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Analysis of combining ability for yield and its attributing characters in red cowpea (*Vigna unguiculata* (L.) Walp)

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Abstract
A study was conducted to determine combining ability and association of yield and yield related attributes among crosses that were derived from five lines and three testers of red cowpea parents and fifteen hybrids. Hybrids and their parents were studied for the combining ability. The results indicated that general combining ability (GCA) and specific combining ability (sca) were significant for certain characters indicating the importance of both additive and non-additive gene components. Twelve traits except days to initiation of flowering, days to maturity, pod length and number of grains per pod involved in the present investigation exhibited a ratio of $\sigma^2 g / \sigma^2 s$ of less than unity thereby indicating the preponderance of non-additive gene action which can be improved through heterosis breeding indicating the presence of non-addictive gene action. Whereas, the remaining four characters *viz.,* days to initiation of flowering, days to 50% flowering, days to maturity and pod length showed the $\sigma^2 g / \sigma^2 s$ ratio greater than one which highlights the additive gene action and hence, can be improved through selection. All the characters under study exhibited high (30-60%) to very high (>60%) broad sense heritability, whereas, ten characters out of sixteen showed <20% narrow sense heritability indicating that the dominance proportion was too high to effect the overall heritability.

Keywords: Line X tester, red cowpea, GCA, sca, combining ability, heritability, yield

Introduction
Cowpea (*Vigna unguiculata* (L.) Walp. (2n=22) is an early, multipurpose and the most widely adapted, versatile and nutritious grain legume crop; belongs to family Leguminosae. Cowpea is a multi-utility, drought tolerant, nitrogen fixing crop and prominent among grain legumes since it is an excellent source of low-cost protein (Deepa Priya *et al.,* 2018) [4]. It is a fast growing, highly palatable and nutritious grain, fodder and vegetable crop. The crop is gaining popularity in developing and under developed countries, especially in arid regions of the world due to its nutritional value. Like other legumes, cowpea fixes atmospheric nitrogen, and thus contributes to the available nitrogen levels in the soil. (Nagalakshmi *et al.,* 2010) [11].

General combining ability is a good estimate of additive gene action, whereas specific combining ability is a measure of non- additive gene action. Various biometrical methods have been successfully employed to assess the genetic make-up of different genotypes for developing suitable breeding methodology. Out of several methods, line x tester analysis provides valid information on combining ability effect of the genotypes (Pethe *et al.,* 2018) [17]. Combining ability analysis, as proposed by Sprague and Tatum (1942) [21] was carried out in the present investigation in order to identify good general combiners as well as to select the proper parentage for the breeding programme. This will help to know the nature of the gene action involved in the inheritance of various traits. Partitioning the total genetic variance into the variance due general and specific combining ability helps to know the proportion of additive and non-additive components and thereby to implicate an appropriate breeding method. In highly self-pollinated crops like cowpea, hybridization is useful to exploit the variability present in the breeding material. The *gca* effects are indicative of additive and additive x additive components of genetic variance whereas *sca* effects are important when based on additive x dominant gene effects. Thus, in short, combining ability analysis was carried out in order to know the best general combiners as well as to identify the superior cross combinations that may produce transgressive segregants.

The combining ability analysis is useful to find out the general combiners for yield and its components, nature and magnitude of gene action governing the expression of yields and its

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components which in turn helps in identification of proper breeding methodology (Uma and Kalubowila, 2010) [22].

Materials and Methods
The present investigation entitled "Analysis of Combining Ability for yield and its attributing Characters in red Cowpea (*Vigna unguiculata* (L.) Walp) was carried out to assess combining ability in red cowpea for phenological traits, yield and yield contributing characters and quality attributes. Experiments were conducted during 2019-20 and 2020-21 at Research Farm, Department of Agril. Botany, College of Agriculture, Dapoli (MS).
Geographically, it is situated in the tropical region on the $17°$ 45.119" North latitude and 73°11" East longitude having elevation of 240 meters above mean sea level with warm and humid conditions throughout the year. The mean annual rainfall ranges from 3000 to 4000 mm which is generally received from June to September. The soil of experimental site was lateritic having pH of about 5.6 to 8.0. Average minimum temperature ranges from 21 to 25^0C and maximum temperature between 31 to 35^0C. The crossing programme between five selected lines and three testers was undertaken during *Rabi* 2020-21. Evaluation of fifteen hybrids, eight parents and three checks carried out at same place during *Summer* 2021. The experimental material comprised of 32 genotypes including three check varieties *viz.,* Phule Pandhari, Konkan Sadabahar and Konkan Safed. The fifteen F_1s were obtained by crossing eight genotypically different parents in line x tester design (5 lines and 3 testers) during *Rabi* 2020-21.

Results and Discussion
Analysis of variance for combining ability
Analysis of variance for combining ability for all the characters under study was carried out as per the line x tester analysis proposed by Kempthorne (1957) [8] and presented in Table 1.
The mean sum of square due to lines was significant for all the characters except for days to maturity. Mean sum of square due to testers was also significant for all the characters except for days to 50% flowering and days to maturity while in case of line vs. testers, mean sum of square was non-significant for characters days to maturity, plant height, number of pods per plant, number of grains per pod and protein content. In hybridization of cowpea, proper selection of parents is of vital importance. Certain parents produce good progenies; however some are poor in producing progenies. The valuable gene combinations having higher combining ability are proved to be important in crop improvement. The combining ability studies provide useful information for the selection of high order parents for effective breeding besides deciding the nature and magnitude of gene action governing the expression of quantitative characters of economic importance. Thus, the analysis of variance is a powerful tool to identify good as well as poor combinations and choose an appropriate parent in any breeding programme.
The concept of general and specific combining ability as a measure of gene action was proposed by Sprague and Tatum (1942) [21]. The resulting total genetic variance is partitioned into the variance due to GCA and SCA. The general combining ability is a good estimate of additive gene action whereas specific combining ability is a measure of non-additive gene action.

Various biometrical methods have been successfully employed to assess the genetic makeup of different genotypes for developing suitable breeding methodology. The line x tester analysis as proposed by Kempthorne (1957) [8] is a powerful tool to distinguish in between good and poor combiners. This provides valid information on combining ability effects of the genotypes.
As cowpea is a self-pollinated crop, the GCA effects are more important as they are attributed to additive and additive x additive interaction while the SCA effects are useful only when they are based on additive x dominance gene effect. The cross combinations with higher SCA effects having good *per se* performance and involving at least one good general combiner parent may possibly produce desirable transgressive sergeants.
In the present investigation based on combining ability, mean sum of squares for different characters in red cowpea, it is observed that in case of general combining ability for the five lines, all the characters were significant except for days to maturity which was non-significant. The mean sum of squares for three testers indicated that all the characters were significant except days to 50% flowering and days to maturity. These results were in accordance with the results obtained by Chaudhari *et al.,* (2013) [3], Idahosa and Alika (2013) [6], Mukati *et al.,* (2014) [10], Satish Kumar *et al.,* (2017) [20] and Pethe *et al.,* (2018) [17]. The significant performance of almost all characters studied indicates that there is substantial extent of variability in the lines and testers which forms a broad base for crop improvement.
Similarly, the observations in mean sum of squares due to lines vs. testers interaction were found to be significant for all the characters except for days to maturity, plant height, number of pods per plant, number of grains per pod and protein content which were non-significant. The harvest index was observed to be significant. Similar results were also recorded by Ushakumari *et al.,* (2010) [23] and Get *et al.,* (2021) who observed significant mean sum of squares for lines vs. testers for all traits, Satish Kumar *et al.,* (2017) [20] reported significant mean sum of squares for lines vs. testers for all traits except number of primary and secondary branches, number of pods per plant, number of seeds per pod, pod length, test weight and dry matter content. Varan *et al.,* (2017) [24] and Pethe *et al.,* (2018) [17] also reported non-significant MSS due to lines vs. testers for trait plant height.

Combining ability effects
The estimation of general combining ability for Lines and testers is presented in Table 2 and the specific combining ability for the hybrids is mentioned in Table 3.

A. Phenological characters
In the present investigation, based on the analysis of general combining ability effects, considering the duration of the crop, the earliness contributing characters are days to initiation of flowering, days to 50% flowering and days to maturity. Among the five lines tested, the line GC 8910 was observed to be a good general combiner for earliness contributing characters showing desirably negative significant performance for all the three characters. Though line TC 210 82 exhibits negative significant performance for days to initiation of flowering, as it approaches maturity, it contrastingly shows highly significant positive performance

thereby showing late maturity and hence, it proves to be a poor general combiner. In case of the three testers under study, the tester CD 209 found to be a good general combiner showing negative significant performance for days to initiation of flowering and days to maturity. These findings are in consonance with Patil *et al.,* (2005) [16], Chaudhari *et al.,* (2013) [3], Mukati *et al.,* (2014) [10], Satish Kumar *et al.,* (2017) [20], Pethe *et al.,* (2018) [17] and Owusu *et al.,* (2018) [13]. The hybrid TC 210 82 x IC 25 90 69 (-5.56) showed negative significant *sca* effect for trait days to initiation of flowering. The line TC 210 82 (-3.25) found desirable and had negative significant *gca* effect while the tester IC 25 90 69 (5.11) in this hybrid was having significant but undesirable *gca* effect. Similarly, the hybrid 4-40-1 x CD 209 (-4.16, -6.51 and -3.16) was next suitable for earliness which is having the *gca* effect of female parent 4-40-1 (5.42, 3.04 and 0.22) undesirable *i.e.,* positive while the male parent *i.e.,* tester CD 209 (-3.29, -1.71 and -3.40) had negative *gca* effect for the traits.

The two lines *viz.,* GC 8910 (-3.78) and KBC-WS-1 (-3.45) and one tester CD 209 (-3.40) showed negative significant *gca* effects for the trait days to maturity. However, surprisingly, no hybrid involving them as one of the parents was found desirably significant considering total days for maturity whereas the hybrid TC 210 82 x IC 25 9104 (-0.03) found to be negatively significant for the trait days to maturity.

Due to the emerging scenario of climate change and considering the limitations in the availability of moisture; while planning breeding strategy of any crop, it is important to focus on earliness in near future. Keeping this in view, it has been observed in the study that the hybrid TC 210 82 x IC 25 90 69 exhibited desirable significant *sca* effect for days to initiation of flowering, 4-40 -1 x CD 209 for days to initiation of flowering and days to 50% flowering while TC 210 82 x IC 25 9104 exhibited desirable significant *sca* effect for the trait days to maturity. Nine hybrids showed negative *sca* effects for trait days to maturity would be useful for breeding for earliness in cowpea. Similar results were also reported by for days to flowering and first picking during both the years, Patil *et al.,* (2005) [16], Chaudhari *et al.,* (2013) [3], Mukati *et al.,* (2014) [10], Satish Kumar *et al.,* (2017) [20] and Pethe *et al.,* (2018) [17].

B. Yield contributing characters
Line GC 8910 exhibited desirable significant *gca* effect for the traits plant height, number of pods per cluster, pod length, test weight, biological yield per plant, grain yield per plant, harvest index and iron content showing good general combining ability for improvement in these traits. For the characters number of clusters per plant, pods per plant, number of grains per pod, biological yield per plant, grain yield per plant, harvest index and protein content, the line TC 210 82 was observed to be the best general combiner among all lines; which can further be used in the breeding programme for improving the yield in cowpea. Thus, two lines GC 8910 and TC 210 82 were good general combiners for the yield contributing characters.

In the present investigation, in the line TC 210 82, it was observed that positive association of the number of clusters per plant and number of pods per plants with the trait number of grains per pod; it influenced and subscribed towards biological yield, grain yield per plant and harvest index. Conversely, positive association of number of clusters per

plant and number of pods per plant is not correlated with the number of grains per pod; it concomitantly reduced biological yield and grain yield per plant along with the harvest index. This analogy was observed in the line CP-210.

Among testers, CD 209 found to be a good general combiner for the traits number of pods per cluster, number of pods per plant and average general combiner for trait plant height. Tester IC 25 9104 was the superior general combiner for the trait plant height, average general combiner for number of pods per plant and good general combiners for grain yield per plant and iron content. While tester IC 25 90 69 was good general combiner for number of primary branches per plant and protein content. These results are in agreement with Patil *et al.,* (2005) [16], Romanus *et al.,* (2008) [19], Chaudhari *et al.,* (2013) [3], Idahosa and Alika (2013) [6], Mukati *et al.,* (2014) [10], Satish Kumar *et al.,* (2017) [20], Deepa Priya *et al.,* (2018) [4] and Pethe *et al.,* (2018) [17]. Owusu *et al.,* (2018) [13] reported similar results for trait grain yield per plant.

The result estimates of the *sca* effect revealed that none of the hybrids showed superiority for all the characters under study (Mukati *et al.,* 2014, Satish Kumar *et al.,* 2017) [10, 20]. Among fifteen hybrids, positive significant *sca* effect was observed for various characters such as in 6 hybrids for number of clusters per plant, 4 hybrids for pods per cluster, 6 hybrids for pods per plant, 2 hybrids for grains per pod, 3 hybrids for test weight and 3 hybrids for the biological yield per plant. Similar results also reported by Patil and Navale (2006) [16] for days to 50% flowering, days to maturity, plant height, plant spread, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, test weight and seed yield per plant.

The hybrid 4-40-1 x IC 25 9104 found to be the superior specific combiner among all 15 cross combinations showing positively significant *sca* effect for the traits number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, test weight, biological yield per plant, grain yield per plant, harvest index, seed protein as well as iron content. Subsequently, the hybrid KBC-WS-1 x CD 209 was observed to be a promising hybrid in respect of traits number of pods per plant, test weight, grain yield per plant, harvest index and highest positive significant estimate for iron content. Positive significant *sca* effect for yield and yield contributing characters were also reported by Patil *et al.,* (2005) [16], Romanus *et al.,* (2008) [19], Chaudhari *et al.,* (2013) [3], Idahosa and Alika (2013) [6], Mukati *et al.,* (2014) [10], Ogunwale and Salami (2015), Satish Kumar *et al.,* (2017) [20], Deepa Priya *et al.,* (2018) [4], Owusu *et al.,* (2018) [13] and Pethe *et al.,* (2018) [17].

Usually, improvement in the yield is one of the objectives of any crop improvement programme. The *sca* effect in 6 hybrids *viz.,* GC 8910 x IC 25 90 69, TC 210 82 x IC 25 90 69, KBC-WS-1 x CD 209, KBC-WS-1 x IC 25 90 69, 4-40-1 x IC 25 9104 and CP-210 x IC 25 9104 were coherent and positively significant for grain yield per plant and harvest index.

C. Quality characters
Quality is another important aspect which is gaining importance next to yield in crop improvement. In this context, the protein and iron content were estimated from fully matured and dried seeds of red cowpea. The lines TC 210 82 and KBC-WS-1 while the tester IC 25 90 69 found to be good

general combiners for trait protein content. Two lines *viz.,* GC 8910 and KBC - WS - 1 and one tester IC 25 9104 exhibited significant *gca* effect for iron content and hence, proved to be good general combiners for the trait iron content. Similar results were reported by Pallavi *et al.,* (2018) [14] for seed iron content in cowpea whereas Baptiste (2019) [2] for iron content in edible leaves of cowpea. Five hybrids *viz.,* GC 8910 x CD 209, TC 210 82 x IC 25 9104, KBC-WS-1 x IC 25 90 69, KBC-WS-1 x IC 25 90 69, 4-40-1 x IC 25 9104 and CP-210 x CD 209 showed higher protein content whereas five hybrids *viz.,* GC 8910 x IC 25 9104, TC 210 82 x IC 25 90 69, KBC-WS-1 x CD 209, 4-40-1 x IC 25 9104 and CP-210 x CD 209 found superior in iron content. Moreover, the hybrid CP-210 x CD 209 exhibited positively significant *sca* effect for both of the quality attributes, protein and iron content, hence, it can be efficiently exploited in cowpea breeding for nutritive improvement in near future. It can be seen that hybrid 4-40-1 x IC 25 9104 performed better in terms of quality characters *i.e.* protein content as well as iron content along with positive significant *sca* effect for grain yield per plant and harvest index and hence, recommended for their utilization in yield as well as quality improvement aspects of cowpea breeding. These results are in conformity with those obtained by Patil *et al.,* (2005) [16], Ushakumari *et al.,* (2010) [23], Chaudhari *et al.,* (2013) [3], Satish Kumar *et al.,* (2017) [20], Pethe *et al.,* (2018) [17] and Deepa Priya *et al.,* (2018) [4] for protein content.

Generally, it is observed that the high yielding hybrids are hardly found superior in quality attributes. However, Hybrids KBC-WS-1 x CD 209 and TC 210 82 x IC 25 90 69 exhibited positive significant *sca* effect for grain yield per plant and iron content while hybrid KBC-WS-1 x IC 25 90 69 showed positive significant *sca* effect for grain yield per plant and protein content. These results are in agreement with Deepa Priya *et al.,* (2018) [4] and Pethe *et al.,* (2018) [17].

Gene action
The nature of gene action is dependent on the relative estimates of general combining ability and specific combining ability. An additive gene action is revealed due to the higher magnitude of general combining ability whereas non-additive gene action results due to higher specific combining ability than the general combining ability. The variances due to general and specific combining ability and dominant component are given in Table 4.

The highest magnitude of $\sigma^2 g$ showed by plant height (129.690) followed by harvest index (24.830) and iron content (18.128) whereas lowest estimates of $\sigma^2 g$ were produced by the trait number of grains per pod (0.110) followed by number of pods per cluster (0.040).

The character plant height (542.055) showed the highest magnitude of $\sigma^2 s$ followed by iron content (234.027) and harvest index (152.101) and whereas lowest estimates were observed in case of number of grains per pod (0.435) and number of pods per cluster (0.092).

In the present investigation, in case of the twelve traits except days to initiation of flowering, days to maturity, pod length and number of grains per pod involved in the present investigation, indicating the presence of non-addictive gene action. Also, the ratio of $\sigma^2 g / \sigma^2 s$ was less than unity and for the twelve characters indicating the preponderance of non-additive gene action due to which, these traits can be improved through heterosis breeding whereas remaining four characters *viz.,* days to initiation of flowering, days to 50%

flowering, days to maturity and pod length showed the $\sigma^2 g / \sigma^2 s$ ratio greater than one which highlights the additive gene action and hence, can be improved through selection.

Considering the improvement in any trait, knowledge of the nature of gene action is of immense importance. Combining ability analysis is exploited in order to have an indication of relative magnitude of additive and non- additive variances. The significance of the *gca* and *sca* variances for the characters studied indicated that both additive as well as non-additive type of gene actions were involved in the expression of these traits. Similar finding has also been obtained by Mukati *et al.* (2014) [10] and Satish Kumar *et al.* (2017) [20].

Out of sixteen characters studied in the present investigation, twelve characters *viz.,* plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of grains per pod, test weight, biological yield per plant, grain yield per plant, harvest index, protein content and iron content exhibited the $\sigma^2 g / \sigma^2 s$ ratio as less than unity revealing the preponderance of non- additive gen action whereas remaining four characters *viz.,* days to initiation of flowering, days to 50% flowering, days to maturity and pod length showed the $\sigma^2 g / \sigma^2 s$ ratio greater than one which highlights the additive gene action and hence, can be improved through selection. These findings are in consonance with Romanus *et al.,* (2008) [19], Ogunwale and Salami (2015) [12] Meena *et al.* (2009) [9], Uma and Kalibowilla (2010), Chaudhari *et al.,* (2013) [3] and Pethe *et al.,* (2018) [17].

In case of the twelve traits except days to initiation of flowering, days to maturity, pod length and number of grains per pod involved in the present investigation, the estimates of *sca* variances were higher than *gca* variances indicating the presence of non-additive gene action due to which these traits can be improved through heterosis breeding. Similar results were also reported by Meena *et al.* (2009) [9], Uma and Kalibowilla (2010), Chaudhari *et al.* (2013) [3] and Pethe *et al.* (2018) [17].

However, cowpea being a highly self-pollinated crop, hybrid seed production is a difficult task without CMS line and hence, fixation of heterosis is not feasible. Thus, hybridization followed by selection in coming generations may be fruitful in further crop improvement. These findings are also supported by Meena *et al.* (2009) [9], Uma and Kalibowilla (2010), Chaudhari *et al.* (2013) [3] Idahosa and Alika (2013) [6], Kadam *et al.* (2013) and Pethe *et al.* 2018) [17].

Heritability
Heritability estimates the degree of variation in a phenotypic trait in a population that is due to genetic variation between the individuals in the population. In any breeding programme, the selection becomes useful only when the character to be transmitted is desirably inherited to the next generations. Thus, the knowledge of heritability *i.e.* the genetic and non-genetic factors governing the phenotypic expression of the trait is of immense importance for choice of the breeding programme. The heritability of a character has a major impact on methods chosen for population improvement, inbreeding and other aspects of selection may be effective for a character with low heritability (5-10%), medium heritability (10-30%), high heritability (30-60%) and very high heritability (above 60%) (Robinson, 1966). The heritability estimates in the present investigation are mentioned in Table 5. Accordingly, in this experiment, the two traits, *viz.,* days to initiation of

flowering (64.00) and pod length (70.17) were very highly heritable whereas five traits *viz.,* days to 50% flowering (44.58), days to maturity (53.84), plant height (32.19), number of pods per cluster (44.63) and test weight (46.19) showed high heritability. Remaining nine characters including grain yield per plant and quality attributes like protein and iron content showed medium heritability in the present investigation.

As per the heritability index given by Robinson (1966) all the characters under study exhibited high (30-60%) to very high (>60%) broad sense heritability whereas, ten characters out of sixteen showed less than 20% narrow sense heritability (Table 5) which indicates that the dominance proportion was too high to effect the overall heritability. Hence, these hybrids cannot be used directly for hybridization Ayo-Vaughan *et al.,* (2013). The results obtained are in consonance with the findings obtained by Uma and Kalibowilla (2010), Chaudhari *et al;* (2013) [3] and Pethe *et al;* (2018) [17].

Table 1: ANOVA for combining ability of lines and testers for different characters in red cowpea

Sr. No.	Characters	Mean Sum of squares			
		Lines (4)	Testers (2)	L vs. T (1)	Error (44)
1	Days to initiation of flowering	80.07**	117.44**	162.70**	11.66
2	Days to 50% flowering	53.23*	1.78	238.46**	16.35
3	Days to maturity	47.27	26.78	11.38	24.77
4	Plant height (cm)	209.42**	648.07**	0.01	12.70
5	No. of Primary branches per plant	5.51**	0.55**	2.03**	0.11
6	No. of clusters per plant	8.07**	13.55**	10.46**	0.35
7	No. of pods per cluster	0.14**	0.13**	0.13**	0.01
8	No. of pods per plant	44.40**	93.32**	0.73	0.96
9	Pod length (cm)	21.67**	15.42**	9.30**	1.00
10	No. of Grains per pod	3.80*	8.54**	0.13	1.33
11	Test weight (g)	12.10**	6.40**	12.30**	0.63
12	Biological yield per plant (g)	84.11*	114.98 *	276.22**	28.23
13	Grain yield per plant (g)	123.00**	61.52**	117.79**	5.04
14	Harvest Index (%)	194.23**	68.17**	40.79*	8.96
15	Protein content (%)	20.63**	28.40**	0.48	0.40
16	Iron content (ppm)	282.96**	831.07**	761.31**	8.26

* Significant at 5% LS and ** Significant at 1% LS

Table 2: Estimation of General combining ability of eight cowpea genotypes (lines and testers)

Sr. No.	Genotypes	Days to initiation of flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of Primary branches per plant	No. of Clusters per plant	No. of Pods per Cluster	No. of Pods per plant
		Lines							
L1	GC 8910	-69 **	-5.07**	-3.78*	- 16.96**	-0.19	-2.53**	0.51**	-1.07**
L2	TC 210 82	-3.25**	-0.62	6.89**	26.19**	-1.22**	1.99**	0.03	3.42**
L3	KBC-WS-1	-0.25	-1.07	-3.45*	-10.39**	0.17	-0.41*	-0.17**	-1.47**
L4	4-40-1	5.42**	3.04*	0.22	3.40**	1.57**	-0.34	-0.29**	-2.44**
L5	CP-210	1.76	3.71*	0.11	-2.24	-0.34**	1.29**	-0.09*	1.56**
	S.E. ±	1.14	1.35	1.66	1.19	0.11	0.2	0.04	0.33
		Testers							
T1	CD 209	-3.29**	-1.71	-3.401*	-1.31	-0.12	0.27	0.091**	0.760**
T2	IC 25 9104	-1.823*	-0.78	0.47	-5.92**	-0.202*	0.27	-0.072*	0.33
T3	IC 25 90 69	5.11**	2.489*	2.933*	7.23**	0.32**	-0.540**	-0.02	-1.09**
	S.E.±	0.88	1.04	1.29	0.92	0.08	0.15	0.03	0.25

*Significant at 5% LS and **Significant at 1% LS

Table 2: Contd…

Sr. No.	Genotypes	Pod Length (cm)	No. of Grains per pod	Test Weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest Index (%)	Seed Protein content (%)	Seed Iron content Fe (ppm)
		Lines							
L1	GC 8910	2.78**	-0.45	3.27**	2.68	3.43**	5.49**	0.22	6.97**
L2	TC 210 82	-0.56	1.23**	-0.58*	4.80*	6.27**	8.39**	1.16**	-1.04
L3	KBC-WS-1	0.54	-0.24	0.50	-0.79	-1.35	-1.85	1.68**	5.47**
L4	4-40-1	-0.69*	-0.39	-0.53	-0.47	-5.05**	-11.30**	-2.41**	-3.03**
L5	CP-210	-2.07**	-0.15	-2.66	-6.22**	-3.31**	-0.73	-0.65**	-8.37**
	S.E.±	0.33	0.39	0.27	1.77	0.75	1.00	0.21	0.96
		Testers							
T1	CD 209	0.06	0.23	-0.29	-0.43	0.48	1.39	0.03	0.63
T2	IC 25 9104	-0.11	0.03	0.19	1.34	1.22*	1.47	-0.54**	2.13**
T3	IC 25 90 69	0.05	-0.25	0.09	-0.91	-1.70**	-2.85**	0.51**	-2.77**
	S.E.±	0.26	0.30	0.21	1.37	0.58	0.77	0.16	0.74

*Significant at 5% LS and **Significant at 1% LS

Table 3: Estimation of Specific combining ability effects for different characters in fifteen hybrids of red cowpea

Sr. No.	Characters / Hybrids	Days to initiation of flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of Primary branches per plant	No. of Clusters per plant	No. of Pods per Cluster	No. of Pods per plant
1	GC 8910x CD 209	2.62	1.27	-2.15	11.84**	-0.27	-1.89 **	0.10	-3.43**
2	GC 8910x IC 25 9104	1.16	0.67	-5.36	-6.88 **	-0.55 **	1.45**	-0.37 **	0.93
3	GC 8910xIC 25 90 69	-3.78	-1.94	7.51 *	-4.96 *	0.82 **	0.44*	0.27**	2.49 **
4	TC 210 82xCD 209	5.18 *	4.49*	1.51	-12.54 **	2.06**	-0.29	0.05	1.02
5	TC 210 82xIC 25 9104	0.38	-1.11	-0.03*	-29.02**	-1.17 **	-3.49**	0.16 *	-4.56 **
6	TC 210 82xIC 25 90 69	-5.56 **	-3.38	-1.49	41.56**	-0.89 **	3.78**	-0.20 **	3.54**
7	KBC-WS-1xCD 209	-0.82	1.60	3.84	8.74 **	0.17	0.70	0.10	2.37 **
8	KBC-WS-1xIC 25 9104	0.71	-3.67	-0.36	-0.07	-0.22	-0.88 *	-0.27 **	-3.80 **
9	KBC-WS-1xIC 25 90 69	0.11	2.07	-3.49	-8.66 **	0.05	0.18	0.16 *	1.43*
10	4-40-1xCD 209	-4.16 *	-6.51 **	-3.16	-8.25 **	-2.57 **	1.84**	-0.35 **	-0.65
11	4-40-1xIC 25 9104	-0.96	2.56	3.31	26.37**	2.52**	0.84*	0.48**	4.98 **
12	4-40-1xIC 25 90 69	5.11 *	3.96	-0.16	-18.12 **	0.05	-2.68**	-0.13	-4.33 **
13	CP-210xCD 209	-2.82	-0.84	-0.05	0.22	0.61 **	-0.36	0.10	0.69
14	CP-210xIC 25 9104	-1.29	1.55	2.42	9.60 **	-0.58 **	2.07**	-0.01	2.44 **
15	CP-210xIC 25 90 69	4.11 *	-0.71	-2.38	-9.82**	-0.04	-1.72 **	-0.09	-3.13**
	SE	2.0	2.3	2.9	2.1	0.2	0.3	0.1	0.6

* Significant at 5% LS and ** Significant at 1% LS

Table 3: Contd…

Sr. No.	Characters / Hybrids	Pod Length (cm)	No. of Grains per pod	Test Weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest Index (%)	Seed Protein content (%)	Seed Iron content Fe (ppm)
1	GC 8910x CD 209	1.08	0.40	2.55 **	1.10	-1.48	-4.12*	2.89 **	-7.97**
2	GC 8910x IC 25 9104	0.38	0.18	-1.91**	-1.34	-1.21	-1.42	-2.67 **	17.04 **
3	GC 8910xIC 25 90 69	-1.46 *	-0.58	-0.64	0.24	2.69 *	5.53**	-0.22	-9.07**
4	TC 210 82xCD 209	-0.65	0.14	-0.36	0.67	1.38	2.12	-3.97 **	-1.47
5	TC 210 82xIC 25 9104	0.22	0.65	-0.13	-7.39 *	-7.51**	-7.32 **	6.01 **	-2.47
6	TC 210 82xIC 25 90 69	0.43	-0.79	0.49	6.72*	6.13 **	5.20**	-2.04 **	3.94 *
7	KBC-WS-1xCD 209	0.52	-0.37	0.94*	3.08	5.10 **	10.05 **	0.56	21.54 **
8	KBC-WS-1xIC 25 9104	-1.27*	-1.07	-1.20*	-6.07 *	-10.13 **	-16.81 **	-4.13 **	-20.47 **
9	KBC-WS-1xIC 25 90 69	0.75	1.44 *	0.26	2.99	4.13 **	6.76 **	3.57 **	-1.07
10	4-40-1xCD 209	-0.92	-0.70	-3.28**	-9.42 **	-7.31**	-7.61 **	-0.61	-16.47 **
11	4-40-1xIC 25 9104	0.59	-0.04	2.49 **	8.82 **	13.83**	20.19**	0.83*	13.53 **
12	4-40-1xIC 25 90 69	0.33	1.74 *	0.79	0.59	-6.52**	-12.58 **	-0.22	2.93
13	CP-210xCD 209	-0.03	0.53	0.14	4.57	1.42	-0.45	1.14**	4.37 *
14	CP-210xIC 25 9104	0.08	0.28	0.76	5.98 *	5.02**	5.36 **	-0.04	-7.63**
15	CP-210xIC 25 90 69	-0.05	-0.81	-0.90	-10.55 **	-6.43 **	-4.91 **	-1.10**	3.27
	SE±	0.58	0.67	0.46	3.07	1.30	1.73	0.37	1.66

* Significant at 5% LS and ** Significant at 1% LS

Table 4: Estimates of *gca* and *sca* variances, additive and dominance variance components and their ratio for different characters in red cowpea. (Fixed Effect Model)

Genetic Parameters	Days to Initiation of flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of Primary branches plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant
$\sigma^2 g$ (GCA)	16.930	6.390	11.210	129.690	0.430	1.260	0.040	2.700
$\sigma^2 s$ (SCA)	15.156	10.429	10.965	542.055	2.606	6.425	0.092	16.609
$\sigma^2 a$ (F = 1)	33.851	12.771	22.421	259.381	0.859	2.526	0.078	5.403
$\sigma^2 D$ (F = 1)	15.156	10.429	10.965	542.055	2.606	6.425	0.092	16.609
$\sigma^2 a / \sigma^2 D$	2.233	1.225	2.045	0.479	0.329	0.393	0.847	0.325
Heritability (Narrow Sense) %	64.00	44.58	53.84	32.19	24.53	27.86	44.63	24.20

Genetic Parameters	Pod length	Number of grains per pod	Test weight (g)	Biologic yield per plant (g)	Grain yield per plant (g)	Harvest Index (%)	Seed Protein content (%)	Seed Iron content (ppm)
$\sigma^2 g$ (GCA)	1.150	0.110	1.730	5.070	9.400	24.830	1.118	18.128
$\sigma^2 s$ (SCA)	0.647	0.435	3.827	52.255	75.563	152.101	13.032	234.027
$\sigma^2 a$ (F = 1)	2.304	0.212	3.466	10.138	18.798	49.656	2.236	36.255
$\sigma^2 D$ (F = 1)	0.647	0.435	3.827	52.255	75.563	152.101	13.032	234.027
$\sigma^2 a / \sigma^2 D$	3.563	0.487	0.906	0.194	0.249	0.326	0.172	0.155
Heritability (Narrow Sense) %	70.17	19.40	46.19	14.12	19.57	24.25	14.52	13.28

Table 5: Genetic parameters for different characters in red cowpea

Observations Recorded	Genetic Parameters								
	Var. Environ - mental	ECV	Var. Genotypical	GCV	Var. Phenotypical	PCV	h2 (Broad Sense)	Genetic Advancement 5%	Gen. Adv. as % of Mean 5%
Days to initiation of flowering	12.32	7.87	28.83	12.05	41.15	14.39	70.06	9.26	20.77
Days to 50% flowering	16.19	7.24	15.19	7.01	31.37	10.08	48.41	5.59	10.05
Days to maturity	28.96	6.81	20.60	5.74	49.56	8.91	41.57	6.03	7.63
Plant height (cm)	12.33	7.50	412.88	43.38	425.21	44.02	97.10	41.25	88.06
Number of Primary branches per plant	0.10	8.95	1.81	37.54	1.91	38.59	94.63	2.70	75.23
Clusters per plant	0.33	6.74	5.53	27.73	5.86	28.54	94.43	4.71	55.52
Number of Pods per cluster	0.02	7.72	0.10	19.34	0.11	20.83	86.27	0.60	37.01
Number of Pods per plant	0.86	6.87	14.30	28.11	15.15	28.94	94.36	7.57	56.26
Pod length	0.96	6.60	3.62	12.85	4.57	14.44	79.11	3.49	23.54
Number of grains per pod	1.21	6.92	3.01	10.92	4.21	12.93	71.31	3.02	18.99
Test weight (g)	0.67	7.79	4.84	21.02	5.51	22.41	87.91	4.25	40.59
Biological yield per plant (g)	27.17	11.21	58.28	16.42	85.45	19.88	68.21	12.99	27.93
Grain yield per plant (g)	5.73	10.85	50.49	32.21	56.22	33.99	89.81	13.87	62.89
Harvest Index (%)	8.12	6.09	92.53	20.58	100.64	21.46	91.94	19.00	40.64
Protein content (%)	0.44	4.10	9.24	18.75	9.69	19.20	95.44	6.12	37.74
Iron content (ppm)	7.859	6.391	162.852	29.092	170.712	29.786	95.396	25.676	58.533

Conclusion

As cowpea is a self-pollinated crop, the GCA effects are more important as they are attributed to additive and additive x additive interaction while the SCA effects are useful only when they are based on additive x dominance gene effect. The cross combinations with higher SCA effects having good *per se* performance and involving at least one good general combiner parent may possibly produce desirable transgressive sergeants.

It is revealed that in case of general combining ability for the five lines, all the characters were significant except for days to maturity which was non-significant. The mean sum of squares for three testers indicated that all the characters were significant except days to 50% flowering and days to maturity. The significant performance of almost all characters studied indicates that there is substantial extent of variability in the lines and testers which forms a broad base for crop improvement.

References

1. Ayo-Vaughan MA, Johnson OA, Christopher OA. Combining ability and genetic components for pod and seed traits in cowpea line. Italian Journal of Agronomy, 2013;8(2):e10. Article DOI: 10.4081/ija.2013.e10.
2. Baptiste Jean Tchiagam Noubissie, Ange Ndogonoudji Alladoum and Joseph Martin Bell. Genetics of four Mineral Micronutrients contents inedible leaves of Cowpea (*Vigna unguiculata* (L.) Walp) genotypes. East African Scholars Journal of Agriculture and Life Sciences. 2019;2(3):104-113.
3. Chaudhari SB, Naik MR, Patil SS, Patel JD. Heterosis in cowpea for seed yield and its attributes over different environment. Trends in Biosciences. 2013;6(4):464-466.
4. Deepa Priya R, Thangaraj K, Gnanamalar RP, Senthil N. Combining ability studies for grain yield and its component traits in cowpea (*Vigna unguiculata* (L.) Walp) Electronic Journal of Plant Breeding. 2018;9(3):941-947.
5. Get Sonu SS, Shekhawat DK, Gothwal Jogendra Singh, Madhu Yadav, Madhu Choudhari. Heterosis for seed yield and associated traits in cowpea [*Vigna unguiculata* (L.) Walp.] genotypes under rainfed condition of Rajasthan. The Pharma Innovation journal. 2021;10:(7):369-373.
6. Idahosa Daniel Osadeyandhian, Alika Joseph Eke. Diallel analysis of six agronomic characters in *Vigna unguiculata* (L.) Walp genotypes. African Journal of Plant Breeding. 2013;1(1):001-007.
7. Kadam YR, Patel AJ, Chaudhari PP, Patel JM, More SJ. Combining ability study in vegetable cowpea (*Vigna unguiculata* (L.) Walp.) Crop Res. 2013;45(1, 2 & 3):196-201.
8. Kempthorne O. An introduction to genetic statistics. John Wiley and Son Inc. Newyork, Champman and Hall Ltd. London, 1957, pp. 468-470.
9. Meena Ramesh, Pithia MS, Savaliya JJ, Pansuriya AG. Heterosis in vegetable Cowpea (*Vigna unguiculata* (L.) Walp), Crop Improv. 2009;36:47-50.
10. Mukati AK, Patel SR, Patil SS, Jadhav BD. Combining ability and gene action studies for seed yield and contributing characters in cowpea (*Vigna unguiculata* (L.) Walp). Trends in Biosci. 2014;7:1479-1484.
11. Nagalakshmi RM, Kumari RU, Boranayaka MB. Assessment of genetic diversity in cowpea (*Vigna unguiculata* (L.) Walp). Electronic Journal of Plant Breeding. 2010;1(4):453-461.
12. Ogunwale GI, Salami AE. Combining ability for days to flowering and grain yield among cowpea (*Vigna unguiculata* (L.) Walp) of different maturity periods. Journal of Agriculture, Forestry and the Social Sciences. 2015;13(1):38-43.
13. Owusu EY, Amegbor IK, Darkwa K, Oteng-Frimpong R, Sie EK. Gene action and combining ability studies for grain yield and its related traits in cowpea (*Vigna unguiculata* (L.) Walp). Cogent Food & Agriculture. 2018;4:1519973.
14. Pallavi YV, Singh Alka Verma, Manoj Kumar Bansala. Analysis of Combining Ability for Yield and its attributing characters in Cowpea (*Vigna unguiculata* (L.) Walp). Pharma Innovation. 2018;7(7):202-204.
15. Patil HE, Nawale PA. Combining ability in cowpea (*Vigna unguiculata* (L.) Walp). Legume Research. 2006;29:270-273.

16. Patil HE, Navale PA, Reddy NBR. Heterosis and combining ability analysis in cowpea (*Vigna unguiculata* (L.) Walp). J Maharashtra Agric. Univ. 2005;30(1):88-90.
17. Pethe UB, Dodiya1 NS, Bhave SG, Dalvi VV. Line X Tester Analysis for Combining Ability in Cowpea (*Vigna unguiculata* (L.) Walp) J Curr. Microbiol. App. Sci. 2018;7(1):511-515.
18. Robinson HF. Quantitative genetics in relation to breeding of the centennial of Mendalism. Indian J Genet. 1966;26:171-187.
19. Romanus KG, Hussein S, Mashela WP. Combining ability analysis and association of yield and yield components among selected cowpea lines. Euphytica, 2008;162(2):205-210.
20. Satish Kumar K, Sridhar Vinod Kumar, Kulkarni NS. Combining ability analysis in dual purpose cowpea (*Vigna unguiculata*) Plant Archives. 2017;17(2):919-923.
21. Sprague GF, Loyd A, Tatum. General vs. Specific Combining Ability in Single Crosses of Corn. 1942.
22. Uma MS, Kalubowila I. Line x tester analysis for yield and rust resistance in Cowpea (*Vigna unguiculata* L. Walp). Electronic Journal of Plant Breeding. 2010;1(3):254-267.
23. Ushakumarin R, Vairam N, Anandakumar CR, Malini N. Studies on hybrid vigour and combining ability for seed yield and contributing characters in cowpea (*Vigna unguiculata*). Electronic Journal of Plant Breeding. 2010;1(4):940-947.
24. Varan R, Jain VK, Singh YV, Bisen P. Heterosis studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp.] For yield and quality traits. Indian Journal of Ecology. 2017;44(4):190-194.