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Unraveling heterosis and combining ability for enhancing yield and its component traits in Cowpea (*Vigna unguiculata* L. Walp)

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Abstract

The present study explores heterosis, combining ability, gene action, and proportional contribution of lines, testers and their interactions for yield and its contributing traits in cowpea (*Vigna unguiculata* L. Walp). Evaluating 24 F_1 populations, 11 parents (3 lines and 8 testers), and a standard check (Phule Rakhumai) in Randomized Block Design during *Summer* 2024. The results revealed that line PL 4, tester NIC 23105, and crosses, PL 4 × IC 259084, Phule Vithai × IC 263015, and Phule Sonali × EC 738083, were found superior for yield and its component traits based on GCA and SCA estimates, respectively. Further, PL 4 × IC 259084, PL 4 × NIC 23105, Phule Vithai × IC 263015, Phule Sonali × NIC 23105, and Phule Sonali × V 240 were identified as superior crosses for yield/plant based on estimates of standard heterosis. The gene action studies indicated that non-additive gene action predominantly controls most quantitative traits, as the dominant variance (σ2 D) was more than the additive variance (σ2 A) and the variance ratio was less than unity for most of the quantitative traits except days to maturity and 100 seed weight. While the higher contribution of line × tester interactions also highlighted the effective role of testers. Heterosis breeding can thus be commercially exploited to develop superior cowpea hybrids.

Keywords: Cowpea, heterosis, combining ability and gene action

Introduction

Cowpea (*Vigna ungiculata* L.) is a highly self-pollinated multipurpose grain legume belonging to the family Papilionaceae with a chromosome number of 2n=22. Cowpea is called as poor man's meat and is drought tolerance, nitrogen fixing crop implies it to be a major grain legume (Deepa Priya *et al*. 2018) [8]. Cowpea grain possesses about 24.8% protein, 1.9% fat and 63.6% carbohydrates and is excellent source of calcium and iron (Davis *et al*. 2000, Ajayi *et al*. 2011) [7, 1]. It is recognized as an important component of cropping systems in the world's tropical and subtropical areas and its relevance in being a nourishing legume can never be overemphasized (Sanchez- Navarro *et al*. 2019) [32]. Globally, cowpea is grown in an area of 14.5 million ha with the production of 6.2 Million tonnes (Boukar *et al*. 2018) [5]. A breeder is challenged at the outset, by a rather complex problem normally the choice of choice of parents for hybridization, because yield is a complex trait, encompassing a number of components each of which is a polygenically controlled and consequently, particularly subject to environmental changes. A study on combining ability is needed to break the prevailing production plateau in cowpea crop. The combining ability studies offer useful information for the selection of high order parents for effective breeding alongside demonstrating the type and extent of gene action governing the expression of quantitative features of economic value. Most of the crop improvement programmes utilized conventional breeding approaches which utilized only the natural variability available in the germplasm (Kumar V. A. *et al*. 2010) [19]. The ability to accumulate the variability by recombination and isolation of desired genotypes from segregating population hold the key to success of any crop improvement programme. (Kurer *et al*. 2010, Fasahat *et al*. 2016) [20, 12]. Identification of the best performing lines (for commercial release) and lines which can be employed as parents in future crosses are two principal objects in most crop breeding initiatives. Heterosis breeding has demonstrated to be a possible strategy of enhancing yield in

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majority of the self-fertilized crops. Dominance gene effects and greater GCA effects imply a greater impact of additive gene effects governing these traits. Heterosis is the genetical phenomena referred to describe an expression of greater vigour. The overall effect of plant breeding on genetic diversity has been a long operating concern in the evolutionary biology of crop plants (Simmonds, 1962) [36]. Among different mating designs, line x tester analysis offers pertinent data on combining ability effect of the genotypes. The line × tester analysis technique (Kempthorne, 1957) [16] provides a systematic approach to assess the heterosis and combing ability of parents and crosses for different quantitative characteristics. The additional advantage of this method is that it presents an overall view of the experimental material under investigation in single generation and a more number of genotypes can be analysed at a time. In light of this perspective, the present research was undertaken for assessing the effects of combining ability effect, the magnitude of gene action and heterotic response for different characteristics in cowpea.

Materials and Methods

The present research was carried out at Experimental Farm of Agriculture Research Station, Badnapur, Maharashtra, India. The most divergent cowpea genotypes consisting of 3 lines and 8 testers selected based on morphological characterization (Table 1). Genotypes were crossed in a line × tester mating design during *Kharif*-2023, producing 24 F_1 crosses. During *Summer*-2024, these crosses, along with their 11 parents and a standard check (Phule Rakhumai), were sown in a Randomized Block Design with two replications. The row length was 2.00 m. The inter and intra row spacing was kept at 45 cm and 10 cm, respectively. Observations were recorded on five randomly selected plants from two replications of each genotype for all the ten quantitative traits under study namely, days to 50% flowering, days to maturity, plant height, number of primary branches, number of clusters/ plant, number of pods/ plant, number of seeds/ pod, pod length, 100 seed weight and seed yield/ plant. The mean data was subjected to line × tester analysis by Kempthorne (1957) [16] and modified by Arunachalam (1974). Test of significance was applied as per Panse and Sukhatme (1985) [27]. The GCA:SCA ratio was computed to analyze the effects and gauge the relative significance of additive and non-additive gene effects, following the methodology outlined by Singh and Chaudhary (1977) [37].

Results and Discussion

Combining ability studies

The analysis of variance indicated significant mean squares due to genotypes, parents, and crosses for all the traits, revealing the existence of sufficient variation among the parents and crosses. (Table 2). The existence of variation among the experimental genotypes were in conformity with the results reported by Idahosa and Alika (2013) [13], Mukati *et al.* (2014) [23], Kumar *et al.* (2017) [17], and Pethe *et al.* (2018) [30]. Combining ability plays a critical role in identifying appropriate parents in breeding programs and studying gene influences on quantitative traits. The results obtained in general combining ability effect (Table 4) indicated that among the lines, PL 4 was good general combiners for the characters days to 50% flowering, days to maturity, number of clusters/plant, number of pods/plant, 100 seed weight seed, and yield/plant. While, among testers, NIC 23105 was shown to be a good general combiner for the characters days to maturity, number of primary branches/plant, number of clusters/plant, number of pods/plant, and seed yield/plant. The results obtained in specific combining ability effect indicated that among the 24 F_1 crosses, the highest magnitude of negative SCA effect for days to 50% flowering was exhibited for cross PL 4 × IC 68786 (- 4.877), followed by Phule Sonali × EC 38214 (-4.019), while the highest SCA for days to maturity was observed in cross Phule Sonali × NIC 23105 (-4.583), followed by PL 4 × IC 259084 (-3.750), and Phule Vithai × IC 263015 (-3.500). The negative SCA effect is favourable since early flowering and maturity than the parents is favourable for producing early varieties. The top performer cross combination for yield component were observed in crosses *viz*., Phule Vithai × EC 244130 (1.703) for number of primary branches/plant, Phule Vithai × IC 263015 (3.146) for number of clusters / plant, Phule Vithai × IC 263015 (19.593) for number of pods/plant, Phule Sonali × EC 738083 (1.690) for pod length, PL 4 × IC 68786 (1.300) for number of seeds/pod, and Phule Vithai × IC 263015 (14.919) for 100 seed weight. The estimates of the SCA effect revealed that none of the cross was consistently to be superior for all the characteristics. For the trait like seed yield, in general, it was observed that the top-ranking heterotic crosses, Phule Vithai × IC 263015 (14.919) and PL 4 × IC 259084 (14.309), manifested significant positive SCA effects and also showed heterotic response over the standard check for yield, and most of the yield components had poor × average and good × average general combiners. The heterotic effects for yield in these crosses might have resulted from epistatic, additive × dominance gene interaction enticing high heterosis for seed yield. Furthermore, the crosses like PL 4 × NIC 23105 and PL 4 × EC 38214 exhibited standard heterosis for seed yield, positive but non-significant SCA effects for seed yield with high × high GCA parent. These imply that good GCA parents did not always generate the best SCA combination for yield. Similarly, the finding was in accordance with Kumar *et al.* (2017) [17], who reported the cross MFC-09-12 × UPC-9202 with good × good GCA parents and a non-significant SCA effect for seed yield. Overall, this appears appropriate, as grain yield being a complex character depends on a number of component traits. It is also apparent that the high degree of non-additive gene action for seed yield and its component traits observed in the present study implies a hybrid breeding program. These findings are in agreement with the preceding findings of Pandey and Singh (2010) [26], Meena *et al.* (2010) [22], Uma and Kalibowilla (2010) [39], and Chaudhari *et al.* (2013) [6].

Heterosis studies

Knowledge on the magnitude of heterosis for various characters is essential to locating better combinations to exploit them through heterosis breeding. In order to identify the true heterotic cross combinations, the heterotic response over standard variety is desirable. Commercial superiority of the hybrid can be assessed by evaluating with a standard commercial check (Swaminathan *et al.* 1972) [38]. Rather than mid-parent heterosis and heterobeltiosis, the standard heterosis, reflecting the actual superiority over the best existing cultivar, appears to be more relevant and practical. With this point of view, Phule Rakhumai was chosen as a check for the present study. The estimates of heterosis for 24 F_1 crosses, compared to the standard check, revealed significant heterosis in desirable directions for all quantitative traits (Table 5). Among all 24 cross combinations, 14 for days to 50% flowering and days to maturity, 3 for number of primary branches/plant, 15 for number of clusters/plant, 10 for number of pods/plant, 4 for pod length, 6 for number of seeds/plant, 12 for 100 seed weight, and 3 for seed yield/plant exhibited significant and positive standard heterosis over check

Phule Rakhumai. The top most significant negative standard heterosis in positive direction was observed in the crosses Phule Sonali × IC 25908 (-27.52%) for days to 50% flowering, PL 4 × IC 68786 (-17.06%) for days to maturity, and Phule Sonali × IC 263015 (-26.16%) for plant height. Previously, these results were in consonance with those obtained by Shashibhushan and Chaudhari (2000) [34], Bhushana *et al.* (2000) [4] for days to 50% flowering, Meena *et al.* (2009) [21], and Raut *et al.* (2017) [31] for days to maturity. The desirable top ranking significant positive heterosis was manifested by Phule Vithai × EC 38214 (130.34%) for number of primary branches/plant, PL 4 × IC 259084 (207.33%) for number of clusters/plant, Phule Vithai × IC 263015 (87.86%) for number of pods/plant, Phule Sonali × EC 738083 (37.92%) for pod length, Phule Sonali × V 240 (20.69%) for number of seeds/pod, and PL 4 × EC 73808 (90.77%) for 100 seed weight. Seed yield is the most economic character in cowpea. The crosses, *viz*., PL 4 × IC 259084 (63.54%), followed by PL 4 × NIC 23105 (62.32%), Phule Vithai × IC 263015 (45.31%), Phule Sonali × NIC 23105 (30.83%), and Phule Sonali × V 240 (26.68%), were regarded as the top five crosses for seed yield/plant based on standard heterosis over standard check Phule Rakhumai. Such crosses can be utilized for future breeding programme in cowpea. Significant standard heterosis for one and more yield component traits was previously reported by Sarath *et al.* (2017) [33], Dinakar *et al.* (2021) [10], Wankhade *et al.* (2018) [40], Shirisha *et al.* (2022) [35], and Jahun *et al.* (2023) [14], indicating the potentiality for increasing cowpea yield.

Gene action

Analysis showed that SCA variance (σ2 s) was greater than GCA variance (σ2 g) for days to 50% flowering, plant height, number of primary branches/plant, number of clusters per/plant, number of pods/plant, pod length, number of seeds/pod and seed yield/plant indicating they were governed by non-additive gene action. (Table 6). These findings were further confirmed by the higher dominant variance (σ2 D) compared to additive variance (σ2 A) and variance ratios less than one for most traits, demonstrating their non-additive gene action. Therefore, heterosis breeding can be effectively used to improve yield and its components. These results were in conformity with past studies by Meena *et al.* (2010) [22], Uma and Kalibowilla (2010) [39], Chaudhari *et al.* (2013) [6]. Idahosa and Alika (2013) [13], Kadam *et al.* (2013) [15], Patel *et al.* (2013a) [28], Patel *et al.* (2013b) [28] and Dhare *et al.* (2024) [9] who reported non-additive gene action for yield and its components. Conversely, traits *viz*., days to maturity and 100 seed weight had higher σ2 g, suggesting role of additive gene action in the inheritance of these characters. Thus, it is suggesting that generation testing of genotypes would be efficient and promising hybrids can be identified and selected based on their prediction from GCA effects. Similar finding for aadditive gene action controlling days to maturity and 100 seed weight has been reported by Amegbor *et al.* (2017) [2], Owusu *et al.* (2018) [24] and Pallavi *et al.* (2018) [25] in cowpea.

Proportional contribution of lines, testers and their interactions (%)

The proportional contribution of lines was higher in magnitude compared to testers for the number of primary branches per plant (24.92). However, testers had a higher contribution in magnitude compared to lines for the characters *viz*., days to 50% flowering (67.80), days to maturity (63.83), plant height (18.62), number of clusters per plant (50.02), number of pods per plant (62.23), pod length (73.16), number of seeds per pod (52.26), 100 seed weight (76.50) and seed yield per plant (31.85). (Table 6). These indicating the effective role of testers in heterosis breeding programs. The contribution of line × tester interactions was higher for the traits like plant height (77.16) followed by number of primary branches (61.65) and seed yield per plant (52.43).

Table 1: Features of parental lines and check.

Sr. No.	Genotype	Characters
Lines		
1.	PL 4	High yielding, short duration and erect growth habit
2.	Phule Vithai	High yielding, indeterminate, dark purple flowers
3.	Phule Sonali	High yielding
Testers		
4.	IC 68786	High yield, good number of pods
5.	IC 259084	Long pod
6.	IC 263015	White creamy seeded
7.	NIC 23105	Long pod, Brown seeded
8.	EC 38214	Red seeded
9.	EC 244130	Red seeded
10.	EC 738083	White seeded
11	V 240	Red seeded
Check		
12	Phule Rakhumai	High yielding, white seeded

Table 2: ANOVA for combining ability in a Line × Tester analysis for yield and its component in cowpea.

Source	D.F.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	No. of clusters per/plant	No. of pods /plant	Pod length (cm)	No. of seeds/pod	100 seed weight (g)	Seed yield/plant (g)
Replications	1	3.36	0.18	3.70	1.13	0.028	2.42	0.10	1.02	1.64	1.77
Genotypes	34	52.80**	66.70**	4643.74**	5.26**	8.60**	394.28**	6.76**	3.99**	30.60**	273.28**
Parents	10	37.58**	45.73**	6932.48**	2.36**	0.44**	241.47**	5.11**	4.53**	56.05**	146.02**
Crosses	23	47.64**	70.69**	2940.94**	4.10**	8.93**	335.96**	7.06**	3.80**	20.30**	178.99**
Parents v/s Crosses	1	323.45**	184.60**	2092.87**	59.36**	82.62**	3263.61**	16.45**	3.80	12.98**	37.14**
Error	34	1.51	3.42	55.50	0.37	0.08	10.92	0.30	0.37	0.29	24.58

Table 3: General combining ability (GCA) effects for yield and yield contributing characters for line and testers in cowpea.

Sr. No	Parents	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of clusters/ plant	No. of pods/ plant	Pod length (cm)	No. of Seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)
1.	**Lines**										
2.	PL 4	-0.123**	-2.917**	1.852	-0.507**	0.611**	1.900*	-0.322*	0.023	1.451**	4.940**
3.	Phule Vithai	-1.229**	2.333**	8.371**	0.999**	-0.243**	-0.859	0.139	0.144	-0.356*	-3.856**
4.	Phule Sonali	1.352**	0.583	-10.224**	-0.491**	-0.369**	-1.041	0.184	-0.167	-1.094**	-1.084
5.	**Testers**										
6.	IC 68786	-3.960**	-8.063**	37.543**	-0.311	-1.267**	-4.491**	0.151	0.328	-1.017**	0.592
7.	IC 259084	-5.794**	-3.063**	-9.098**	-0.155	2.648**	3.675*	-1.716**	-0.328	-1.184**	1.073
8.	IC 263015	-4.844**	-2.563**	2.934	-0.078	0.998**	7.542**	-1.499**	-1.107**	-2.875**	1.670
9.	NIC 23105	2.106**	-2.271**	-18.624**	0.0802**	1.491**	16.984**	-1.444**	-0.996**	-1.417**	9.577**
10.	EC 38214	1.706**	-0.396	-8.109*	0.822**	-0.485**	4.855**	-0.199	-0.502	-1.057**	-7.165**
11.	EC 244130	5.206**	0.271	-2.499	-0.651*	-1.709**	-13.958**	1.284*8	0.734**	3.688**	-4.073
12.	EC 738083	2.040**	2.604**	8.341*	0.089	-0.209	-14.281**	3.288**	-0.241	5.443**	-5.995**
13.	V 240	3.540**	8.938**	-10.488**	-0.518	-1.459**	-0.325	0.134	2.086**	-1.582**	4.322*

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

Table 4: Specific combining ability (SCA) effects for yield and yield contributing characters for crosses in cowpea.

Sr. No.	Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	No. of clusters/ plant	No. of pods/ plant	Pod length (cm)	No. of Seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)
1.	PL 4 × IC 68786	-4.877**	0.750	-58.968**	0.574	1.097**	1.566	50.372	1.301**	0.701	-1.638
2.	PL 4 × IC 259084	-2.544**	-3.750**	-13.753*	0.537	1.152**	13.600**	-0.261	1.259**	1.141**	14.390**
3.	PL 4 × IC 263015	1.006	4.250**	3.861	-1.210*	-0.818**	-10.867**	0.022	0.216	1.633**	-4.711
4.	PL 4 × NIC 23105	3.756**	-1.083	38.929**	1.500**	0.539*	5.891*	-1.668**	-1.403**	-1.751**	5.372
5.	PL 4 × EC 38214	0.456	2.083	-3.576	-1.110*	1.115**	-3.580	1.322**	0.869	0.264	5.124
6.	PL 4 × EC 244130	1.956*	1.917	14.199*	-0.446	-1.711**	-5.967*	0.339	-0.883	0.329	-8.898*
7.	PL 4 × EC 738083	0.123	-0.917	8.024	1.124*	-0.561*	2.156	0.235	2.017	0.314	-4.046
8.	PL 4 × V 240	0.123	-3.250*	11.283*	-0.970*	-0.811**	-2.800	-0.361	-0.340	-1.231**	-5.593
9.	Phule Vithai × IC 68786	3.229**	-3.000*	-32.211**	-1.632**	-1.524**	-6.374*	0.511	0.863	0.131	-2.732
10.	Phule Vithai × IC 259084	-2.438*	2.500	-34.896**	0.061	-2.114**	-14.041**	1.128**	-0.122	-1.202**	-12.109**
11.	Phule Vithai × IC 263015	-1.538	-3.500*	50.247**	0.685	3.146**	19.593**	0.561	0.018	0.040	14.919**
12.	Phule Vithai × NIC 23105	-2.838**	5.667**	-9.080	-2.395**	-1.857**	-7.724**	0.756	0.851	2.131**	-3.522
13.	Phule Vithai × EC 38214	3.563**	-0.167	12.940*	1.535**	-1.680**	2.379	-1.689**	-1.037*	-0.774	-0.981
14.	Phule Vithai × EC 244130	0.563	0.667	6.275	1.703**	2.043**	-0.107	0.428	-0.329	-0.424	3.933
15.	Phule Vithai × EC 738083	-1.771	-2.667	7.945	0.218	1.143**	7.916**	-1.925**	-0.204	-1.649**	-3.441
16.	Phule Vithai × V 240	1.229	0.500	-1.221	-0.175	0.843**	-1.641	0.228	-0.040	1.746**	3.933
17.	Phule Sonali × IC 68786	1.648	2.250	91.179**	1.058*	0.427*	4.808	-0.848*	0.439	0.569	4.370
18.	Phule Sonali × IC 259084	4.981**	1.250	48.649**	-0.599	0.962**	0.441	-0.867*	-1.136*	0.061	-2.281
19.	Phule Sonali × IC 263015	0.531	-0.750	-54.108**	0.525	-2.328**	-8.726**	-0.584	0.199	-1.672**	-10.208**
20.	Phule Sonali × NIC 23105	-0.919	-4.583**	-29.850**	0.895	1.319**	1.833	0.911*	0.552	-0.381	-1.850
21.	Phule Sonali × EC 38214	-4.019**	-1.917	-9.365	0.425	0.565*	1.201	0.366	0.169	0.509	-4.143
22.	Phule Sonali × EC 244130	-2.519**	-2.583	-20.475**	-1.257**	-0.331	6.074*	-0.767	1.212**	0.094	4.965
23	Phule Sonali × EC 738083	1.648	3.583*	-15.970**	-1.345**	-0.581**	-10.072**	1.690**	-1.813**	1.334**	7.487*
24	Phule Sonali × V 240	-1.352	2.750*	-10.061	1.145*	-0.031	4.441	0.133	0.380	-0.516	1.660

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

Table 5: The estimates of heterosis over better standard check (SH) for various characters in Cowpea.

Sr. No.	Crosses	Days to 50% flowering	Days to Maturity	Plant height	No. of primary branches /plant	No. of clusters/plant	No. of pods /plant	Pod length	No. of seeds /pod	100 seed weight	Seed yield/plant
1.	PL 4 × IC 68786	-26.61**	-17.06**	-2.26	49.44**	75.00**	15.62	1.02	-4.78	14.10*	24.30
2.	PL 4 × IC 259084	-25.69**	-16.47**	-3.07	52.13**	207.33**	69.07**	-15.93**	10.34*	31.28**	63.54**
3.	PL 4 × IC 263015	-17.43**	-6.47**	13.87**	14.61	86.33**	14.57	-12.54**	-7.52	18.97**	19.55
4.	PL 4 × NIC 23105	0.37	-7.06**	21.59**	95.28**	148.33**	83.89**	-23.63**	-15.95**	-0.77	62.32**
5.	PL 4 × EC 38214	-6.42**	-6.47**	3.31	37.08*	101.67**	26.74**	5.08	5.72	23.59**	21.93
6.	PL 4 × EC 244130	2.75	-5.88*	16.67**	18.88	-33.33**	-29.36**	8.47*	1.68	72.92**	-4.05
7.	PL 4 × EC 738083	-6.42**	-6.47**	19.34**	70.79**	55.00**	-8.72	21.36**	16.77**	90.77**	2.91
8.	PL 4 × V 240	-3.67	-1.76	10.44*	10.11	5.00	15.09	-4.07	16.54**	2.87	23.76
9.	Phule Vithai × IC 68786	-13.76**	-15.29**	16.76**	33.71*	-40.83**	-12.69	5.08	13.13*	4.10	0.78
10.	Phule Vithai × IC 259084	-27.52**	-2.94	-11.43*	75.28**	70.00**	-11.36	-3.39	0.47	-11.28	-20.36
11.	Phule Vithai × IC 263015	-24.13**	-9.41**	44.10**	91.01**	190.00**	87.86**	-5.76	-4.74	-15.90**	45.31**
12.	Phule Vithai × NIC 23105	-13.76**	7.06**	-2.12	41.57**	40.00**	40.56**	-4.07	2.66	20.51**	20.27
13.	Phule Vithai × EC 38214	-2.75	-2.94	-16.47**	130.34**	-20.00*	35.20**	-12.20**	-8.27	-5.59	-13.49
14.	Phule Vithai × EC 244130	-1.83	-1.18	15.87**	101.01**	63.33**	-21.15*	12.20**	6.97	46.67**	5.54
15.	Phule Vithai × EC 738083	-11.93**	-2.35	23.02**	84.27**	83.33**	-0.78	9.83*	0.31	52.10**	-16.56
16.	Phule Vithai × V 240	-3.67	8.82**	7.02	61.80**	31.67**	10.86	3.05	19.83**	14.87*	25.50*
17.	Phule Sonali × IC 68786	-11.93**	-11.18**	76.64**	60.67**	20.00*	16.42	-4.07	7.37	1.03	24.26
18.	Phule Sonali × IC 259084	-9.17**	-6.47**	25.69**	26.97	168.33**	26.47**	-16.61**	-9.91*	-5.90	9.59
19.	Phule Sonali × IC 263015	-15.60**	-8.24**	-26.16**	53.93**	3.33	12.45	-13.22**	-5.76	-41.03**	-7.83
20.	Phule Sonali × NIC 23105	-5.50	-7.06**	-24.61**	82.02**	141.67**	65.37**	-2.71	-2.12	-12.82*	30.83*
21.	Phule Sonali × EC 38214	-11.93**	-7.06**	-6.90	52.81**	50.67**	31.60**	2.03	-1.25	0.00	-14.42
22.	Phule Sonali × EC 244130	-2.75	-7.06**	-10.04*	1.01	-20.00*	-5.28	2.41	16.61**	44.41**	14.58
23.	Phule Sonali × EC 738083	-0.92	2.94	-1.27	15.73	21.67*	-48.86**	34.64**	-14.73**	75.13**	16.01
24.	Phule Sonali × V 240	-3.67	9.41**	-8.66	57.98**	-1.67	26.47**	2.71	20.69**	-15.90**	26.68*

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

Table 6: Estimates of genetic components of variance and proportional contribution of lines, testers and their interactions to sum of squares of the crosses for quantitative traits in cowpea.

Sr. No.	Characters	σ2 g	δ2 s	Σ2 A	σ2 D	(δ2 g) / (δ2 s)	Per cent contribution of		
							Lines	Testers	Lines × Testers
1	Days to 50% flowering	5.90	9.92	11.8151	9.9268	0.59	4.89	67.80	27.29
2	Days to maturity	11.62	11.11	23.2508	11.1190	1.05	14.06	63.83	22.09
3	Plant height (cm)	141.48	1836.44	282.96	1836.44	0.08	4.21	18.62	77.16
4	No. of primary branches/plant	0.59	1.92	1.18	1.92	0.31	24.92	13.41	61.65
5	No. of clusters per/plant	0.86	3.30	1.73	3.30	0.26	4.42	50.02	45.54
6	No. of pods /plant	32.20	95.66	64.41	95.66	0.34	1.12	62.23	36.63
7	Pod length (cm)	0.80	1.31	3.20	5.25	0.61	1.54	73.16	25.29
8	No. of seeds/pod	0.28	1.27	1.12	5.10	0.22	0.89	52.26	46.83
9	100 seed weight (g)	3.54	1.81	14.16	7.25	1.96	11.74	76.50	11.75
10	Seed yield/plant (g)	20.96	64.79	41.97	64.79	0.32	15.71	31.85	52.43

Where, 1. σ2 g= General combining ability (GCA) variance, σ2 s= Specific combining ability variance, σ2 A= Additive variance, σ2 D= Dominance variance and (σ2 g)/(σ2 s) = Variance ratio.

Conclusion

The study concluded that line PL 4 and tester NIC 23105 are superior for seed yield and yield components based on general combining ability. These can be used for future heterosis breeding in cowpea. The crosses PL 4 × IC 259084, PL 4 × NIC 23105, Phule Vithai × IC 263015, Phule Sonali × NIC 23105, and Phule Sonali × V 240 were top crosses for seed yield based on standard heterosis and can be further used for their commercial exploitation in cowpea. Gene action studies revealed non-additive gene action for most of the traits, highlighting the role of heterosis breeding in improving quantitative traits.

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