



Analysis of Combining Ability and Gene Action for Seed Yield and its Component Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]

T.L. Chaudhary¹, P.R. Patel², D.G. Patel³, D.M. Suthar¹

10.18805/ag.D-6012

ABSTRACT

Background: Pigeonpea is one of India's most essential pulse crops and it is the handiest food legume with widespread uses as food, feed, fodder and fuel. To fulfil the peoples nutrient demand, the urgent need for developing nutritious and higher productive cultivar become imperative. Therefore, this research paper seeks to explore the combining ability with the ultimate goal of advancing the development of improved varieties.

Methods: An experiment was carried out in pigeonpea using Line $\times$ Tester mating design to estimate combining ability. 20 hybrids were developed by using five female lines crossed with four male testers.

Result: The analysis of variance revealed significant differences of genotypes for all characters studied, indicating sufficient genetic variability for the characters. Based on results, Seed yield per plant showed a positive and significant correlation with the number of pods per plant, pod length and the number of seeds per pod. While, parents GT 102, Vaishali, GT 1 and BDN 2004-01 were found to be good general combiners. Whereas, crosses viz., GT 102 $\times$ SKNP 1408 and GT 103 $\times$ BDN 2004-01 were the most promising specific combiners for seed yield per plant.

Key words: Combining ability, Line $\times$ tester, Pigeonpea.

INTRODUCTION

Pulses play a crucial role in the vegetarian Indian diet, serving as essential components that contribute significantly to protein and calorie intake. Pigeonpea is famous with different names as tur, red gram and arhar. Barbados gave the name "pigeonpea" to the plant because its seeds are used to make pigeon feed (Gowda *et al.*, 2011). Pigeonpea belongs to the family 'Fabaceae' and sub-family 'Faboideae'. Pigeonpea crop is diploid ($2n = 2x$), with a chromosomal number of 22. It is an often-cross-pollinated crop in which 25 to 70 per cent natural out-crossing observed (Saxena *et al.*, 1990). Worldwide, pigeonpea is mostly traded for food. The protein content of commonly grown pigeonpea cultivars range from 17.9 to 24.3 per cent for whole grain and split-grain (Sinha, 1977). One of the factors attributed to the low productivity levels is the inherent low yield potential of the currently accessible cultivars *vis-à-vis* cultivation on marginal land and lack of robust, high-yielding varieties. For that reason must need arise to develop high-yielding and stable cultivars through efficient breeding programme to eliminate this factor.

Conducting combining ability studies assumes paramount importance in this context, as they furnish crucial insights into identifying optimal parental candidates for robust hybridization programme, while also shedding light on the intricacies of gene action, encompassing both its nature and magnitude. Correlation analysis offers valuable insights into the nature and strength of the relationships between various morphological traits, including yield.

¹Department of Genetics and Plant Breeding, C P College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar-385 506, Gujarat, India.

²Pulses Research Station, S D Agricultural University, Sardarkrushinagar-385 506, Gujarat, India.

³Cotton Research Station, S D Agricultural University, Talod-383 215, Gujarat, India.

Corresponding Author: P.R. Patel, Pulses Research Station, S D Agricultural University, Sardarkrushinagar-385 506, Gujarat, India. Email: prpatel@sdau.edu.in
ORCID: 23470803400

How to cite this article: Chaudhary, T.L., Patel, P.R., Patel, D.G. and Suthar, D.M. (2024). Analysis of Combining Ability and Gene Action for Seed Yield and its Component Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]. Agricultural Science Digest. 1-7. doi: 10.18805/ag.D-6012.

Submitted: 02-04-2024 **Accepted:** 21-10-2024 **Online:** 27-12-2024

Various breeding designs, such as diallel, test crosses, bi-parental crosses, line $\times$ tester and multiple crosses, are systematically employed to assess the breeding material. The Line $\times$ Tester design represents a refined iteration of the top cross design, originally devised by Kempthorne in 1957 to ascertain combining ability (both General and Specific) and identify superior parental lines based on hybrid performance, along with estimating diverse gene activities. Widely recognized for its efficacy, this design facilitates the simultaneous evaluation of numerous germplasm lines, offering insights into combining ability variances and effects, as highlighted by Singh (1978).

The present study was conducted with the aim to assess relationship and combining ability for seed yield and yield contributing characters among cross-combinations of nine selected parents.

MATERIALS AND METHODS

The five females (Banas, GT 102, GT 103, GT 100 and GT 1) used as lines and four males (SKNP 1408, SKNP 1406, Vaishali and BDN 2004-01) used as testers were crossed in Line $\times$ tester mating design to produce 20 F₁'s under insect proof net house (to avoid outcrossing) at Pulse Research Station (PRS), Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, during *Kharif*-2019. Thus, the 29 genotypes including 9 parents and 20F₁'s were grown during *kharif*-2020.

The experimental material comprising of 29 entries including 9 parents and 20 crosses were raised in a Randomized Block Design with three replications. Each male and female lines were grown in a single row of 3.0 m length keeping an inter-row and intra-row distance of 60 cm and 20 cm respectively. Observations were recorded from five randomly chosen plants for each genotype in each replication for various characters, including number of branches per plant, number of pods per plant, length of the pods, number of seeds per pod, plant height, seed index, seed yield per plant, biological yield per plant, harvest index, total protein content and leaf area per plant. The data were compiled for analysis of the variance of different traits using the method suggested by Panse and Sukhatme (1978). Combining ability was analyzed as suggested by Kempthorne (1957). Correlation coefficients were calculated at both the genotypic (r_g) and phenotypic (r_p) levels as method described by Al-Jibouri *et al.* (1958).

RESULTS AND DISCUSSION

The analysis of variance presented in Table 1 outlines the variations observed among both parental lines and hybrids across 13 attributes assessed. Notably, the results unveiled significant mean squares attributed to genotypes across all traits, underscoring the ample genetic variability inherent in the studied materials. Furthermore, the mean sum of squares pertaining to parents versus hybrids exhibited significance across most attributes, with the exceptions being days to flowering, days to maturity and plant height. Following this, a pivotal aspect in any breeding programme entails the strategic selection of an appropriate breeding strategy to effectively harness the observed variability. This decision-making process heavily relies on discerning the type of gene action prevailing within the population concerning the traits targeted for genetic improvement, subsequent to the identification of suitable parent plants and prospective crosses (Cockerham 1961; Sprague 1966).

The results of an analysis of variance for combining ability for thirteen characters are presented in Table 2. The significance of mean squares attributed to various factors

Table 1: Analysis of variance showing mean sum of squares for different characters in pigeonpea.

Source of variation	d.f.	Days to flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Pod length	Number of seeds per pod	Test weight	Seed yield per plant	Biological yield per plant	Harvest index	Total protein content	Leaf area per plant
Replications	2	6.36	39.18	66.70	0.23	25.67	0.20	0.10	0.24	20.23	48.28	31.52	0.06	52723.25
Genotypes	28	334.00**	349.41**	1241.08**	3.75**	4604.87**	1.62**	0.74**	3.02**	767.63**	5003.31**	266.04**	2.28**	1487952.57**
Parents (P)	8	578.73**	578.50**	1847.52**	0.87**	2514.68**	1.10**	0.72**	1.76**	862.12**	3421.00**	261.81**	3.51**	638528.05**
Lines (L)	4	721.77**	976.90**	2037.23**	1.22**	2031.20**	1.46**	0.78**	0.74**	1327.63**	6167.85**	365.95**	6.26**	339517.77*
Testers (T)	3	158.75**	111.78**	1995.45**	0.69	3992.65**	0.42	0.31*	3.36**	412.69**	319.04*	204.58**	0.95**	1155379.41**
Lines vs Testers	1	1266.54**	385.07**	644.85*	0.04	14.70	1.73**	1.69**	1.04**	348.37**	1739.46**	16.95	0.16	284015.06
Parents vs Hybrids	1	9.81	39.45	0.52	7.72**	15943.88**	12.03**	6.92**	25.55**	3255.04**	13784.38**	250.59**	9.33**	13655255.71**
Hybrids (H)	19	248.01**	269.27**	1051.03**	4.75**	4888.16**	1.29**	0.43**	2.37**	596.93**	5207.38**	268.64**	1.40**	1205220.62**
Error	56	5.12	22.73	135.22	0.25	81.10	0.17	0.10	0.13	20.07	81.77	16.00	0.11	128130.27
Total	86	112.22	129.48	493.68	1.39	1552.67	0.64	0.31	1.07	263.47	1683.35	97.77	0.81	569109.46

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

in the experimental study was notable across multiple traits, with exceptions noted for specific characteristics such as the number of branches per plant. Notably, testers exhibited significant influence on most traits, except for a few like the number of branches per plant, number of seeds per pod and harvest index. Moreover, the interaction between lines and testers significantly impacted traits like the number of pods per plant, test weight, seed yield per plant, harvest index and total protein content, underscoring the importance of hybrid combinations in determining specific combining abilities.

In terms of contribution, female lines displayed a higher mean square compared to testers for several traits including days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, biological yield per plant, harvest index and total protein content. This indicates a predominant influence of female parents on these characteristics. Conversely, testers played a more prominent role in traits such as the number of seeds per pod, test weight, seed yield per plant and leaf area per plant, as reflected by their higher mean squares.

Furthermore, the interaction variances due to lines $\times$ testers were exceptionally significant for traits such as the number of pods per plant, test weight, seed yield per plant, harvest index and total protein content. This underscores the importance of specific combining ability variances in the inheritance of significant traits, highlighting the complex interplay between parental lines and testers in hybrid performance. By elucidating the differential contributions of parental lines and testers to various traits and emphasizing the significance of their interaction in hybrid performance.

The ratio of $\sigma^2_{gca} / \sigma^2_{sca}$ being more than unity was found for number of pods per plant, length of the pods, number of seeds per pod, seed index, seed yield per plant, biological yield per plant, harvest index and leaf area per plant, which indicates preponderance of additive gene action (Table 2). This is supported by Khorgade *et al.* (2000). While, the ratio of $\sigma^2_{gca} / \sigma^2_{sca}$ being less than unity was observed for days to maturity, plant height, number of branches per plant and total protein content, which indicate preponderance of non-additive gene action. These results are in concordance with Baskaran and Muthiah (2007); Chandra *et al.* (2024). Therefore, for enhancing these traits, employing bi-parental mating followed by recurrent selection would prove fruitful in obtaining desirable recombinants. Given the simultaneous role played by additive and non-additive genetic effects in determining the inheritance of different characters, utilising both additive and non-additive genetic variances through biparental crosses and modified recurrent selection in population breeding may lead to greater genetic improvement.

The estimates of general combining ability effects of the parents for various characters are presented in Table 3. The parents viz. GT 102, Vaishali, GT 1 and BDN 2004-01 were found good general combiners for seed yield and its

Table 2: Analysis of variance for combining ability for different characters in pigeonpea.

Source of variation	d.f.	Days to flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Pod length	Number of seeds per pod	Test weight	Seed yield per plant	Biological yield per plant	Harvest index	Total protein content	Leaf area per plant
Replications	2	11.85	16.07	6.62	0.98	52.49	0.13	0.32*	0.30	10.42	120.24	26.16	0.06	56021.83
Lines	4	1101.11**	1149.81**	3079.43**	5.56	12471.45**	4.64**	0.51*	4.12**	1376.37**	22007.87**	1037.96**	3.15*	803107.33*
Testers	3	69.82**	106.38**	2028.98**	2.45	11377.96**	1.19**	1.48	7.88**	1588.55**	3164.84**	128.38	2.31*	5803880.62**
Lines $\times$ Testers	12	8.20	16.48	130.42	5.05	737.95**	0.20	0.13	0.41**	89.21**	117.84	47.27**	0.59**	189593.38
Error	38	5.04	23.54	1171.48	0.20	90.23	0.17	0.09	0.12	24.01	93.08	16.30	0.10	150354.25
Components of variance														
σ^2 Lines		91.08**	94.44**	245.75**	-0.04	977.79**	0.37**	0.03*	0.31**	107.26**	1824.17**	82.56**	0.21*	51126.16*
σ^2 Testers		4.11**	5.99**	126.57**	-0.17	709.33**	0.07**	0.09**	0.50**	99.96**	203.13**	5.41	0.12*	374285.82**
σ^2_{gca}		42.76	45.31**	179.54**	-0.08	828.65**	0.20**	0.06**	0.41**	103.20**	923.59**	39.70**	0.16**	230659.30**
σ^2_{sca}		1.05	-2.36	-13.69	1.62	215.90**	0.01	0.02	0.09**	21.73**	8.26	10.32	0.16**	13079.71
$\sigma^2_{gca} / \sigma^2_{sca}$		40.67	-19.24	-13.12	-0.05	3.84	17.81	3.95	4.37	4.75	111.88	3.85	0.97	17.63

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

contributing traits like number of pods per plant, number of seeds per pod, test weight, harvest index and leaf area per plant. Banas, GT 102, SKNP 1408 and SKNP 1406 emerged as superior performers in terms of early flowering, evidenced by their markedly significant and negative general combining ability (GCA) effects. This observation underscores their potential for imparting early flowering characteristics to their progeny. Moreover, concerning days to maturity, a similar trend in GCA effects was observed specifically with parent GT 102. The minimum number of days to flowering and maturity is preferred to reduce the crop growth period. While, for days to flowering and days to maturity line GT 102 exhibited significant negative gca effect for both these traits. Therefore, these lines could be used in the synthesis of early maturing hybrids. Parents *viz*, GT 100, SKNP 1408, Vaishali and BDN 2004-01 are good combiners for plant height in desired direction. Banas and SKNP 1406 are good combiners for the number of branches per plant. GT 102 for number of pods per plant along with GT 1, Vaishali and BDN 2004-01 for number of pods per plant, number of seed per pod, test weight, harvest index and leaf area per plant, recorded as good combiners as they ultimately lead to increase of seed yield by producing superior hybrids. These results are in concordance with Chaudhary *et al.* (2016) and Soni and Patel (2016). While, for protein content, Banas, SKNP 1408 and Vaishali considered as good combiners to producing hybrids which contains good amount of protein, which is beneficial for reducing the Kwashiorkor disease. These results were supported by Soni and Patel (2016) and Patel *et al.* (2020) for total protein content.

Specific combining ability effect is a very important estimate for determining the potentiality of cross combination. The results of SCA effects of the hybrids for various characters are presented in Table 4. Out of the 20 cross combinations, GT 102 × SKNP 1408 and GT 103 × BDN 2004-01 were found to be positive and significant specific combiners for seed yield per plant. The results were found similar with work done by Patil *et al.* (2015), Soni and Patel (2016), Patel *et al.* (2020) and Kumar *et al.* (2001). While, none of the crosses exhibited negative and significant SCA effects for days to flowering, days to maturity and plant height. But some crosses exerted negative value of sca effect which indicates that they are average specific combiner. The results are in accordance with similar findings of Thiruvengadam and Muthiaha (2012) and Chaudhary *et al.* (2016). Crosses *viz.*, Banas × SKNP 1406, GT 1 × Vaishali and GT 100 × SKNP 1406 for branches per plant, GT 1 × BDN 2004-01, GT 100 × BDN 2004-01 and GT 103 × SKNP 1406 for number of pods per plant, GT 100 × Vaishali (0.68) and Banas × SKNP 1408 for test weight, GT 100 × SKNP 1406, GT 102 × SKNP 1408 and GT 1 × Vaishali for harvest index and GT 103 × SKNP 1408 for total protein content, exhibited positive and significant sca effect which reveals they are good specific combiner and further they used as potential variety. While, some crosses exhibited positive but non-significant value of sca effect for traits likes,

Table 3: The estimates of general combining ability (GCA) effects of the parents for various characters in pigeonpea.

Parents	Days to flowering	Days to maturity	Plant height	No. of branches per plant	No. of pods per plant	Pod length	No. of seeds per pod	Test weight	Seed yield per plant	Biological yield per plant	Harvest index	Total protein content	Leaf area per plant
Lines													
Banas	-4.03**	0.68	6.05	1.05**	-14.85**	-0.68**	-0.06	-0.80**	-8.28**	-20.59**	1.96	0.76**	-45.78
GT 102	-12.20**	-15.73**	14.93**	0.15	46.13**	-0.18	0.05	0.60**	11.15**	3.60	4.88**	0.10	12.27
GT 103	2.97**	6.93**	-0.07	-0.54**	-0.79	-0.02	-0.26**	-0.29**	0.78	72.51**	-13.49**	-0.04	-0.71
GT 100	-0.62	-1.15	-27.01**	-0.67**	-41.16**	-0.14	-0.03	-0.05	-13.20**	-34.87**	-1.06	-0.17	-346.81**
GT 1	13.88**	9.27**	6.11	0.01	10.67**	1.02**	0.30**	0.54**	9.54**	-20.64**	11.63**	-0.66**	381.03**
S.Em.±	0.65	1.40	3.78	0.13	2.74	0.12	0.08	0.10	1.41	2.79	1.17	0.09	111.94
Testers													
SKNP 1408	-1.33*	-2.17	-12.74**	-0.44**	-0.50	0.22*	-0.07	-0.29**	-1.86	-0.89	-0.94	0.25**	-293.06**
SKNP 1406	-2.07**	-1.90	6.85*	0.51**	-36.40**	-0.39**	-0.41**	-0.86**	-13.62**	-19.26**	-3.73**	-0.50**	-719.56**
Vaishali	2.73**	3.57**	-8.26*	0.10	30.06**	0.19	0.31**	0.78**	9.84**	15.47**	2.43*	0.37**	655.36**
BDN 2004-01	0.67	0.50	-11.33**	-0.17	6.84**	-0.01	0.17*	0.37**	5.64**	4.68	2.24*	-0.11	357.26**
S.Em.±	0.58	1.25	3.38	0.12	2.45	0.10	0.08	0.09	1.27	2.49	1.04	0.08	100.12

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

Table 4: Estimates of specific combining ability (SCA) effects of the hybrids for various characters in pigeonpea.

Hybrids	Days to flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Pod length	Number of seeds per pod	Test weight	Seed yield per plant	Biological yield per plant	Harvest index	Total protein content	Leaf area per plant
Banas x SKNP 1408	-1.50	-3.42	-3.97	-0.85 **	1.11	-0.42	0.09	0.46*	-1.48	-3.80	-0.02	-0.26	-82.73
Banas x SKNP 1406	2.23	-2.02	-5.88	2.61 **	10.02	0.35	-0.38*	-0.06	0.27	-1.59	-0.69	0.16	-133.11
Banas x Vaishali	-0.90	2.18	4.16	-0.85 **	9.09	-0.03	0.17	-0.15	2.38	5.31	0.60	0.27	98.39
Banas x BDN 2004-01	0.17	3.25	5.69	0.91 **	-20.22**	0.10	0.12	-0.24	-1.17	0.09	0.10	-0.17	117.45
GT 102 x SKNP 1408	2.33	1.67	-3.02	0.32	-7.06	0.32	0.04	-0.14	7.60**	-2.02	5.57*	-0.02	-23.86
GT 102 x SKNP 1406	-2.27	0.07	-4.37	-0.49	4.38	-0.36	0.24	0.08	3.22	9.04	-0.32	-0.25	-156.12
GT 102 x Vaishali	0.60	1.60	4.81	0.52	1.22	0.13	-0.15	-0.18	-5.09	-2.26	-2.98	-0.09	109.61
GT 102 x BDN 2004-01	-0.67	-3.33	2.58	-0.35	1.47	-0.09	-0.13	0.25	-5.73*	-4.76	-2.27	0.36	70.37
GT 103 x SKNP 1408	0.50	0.33	0.71	0.07	1.40	-0.08	0.09	0.06	-2.40	-0.37	-0.50	1.03**	106.69
GT 103 x SKNP 1406	0.90	-0.93	3.60	-1.54 **	12.10*	0.24	-0.24	0.24	-8.03**	-1.87	-3.78	-0.17	191.52
GT 103 x Vaishali	-0.57	-0.40	0.88	0.74 **	-0.76	0.00	0.10	-0.31	3.92	4.23	1.25	-0.42*	-180.94
GT 103 x BDN 2004-01	-0.83	1.00	-5.19	0.74 **	-12.74*	-0.16	0.05	0.13	6.50*	-1.99	3.03	-0.44*	-117.27
GT 100 x SKNP 1408	-1.58	-0.25	9.39	0.34	1.10	0.18	-0.01	-0.34	1.80	0.54	0.96	-0.46*	306.56
GT 100 x SKNP 1406	0.15	1.15	6.54	0.92 **	5.00	0.00	0.26	0.12	4.52	-9.65	5.59*	0.19	270.80
GT 100 x Vaishali	-0.65	-1.65	-12.78	-1.53 **	-18.59**	-0.15	-0.13	0.68**	-4.41	2.48	-3.68	0.19	-268.60
GT 100 x BDN 2004-01	2.08	0.75	-3.15	0.27	12.50*	-0.03	-0.12	-0.46*	-1.91	6.63	-2.87	-0.01	-308.75
GT 1 x SKNP 1408	0.25	1.67	-3.10	0.12	3.46	-0.00	-0.21	0.09	-5.52	5.65	-6.01*	-0.30	-306.67
GT 1 x SKNP 1406	-1.02	1.73	0.11	-1.49 **	-31.50**	-0.00	0.12	-0.37	0.02	4.07	-0.80	0.06	-173.08
GT 1 x Vaishali	1.52	-1.73	2.93	1.12 **	9.04	0.05	0.00	-0.03	3.19	-9.75	4.80*	-0.02	241.54
GT 1 x BDN 2004-01	-0.75	-1.67	0.06	0.25	19.00**	0.18	0.08	0.31	2.31	0.03	2.01	0.26	238.20
Range Minimum	-2.27	-3.42	-12.78	-1.54	-31.50	-0.42	-0.38	-0.46	-8.03	-9.75	-6.01	-0.46	-308.75
Maximum 2.33	3.25	9.39	2.61	19.00	0.35	0.26	0.68	7.60	9.04	5.59	1.03	306.56	
S.E.m ±	1.30	2.80	7.56	0.26	5.48	0.23	0.17	0.20	2.83	5.57	2.33	0.18	223.87
No. of +ve significant	0	0	0	6	3	0	0	2	2	0	3	1	0
No. of -ve significant	0	0	0	5	4	0	1	1	2	0	1	3	0

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

Table 5: Genotypic and phenotypic correlation coefficient among thirteen characters in pigeonpea.

Charact.	DFF	DM	PH	BPP	PPP	PL	SPP	TW	BYPP	HI	TPC	LAPP	SYPP
DF	1	0.930**	-0.292	0.087	-0.108	0.489**	0.108	0.009	-0.099	0.421*	-0.188	-0.089	0.227
DM	0.860**	1	-0.264	0.061	-0.154	0.332	0.028	0.027	-0.068	0.235	-0.160	-0.041	0.141
PH	-0.258*	-0.207*	1	-0.092	0.326	0.411*	0.056	0.029	0.272	-0.223	0.214	0.180	0.187
BPP	0.069	0.052	-0.067	1	-0.089	-0.130	0.322	-0.088	-0.112	-0.031	0.129	0.281	-0.113
PPP	-0.099	-0.140	0.250*	-0.095	1	-0.074	0.116	-0.114	0.769**	0.019	-0.077	0.165	0.860**
PL	0.389**	0.251*	0.285**	-0.108	-0.088	1	0.298	0.279	0.085	0.215	0.141	0.031	0.244*
SPP	0.486	0.082	-0.702	0.302**	0.093	0.303**	1	0.103	0.267	-0.188	-0.074	0.281	0.149**
TW	0.034	-0.015	0.021	-0.092	-0.105	0.238*	0.089	1	0.093	0.073	-0.054	0.155	0.089
BYPP	-0.091	-0.058	0.255*	-0.111	0.732**	0.077	0.251*	0.086	1	-0.445	-0.149	0.254	0.725
HI	0.361**	0.151	-0.177	-0.030	0.019	0.153	-0.147	0.074	-0.433**	1	0.078	-0.283	0.267
TPC	-0.176	-0.151	0.160	0.117	-0.068	0.126	-0.066	-0.061	-0.133	0.055	1	0.071	-0.074
LAPP	-0.085	-0.042	0.163	0.263*	0.156	0.031	0.268**	0.144	0.246*	-0.250*	0.073	1	0.085
SYPP	0.207	0.096	0.177	-0.107	0.795**	0.208*	0.148**	0.086	0.683	0.331	-0.068	0.079	1

Upper side: Genetic correlation. Lower side: Phenotypic correlation. *, ** Significant at 5 per cent and 1 per cent levels of significance, respectively.

pod length, number of seeds per pod, biological yield per plant and leaf area per plant, which indicates that they are average specific combiner and there is need to further utilized them with proper breeding methods for betterment of their combining ability. Soni and Patel (2016) and Patel *et al.* (2020) obtained similar result for above traits.

The phenotypic correlation represents the observable relationship between two traits, while the genotypic correlation reflects the inherent association that can enhance the genetic makeup of genotypes through selection for seed yield and its contributing traits. The estimate of genotypic and phenotypic correlation coefficients was presented in Table 5. The higher magnitude of genotypic correlation coefficients compared to phenotypic correlation coefficients for almost all studied traits suggested a strong inherent association between these characters, indicating minimal environmental influence on their expression. Seed yield per plant showed positive and significant correlation with number of pods per plant, pod length and number of seeds per pod at both genotypic and phenotypic levels. Therefore, more preference is given to entries which exhibits high value for above traits in future breeding programme. Similar results recorded by Vanniarajan *et al.* (2023).

CONCLUSION

The breeding programme for pigeonpea can leverage specific parent combinations and hybridizations to enhance seed yield per plant and other yield components. Seed yield per plant showed a positive and significant correlation with the number of pods per plant, pod length and the number of seeds per pod. Therefore, entries with high values for these traits should be prioritized in future breeding programs. Parents such as GT 1, GT 102, Vaishali and BDN 2004-01 exhibit significant general combiner effects, highlighting their potential for contributing to desirable traits. It's recommended to initially select parents based on per se performance and general combining ability (GCA) effects, followed by recurrent selection to exploit both additive and non-additive gene actions simultaneously. While, Crosses viz., GT 102 × SKNP 1408 and GT 103 × BDN 2004-01 were found to be positive and significant specific combiners for seed yield per plant. Hence, these crosses were identified as potential for getting good transgressive segregants for seed yield per plant and its component traits and suggested for further evaluation in future breeding programme.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

All animal procedures for experiments were approved by the Committee of Experimental Animal care and handling techniques were approved by the University of Animal Care Committee.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

REFERENCES

- Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variances in upland cotton cross of inter specific origin. *Agronomy Journal*. 50: 633-635.
- Baskaran, K., Muthiah A.R. (2007). Studies on combining ability in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*. 30(1): 67-69.
- Chandra, D., Verma, S.K., Gaur, A.K., Bisht, C., Gautam, A., Chauhan, C. and Yadav H. (2024). Heterosis, Combining Ability, Genetic Diversity and their Interrelationship in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Legume Research*. 47(2): 183-189. doi: 10.18805/LR-4628.
- Chaudhary, R.G., Joshi, D.J. and Patel, A.M. (2016). Combining ability studies comprising male sterile lines in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Advances in Life Sciences*. 5(17): 6739-6744.
- Cockerham, C. (1961). Implications of genetic variances in a hybrid breeding programme. *Crop Science*. 1: 47-52.
- Gowda, C.L.L., Saxena, K.B., Srivastava, R.K., Upadhyaya, H.D. and Silim, S.N. (2011). Pigeonpea: From an orphan to leader in food legumes. In *Biodiversity in Agriculture: Domestication, Evolution and Sustainability*. Cambridge University Press. University of California, Davis, USA. pp. 361-373.
- Kemphorne, O. (1957). *An introduction to genetic statistics*. John Wiley and Sons, Inc. New York. Champan and Hall, Ltd.
- Khorgade, P.W., Wankhade, R.R. and Wanjari, K.B. (2000). Combining ability analysis in pigeonpea using male sterile lines. *Indian Journal of Agricultural Research*. 34(2): 112-116.
- Kumar, A., Shrivastava, D.P., Singh, I.P. and Dixit, G.P. (2001). Combining ability analysis of male sterile lines and hybrids in pigeonpea. *Legume Research*. 24(3): 178-181.
- Panase, V.G. and Sukhatme, P.V. (1978). *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research. New Delhi.
- Patel, H.S., Patel, A.M., Chaudhary, N.B. and Kugashiya, K.G. (2020). Exploitation of heterosis in hybrids developed using cytoplasmic genetic male sterility (CGMS) system in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Journal of Pharmacognosy and Phytochemistry*. 9(4): 1147-1151.
- Patil, S.B., Hingane, A.J., Sameer Kumar, C.V., Mula Myer, R., Kumar, Vijaya and Saxena, K.B. (2015). Combining ability studies of pigeonpea CGMS lines with an obcordate leaf Marker. *Journal of Food Legumes*. 28(2): 7-12.
- Saxena, K.B., Singh, L. and Gupta, M.D. (1990). Variation for natural out-crossing in pigeonpea. *Euphytica*. 46: 143-148.
- Singh, P. (1978). Line × Tester Analysis in Urd (*Phaseolus mungo* L.). Ph.D. thesis (unpublished), Kanpur University, Kanpur.
- Sinha, S.K. (1977). Food legumes: Distribution, Adaptability and Biology of Yield. In: *FAO Plant Production and Protection Paper 3*, Food and Agriculture Organization (FAO), Rome, Italy. pp. 1-102.
- Soni, N. and Patel, P.T. (2016). Gene action and combining ability of cytoplasmic genic male sterility system-based hybrids in pigeonpea [*Cajanus Cajan* (L.) Millsp.]. *International Journal of Horticulture*. 6(24):1-7.
- Sprague, G.F. (1966). *Quantitative Genetics in Plant Improvement*. In: *Plant Breeding. A Symposium on Plant Breed.* [(Ed.) Kenneth, J. Frey] Iowa State Univ Press Ames, Iowa. pp 315-354.
- Thiruvengadam, V. and Muthiah, R. (2012). Combining ability analysis for yield and its components in pigeonpea using genetic male sterile lines. *Journal of Food Legumes*. 25(3): 171-174.
- Vanniarajan, C., Magudeeswari, P., Gowthami, R., Indhu, S.M., Ramya, K.R., Monisha, K. and Yasin, J.K. (2023). Assessment of genetic variability and traits association in pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm. *Legume Research*. 46(10): 1280-1287. doi: 10.18805/LR-4442.