.002	0.01	0.12	-0.19	0.09
σ^2 Males		4.27	7.94	-5.95	-0.02	47.51	0.003	0.01	0.03	-0.98	0.04	-0.12
σ^2_{gca}		3.50	2.11	28.87*	0.06	126.96	-0.004	0.001	0.01	-0.19	-0.13	0.03
σ^2_{sca}		8.87	41.39**	24.16*	0.96**	1710.48**	0.03	0.01	0.19**	39.36**	3.73**	0.44*
$\sigma^2_{gca} / \sigma^2_{sca}$		0.40	0.05	1.19	0.06	0.07	-0.13	0.04	0.05	-0.01	-0.03	0.07

*, ** Significant at 5 *per cent* and 1 *per cent* levels of significance, respectively.

Table 2 : Estimates of general combining ability (gca) effects of the parents for eleven characters in pigeonpea

Parents	Days to flowering	Days to maturity	Plant height	No. of branch per plant	No. of pod per plant	Pod length	No. of seed per pod	Test weight	Seed yield per plant	Harvest index	Crude protein content
Lines											
CMS GT 301 A	0.93	1.83*	-7.96**	0.21	-21.33**	0.06	0.04	0.13	-2.12**	-0.6*	0.36
CMS GT 307 A	2.27**	1.80*	-3.59	-0.25	4.20*	-0.006	0.02	0.07	2.10**	0.43	-0.20
CMS GT 1609 A	-0.47	-1.53*	4.56*	-0.51**	-5.26*	-0.007	-0.03	-0.21*	-1.42**	-0.25	-0.52*
CMS GT 1615 A	-2.73**	-2.10**	6.99**	0.56**	22.39**	-0.05	-0.03	0.01	1.45**	0.42	0.35
S.Em.±	0.70	0.73	1.84	0.18	2.03	0.08	0.04	0.09	0.53	0.28	0.22
Testers											
ICPL 19018	-2.37*	-5.23**	0.21	0.21	-13.50**	0.09	0.01	-0.048	-0.75	-0.35	-0.04
IPA 15-6	2.22*	4.02**	1.48	-0.57	-15.77**	0.13	0.08	-0.13	-3.09**	-0.96*	-0.42
WRGE 133	-0.62	8.60**	0.11	-0.75*	1.58	0.13	0.11	0.29	-0.55	0.40	0.51
BRG 20-506	-2.87*	-1.98	-6.72*	-0.68*	-24.11**	-0.23	-0.11	0.18	-4.26**	0.59	0.21
BRG 20-511	0.13	-0.98	1.71	0.35	-1.72	-0.23	-0.04	0.01	-0.24	-0.18	-0.08
GT 107	-1.03	1.52	4.71	0.56	5.89	-0.13	0.05	-0.21	2.50**	-2.073**	-0.23
GT 108	4.30**	1.77	0.18	0.10	-10.42**	0.06	-0.16*	-0.38*	-2.31**	0.23	-0.11
NAM 314	3.47**	1.68	-2.10	-0.29	20.65**	0.17	-0.19*	0.07	3.83**	0.98*	-0.28
SKNP 1701	-4.20**	-5.65**	0.50	0.89**	-13.57**	-0.12	0.11	-0.38*	-0.67	-0.48	-0.15
SKNP 1715	0.97	-3.73**	-0.07	0.18	50.97**	0.13	0.13	0.62**	5.55**	1.83**	0.59
S.Em.±	1.10	1.15	2.91	0.29	3.21	0.12	0.07	0.15	0.84	0.44	0.35

*, ** Significant at 5 *per cent* and 1 *per cent* levels of significance, respectively.

Table 3 : Estimates of specific combining ability (sca) effects for eleven characters in pigeonpea

Sr. No.	Hybrids	DF	DM	PH	NBP	NPP	PL	NSP	TW	SYP	HI	CPC
1	CMS GT 301 A × ICPL 19018	-1.93	-0.50	2.71	0.14	0.86	-0.10	-0.09	0.57	1.02	0.09	1.59*
2	CMS GT 301 A × IPA 15-6	-1.52	6.25**	0.37	0.11	15.53*	0.03	-0.09	-0.78*	-1.14	-0.80	1.09
3	CMS GT 301 A × WRGE 133	-0.35	-1.67	-3.30	0.50	-8.96	0.40	0.28	0.54	-4.21*	1.79*	0.08
4	CMS GT 301 A × BRG 20-506	-1.10	0.58	3.73	0.35	16.07*	0.21	-0.10	-0.05	2.90	0.05	1.41*
5	CMS GT 301 A × BRG 20-511	4.57*	2.58	3.81	0.80	4.98	-0.21	-0.17	0.02	4.46**	-2.64**	-0.10
6	CMS GT 301 A × GT 107	-2.27	3.75	7.43	-0.55	8.73	0.12	0.15	-0.10	3.47*	-1.37	-0.80
7	CMS GT 301 A × GT 108	2.07	-3.17	6.83	0.98	2.31	0.41	0.22	0.30	-0.09	1.18	-1.17
8	CMS GT 301 A × NAM 314	2.57	-6.75**	-1.28	0.90	12.28	-0.56*	-0.22	0.19	1.37	-2.55**	-1.02
9	CMS GT 301 A × SKNP 1701	0.57	6.92**	-14.65*	-1.28*	7.83	0.00	0.02	0.00	-1.36	3.16**	-0.24
10	CMS GT 301 A × SKNP 1715	-2.60	-8.00**	-5.65	-1.94**	-59.61**	-0.31	0.00	-0.70*	-6.42**	1.09	-0.84
11	CMS GT 307 A × ICPL 19018	-3.27	-0.47	1.91	1.66**	26.59**	-0.02	0.20	-0.37	3.20	-0.86	0.45
12	CMS GT 307 A × IPA 15-6	0.15	5.62*	8.10	1.44*	16.96**	0.02	0.06	0.61*	0.90	-1.05	0.74
13	CMS GT 307 A × WRGE 133	4.32	3.03	0.60	-0.05	41.74**	-0.04	-0.17	-0.27	8.87**	3.04**	-1.25
14	CMS GT 307 A × BRG 20-506	0.90	-9.38**	-10.64	-0.39	-9.57	0.00	-0.02	0.37	-2.49	1.25	-1.41*
15	CMS GT 307 A × BRG 20-511	1.57	-6.72**	-9.56	-1.75**	-29.06**	0.33	0.11	-0.65*	-5.68**	1.95**	0.37
16	CMS GT 307 A × GT 107	3.73	3.45	-4.94	-0.96	-8.63	-0.05	-0.04	0.73*	0.55	-0.22	1.11
17	CMS GT 307 A × GT 108	-0.27	6.20**	-9.90	-1.23*	-11.33	-0.56*	0.10	-0.27	-2.37	-2.22*	-0.47
18	CMS GT 307 A × NAM 314	2.57	6.62**	2.91	-0.12	4.24	0.57*	0.06	-0.92**	1.25	1.90*	0.33
19	CMS GT 307 A × SKNP 1701	-3.77	-6.38**	18.15**	1.11	18.06**	-0.17	-0.17	0.13	0.55	-1.42	-0.55
20	CMS GT 307 A × SKNP 1715	-5.93**	-1.97	3.38	0.29	-49.01**	-0.08	-0.12	0.63*	-4.77**	-2.35**	0.67
21	CMS GT 1609 A × ICPL 19018	-1.87	-2.47	-5.75	-0.55	1.05	-0.05	-0.16	-0.03	-0.38	1.76*	-1.05
22	CMS GT 1609 A × IPA 15-6	0.55	0.95	-1.92	-0.57	3.25	-0.08	0.04	0.06	4.49**	0.77	-1.05
23	CMS GT 1609 A × WRGE 133	-3.28	1.37	4.95	-0.39	14.20*	-0.15	0.14	0.27	0.66	-3.34**	0.08
24	CMS GT 1609 A × BRG 20-506	-0.03	5.62*	5.51	0.70	12.59	-0.15	-0.18	-0.35	2.93	-0.79	-0.38
25	CMS GT 1609 A × BRG 20-511	-4.70*	3.62	7.86	0.58	27.67**	-0.13	-0.11	0.39	7.51**	3.62**	-0.37
26	CMS GT 1609 A × GT 107	-1.20	-3.88	-2.25	0.57	9.79	-0.13	0.01	-0.19	2.57	0.15	0.57
27	CMS GT 1609 A × GT 108	3.47	-9.47**	2.91	1.30*	18.10**	0.50*	-0.13	0.24	1.78	0.21	0.76
28	CMS GT 1609 A × NAM 314	-0.70	-6.05	-3.10	-0.66	-14.37*	0.06	0.24	0.36	-7.09**	-1.40	0.64
29	CMS GT 1609 A × SKNP 1701	0.30	-3.72	0.06	-0.43	-18.65**	0.19	0.14	0.01	-2.73	-0.30	0.66
30	CMS GT 1609 A × SKNP 1715	7.47**	14.03**	-8.27	-0.56	-53.62**	-0.06	-0.01	-0.76*	-9.75**	-0.69	0.14
31	CMS GT 1615 A × ICPL 19018	7.07**	3.43	1.13	-1.25*	-28.50**	0.17	0.05	-0.18	-3.85*	-0.99	-1.00
32	CMS GT 1615 A × IPA 15-6	0.82	-12.82**	-6.54	-0.98	-35.73**	0.04	-0.02	0.11	-4.25*	1.08	-0.78

33	CMS GT 1615 A × WRGE 133	-0.68	-2.73	-2.24	-0.06	-46.98**	-0.20	-0.25	-0.54	-5.31*	-1.48	1.09
34	CMS GT 1615 A × BRG 20-506	0.23	3.18	1.39	-0.67	-19.09**	-0.06	0.30*	0.03	-3.34	-0.51	0.38
35	CMS GT 1615 A × BRG 20-511	-1.43	0.52	-2.10	0.38	-3.58	0.01	0.17	0.24	-6.29**	-2.93**	0.10
36	CMS GT 1615 A × GT 107	-0.27	-3.32	-0.24	0.93	-9.89	0.06	-0.12	-0.44	-6.60**	1.44	-0.88
37	CMS GT 1615 A × GT 108	-5.27*	6.43**	0.16	-1.04	-9.08	-0.35	-0.19	-0.28	0.68	0.83	0.88
38	CMS GT 1615 A × NAM 314	-4.43*	6.18**	1.47	-0.13	-2.15	-0.07	-0.09	0.37	4.47**	2.04*	0.05
39	CMS GT 1615 A × SKNP 1701	2.90	3.18	-3.56	0.6	-7.23	-0.02	0.02	-0.14	3.54*	-1.44	0.13
40	CMS GT 1615 A × SKNP 1715	1.07	-4.07	10.54	2.21**	162.24**	0.44	0.13	0.82**	20.95**	1.95*	0.03
Range		-5.93 to 7.47	-12.82 to 14.03	-14.65 to 18.15	-1.94 to 2.21	-59.61 to 162.24	-0.56 to 0.57	-0.25 to 0.30	-0.92 to 0.82	-9.75 to 20.95	-3.34 to 3.62	-1.41 to 1.59
S. Em. ±		2.20	2.30	5.83	0.58	6.41	0.24	0.14	0.29	1.69	0.88	0.70

*, ** Significant at 5 *per cent* and 1 *per cent* levels of significance, respectively.

DF = Days to flowering; **DM =** Days to maturity; **PH** = Plant height; **NBP =** Number of branch per plant; **NPP** = Number of pod per plant; **PL** = Pod length; **NSP** = Number of seed per plant; **TW** = Test weight; **SYP** = Seed yield per plant; **HI** = Harvest index and **CPC** = Crude protein content.

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