Assessment of Combining Ability and Gene Action in F_1 Generation for Quantitative and Qualitative Traits of Pigeonpea [*Cajanus cajan* (L). Millsp.]

Talatam Ramya Vardhini [a*], L. K. Sharma [b++], R. S. Tomar [c#] and G. U. Kulkarni [d†]

[a] Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh-362001, Gujarat, India.
[b] Pulses Research Station, Junagadh Agricultural University, Junagadh, India.
[c] ICAR-Directorate of Groundnut Research, Junagadh, India.
[d] Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Original Research Article

ABSTRACT

To estimate combining ability and nature of gene action, twenty four pigeonpea crosses were developed from ten parents in Line **x** Tester fashion during *Kharif* 2022-23 and were evaluated in Randomized Block Design with three replications during *Kharif* 2023-24. The estimates of σ²gca

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[++] *Assistant Research Scientist;*
[#] *Principal Scientist;*
[†] *Associate Professor;*
Corresponding author: E-mail: ramyavardhinit@gmail.com;

were lower than the corresponding σ^2sca for all the twelve characters studied indicating the predominance of non-additive gene action. Among the parents, the line GJP 1915 was found to be good general combiner for seed yield per plant and its yield contributing characters like plant height, number of primary branches per plant and pod length. The tester GJP 1820 was also good general combiner for seed yield per plant and its component traits like plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and 100-seed weight. The cross BDN 2013-41 × UPAS 120 had registered the highest sca effect for seed yield per plant. The sca effect in this cross combination was also accompanied by significant and desirable standard heterosis and high *per se* performance for days to maturity, reproductive phase duration, number of secondary branches per plant, number of pods per plant and number of seeds per pod and significant and desirable heterobeltiosis for days to maturity, reproductive phase duration, number of primary branches per plant, number of pods per plant and 100-seed weight. The cross GJP 1915 × BLACKTUR had registered significant and positive sca effect for seed yield per plant which was also accompanied by highest *per se* performance for pod length. These cross combinations can be potentially utilized in future breeding programmes for exploitation of hybrid vigour.

1. INTRODUCTION

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is the sixth important pulse crop in the world and second important pulse crop in India after chickpea which belong to the family Fabaceae [1]. It is popularly known as tur, pigeonpea or arhar. The seeds contain crude protein (19.0-21.7%), crude fibre (9.8-13.0%), ash (3.9-4.3%) and dry matter (86.6-88.0%) [2] and is also rich in minerals like calcium, magnesium, iron and zinc [3]. The pigeonpea crop is immensely important with respect to diversification of the cropping cycle, low ecological foot print, improvement of soil health, bringing fallow lands under cultivation etc. However, the progress in the genetic improvement of yield potential has been limited and the improved cultivars failed in enhancing the productivity of the crop. Narrow genetic diversity in cultivated genotypes has further hampered the successful exploitation of traditional breeding, consequently pigeonpea referred to as an 'Orphan Crop Legume' [4]. Therefore, an alternative breeding approach such as hybrid technology is pivotal to augment the yield of pigeonpea for assuring food and nutritional security. Most of the economic characters like seed yield, number of pods per plant, days to 50% flowering are mostly governed by polygenes and their inheritance is of complex nature. Therefore, before making attempts for improvement of these characters it is essential to know the nature of gene action controlling these quantitative characters. This information will be helpful to breeders in devising appropriate methods of breeding for crop improvement. Combining ability studies are useful in evaluation of the parental lines and their cross combinations, usually this information aids in selection of parents in terms of performance of hybrids and elucidate the nature and magnitude of various types of gene action involved in the expression of quantitative traits [5]. General combining ability is attributed to additive gene effects and additive × additive epistasis and is theoretically fixable. On the other hand, specific combining ability attributable to non additive gene action may be due to dominance or epistasis or both and is non fixable. Line × Tester mating design, as suggested by Kempthorne [6], is an appropriate method to identify superior parents and hybrids based on gca and sca, respectively and to study nature of gene action. Hence, in the present study, an attempt was made to understand the genetic nature of yield and yield components through studies involving six lines and four testers in Line × Tester mating design. This study is essential for enhancing pigeonpea breeding operations since it quantifies the combining capacity of distinct parent lines, which aids in selecting superior hybrids. Breeders can use it to create varieties with increased yield, disease resistance, and other desirable qualities by using the insights it offers about the gene action affecting critical attributes. Furthermore, this research promotes improved and more effective breeding procedures, which contribute to higher agricultural output and sustainability.

2. MATERIALS AND METHODS

A set of 24 F_1 pigeonpea crosses involving six lines (BDN 2013-41, GRG 152, IBTDRG 7, TDRG 59, GJP 1915, RKVT 322) and four testers (UPAS 120, BLACKTUR, GT 100 and GJP 1820) were generated during *Kharif* 2022-23 following line x tester fashion. These were evaluated in Randomized Block Design with three replications at Pulses Research Station, Junagadh Agricultural University, Junagadh during *Kharif* 2023-24. The parents and F_1's were grown in single row plot with a spacing of 90 x 20 cm. Five plants from each of the parents and their F_1 generation excluding border plants were randomly selected before flowering and tagged for the purpose of recording observations on twelve different characters and their mean values were used for statistical analysis. Observations were recorded for twelve characters namely days to 50% flowering, days to maturity, reproductive phase duration, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, seed yield per plant and protein content. Observations on days to 50% flowering and days to maturity were taken on plot basis. True protein was estimated by Folin-Lowry method [7].

3. RESULTS AND DISCUSSION

The concept of general and specific combining ability as a measure of gene action was proposed by Sprague and Tatum [8]. The total genetic variance is partitioned into the variance due to gca and sca. This helps in ascertaining the relative proportion of additive and non-additive variances in the inheritance of individual traits that is the decisive basis for choosing the appropriate breeding methods for effective exploitation of the available genetic variation.

The analysis of variance for combining ability was carried out for 12 characters and mean sum of squares were presented in Table 1. The mean squares due to lines were found to be significant for all of the characters except for number of secondary branches per plant, pod length and seed yield per plant when tested against error mean squares while significant for days to 50% flowering, reproductive phase duration, number of primary branches per plant, 100-seed weight and seed yield per plant when tested against line x tester interaction mean squares. Among testers, the mean squares were significant for all the characters except for number of seeds per pod and pod length when tested against error mean squares while significant for all characters except for plant height, number of seeds per pod, pod length and protein content when tested against line x tester interaction mean squares. The mean squares due to interaction effects (lines x testers) were found to be significant for all the characters except for plant height, number of seeds per pod and protein content. The estimates of σ^2gca were lower than the corresponding σ^2sca for all the characters. The result was also confirmed by the ratio of σ^2 gca /σ^2 sca for all the traits, which was less than unity. The presence of predominantly large amount of non-additive gene action would be useful for its exploitation in population having considerable necessitating heterozygosity in an often cross pollinated crop like pigeonpea as well as for exploitation of heterosis. The predominance of non-additive gene action for seed yield and its component traits were also reported by Yamanura et al. (2016), Maida et al. [5], Patel et al. [2] and Bisht et al. [9] in pigeonpea.

From Table 2, the contribution towards total hybrid variance was found to be higher from females (lines) than males (testers) for the characters number of seeds per pod, pod length, 100-seed weight and protein content. The contribution towards total hybrid variance was found to be higher from males (testers) than females (lines) for the characters days to 50% flowering, days to maturity, reproductive phase duration, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and seed yield per plant. The proportional contribution of line x tester interaction to the total variance was higher than that of males for the characters number of seeds per pod and pod length. Whereas, the contribution of the line x tester interaction was higher than that of females for days to maturity, number of secondary branches per plant, number of pods per plant, pod length and seed yield per plant. However the contribution of the line x tester interaction was lower than that of females for days to 50% flowering, reproductive phase duration, plant height, number of primary branches per plant, number of seeds per pod, 100-seed weight and protein content. It indicates specific cross combinations interact considerably in the expression of *per se* values for important characters like kernel yield.

Table 1. Analysis of variance (mean squares) for combining ability for different characters in pigeonpea

Source	d.f.	Days to 50% flowering	Days to maturity	Reproductive phase duration	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant
Replications	2	11.36	3.80	7.88	8.36	1.23	1.72
Crosses	23	154.65**	473.70**	355.82**	335.25**	23.05**	28.00**
Lines	5	231.25**++	269.91**	585.99**++	483.75**	23.27**+	26.27
Testers	3	656.83**++	2691.50**++	1049.67**++	1443.50**	107.69**++	93.66**++
Lines × Testers	15	28.68**	98.06**	140.32**	64.10	6.05**	15.45**
Error	66	7.64	10.66	14.06	125.31	1.88	1.59
Estimates of genetic components of variance							
$\sigma^2 l$		16.88	14.32	37.14	34.97	1.43	0.90
$\sigma^2 t$		34.80	144.08	50.51	76.63	5.65	4.34
$\sigma^2 lt$		7.01	29.13	42.09	20.40	1.39	4.62
$\sigma^2 gca$		1.58	4.74	2.71	3.41	0.21	0.15
$\sigma^2 sca$		7.01	29.13	42.09	20.40	1.39	4.62
$\sigma^2 gca/ \sigma^2 sca$		0.22	0.16	0.06	0.17	0.15	0.03

*, ** Significant at 5 % and 1 % levels, respectively
+, ++ Significant at 5% and 1% levels against line × tester interaction, respectively

Table 1: Contd…

Source	d.f.	Number of pods per plant	Number of seeds per pod	Pod length (cm)	100-seed weight (g)	Seed yield per plant (g)	Protein content (%)
Replications	2	22.68	0.01	0.01	0.07	2.59	0.05
Crosses	23	4038.20**	0.26**	0.21**	1.55**	520.77**	0.12
Lines	5	1505.97*	0.54**	0.23	5.95**++	283.73++	0.42**
Testers	3	25642.28**++	0.36	0.23	0.92**++	2287.93**+	0.10**
Lines × Testers	15	561.47*	0.15	0.20*	0.21**	246.35**	0.02
Error	66	288.54	0.11	0.09	0.08	54.70	0.07
Estimates of genetic components of variance							
$\sigma^2 l$		78.71	0.03	0.002	0.48	3.11	0.03
$\sigma^2 t$		1393.38	0.01	0.001	0.04	113.42	0.06

$\sigma^2 lt$	90.97	0.01	0.04	0.04	63.88	0.02
$\sigma^2 gca$	43.84	0.001	0.0001	0.02	3.46	0.001
$\sigma^2 sca$	90.97	0.01	0.04	0.04	63.88	0.02
$\sigma^2 gca / \sigma^2 sca$	0.48	0.10	0.01	0.42	0.05	0.07

*, ** Significant at 5 % and 1 % levels, respectively
+, ++ Significant at 5% and 1% levels against line × tester interaction, respectively

Table 2. Proportional contribution of lines, testers and line × tester interactions to total variance for different characters in pigeonpea

Sr. No.	Characters	% Contribution		
		Lines	**Testers**	**Line × tester**
1.	Days to 50% flowering	32.50	55.40	12.10
2.	Days to maturity	12.39	74.11	13.50
3.	Reproductive phase duration	35.80	38.48	25.72
4	Plant height (cm)	31.37	56.16	12.47
5.	Number of primary branches per plant	21.94	60.93	17.12
6.	Number of secondary branches per plant	20.39	43.62	35.98
7.	Number of pods per plant	8.11	82.82	9.06
8.	Number of seeds per pod	44.87	18.25	36.88
9.	Pod length (cm)	23.25	14.00	62.74
10.	100-seed weight (g)	83.60	7.74	8.65
11.	Seed yield per plant (g)	11.84	57.30	30.85
12.	Protein content (%)	79.15	11.38	9.47

Table 3. Estimation of general combining ability (gca) effect of parents for days to 50% flowering, days to maturity, reproductive phase duration, plant height (cm), number of primary branches per plant and number of secondary branches per plant in pigeonpea

Parents	Days to 50% flowering	Days to maturity	Reproductive phase duration	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant
Females						
BDN 2013-41	3.57**	-5.57**	-9.14**	-2.18	-0.59	0.43
GRG 152	-6.18**	-4.90**	1.28	-0.76	-0.54	0.22
IBTDRG 7	-0.6	4.01**	4.78**	-10.26**	-2.23**	-1.98**
TDRG 59	-4.18**	6.35**	10.36**	-0.26	0.81*	0.02
RVKT 322	3.32**	0.76	-2.56*	6.90*	1.56**	2.38**
GJP 1915	4.07**	-0.65	-4.72**	6.57*	1.00*	-1.06**
SE (g_i)	0.798	0.943	1.083	3.232	0.396	0.364
SE ($g_i - g_j$)	1.128	1.333	1.531	4.570	0.560	0.514
Males						
UPAS 120	-5.13**	-15.57**	-10.33**	-3.76	0.05	1.96**
GT 100	-3.01**	3.32**	6.33**	-5.88*	-0.84*	-1.76**
BLACKTUR	-0.46	-1.63*	-1.17	-3.71	-2.52**	-2.18**
GJP 1820	8.60**	13.88**	5.17**	13.35**	3.30**	1.98**
SE (g_i)	0.651	0.770	0.884	2.639	0.323	0.297
SE ($g_i - g_j$)	0.921	1.088	1.250	3.731	0.457	0.420

*, ** Significant at 5 % and 1 % levels, respectively

Table 4. Estimation of general combining ability (gca) effect of parents for number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g), seed yield per plant (g) and protein content (%) in pigeonpea

Parents	Number of pods per plant	Number of seeds per pod	Pod length (cm)	100-seed weight (g)	Seed yield per plant (g)	Protein content (%)
Females						
BDN 2013-41	12.17**	0.36**	-0.09	-0.47**	-1.28	-0.12
GRG 152	-16.36**	0.13	-0.04	-0.99**	-4.38*	-0.06
IBTDRG 7	-7.72	-0.05	-0.10	0.52**	-6.26**	0.32**
TDRG 59	-2.79	-0.21*	-0.11	0.81**	2.28	-0.22**
RVKT 322	11.61*	-0.15	0.15	0.49**	3.02	0.04
GJP 1915	3.09	-0.08	0.20*	-0.35**	6.63**	0.03
SE (g_i)	4.904	0.094	0.088	0.084	2.135	0.075
SE ($g_i - g_j$)	6.934	0.133	0.124	0.118	3.019	0.106
Males						
UPAS 120	29.47**	0.18*	0.05	-0.05	2.38	-0.01
GT 100	-22.17**	-0.17*	-0.15*	-0.08	-1.47	-0.09
BLACKTUR	-41.64**	0.003	-0.02	-0.19**	-14.11**	0.01
GJP 1820	34.35**	-0.01	0.12	0.33**	13.20**	0.09
SE (g_i)	4.004	0.077	0.072	0.068	1.743	0.061
SE ($g_i - g_j$)	5.662	0.109	0.101	0.096	2.465	0.086

*, ** Significant at 5 % and 1 % levels, respectively

Table 5. Classification of parents based on general combining ability effects for various traits in pigeonpea

Sr. No.	Parents	DF	DM	RPD	PH (cm)	PBP	SBP	PPP	NSP	PL (cm)	TW (g)	SYP (g)	PC (%)
	LINES												
1.	BDN 2013-41	P	G	G	A	A	A	G	G	A	P	A	A
2.	GJP 1915	P	A	G	G	G	P	A	A	G	P	G	A
3.	GRG 152	G	G	A	A	A	A	P	A	A	P	P	A
4.	IBTDRG 7	A	P	P	G	P	P	A	A	A	G	P	G
5.	RVKT 322	P	A	G	A	G	G	G	A	A	G	A	A
6.	TDRG 59	G	P	P	A	G	A	A	P	A	G	A	P
	TESTERS												
1.	BLACKTUR	A	G	A	A	P	P	P	A	A	P	P	A
2.	GJP 1820	P	P	P	G	G	G	G	A	A	G	G	A
3.	GT 100	G	P	P	P	P	P	P	P	P	A	A	A
4.	UPAS 120	G	G	G	A	A	G	G	G	A	A	A	A

G = Good combiner (Significant and desirable direction),
A = Average combiner (non-significant),
P = Poor combiner (Significant and undesirable direction)
DF = Days to 50% flowering
PBP = Primary branches per plant
PL = Pod length (cm)
DM = Days to maturity
SBP= Secondary branches per plant
TW = Test weight (g)
RPD = Reproductive phase duration
PPP= Pods per plant
SYP = Seed yield per plant (g)
PH = Plant height (cm)
NSP= Number of seeds per pod
PC = Protein content (%)

Table 6. Specific combining ability effects for different characters in pigeonpea

Sr. No.	Crosses	DF	DM	RPD	PH (cm)	PBP	SBP	PPP	NSP	PL (cm)	TW (g)	SYP (g)	PC (%)
1.	BDN 2013-41 × UPAS 120	3.88*	-3.1	-7.09**	0.02	3.19**	2.03**	10.95	0.18	0.17	-0.02	22.88**	-0.06
2.	BDN 2013-41 × GT 100	-3.57*	-4.32*	-0.75	-6.55	-0.4	-1.09	23.99*	0.08	0.06	0.15	-1.33	0.01
3.	BDN 2013-41 × BLACKTUR	-1.80	-0.05	1.75	2.63	-0.03	0.07	-13.69	0.06	-0.09	0.04	-13.28**	-0.03
4.	BDN 2013-41 × GJP 1820	1.49	7.46**	6.09**	3.91	-2.78**	-1.01	-21.24*	-0.31	-0.14	-0.18	-8.28	0.07
5.	GRG 152 × UPAS 120	-3.71*	-4.44*	-0.84	-3.07	0.56	.-3.09**	3.27	-0.01	0.21	-0.28	0.39	0.01
6.	GRG 152 × GT 100	2.85	6.35**	3.5	2.71	-0.42	-0.83	-8.03	-0.06	0.14	-0.1	-1.45	0.09
7.	GRG 152 × BLACKTUR	-0.05	6.63**	6.67**	-1.13	-0.08	0.41	-2.2	0.2	0.01	-0.2	-1.23	-0.03
8.	GRG 152 × GJP 1820	0.91	-8.55**	-9.34**	1.49	-0.06	3.52**	6.96	-0.14	-0.36*	0.56**	2.29	-0.06
9.	IBTDRG 7 × UPAS 120	3.38*	-5.69**	-8.67**	0.77	-1.27	3.56**	9.98	-0.05	-0.01	0.1	-7.33	0.05
10.	IBTDRG 7 × GT 100	-2.74	-0.24	2.34	3.88	0.41	0.66	-15.16	0.27	-0.01	0.08	4.34	-0.14
11.	IBTDRG 7 × BLACKTUR	-0.63	3.71	4.17	-7.63	0.51	-0.17	2.06	-0.11	-0.18	0.06	-2.47	0.08
12.	IBTDRG 7 × GJP 1820	-0.02	2.21	2.17	2.99	0.36	.-4.05**	3.13	-0.11	0.19	-0.23	5.47	0.02
13.	TDRG 59 × UPAS 120	-4.05*	6.66**	10.75**	-4.91	-1.64*	-0.49	-9.04	-0.07	-0.11	0.13	-4.87	0.08
14.	TDRG 59 × GT 100	2.85	-1.91	-4.59*	-0.8	0.8	0.98	-10.91	-0.14	0.11	0.21	-0.22	0.05
15.	TDRG 59 × BLACKTUR	1.30	-3.3	-4.42*	6.38	0.92	0.34	14.23	0.01	0.08	-0.15	3.74	0.02
16.	TDRG 59 ×	-0.10	-1.46	-1.75	-0.69	-0.07	-0.83	5.73	0.2	-0.09	-0.19	1.34	-0.14

Sr. No.	Crosses	DF	DM	RPD	PH (cm)	PBP	SBP	PPP	NSP	PL (cm)	TW (g)	SYP (g)	PC (%)
	GJP 1820												
17.	GJP 1915 × UPAS 120	1.71	2.32	0.5	3.27	-0.22	0.43	-10.19	0.11	0.18	0.25	-9.83*	-0.03
18.	GJP 1915 × GT 100	-1.41	-3.24	-1.84	2.71	-0.49	0.55	-5.16	0.11	-0.15	-0.05	1.19	-0.02
19.	GJP 1915 × BLACKTUR	-1.96	1.38	3.34	-3.13	-0.18	-0.24	5.8	-0.08	0.17	0.05	12.97**	-0.03
20.	GJP 1915 × GJP 1820	1.66	-0.46	-2	-2.85	0.89	-0.74	9.55	-0.14	-0.2	-0.25	-4.33	0.08
21.	RVKT 322 × UPAS 120	-1.21	4.24*	5.34*	3.94	-0.63	-2.43**	-4.96	-0.16	-0.44*	-0.2	-1.25	-0.05
22.	RVKT 322 × GT 100	2.02	3.35	1.34	-1.96	0.1	-0.28	15.26	-0.26	-0.16	-0.29	-2.54	0.02
23.	RVKT 322 × BLACKTUR	3.13	-8.38**	-11.50**	2.88	-1.13	-0.4	-6.19	-0.08	0.01	0.2	0.27	-0.03
24.	RVKT 322 × GJP 1820	-3.94*	0.8	4.84*	-4.85	1.66*	3.11**	-4.11	0.5	0.59**	0.28	3.52	0.05
	S. E. (S$_{ij}$)	1.60	1.89	2.17	6.46	0.79	0.73	9.81	0.19	0.18	0.17	4.27	0.15
	S. E. (S$_{ij}$ − S$_{kl}$)	2.26	2.67	3.06	9.14	1.12	1.02	13.86	0.27	0.25	0.24	6.04	0.21

DF = Days to 50% flowering
PBP = Primary branches per plant
PL = Pod length (cm)
DM = Days to maturity
SBP= Secondary branches per plant
TW = Test weight (g)
RPD = Reproductive phase duration
PPP= Pods per plant
SYP = Seed yield per plant (g)
PH = Plant height (cm)
NSP= Number of seeds per pod
PC = Protein content (%)
*, ** Significant at 5 % and 1 % levels, respectively

3.1 General Combining Ability Effects

The estimates of general combining ability effects for different characters were listed in Table 3. The parents were classified as good, average and poor combiners for different characters on the basis of estimates of general combining ability effects for population and are listed in Table 4. It was observed that none of the parent was good general combiner for all the characters. However, the line GJP 1915 and the tester GJP 1820 were found to be good general combiners for seed yield per plant; the lines GRG 152 and TDRG 59 and the testers GT 100 and UPAS 120 for days to 50% flowering; the lines BDN 2013-41 and GRG 152 and the testers BLACKTUR and UPAS 120 for days to maturity; the lines BDN 2013-41, GJP 1915 and RKVT 322 and the tester UPAS 120 for reproductive phase duration; the lines GJP 1915 and RKVT 322 and the tester GJP 1820 for plant height; the lines GJP 1915, RKVT 322 and TDRG 59 and the tester GJP 1820 for number of primary branches per plant; the line RKVT 322 and the testers GJP 1820 and UPAS 120 for number of secondary branches per plant; the lines BDN 2013-41 and RKVT 322 and the testers GJP 1820 and UPAS 120 for number of pods per plant; the line BDN 2013-41 and the tester UPAS 120 for number of seeds per pod; the lines IBTDRG 7, RKVT 322 and TDRG 59 and the tester GJP 1820 for 100-seed weight were found to be good general combiners, as they noted significant and desirable gca effects. For pod length, the line GJP 1915 and none of the testers were found to be good general combiners. For protein content, the line IBTDRG 7 and none of the testers were found to be good general combiners. The high gca effects are related to additive gene effects and additive x additive interaction effect which represent the fixable component of genetic variation. Involving these lines in multiple crossing programmes recombinant population may be developed for isolating high yielding genotypes.

In general, it is evident that the line GJP 1915 which was good general combiner for seed yield per plant was also good general combiner for its component traits like reproductive phase duration, plant height, number of primary branches per plant and pod length. Likewise, the tester GJP 1820 which was good general combiner for seed yield per plant was also good general combiner for plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant

and 100-seed weight. Similar finding of good gca effects for different traits were reported by Kumar et al. [10], Maida et al. [5], Patel et al. [2] and Bisht et al. [9] in pigeonpea.

The parents identified as good general combiners simultaneously for more number of characters can be considered as the potential parents and should be preferred in breeding programme in order to combine more number of characters by involving fewer numbers of parents in crossing programme. It is suggested that population involving these parents in a multiple crossing programme may be developed for isolating desirable recombinants. Further, the varieties or lines showing good general combining ability for particular component may also be utilized in component breeding programme for effective improvement in particular components, ultimately seeking improvement in seed yield itself. This showed that good × average and good × poor combination of parents played lead role to transmit its superior performance to its crosses in segregating generations also (Table 5).

In general, the crosses involving parents with good × good gca effects indicated additive × additive type of interaction; good × average or good × poor gca effects showed additive × dominance type of gene action, while in rest of the cases (*i.e.,* average × average, average × poor and poor × poor) of gca effect revealed dominance × dominance type of gene interaction. It was further observed that crosses involving both poor combiners also resulted in high sca effects for some of the traits. This may be because of the role of high magnitude of non-additive gene action. These crosses could be utilized through intermating in the segregating generations followed by simultaneous selection for desirable plant type for seed yield per plant and its component traits. These findings are in agreement with the earlier findings of Kumar et al. [11], Yamanura et al. [12] and Patel et al. [2] in pigeonpea.

3.2 Specific Combining Ability Effects

Specific combining ability effects helps in the identification of superior cross combinations for development of promising hybrids. The crosses showing high sca effects involving parents with high gca effects, may give rise to desirable segregants in future generations. Since, sca effect of the cross is an estimate, while *per se* performance is the realized value, the later

should also be given due consideration, while making selection of best cross combinations. The sca effects for better cross combinations for various traits were represented in Table 6.

a) Seed yield per plant: The cross BDN 2013-41 × UPAS 120 had registered the highest sca effect for seed yield per plant. The cross GJP 1915 × BLACKTUR had registered significant and positive sca effect for seed yield per plant which was also accompanied by highest *per se* performance for pod length. Hence, these hybrids should be studied in detail for commercial exploitation of heterosis and getting desired segregants during subsequent segregating.

b) Days to 50% flowering: For days to 50% flowering, the cross TDRG 59 × UPAS 120 recorded highest sca effect which was also reported for high *per se* performance in desirable direction for days to 50 % flowering. The cross RVKT 322 × GJP 1820 recorded significant and desirable sca effect involving poor × poor general combiners for this trait and also recorded significant and high *per se* performance for plant height, number of primary branches and secondary branches per plant, number of pods per plant, pod length, 100-seed weight and seed yield per plant. The cross GRG 152 × UPAS 120 recorded significant and desirable sca effect involving good × good general combiners.

c) Days to maturity and Reproductive phase duration: With respect to days to maturity and reproductive phase duration, the cross GRG 152 × GJP 1820 recorded significant sca effect and also recorded high *per se* performance for number of secondary branches per plant. The crosses RVKT 322 × BLACKTUR and IBTDRG 7 × UPAS 120 recorded significant sca effect for days to maturity and reproductive phase duration.

d) Plant height, Number of seeds per pod and Protein content: None of the crosses recorded significant sca effects for the character plant height, number of seeds per pod and protein content.

e) Number of primary branches per plant: The cross BDN 2013-41 × UPAS 120 had exhibited significant sca effect for number of primary branches per plant. The sca effect in this cross combination was also accompanied by high *per se* performance for days to maturity, reproductive phase duration, number of secondary branches per

plant, number of pods per plant, number of seeds per pod and seed yield per plant The cross RVKT 322 × GJP 1820 recorded significant and desirable sca effect involving good × good general combiners for this trait and high *per se* performance for plant height, number of primary branches and secondary branches per plant, number of pods per plant, pod length, 100-seed weight and seed yield per plant.

f) Number of secondary branches per plant: For number of secondary branches per plant, the cross IBTDRG 7 × UPAS 120 recorded significant sca effect and also recorded high *per se* performance for days to maturity and protein content. The cross GRG 152 × GJP 1820 recorded significant sca effect for this trait which involved average × good general combiners and high *per se* performance for number of secondary branches per plant. The cross RVKT 322 × GJP 1820 recorded significant and desirable sca effect involving good × good general combiners for this trait and high *per se* performance for plant height, number of primary branches and secondary branches per plant, number of pods per plant, pod length, 100-seed weight and seed yield per plant.

g) Number of pods per plant: For the trait number of pods per plant, the cross BDN 2013-41 × GT 100 recorded significant and desirable sca effect involving good × poor general combiners.

h) Pod length: For the trait pod length, the cross RVKT 322 × GJP 1820 recorded significant and desirable sca effect involving average × average general combiners for this trait.

i) 100-seed weight: For the trait 100-seed weight, the cross GRG 152 × GJP 1820 recorded significant sca effect for this trait which involved poor × good general combiners.

Better performance of hybrids involving high x low or low x low general combiners indicated dominance x dominance type of gene interaction. The crosses showing high sca effects involving one good general combiner indicated additive x dominance type gene interaction which exhibited the high heterotic performance for yield and yield related traits. Similar results of specific combining ability effects for all the characters have also been reported by Pawar et al. [13], Rashmi et al. [14], Srivarsha et al. [15], Patel et al. [2] and Bisht et al. [9] in pigeonpea.

4. CONCLUSION

From the present study, following broad inferences could be drawn that none of the crosses was consistently superior for all the traits; the crosses displaying significant sca effects did not always involve parents with high gca effects, suggesting that the inter-allelic interactions were also important for the traits; crosses having significant sca effects for seed yield may or may not have high sca effects for all the yield attributing characters; the crosses having high heterotic effects for various traits, in general, involved at least one good or average combining parent for that character; best performing parents were mostly good general combiners for majority of the characters and the crosses exhibiting high heterosis with low inbreeding depression may be exploited for development of high yielding stable lines in pigeonpea. However, high sca effect would not necessarily mean a high performance by the hybrid and the estimation of sca effect seemed to be superfluous, as no additional information was obtained by doing so. Therefore, it is suggested that the selection of parents for further breeding programme should be based on gca effect and due consideration should be given to mean value of the cross combination while selecting crosses for specific combining ability effect.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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