

Full Diallel Analysis and Combining Ability Study in Cowpea (*Vigna Unguiculata* (L.) Walp) For Yield and Its Related Components

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ABSTRACT

Crosses were made between the six parental lines of cowpea using the full diallel-crossing design to generate 15 crosses, 15 reciprocals and 6 parents were evaluated during the cropping season of 2024 and 2025 at Yola and Wukari, Nigeria in a randomized complete block design (RCBD) and replicated three times. Substantial variance existed among the genotypes, parental lines, crosses, and reciprocals for most of the agronomic traits. Both additive genetic effect and non-additive gene effects controlled most traits, but non-additive gene effects were significant and predominant as indicated by the predictability ratio of $\delta^2\text{GCA}/\delta^2\text{SCA}$ which were less than one for all the traits. This work also identified Bossop, Bakwa and Sampea 18 as the best general combiner in term of GCA effects. Sampea 18 x Bossop, Sampea 19 x Bakwa, Bossop x Achishiru recorded the highest SCA effects for the crosses and the reciprocals Achishiru x Bossop and Bossop x Sampea 19 were found the best cross-combination. It was observed that most of crosses and reciprocals involved in this work with high SCA effect of crosses and reciprocal involve at least one of three high general combiners. The preponderance of non-additive genetic effect observed among the traits in the parents, the crosses and reciprocals studied is great tools in choosing the cowpea lines for biparental mating or reciprocal recurrent selection for developing superior genotypes with high yield.

Key word. Diallel; reciprocals; crosses; genotypes; combining ability

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp) a diploid species with somatic chromosome number $2n=22$ (Darlington and Wylie, 1955). It belongs to the order Rosales, family Fabaceae and the genus *Vigna*. It is locally known as wake, southern pea or black eye pea. It is one of the most important pulse crops, native of West Africa (Vavilov, 1951) but Steele (1976) suggested Ethiopia as the primary and Africa as the secondary centre of diversity.

Genetic diversity is very important for any crop improvement programme. The larger the genetic diversity in the crop is, more the opportunity will be for identification of the suitable parents for hybridization in the crop. Further, the genetics of the yield and its contributing traits needs to be well elucidated. In a crop like cowpea, which is an autogamy by pollination, hybridization between selected parents is used to create variability. The selection of parents plays a crucial role in success of hybridization and studies on combining ability and gene action helps to choose superior parents and cross combinations (Priya et al. 2018) as it estimates the breeding value of parental lines to produce hybrids (Owusu et. al. 2018). The GCA (general combination ability) denotes to additive gene action and is used to determine the performance of parents in general terms while SCA (specific combining ability) is determined by non-additive or dominant gene action and is used to indicate the hybrid performance in specific terms. These variance components are used to investigate the gene action and to estimate the genetic prepotency of parents in hybrid combinations. Matting design such as Diallel (Griffing 1956) provide reliable information about the combining ability of parents and their cross combinations (Owusu et. al. 2018; Samadia et al. 2019). Thus, it becomes essential to characterize the genetic nature of various yield and its components and assess potential of parents in hybrid combinations as well.

MATERIALS AND METHODS

Two experimental sites were used for this research work, one location at the Teaching and Research Farm of Crop Production and Horticulture Department, Modibbo Adama University, Yola Adamawa State, located on Latitude $9^{\circ} 14^1$ N and longitude $12^{\circ} 32^1$ E, at an altitude of 200m above sea level and is located within Sudan savannah agro-ecological zone. The soil type of the experimental site is sandy clay loam. The second location will be at Teaching and Research Farm of Crop Production and Protection Department, Federal University Wukari, (latitude $7^{\circ} 51^1$ N and longitude $9^{\circ} 47^1$ E) in northern Guinea Savannah agro-ecological zone, Taraba State.

The materials to study the nature of gene actions, genetic components, estimation of the general combining ability of parents and specific combining ability of crosses, the heterotic effect of F_1 's over better parent for six cowpea genotypes are SAMPEA 15 (IT99K-573-2-1), SAMPEA 18 (1T07K-293-13), SAMPEA 19 (IT08K-150-12), Bakwa, Bossop and Achishuru along with their 15 F_1 's and 15 reciprocals.

The crossing was carried out during cropping season of 2023 at the screen house, Department of Crop Production, Modibbo Adama University Yola. Crosses was carried out among the six (6) genotype according to full diallel mating design fashion (Method 1 Model 1) of Griffings (1956b), to obtain 15 hybrids and their 15 reciprocals

The emasculation and pollination were carried out as per method proposed by Ritchie et al., (1975). Cowpea has cleistogamous flower consisting of sepals, petals, stamens and carpel. Pollen grains are released from the pollen sacs between 8-10 a.m. and pollination generally has taken place when flowers are open. In order to obtain the first generation of seed, method of emasculation and pollination was adopted to achieve the better success. The well-developed flower buds which are about to open in the next morning were selected for emasculation. The bud was gripped gently and a cut above two third of width of the unopened bud with sharp razor blade, starting from its straight edges, this lifts the upper portion of the corolla and stamens and remove anthers by help of the forceps. After these pollens were dusted on stigma. These operations were carried out in the morning hours. Seeds of the F_1 's and reciprocals produced in the dry season of 2023, along with their six parents were grown in 2024 and 2025 cropping seasons for evaluation.

The six parents, fifteen F_1 's and fifteen reciprocals were grown for evaluation at two locations, Yola ($9^{\circ}14^1$ N, $12^{\circ} 29^1$ E) in Sudan savannah, and Wukari, (latitude $7^{\circ} 51^1$ N and longitude $9^{\circ} 47^1$ E) in northern Guinea Savannah agro-ecological zone of Nigeria in 2024 and 2025 cropping seasons. The three locations provide differences in soil type and rainfall respectively. The materials were grown for field evaluation in a Randomized Complete Block Design (RCBD) with three replications at both the locations. The plot consists of 3m x 2m. Each plot contains 21 plants. Row spaced of 75cm apart and distance between hills in the rows was 30cm and alley of 1.0m between block. Seed were sown by hand; the seed were treated with Apron Star (Metaxyl) at the rate of 15grams for every 1kg of seed in order to prevent seedling damage by pathogenic micro-organism and ensure excellent germination and establishment. Weed control was done as when required to keep the weed pressure low. N: P: K (15:15:15) fertilizer was applied at rate of 100kg per hectare as basal dose. Magic force (Lamda-cyhalothrin 15g/l plus Dimethoate 300g/l) was used at different growth stages to control insect pests at appropriate time.

The observations were recorded from five consecutive plants on the net plots on each parent, cross and reciprocal from each replication on days 50% flowering, days to maturity, vine length, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, pods weight per plant, 100- seed weight, seed yield per plant, seed yield per unit area. Statistical analyses were performed based on plot mean values for all the parameters according to Griffing (1956b) Method 1 model 1 using SAS 2005 package from Zhang et al (2005).

RESULTS AND DISCUSSION

The mean squares from the analysis of variance (ANOVA) for combining ability in a full diallel cross of cowpea combined across locations and years for all the eleven traits are presented in Table 4.1. The mean square values

for year were highly significant ($P < 0.01$) for all the traits except 100 seed weight. Highly significant mean square for locations were observed for number of branches per plant, pod length, seed yield per plant while significant ($P < 0.05$) mean square existed in days to 50% flowering, pods per plant, 100 seed weight and seed yield per unit area. No significant mean square existed in location for days to maturity, vine length, number of pods per plant and number of seed per pod. The mean square values for Genotype and year x genotype were highly significant for all the eleven agronomic traits studied. The three-way interaction between Year x Loc x Gen only showed significant ($P < 0.05$) for days to maturity and seed yield per unit area.

The mean square values for crosses and crosses x Loc were significant for all the traits. The general combining ability (GCA) and specific combining ability (SCA) mean squares were highly significant for all the traits. Mean square values for Maternal (MAT) and Non-maternal (NMAT) effects were highly significant ($P < 0.01$) except number of seeds per pod. It was also observed that both Reciprocals and REC x Environment were highly significant except for number of seeds per pod and 100 seed weight. The mean square for analysis of variance for interaction revealed that GCA x Environment and GCA x Environment and SCA x Environment were highly significant ($P < 0.01$) except pod length and number of branches per plant, pod length, number of seed per plant and 100 seed weight in MAT x Environment and NMAT x Environment respectively.

Highly significant differences observed among the genotypes, parental lines, crosses, and reciprocals for most of the agronomic traits indicated that an appreciable amount of variability existed in the population used for this study, suggesting that they can be responsive to selection pressure and thus there has been chance for improvement. Falconer (1989) had observed that the amount of improvement that is obtained by selection among a number of crosses is dependent on the amount of variability between the crosses and the intensity of selection applied.

Substantial variance existed for year, location and the interaction between year x genotype, location x genotype, crosses x location was highly significant for most of the traits under study. This further suggested that the materials used for this study performed differently in the respective location and year. Similar results were observed by Emmanuel et al. (2021), Patil et al. (2018), and Gowda et al. (2012).

Higher level of significant variability observed for all the traits in general combining ability (GCA) and specific combining ability (SCA) variances, indicating the importance of GCA variance additive and additive x additive types of gene action while SCA variance involves both dominant and epistasis types of gene action which constitute the non-additive genetic effects (Ogunwale, 2013). This portrayed that both additive and non-additive gene effects played major roles in cowpea yield and its related traits as observed by Dokashi et al. (2003) and Singh et al. (2004).

Highly significant variance recorded by Maternal (MAT) and non-maternal (NMAT) effects indicated that environment has no influence on the traits studied. The significance of GCA x Environment, SCA x Environment, MAT x Environment and NMAT x Environment were also observed by Singh et al. (1997), Francis (2006), Olapade et al. (2002) etc.

The findings revealed that such results were probably because the parental lines used for the study were selected based on the exact knowledge of genetic architecture of the materials, the basic genetic mechanism involved in generating variability, the selection of the parents, and the information regarding nature and magnitude of gene action. This study is in line with the findings of Griffing (1956b) which stated that if the parents were selected based on performance, then method 1 should be used with Model 1. Griffing's analysis on combining ability requires the combining potentials of parents (Niehuis et al., 1986). The possibility of isolating superior true breeding genotypes is supported by preponderance of additive genetic variance in many self-fertilizing species (Joshi et al, 1986).

The preponderance of GCA mean variance over SCA variance for traits such as days to 50% flowering, days to maturity, pod length, 100 seed weight, seed yield per plant, and seed yield per unit area indicate that additive genetic effects are more than non-additive gene effects in the inheritance of these traits. Similar results were reported by Raut et al. (2017) and Amegbor et al. (2017). The prevalence of GCA variance over SCA variance

suggests that early generation testing of genotype would be efficient and promising hybrids can be identified and selected based on their prediction of GCA variance (Amegbor et al., 2017; Fasahat et al., 2013).

The predominance of SCA variance over GCA variance for vine length, number of branches per plant, number of pods per plant, pods length, number of seed per pod, and pods weight per plant suggests the non-additive gene action is more important in controlling the inheritance of these traits. These findings are in agreement with Raut et al. (2017) and Singh et al. (2006). However, the differences in the two results could be attributed to the differences in the genetic materials used and also the research conditions (environment) under which the study were conducted.

The components of genetic variance are presented in Table 4.2. The result revealed that the relative magnitude of GCA and SCA for all the traits studied showed that SCA consistently had higher values than the GCA. However, when the components of variance were computed to estimate the predictability ratio of GCA: SCA all the estimate were less than one.

Non-additive variance (δ^2D) was consistently higher than the Additive variance (δ^2A) for all the traits. The dominant ratio ($H_1/D^{1/2}$) were greater than one in all the traits except with number of branches per plant and number of pods per plant which recorded zero value.

The wide range of variability was noticed in all the traits among the genotypes studied which showed that the parental lines with diverse variation were included in the present investigation which provide sufficient scope for further selection for improvement on these traits. This variability could be harnessed to gain improvement in yield and its contributing traits following appropriate breeding method. Result from this work indicated that the component variance due to SCA was consistently higher than the component variance of GCA in all the traits studied, suggesting that non-additive gene action is more important in controlling the inheritance of the traits. These findings are in agreement with Raut et al. (2017), Singh et al. (2006).

This further emphasized the existence of genetic diversity among the parents tested and demonstrated the impact of dominance and/or epistatic effect which signify the non-fixable components of the genetic variation related to heterosis (Pandey et al. 2015). Singh et al. (2006), postulated that non-additive gene action can be explored by multiple crosses followed by inter-mating among desirable segregants. Selection should therefore be deferred till later generations when these impacts are fixed in the homozygous level (Ertiro et al. 2013). The preponderance of SCA than GCA could be ascribed to repulsion phase linkage and linkage disequilibrium (Sokol et al. 1977). Furthermore, higher SCA than GCA can be elucidated by the usage of closely related parents (Azad et al 2014).

The $H_1/D^{1/2}$ ratio were greater than one for all the traits except number of branches per plant and number of pods per plant where the dominance ratio was zero. Revealed the superior dominance of these genes. The fact that $\delta^2GCA / \delta^2SCA$ ratio was less than one and the $H_1/D^{1/2}$ ratio was greater than one shows that the non-additive gene effect is effective in the inheritance of these traits. Likewise, $H_1/D^{1/2}$ ratio being greater than one indicated the superior dominance of these genes. However, selection could be started in the future generations. The results are in agreement with Badhe et al. (2016) and Purnamasari et al. (2017).

The estimates of general combining effects of the parental lines for the eleven agronomic traits studied in the combined analysis across locations and years are presented in Table 4.6. The results revealed that Bossop is the best general combiner among the parents, because it showed significant positive GCA effect for all the traits. Bakwa and Sampea 18 ranked second and third best general combiners. Bakwa showed significant positive GCA effects with days to 50% flowering, days to maturity, vine length, pod length, pods weight per plant, 100 seed weight, seed yield per plant and seed yield per unit area. While Sampea 18 exhibited positive significant GCA effect with number of branches per plant, pod length, number of pods per plant, pod length, pods weight plant, 100 seed weight, seed yield and seed yield per unit area. It also showed significant negative GCA effect with days to 50% flowering. Parental lines Achishiru and Sampea 15 were the fourth and fifth, which although showed negative values for almost all agronomic traits. Both Achishiru and Sampea 15 recorded significant negative GCA effects with days to 50% flowering and days to maturity, indicating earliness.

However, Sampea 19 is considered the least general combiner because it only showed significant negative GCA effects with days to 50% flowering and days to maturity also indicating earliness. Worthy to note, parental lines Sampea 15, Sampea 19 and Achishiru showed significant negative GCA effect with vine length. Ironically however, the best general combiners (that is GCA effects) did not always give best performance in the trait, considering the per se performance. This can be affirmed by the level of correlation existing between the per se performance and the GCA effect of the parents.

General combining ability of a parent refers to the capacity of a parent to produce superior hybrids or otherwise when crossed with another parent. It is a vital tool for identifying superior parental lines based on their hybrids' performance. This helps in the selection of the best parent which, when crossed, will give rise to more desirable segregates. The high general combiners for any of the measured traits identified in this study should produce desirable segregates for selection when crossed together. Azad et al. (2014) and Raut et al. (2017) suggested that parents showing positive GCA effects means continuous progress should be achieved through breeding of traits under study. However, the identification of parental lines having superior hybrids is costly and time-consuming in extensive field tests in hybrid breeding programs. This ("hard way is the only way") still remains the case in third world countries around the world.

The results revealed that Sampea 15, Sampea 19, and Achishiru were good general combiners for earliness because these parental lines had highly significant and negative GCA effects for days to 50% flowering and days to maturity. Hybridizing these parental lines therefore will likely result in early or extra-early maturing crosses in cowpea. Ogunwale (2013), and Okunlola (2014) also reported similar results in cowpea. Since many workers reported maturity period as an important factor affecting grain yield, this study suggests the possibility of developing genotypes that combine shortest duration and highest seed yields.

The parental lines Sampea 15, Sampea 19, and Achishiru recorded negative and significant GCA effects for vine length. Negative GCA effect for vine length could also be desirable. This finding is in agreement with Patel et al. (2008) and Verma et al. (2020). The parental lines Bossop, Bakwa, and Sampea 18 were identified to be the best general combiners for yield and yield components in cowpea. This indicated that these genotypes are good parents that can be used in cross combinations to generate superior crosses. This result is in agreement with the one of Patel et al. (2013) and Joshi et al. (2022).

In any systematic breeding programme, selection of parents with desirable traits having good general combining ability effects for yield and yield contributing traits and cross combinations having high heterosis estimate along with high estimate of SCA effects also help in formulating of an efficient and sound breeding procedure for rapid and effective isolation of superior genotypes in crossing programme, selected individuals should be taken care of with to avoid the risk in losing a high level of performance. This indicates the importance of testing the parents for their nicking ability because many a times, the high yielding parents may not combine well to give good segregants.

The Specific Combining Ability (SCA) effects for the fifteen crosses, for the eleven agronomic traits in the combined analysis are presented in Table 4.7. The results revealed that there was significant difference for the crosses in all the traits studied. Of the 15 crosses, only six showed positive significant SCA effects for seed yield per plant. The highest were obtained from Sampea 18 x Bossop, closely followed by Sampea 19 x Bakwa, and Bossop x Achishiru. The crosses Sampea 15 x Bakwa, Sampea 15 x Bossop, Sampea 18 x Achishiru, Sampea 19 x Bossop, Bakwa x Bossop and Achishiru showed significant SCA effect for days to 50% flowering. Three crosses: Sampea 15 x Sampea 19, Sampea 15 x Bakwa, and Sampea 19 x Bossop exhibited significant negative SCA effects for days to maturity. As for number of branches per plant, five crosses recorded significant positive SCA effect, the highest among them were Sampea 18 x Bossop, Sampea 19 x Bakwa, Bossop x Achishiru, Bakwa x Achishiru and Sampea 15 x Sampea 18. On the other hand, the highest significant negative SCA effect for branches per plant was recorded by Sampea 15 x Sampea 19, Sampea 18 x Sampea 19, followed by Sampea 15 x Bossop, Sampea 15 x Achishiru, Sampea 15 x Sampea 19, Sampea 19 x Bossop, Sampea 18 x Achishiru and Bakwa x Bossop. 7 out of 15 crosses showed positive significant SCA effect for pod weight. The highest was recorded in Sampea 18 x Bossop, Sampea 19 x Bakwa and Bossop x Achishiru while the lowest significant negative SCA effects for pod weight was recorded in the crosses Sampea 18 x Sampea 19. Worthy to note, all

the crosses that gave the highest per se performance in a particular trait were also the crosses that produced the highest SCA effect.

Specific combining ability effects are usually used to identify the best cross combinations for hybrid seed production. In this study, it was observed that the best cross combinations in terms of SCA effects involved one or both of the high general combiners as parents. Most of the crosses involved in this work with high SCA effects involve at least one of the three high general combiners, namely Bossop, Bakwa, and Sampea 18. However, poor general combiners such as Sampea 15 and Sampea 19 gave good cross combinations when they were crossed with high general combiners, such as observed from Bossop x Achishiru, Sampea 19 x Bakwa, and Sampea 19 x Bossop. Kadams (1999) reported similar results where a hybrid with high SCA effects involved one or both of the good general combiners as parents. Emmanuel et al. (2021), Rocha et al. 2017, and Kadams et al. (2013) report similar results in cowpea.

This work observed that most the best performing parents to some extents were also found to be the best general combiners, though their relative rankings were changed. However, the best general combiners or best performing parents provide best specific combinations for majority of the traits. Thus, a critical examination of relative magnitude of GCA and SCA variance and their effects provided guidelines for development of genotypes. With the availability of high yielding parents involved in the production of best Specific Combination observed in Sampea 18 x Bossop, Sampea 19 x Bakwa, Bossop x Achishiru, Sampea 18 x Bakwa, and Sampea 15 x Bakwa, the interaction of high x high, high x low, and low x low combinations, particularly those having highly significant and higher magnitude of SCA values, could be exploited for practical breeding which is expected to throw stable performing transgressive segregates carrying fixable genes. Similar work was reported by Raut et al. (2017) and Owusu et al. (2020). In this situation, selection of superior segregates followed by recurrent selection or multiple crossing will be useful in harnessing both additive and non-additive gene effects in the present collection of biological material.

The specific combining ability effects of the 15 reciprocals for eleven agronomic traits in the combined analysis across locations and years are presented in Table 4.8. The result revealed that out of 15 reciprocals, only four showed positive significant SCA effects for seed yield per plant and seed yield per unit area. While eight others showed negative significant effects. Among these reciprocals, Achishiru x Bossop showed the highest positive SCA effect for both seed yield per plant and seed yield per unit area, and was followed by Bossop x Sampea 19, Bakwa x Sampea 18 and Sampea 18 x Sampea 15. While Bossop x Sampea 18 recorded the highest negative SCA effect for both seed yield per plant and seed yield per unit area, followed by Sampea 19 x Sampea 18, Bossop x Bakwa, Achishiru x Sampea 19 and Achishiru x Sampea 15. It is worthy to note that each of these reciprocals involved at least one or both high general combiners in the reciprocal.

The reciprocals Sampea 19 x Sampea 18, Bakwa x Sampea 19, Bossop x Sampea 18 and Bossop x Bakwa showed significant negative SCA effects for days to 50% flowering. However, Sampea 19 x Sampea 15, Bossop x Sampea 15, Bossop x Sampea 18, Bossop x Bakwa and Achishiru x Sampea 15 exhibited significant negative SCA effects for days to maturity. Nine reciprocals exhibited positive significant SCA effects for vine length, among them are: Sampea 18 x Sampea 15, Sampea 19 x Sampea 15, Bossop x Sampea 19, Achishiru x Sampea 19, Bakwa x Sampea 19, Bossop x Sampea 15 and Achishiru x Bossop while 2 reciprocals gave negative SCA effect, they are Achishiru x Sampea 15 and Bakwa x Sampea 18. 3 out of 15 reciprocals had positive significant SCA effects for number of branches, the highest among them was Achishiru x Bossop, followed by Bossop x Sampea 19 and Sampea 18 x Sampea 15. The reciprocals Achishiru x Bakwa, Achishiru x Bossop, Bossop x Sampea 19 and Sampea 18 x Sampea 15 showed high positive significant SCA effects for number of pods per plant. 4 out of 15 reciprocals recorded significant positive SCA effects for pods weight per plant, the highest was observed in the reciprocal Achishiru x Bossop, Bossop x Sampea 19, Bakwa x Sampea 18 and Sampea 18 x Sampea 15. Most of the reciprocals which produced the highest per se performance in a particular trait also had high SCA effect of reciprocals.

Specific combining ability effects are used to identify the best cross combination of the reciprocal seed production. The study also observed that the best cross combination in terms of SCA effects of the reciprocals involved one or two of the three best combiners as parents, viz. Bossop, Bakwa, and Sampea 18. However, poor

general combiners such as Sampea 15, Achishiru, and Sampea 19 also gave good cross combinations when they were crossed with high general combiners, such as observed from Bossop x Sampea 19 and Achishiru x Bossop arising from parents with high $\times$ low and low $\times$ high GCA values for yield and other traits might be due to complementation of high and low combining loci (Raut et al. 2017). Parents of these crosses can be used for biparental mating or reciprocal recurrent selection for developing superior varieties with high yield (Azad et al., 2014).

Considering the SCA effects of the crosses in the F_1 generation, Sampea 18 x Bossop and Sampea 19 x Bakwa were the best cross combinations showing positive and highly significant in yield and these combinations are genotypes with breeding potential for yield related components. But when SCA reciprocal effects are examined, Bossop x sampea 18 and Bakwa x Sampea 19 cross combinations were found negative significant in yield and most of the yield components. This indicated that cytoplasmic inheritance or cytoplasmic $\times$ nuclear interactions causes significant changes in these features as a result of better mother plant that influences seed traits, vigour and yield and this direct maternal inheritance effect is useful in breeding system. These findings are in agreement with Owusu et al. (2020), Pallavi et al. (2020), and Verma et al. (2020).

Table 4.1: Mean Square of Entries and Analysis of Variance for Combining Ability in 6x6 Diallel Cross of Cowpea, Combined Across Locations and Years

Source of variation	df	Days to 50% flowering	Days to maturity	Vine length (cm)	No. of branches/plant	No. of pods/plants	Pods length (cm)	No. of seeds/pod	Pods weight/plant (g)	100 seed weight (g)	Seed yield/plant (g)	Seed yield/unit area (kg)
Year	1	119.28**	416.15**	851.55**	74.92**	997.40**	1.22*	72.28**	218.48**	0.59 ^{ns}	293.07**	194.14**
Location	1	9.19*	0.33 ^{ns}	8.90 ^{ns}	36.11**	129.58 ^{ns}	1.47**	1.34 ^{ns}	239.56*	2.58*	97.98**	148.92*
Rep (y $\times$ loc)	8	8.10 ^{ns}	17.09*	726.73**	147.76**	974.04**	1.71**	8.76**	502.67**	14.60**	363.98**	169.36**
Genotypes	35	798.35**	659.27**	252.15**	360.25**	124.20**	25.37**	12.42**	708.08**	192.14**	417.13**	194.81**
Year $\times$ Gen	35	33.19**	35.06**	345.51**	93.12**	340.30**	3.67**	7.90**	117.15**	10.45**	73.77**	345.20**
Loc $\times$ Gen	35	7.33 ^{ns}	18.41*	170.54 ^{ns}	3.06 ^{ns}	226.77*	0.21 ^{ns}	6.00 ^{ns}	53.67 ^{ns}	1.88 ^{ns}	21.87 ^{ns}	98.63*
Year $\times$ Loc $\times$ Gen	35	4.73 ^{ns}	16.55*	170.40 ^{ns}	14.64 ^{ns}	203.84 ^{ns}	0.23 ^{ns}	6.15 ^{ns}	102.54 ^{ns}	1.58 ^{ns}	39.56 ^{ns}	119.94*
Crosses	14	798.39**	659.29**	252.03*	357.12**	124.10**	25.76**	12.30**	707.78**	192.59**	437.29**	195.24*
Crosses $\times$ location	14	15.75**	23.35**	126.93**	36.88**	256.15**	1.41**	6.69*	443.85**	4.65**	265.57**	120.59**
GCA	5	488.61**	417.62*	114.25**	407.02.86**	593.06**	154.20**	16.12**	139.80**	122.18**	878.72**	385.75**
SCA	14	90.62**	89.02*	138.12**	421.63**	1650.78**	4.11**	19.43**	868.92**	34.59**	526.93**	236.44**
Reciprocals	15	143.49**	57.24**	691.01**	275.98**	104.72**	4.60**	3.89 ^{ns}	316.70**	7.49**	200.50**	905.30*
Maternal	5	161.36**	53.70**	703.86**	403.17**	153.19**	9.76**	5.70 ^{ns}	458.85**	6.63**	281.58*	128.91*
Non-Maternal	10	134.55**	59.02**	684.60**	212.39**	804.80**	2.20*	2.98 ^{ns}	245.62**	7.93**	1599.58**	713.38**
GCA $\times$ E	15	46.44**	27.18**	213.66**	82.48**	239.12**	2.44**	12.19**	673.25**	4.31*	407.27**	191.78**
SCA $\times$ E	45	12.16**	23.97*	101.40*	30.64*	212.00**	1.10 ^{ns}	9.66**	481.56**	6.27**	241.40*	107.43**
REC $\times$ E	14	9.11**	21.45*	123.54**	27.92*	306.00**	1.39*	1.88**	329.67**	3.15 ^{ns}	242.51*	110.00**
MAT $\times$ E	5	7.99**	28.83*	133.09**	21.36 ^{ns}	329.43**	0.78 ^{ns}	1.89 ^{ns}	462.61**	3.04 ^{ns}	328.81**	152.87**
NONM $\times$ E	30	9.67**	17.76**	118.77**	31.20*	294.28**	1.69*	1.87 ^{ns}	263.20**	3.20 ^{ns}	199.36*	885.66**
Pool Error	280	13.67.	20.41	99.83	27.43	27.62	1.16	6.65	43.34	4.11	24.79	11.04

Table 4.2: Components of genetic variance for eleven characters of cowpea, combined across locations and years

Sources of variation	Days to 50% flowering	Days to maturity	Vine length (cm)	No. of branches/plant	No. of pods/plants	Pods length (cm)	No. of seeds/pod	Pods weight/plant (g)	100 seed weight (g)	Seed yield/plant (g)	Seed yield/unit area (kg)
δ^2_{gca}	33.08	28.38	692.57	0.00	0.00	1.03	0.00	37.26	8.27	24.40	102.89
δ^2_{sca}	235.84	200.91	5479.23	18.21	18.44	7.41	0.31	653.14	58.82	413.51	1814.54
$\delta^2_{gca} / \delta^2_{sca}$	0.01	0.14	0.13	0.00	0.00	0.14	0.00	0.06	0.14	0.06	0.06
δ^2_A	66.16	56.75	1385.14	0.00	0.00	2.07	0.00	74.51	16.53	48.81	205.77
δ^2_D	235.83	200.91	5479.23	18.21	18.44	7.41	0.31	653.14	58.82	413.51	1814.54
H_1/D^1 ratio	2.67	2.66	2.81	0.00	0.00	2.68	0.00	4.19	2.67	4.12	4.20

Table 4.6: Estimate of General combining ability effects for yield and yield components in 6 genotypes, combined across locations and years

S / N o.	Parental lines	Days to 50% flowering	Days to maturity	Vine length (cm)	No. of branches/plant	No. of pods/plants	Pods length (cm)	No. of seeds/pod	Pods weight/plant (g)	100 seed weight (g)	Seed yield/plant (g)	Seed yield/unit area (kg)
1	Sampea 15	-6.218	-6.938	-32.254	-2.645	-3.663	-0.053	-0.169	-8.557	-0.787	-5.567	-114.578
2	Sampea 18	-0.773	0.000	0.300	1.687	1.801	0.378	-0.301	6.294	1.542	6.134	127.388
3	Sampea 19	-4.336	-3.000	-20.582	-0.186	-0.829	-0.224	-0.213	-0.141	-0.063	-0.723	-15.662
4	Bakwa	7.817	6.806	39.230	0.050	0.784	1.157	-0.348	9.182	3.215	6.925	145.305
5	Bossop	6.463	5.847	27.576	1.927	1.589	0.601	0.474	8.128	1.323	5.701	119.928
6	Achishiru	-2.954	-2.715	-14.270	-0.734	0.318	-1.859	0.220	-14.906	-5.229	-12.471	-262.381
	SE	0.281	0.344	2.404	0.398	1.264	0.082	0.196	1.584	0.154	1.198	25.281

Table 4.7: Estimates of Specific Combining Ability effects for yield and yield components of 15 Crosses, combined across locations and years

S/ N o	hybrids	pedigree	Days to 50% flowering	Days to maturity	Vine length (cm)	No. of branches/plant	No. of pods/plants	Pods length (cm)	No. of seeds/pod	Pods weight/plant (g)	100 seed weight (g)	Seed yield/plant (g)	Seed yield/unit area (kg)
1	1x2	Sampea x Sampea 18	-0.613	3.618	16.356	0.925	3.047	0.153	0.817	3.396	-1.178	1.958	40.628

2	1x3	Sampea 15 x Sampea 19	-0.009	- 1.549	4.3169	-1.510	-2.451	- 0.664	-0.222	-6.445	-0.515	- 5.481	- 117.0 35
3	1x4	Sampea 15 x Bakwa	-1.602	- 2.146	11.475	0.562	2.906	0.500	0.355	7.211	0.153	5.500	113.2 10
4	1x5	Sampea 15 x Bossop	1.0440	- 0.604	10.272	-1.135	-0.520	0.406	-0.493	2.587	1.225	3.353	67.57 1
5	1x6	Sampea 15 x Achishir u	-0.414	- 0.250	-14.462	-1.329	-3.536	- 0.087	-0.938	-2.976	1.726	- 1.609	- 19.08 8
6	2x3	Sampea 18 x Sampea 19	1.607	0.722	2.138	-1.130	-0.012	0.472	0.753	-5.046	0.102	- 3.249	- 66.73 4
7	2x4	Sampea 18 x Bakwa	1.412	0.125	-18.466	0.534	-2.854	0.228	0.039	10.894	0.687	8.715	184.0 79
8	2x5	Sampea 18 x Bossop	1.933	0.167	23.960	9.524	15.708	- 0.114	-1.022	34.578	0.996	27.43 5	588.4 14
9	2x6	Sampea 18 x Achishir u	-0.859	- 0.354	18.384	-2.682	-4.088	- 0.293	-0.192	15.080	-0.078	- 10.82 7	- 246.0 11
10	3x4	Sampea 19 x Bakwa	0.141	0.250	15.854	5.952	10.110	0.205	-0.154	31.203	1.812	25.66 4	538.2 82
11	3x5	Sampea 19 x Bosop	-3.671	- 2.250	-29.521	-1.882	-2.166	- 0.523	-0.811	-12.896	-1.937	- 10.64 6	- 223.4 87
12	3x6	Sampea 19 x Achishir u	0.912	3.354	26.720	0.795	-0.633	- 0.216	-0.610	2.308	0.981	1.905	40.29 2
13	4x5	Bakwa x Bossop	-2.324	0.153	-7.104	-3.689	-9.021	- 0.325	-0.717	-18.723	0.385	- 14.32 7	- 299.3 66
14	4x6	Bakwa x Achishi ru	0.843	0.007	12.191	2.646	12.225	- 0.206	0.413	4.993	-1.922	2.486	52.63 8
15	5x6	Bossop x Achishi ru	-1.137	- 0.076	23.909	4.157	8.174	0.513	-0.118	24.290	-0.188	16.38 5	345.5 24
		SE	0.641	0.736	5.481	0.909	2.883	0.187	0.447	3.611	0.352	2.731	57.65 0

Table 4.8: Estimate of Specific Combining Ability effect for yield and yield components of 15 reciprocals, combined across locations and years

S/NO.	Reciproca ls	pedigree	Days to 50% flowering	Days to maturity	Vine length (cm)	No. of branches/ plant	No. of pods/ plants	Pods length (cm)	No. of seeds/ pod	Pods weight/ plant (g)	100 seed weight (g)	Seed yield/ plant (g)	Seed yield/unit area (kg)
1	2x1	Sampea 18 x Sampea 15	0.042	-0.875	11.725	2.071	5.333	- 0.504	- 0.150	5.579	-0.588	3.513	74.096
2	3x1	Sampea 19 x Sampea 15	-0.708	-1.042	9.813	-0.629	0.488	- 0.679	- 0.808	-0.413	0.321	0.225	4.867
3	3x2	Sampea 19 x Sampea 18	-0.833	-0.250	0.146	-1.958	-5.167	0.404	- 0.238	- 14.979	-0.158	- 11.133	-234.633
4	4x1	Bakwa x Sampea 15	-0.333	-0.333	11.367	0.354	-0.008	- 0.308	- 0.442	-4.842	0.258	-3.596	-76.013
5	4x2	Bakwa x Sampea 18	0.125	0.875	- 14.379	-1.000	-0.454	- 0.192	0.021	5.850	-0.254	4.996	104.829
6	4x3	Bakwa x Sampea 19	-1.042	-0.167	14.850	-1.938	-6.679	- 0.258	- 0.433	-2.033	0.908	-0.979	-41.442
7	5x1	Bossop x Sampea 15	0.042	-1.333	11.575	-0.508	-0.671	- 0.900	- 0.525	-6.371	-0.879	-4.992	-103.429
8	5x2	Bossop x Sampea 18	-4.042	-3.042	-5.000	-9.933	- 15.629	- 0.056	0.133	- 24.271	-0.321	- 20.633	-445.179
9	5x3	Bossop x Sampea 19	5.375	3.792	47.346	4.346	6.233	- 0.267	- 0.633	13.921	0.550	10.346	218.563
10	5x4	Bossop x Bakwa	-4.292	-1.750	0.500	-3.067	-4.034	- 0.596	- 0.642	- 16.558	-0.650	- 10.513	-221.692
11	6x1	Achishiru x Sampea 15	0.250	-1.292	- 22.288	-1.496	-3.475	- 0.104	0.033	-7.767	0.088	-5.233	-93.546
12	6x2	Achishiru x Sampea 18	1.000	1.208	8.879	-0.717	-5.913	0.463	- 0.192	-8.054	0.638	-4.800	-118.304
13	6x3	Achishiru x Sampea 19	3.875	0.417	21.067	0.996	-0.779	- 0.521	0.096	- 10.975	-0.917	-6.075	-129.200
14	6x4	Achishiru x Bakwa	2.542	0.792	2.275	-0.508	11.083	- 0.146	- 0.350	-2.717	-0.617	-0.288	-5.221
15	6x5	Achishiru x Bossop	1.042	0.750	10.154	5.279	9.163	0.208	0.192	17.642	0.133	17.871	376.163
		SE	0.755	0.922	6.450	1.069	3.393	0.220	0.526	4.249	0.414	3.214	67.837

CONCLUSION

It has been revealed that the traits involved in cowpea population evaluated are controlled by both additive and non-additive genetics effect. However, non-additive gene effect, were found to be most significant and predominant as indicated by the predictability ratio of $\delta^2\text{GCA}/\delta^2\text{SCA}$ which were all less than one. Since component of variance due GCA was lower than that due to SCA it also means that non-additive genetic effect, were more stable than additive genetic effect over the environment suggesting that more than one test environment is not necessary to get any reliable information on the traits involved among these population. It could be ascribed to repulsion phase linkage and linkage disequilibrium. Under such situation, selection should be therefore deferred till later generations when these impacts are fixed in homozygous level.

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