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## Analysis of combining ability and gene action for seed yield and biochemical traits in pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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### Abstract

Information on magnitude of combining ability and gene action were obtained for seed yield and biochemical attributes; involving twelve parents and their 32 F<sub>1</sub> hybrids along with a commercial hybrid check 'ICPL-87119' of pigeonpea in randomized block design with three replications. The magnitude of *sca* variance was higher than *gca* variance for all the traits revealed preponderance of non-additive gene action for all the traits. The estimation of *gca* effects indicated that parents *viz.*, RKPV-702-16, RKPV-807, RKPV-808 and ICPL-8039 were good general combiner for seed yield and biochemical attributes. The estimation of *sca* effects indicated that hybrids, *viz.*, RKPV-702-16 x ICPL-88039, RKPV-705 x ICPL-88039, RKPV-807 x PA-291, RKPV-808 x UPAS-120 and RKPV-821-01 x ICPL-88039 were exhibited high heterosis coupled with high *sca* effects also.

**Keywords:** Heterosis, combining ability, *gca* and *sca*

### Introduction

Redgram (*Cajanus cajan* (L.) Millsp.), commonly known as Arhar, Tur, or Pigeonpea, belongs to the Fabaceae family. It is an often-cross pollinated crop, with a cross-pollination rate ranging from 20–70%. This diploid species has a chromosome number of 2n = 22 and a genome size of 1C = 858 Mbp. In India, Redgram ranks as the second most cultivated legume after chickpea, contributing approximately 20% to the nation's total pulse production (M. Aarif *et al.*, 2021) [1].

In 2019–2020, India recorded a total pigeonpea cultivation area of 4.23 million hectares, producing 3.89 million tons with an average productivity of 919 kg/ha. Maharashtra emerged as the leading producer, contributing approximately 32% of the total production. Other significant contributors included Karnataka (17%), Madhya Pradesh (15%), Uttar Pradesh (11%), Gujarat (10%), Telangana (7%), and Jharkhand (6%). During the same period, Rajasthan cultivated pigeonpea over 0.168 lakh hectares, achieving a production of 0.132 lakh tons and a productivity of 785 kg/ha (Anonymous, 2021) [3].

Combining ability refers to a parent's capacity to transmit its performance traits to offspring. This ability depends on complex gene interactions, where certain combinations result in superior offspring, while others, even among promising parents, may fail to meet expectations. Sprague and Tatum (1942) [18] introduced the concept, distinguishing between general combining ability (GCA) and specific combining ability (SCA). GCA reflects a parent's average performance across multiple crosses, primarily influenced by additive gene effects. In contrast, SCA pertains to performance deviations caused by inter-allelic interactions. Line x Tester analysis is an efficient tool for studying the genetic basis of polygenic traits and determining parent prepotency.

### Materials and Methods

The present study consists of 8 females (RKPV-702-16, RKPV-705, RKPV-807, RKPV-808, RKPV-810-01, RKPV-816-01 RKPV-817-01 and RKPV-821-01) and 4 males (UPAS-120, PA-291, PAU-881 and ICPL-88039) following line x tester mating design during *kharif* 2022-23 at Research Field of AICRP on Pigeonpea, Agricultural Research Station,

Ummadganj, Agriculture University, Kota. A total of 45 genotypes, including eight lines, four male lines, 32 resultant hybrids, and a standard check variety (ICPL-87119), were evaluated in a Randomized Block Design (RBD) with three replications. Each genotype was sown in 3-meter-long rows with an inter-row spacing of 60 cm and an intra-row spacing of 30 cm with recommended agronomic practices and plant protection measures were adopted to ensure optimal crop health.

Ten competitive plants from each genotype were randomly selected in each replication for recording the observations of characters *viz.*, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100 seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%). The observation on days to 50% flowering and days to maturity was recorded on whole plot basis. The general combining ability (GCA) and specific combining ability (SCA) variances were calculated using the method outlined by Kempthorne (1957) [5].

### Results and Discussion

The analysis of variance for combining ability for different traits was presented in Table 1. The analysis of variance for combining ability revealed that mean sum of square due to general combining ability for some traits and specific combining ability were significant for all the traits under study. It revealed that involvement of both additive as well as non-additive gene action responsible for inheritance of seed yield and yield related traits in pigeonpea. However, the magnitudes of variance *gca* were lower than variance *sca* for all the traits indicating the predominance of the non-additive gene action, for all the traits.

The mean sum of square due to genotype, parents and crosses were significant for all trait under investigation. The analysis of variance for combining ability revealed significant differences in the line x tester component for all evaluated traits, indicating substantial variability in the selected material for the traits under investigation. The mean sum of squares due to lines were significant for days to 50% flowering and plant height. The mean sum of squares due to testers was significant for number of primary branches per plant.

The variance ratio ( $\sigma^2_{gca}/\sigma^2_{sca}$ ) being less than unity for all traits, indicated a predominance of non-additive gene action. Thus, it emphasizes, the use of recurrent selection, it would be advantageous to develop a population by inter-mating these parents inter se prior to initiating random mating in the F<sub>2</sub> generation. The predominance of non-additive gene action for the majority of traits observed was found to be consistent with previous finding with Kumar *et al.*, (2003) [7], Reddy *et al.*, (2004) [15] and Phad *et al.*, (2009) [14].

The estimates of general combining ability effects for each parent are presented in table 2. Parents were grouped as good, average, or poor general combiners based on their GCA effects: significant in the desired direction (good), non-significant in the desired direction (average), and significant in the undesired direction (poor). Crosses followed the same classification for seed yield and its contributing traits.

In the present investigation, among lines RKPV-702-16, RKPV-807 were good general combiners for seed yield per plant & biological yield per plant; RKPV-702-16, RKPV-705, RKPV-807 for days to 50% flowering & days to maturity; RKPV-705, RKPV-807 for plant height; RKPV-

807, RKPV-808 & RKPV-821-01 for number of primary branches per plant; RKPV-702-16, RKPV-808, RKPV-821-01 for number of pods per plant & 100-seed weight; RKPV-808 for number of seed per pod & pod length; RKPV-821-01 for harvest index; RKPV-705 for protein content; RKPV-702-16, RKPV-705, RKPV-808 for total carbohydrate content. Among testers RKPV-821-01 was good general combiner seed yield per plant and its component traits. Similar result was reported by Pandey *et al.*, (2014) [9], Soni and Patel (2016) [17], Maida *et al.*, (2017) [8] and Patel *et al.*, (2020) [11] in pigeonpea.

Specific combining ability effect (Table-3) helps in identification of superior cross combination (good specific combiners) for commercial exploitation of heterosis. In present investigation, Out of thirty two hybrids evaluated, nine hybrids registered significant positive SCA effects for seed yield per plant. The best five hybrids on the basis of significant positive SCA effects for seed yield per plant were RKPV-702-16 x ICPL-88039 (G x G), RKPV-705 x ICPL-88039 (A x G), RKPV-807 x PA-291 (G x P), RKPV-808 x UPAS-120 (A x A) and RKPV-821-01 x ICPL-88039 (A x G). However, Crosses with high SCA effects did not consistently involve parents with high GCA effects, indicating the presence of intra-allelic gene interactions. Additionally, undesirable SCA effects in certain crosses could result from a lack of cooperation between the desirable alleles of the parents. As a result, a cross from good general combiner parents may exhibit poor *sca* effects. Similar result was reported by Srinivas *et al.*, (2000) [19], Kumar *et al.*, (2001) [6], Kumar *et al.*, (2003) [7], Pandey (2004) [9], Vaghela *et al.*, (2009) [21], Phad *et al.*, (2009) [14], Gupta *et al.*, (2011) [4], Parmar *et al.*, (2012) [10], Patil *et al.*, (2014) [13] and Tikle *et al.*, (2016) [20].

For various yield contributing traits significant and desirable *sca* effect found in several hybrids for days to 50% flowering (thirteen), days to maturity (twelve), for plant height (two), for primary branches per plant (eight), for pods per plant (Nine), number of seeds per pod (six), for pod length (seven), 100-seed weight (twelve), biological yield (ten), harvest index (two), for protein content (nine), carbohydrate content (nine).

The hybrids *viz.*; RKPV-821-01 x ICPL-88039 (poor x average) for days to 50% flowering; RKPV-808 x UPAS-120 (average x good) for days to maturity; RKPV-702-16 x ICPL-88039 (average x good) for plant height; RKPV-807 x PA-291 (good x poor) for primary branches per plant; RKPV-807 x PA-291 (average x average) for pods per plant; RKPV-807 x PA-291 (average x average) for number of seeds per pod; RKPV-807 x PA-291 (average x average) for pod length, RKPV-807 x PA-291 (average x poor) for 100-seed weight, RKPV-808 x UPAS-120 (average x average) for seed yield, RKPV-808 x UPAS-120 (average x average) for biological yield, RKPV-702-16 x ICPL-88039 (average x average) for harvest index, RKPV-807 x PA-291 (average x average) for protein content and RKPV-807 x ICPL-88039 (poor x good) for total carbohydrate content exhibited higher *sca* effects.

An appraisal of the data revealed that, for most traits, hybrids with higher SCA effects for seed yield and yield-contributing characters involved average x poor, good x poor, and average x average combiner parents. This suggests the involvement of both additive and non-additive gene effects in controlling fruit yield and its contributing traits. These results are in agreement with Srinivas *et al.*, (2000) [19], Sekhar *et al.*, (2004) [16] and Acharya *et al.*, (2009) [2].

**Table 1:** Analysis of variance (MSS) for combining ability in respect to various characters in pigeonpea

Sources	DF	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Pod length	100-Seed weight	Seed yield per plant	Biological yield per plant	Harvest index	Protein content	Total carbohydrate content
Replicates	2	0.51	3.76	7.53	0.46	49.00	0.15	0.13	0.02	9.41	129.88	0.39	0.05	1.08
Genotype	43	211.49**	456.61**	414.24**	6.22**	1895.69**	0.68**	0.77**	2.83**	89.97**	1142.15**	6.92**	5.15**	96.25**
Parents	11	179.36**	255.96**	343.55*	3.59**	643.05**	0.24*	0.52**	1.09**	31.69**	656.17**	5.29*	2.11**	99.62**
Parents vs. crosses	1	232.38**	896.22**	0.44	3.85**	6087.02**	0.26	0.38	2.15**	103.57**	2540.22*	0.22	18.16**	0.52
Crosses	31	222.21**	513.63**	452.68**	7.23**	2204.97**	0.85**	0.88**	3.48**	110.21**	1269.49**	7.72**	5.81**	98.14**
Line Effect	7	445.99*	698.89	681.50*	4.41	31.71	0.32	0.48	2.36	51.36	640.94	4.76	1.27	122.58
Tester Effect	3	247.04	747.48	456.74	30.16**	5114.57	1.92	1.48	8.65	86.85	978.14	6.97	4.99	38.09
Line x Tester Eff.	21	144.07**	418.47**	375.82**	4.89**	913.73**	0.88**	0.92**	3.11**	133.16**	520.63**	8.81**	7.44**	98.58**
Error	62	1.91	4.07	157.53	0.37	160.83	0.10	0.11	0.09	8.24	125.67	2.88	0.51	1.45
<b>Components of variance</b>														
$\sigma^2_{gca}$	-	19.12**	39.91*	23.41*	0.94**	184.59**	0.06	0.05	0.30*	3.41	38.41	0.18	0.15	4.39
$\sigma^2_{sca}$	-	47.32**	137.88**	76.05**	1.52**	587.59**	0.26**	0.27**	1.00**	41.84**	467.47**	2.08**	2.31**	32.42**
$\sigma^2_{gca}/\sigma^2_{sca}$	-	0.40	0.29	0.30	0.62	0.31	0.22	0.19	0.30	0.08	0.08	0.09	0.06	0.14

\*-Significant at 5% and \*\*-Significant at 1%

**Table 2:** General combining ability effects for different characters in pigeonpea

Parents	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Pod length	100-Seed weight	Seed yield per plant	Biological yield per plant	Harvest index	Protein content	Total carbohydrate content
<b>FEMALES (LINES)</b>													
RKPV-702-16	-8.48**	-9.16**	-0.82	0.30	7.91*	-0.01	0.14	0.32**	2.35**	7.98*	0.29	0.01	1.78**
RKPV-705	-6.90**	-8.07**	7.68*	-0.28	-5.57	0.01	-0.18	-0.07	-0.87	-1.56	-0.66	0.70**	6.31**
RKPV-807	-4.15**	-6.91**	7.30*	0.37*	5.09	0.14	-0.14	-0.05	2.36**	10.12*	0.10	-0.27	-0.81*
RKPV-808	-0.40	-1.16	5.36	0.82**	7.39*	0.24**	0.27**	0.77**	1.46	2.62	0.55	-0.11	1.37**
RKPV-810-01	6.77**	10.01**	-3.76	-0.72**	-12.69**	-0.22*	-0.13	-0.33**	-0.73	-1.77	-0.32	-0.40	-3.00**
RKPV-816-01	6.94**	8.84**	-10.54**	-0.90**	-20.04**	-0.21*	-0.25*	-0.69**	-2.83**	-7.12*	-1.09*	0.01	0.03
RKPV-817-01	5.35**	5.51**	-10.26**	-0.10	-0.29	-0.06	0.16	-0.21*	-2.59**	-11.92**	0.47	0.05	-3.50**
RKPV-821-01	0.85*	0.93	5.04	0.52**	18.21**	0.09	0.13	0.23*	0.85	1.65	0.66*	0.01	-2.17**
<b>SE</b>	0.41	0.63	3.51	0.16	3.55	0.09	0.10	0.09	0.80	3.14	0.46	0.20	0.33
<b>MALES (TESTERS)</b>													
UPAS-120	0.27	-2.49**	1.28	-0.21	-3.91	0.02	0.10	0.22**	0.18	3.82	-0.54	-0.05	0.61*
PA-291	1.52**	4.30**	-5.48*	-0.46**	-2.57	-0.07	-0.13	-0.57**	-1.79**	-6.32**	-0.28	-0.24	-0.90**
PAU-881	2.77**	4.88**	-0.77	-0.95**	-14.03**	-0.31**	-0.26**	-0.39**	-0.97	-4.43	0.14	-0.37*	-1.18**
ICPL-88039	-4.56**	-6.70**	4.98*	1.62**	20.51**	0.37**	0.30**	0.74**	2.58**	6.93**	0.69*	0.66**	1.47**
<b>SE</b>	0.30	0.45	2.48	0.11	2.51	0.06	0.07	0.07	0.56	2.22	0.33	0.14	0.23

\*-Significant at 5% and \*\*-Significant at 1%

**Table 3:** Specific combining ability effects parental combination for different characters in pigeonpea

Sr. No.	Hybrids	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Pod length	100-Seed weight	Seed yield per plant	Biological yield per plant	Harvest index	Protein content	Total carbohydrate content
1.	RKPV-702-16 X UPAS-120	1.40	-2.09	-10.57	-0.04	-13.24	-0.07	-0.30	0.31	-8.95**	-21.94**	-3.58**	-0.28	6.57**
2.	RKPV-702-16 X PA-291	6.15**	4.11**	3.93	-0.39	16.08*	-0.11	0.38	-0.12	-0.39	-9.72	2.16*	-0.69	-6.86**
3.	RKPV-702-16 X PAU-881	-3.10**	-5.47**	-9.04	-0.90**	-18.58*	-0.53 **	-0.52**	-1.09**	3.05	13.25*	-0.04	0.11	-0.48
4.	RKPV-702-16 X ICPL-88039	-4.44**	3.44**	15.67*	1.33**	15.74*	0.71**	0.44*	0.90**	6.29**	18.42**	1.46	0.86*	0.77
5.	RKPV-705 X UPAS-120	-0.52	14.15**	1.66	0.01	2.91	0.05	-0.05	0.82**	-4.58**	-15.07*	-0.97	-0.65	1.17
6.	RKPV-705 X PA-291	-0.44	-6.30**	6.10	0.06	-1.23	0.21	-0.14	-0.57**	4.34**	16.28*	0.80	0.92*	-5.38***
7.	RKPV-705 X PAU-881	3.98**	0.78	-3.60	-0.58	-20.77**	-0.62**	-0.26	-0.65**	-7.58**	-26.51**	-1.51	0.57	1.54*
8.	RKPV-705 X ICPL-88039	-3.021**	-8.63**	-4.15	0.52	19.09**	0.36	0.45*	0.40*	7.82**	25.30**	1.67	-0.85*	2.67**
9.	RKPV-807 X UPAS-120	9.06**	10.99**	-10.50	-1.84**	-49.09**	-0.75**	-0.86**	-1.47**	-0.90	3.72	-1.39	-1.42**	-3.89**
10.	RKPV-807 X PA-291	-7.52**	-8.47**	6.05	2.54**	38.90**	1.07**	1.10**	1.82**	7.31**	22.61**	1.48	2.84**	-1.56*
11.	RKPV-807 X PAU-881	0.56	-2.38	0.43	-0.23	9.70	0.31	-0.05	0.21	-2.72	-14.15*	0.53	-0.35	-6.29**
12.	RKPV-807 X ICPL-88039	-2.1*	-0.13	4.01	-0.47	0.50	-0.63**	-0.19	-0.56**	-3.69*	-12.18	-0.62	-1.07*	11.74**
13.	RKPV-808 X UPAS-120	-11.35**	-20.76**	14.85*	1.91**	44.75**	0.61**	0.33	1.75**	11.03**	35.02**	1.97*	1.14**	-6.56**
14.	RKPV-808 X PA-291	2.40**	3.781**	-15.78*	-0.71*	-26.19**	-0.03	-0.41*	-1.19**	-8.18**	-25.36**	-2.11*	-0.56	6.35**
15.	RKPV-808 X PAU-881	-3.19**	-3.47**	-7.63	-0.88**	-10.46	-0.05	0.22	0.59**	2.68	7.48	0.98	0.26	2.65**
16.	RKPV-808 X ICPL-88039	12.15**	20.45**	8.56	-0.32	-8.09	-0.53**	-0.15	-1.15**	-5.53**	-17.15**	-0.84	-0.85*	-2.44**
17.	RKPV-810-01 X UPAS-120	3.15**	8.40**	0.57	0.91**	3.75	0.41*	0.47*	-0.86**	3.83*	12.48	0.82	1.48**	-3.48**
18.	RKPV-810-01 X PA-291	-8.44**	-18.72**	4.80	-0.91**	-20.92**	-0.49**	-0.73**	-0.29	-2.72	-9.90	-0.36	0.96*	9.19**
19.	RKPV-810-01 X PAU-881	2.31**	8.70**	7.89	1.25**	9.15	0.28	0.85**	0.56**	7.92**	28.67**	0.94	-0.93*	-3.98**
20.	RKPV-810-01 X ICPL-88039	2.98**	1.61	-13.26	-1.25**	8.01	-0.20	-0.59**	0.60**	-9.03**	-31.25**	-1.41	-1.51**	-1.73*
21.	RKPV-816-01 X UPAS-120	-2.35**	-10.09**	11.48	-0.24	14.97*	0.40*	0.49*	0.49*	5.59**	15.16*	1.83	-1.95**	0.28
22.	RKPV-816-01 X PA-291	5.06**	15.45**	2.79	-0.59	-9.63	-0.64**	-0.29	-0.08	-3.81*	-15.36*	-0.50	-1.48**	1.31
23.	RKPV-816-01 X PAU-881	-3.52**	-5.13**	-1.92	1.77**	15.77*	0.33	0.27	0.66**	-1.39	3.41	-1.97*	2.68**	5.85**
24.	RKPV-816-01 X ICPL-88039	0.81	-0.22	-12.34	-0.93**	-21.11**	-0.08	-0.47*	-1.07**	-0.39	-3.21	0.64	0.74	-7.44**
25.	RKPV-817-01 X UPAS-120	-5.44**	-6.76**	-5.73	-0.97 **	-10.44	-0.08	-0.13	-0.32	-2.12	-10.11	0.44	1.44**	6.41**
26.	RKPV-817-01 X PA-291	0.98	5.45**	10.83	0.87**	7.61	-0.06	0.29	0.84**	2.05	5.64	0.61	-0.22	-2.77**
27.	RKPV-817-01 X PAU-881	-2.60**	-1.80	2.72	0.57	34.35**	0.25	-0.10	-0.33	3.14	10.41	0.52	-1.33**	-0.52
28.	RKPV-817-01 X ICPL-88039	7.06**	3.11*	-7.83	-0.47	-31.52**	-0.10	-0.05	-0.18	-3.07	-5.95	-1.57	0.12	-3.13**
29.	RKPV-821-01 X UPAS-120	6.06**	6.16**	-1.77	0.27	6.39	-0.57**	0.05	-0.72**	-3.90*	-19.27**	0.88	0.24	-0.51
30.	RKPV-821-01 X PA-291	1.81*	4.70**	-18.7**	-0.87**	-4.62	0.06	-0.20	-0.41*	1.40	15.81*	-2.07*	-1.78**	-0.28
31.	RKPV-821-01 X PAU-881	5.56**	8.78**	11.16	-0.98**	-19.15**	0.03	-0.42*	0.07	-5.10**	-22.55**	0.53	-1.02*	1.24
32.	RKPV-821-01 X ICPL-88039	-13.44**	-19.63**	9.34	1.58**	17.38*	0.48*	0.57**	1.06**	7.60**	26.02**	0.66	2.56**	-0.45
	SE	0.84	1.27	7.02	0.32	7.09	0.18	0.19	0.19	1.60	6.28	0.92	0.41	0.66



Negative and significant SCA effects observed in crosses between average x poor, average x average, and good x poor combiners likely reflect a lack of co-adaptation between the favorable alleles of the parents. In contrast, positive and significant SCA effects in crosses involving poor x poor, good x good, average x poor, and good x average combiners can be attributed to improved complementation of favorable alleles between the parents. [Patel and Mehta (1985)]<sup>[12]</sup>.

The high per se performance exhibited by these parents and hybrids highlights their potential for trait improvement. Specifically, hybrids derived from good x good combinations can be effectively exploited using the simple pedigree method. On the other hand, combinations involving poor x good or poor x poor crosses would require approaches such as diallel selective mating or intermating in segregating populations, followed by cyclic selection cycles, to achieve consistent improvement in this trait.

### Conclusion

Overall results revealed that the lines RKPV-702-16, RKPV-807, RKPV-808 and ICPL-8039 were good general combiner for seed yield and biochemical attributes in pigeonpea. Based on mean performance and significant SCA effect for seed yield and biochemical attributes, the hybrids RKPV-702-16 x ICPL-88039, RKPV-705 x ICPL-88039, RKPV-807 x PA-291, RKPV-808 x UPAS-120 and RKPV-821-01 x ICPL-88039 was found most promising. Therefore, it needs to be exploited in future breeding programme of pigeonpea.

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