Estimation of Genetic Parameters of Yield Traits in Crosses of Cowpea

Olunloyo A. A.

Department of Agricultural Technology, Federal College of Forestry, Ibadan, Oyo State, Nigeria.
Corresponding author email: akinrinade_zone@hotmail.com

ABSTRACT

The experiment was conducted in understanding and describing the nature and extent of genotypic and phenotypic variation, heritability, expected genetic advance, as well as gene effects between yield and yield components of cowpea. The experiments were conducted in the Department of Agricultural Technology, Federal College of Forestry, Jericho, Ibadan, Nigeria. Five generations (P_1, P_2, F_1, F_2 and F_3) of three crosses from three cowpea lines (TVu1xTVu14019, TVu1xTVu3629 and TVu3629xTVu14019).

In days to flowering, there was no epistatic effect in the cross TVu3629 x TVu14019. All the crosses exhibited high broad sense heritability and moderate genetic advance as percentage of mean for pod length, number of seeds per pod and 100 seed weight while cross TVu1 x TVu14019 and TVu1 x TVu3629 also in seed yield per plant. There was significant complementary and duplicate epistatic gene effect in days to flowering, pod length, number of seeds per pod in the cross involving TVu1 with TVu3629 and TVu14019. There was significant epistasis gene effect in the cross of TVu3629 x TVu14019 in pod length, number of seeds per pod and 100 seed weight.

High magnitude of broad sense heritability along with moderate to high genetic advance as percentage of mean recorded for days to flowering, pod length, number of seeds per pod,

100 seed weight and seed yield per plant indicated that these characters can be improved through selection in advanced generations. Since different gene effects were responsible for the inheritance of the same character in different crosses and for the different characters in the same cross specific handling of individual crosses for different characters would be advantageous for the improvement of these characters. The characters controlled by both additive and non-additive gene effects can be successfully improved by utilizing hybrid vigour or biparental mating method of breeding.

Keywords: genotypic and phenotypic variation, heritability, genetic advance, gene effects, epistasis, yield

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp.) is of major importance to the livelihoods of millions of people in the tropics. Resource-poor small-holder farmers derive food, animal feed, cash and manure from the crop. Cowpea has the potential to function as a key integrating factor in intensifying systems through supplying protein in human diets and fodder for livestock, as well as bringing Nitrogen into the farming system through biological fixation (Singh *et al*., 2003). In spite of the significance of cowpea as a food crop to millions of people on the continent, grain yields today remain low

International Journal of Research Available at
https://journals.pen2print.org/index.php/ijr/

e-ISSN: 2348-6848
p-ISSN: 2348-795X
Volume 06 Issue 10
September 2019

averaging 0.3 tones/ha due to several biotic and abiotic factors. In the humid tropics, seed yield of cowpea is low due to unfavorable environmental conditions such as high rainfall, high disease incidence, reduced sunshine hour, poor soil fertility level etc. (Singh *et al*., 2005). Furthermore, the general grain yield of cowpea especially in marginal areas is still low and no single variety can be suitable for all growing conditions; whereby varietal requirements in terms of plant type, seed type, maturity and use pattern are highly diverse from region to region and these makes cowpea breeding programs more complex than any other crops (Singh *et al*., 1997).

The prime objective the crop improvement programme is to improve genotypes /hybrids or population of genotypes to develop crop varieties that are superior in one or more aspects than the cultivated best varieties/hybrids in the crop. Cowpea plays a significant role in the livelihood of millions of people in Africa and other parts of the developing world where it is a major source of dietary protein that nutritionally complements low-protein staples like cereal and tuber crops (SARI, 1996 and 1997). Improving cowpea against constraints without farmer/consumer preference may result in the rejection of such varieties by farmers since farmer/consumer choice is very significant in utilization of cowpea in Nigeria and the world at large.

Considering the farmer/consumer preference of dearly maturity, colour and seed yield makes cowpea improvement programme more complex and as such no single variety can be suitable for the farmer/consumer preference. The objective of any breeding program is to develop desirable genotypes with high yield potential. Selection is an integral part of breeding program by which genotypes with high productivity in a given environment are selected. So, selection for high yield is made difficult by the complex nature of this trait. Yield per unit area is the end product of components of several yield contributing characters. But the study of the genetic parameters controlling the expression of yield and its components are essential in determining the effect of such genetic parameters in enhancing the seed yield of cowpea (Katiyar *et al*., 1977). One of the important strategies plant scientists adopted to overcome the problem of getting a better yield is to exploit genetic variability of the available germplasm to identify high yielding genotypes that may give a reasonable yield on different soil and environmental conditions (Kaur *et al*., 2007). Therefore, this research attempted to investigate the genetic variability of cowpea genotypes in relation to yield and yield related agronomic traits. The reason for selecting cowpea is that no sufficient work has been done for understanding and describing the nature and extent of genotypic and phenotypic variation, heritability, expected genetic advance, as well as gene effects between yield and yield components of cowpea.

MATERIALS AND METHODS
Location of Study

The experiments were conducted in the Department of Agricultural Technology, Federal College of Forestry, Jericho, Ibadan, Nigeria. Five generations (P_1, P_2, F_1, F_2 and F_3) of three crosses from three cowpea lines (Table 1) that were collected from the International Institute of

Tropical Agriculture (IITA), Ibadan, Nigeria for their contrasting traits in seed colouration.

The experimental design was completely randomized design with six replicates with each cross forming the blocks. Each block contains the five generations of each cross. A single replication had one row each of the parents and F_1 generation, two rows of F_2 generation and three rows of F_3 generation. There were ten plants in a row with spacing of 50cm and 20cm was used. Plastic pots of 25cm diameter filled with garden soil weighing 4.5kg. Thinning to one plant per pot was done at two weeks after planting.

Cultural practices such as daily watering was carried out for potted plants, while hand weeding and spraying were carried out when necessary in the pot and field experiments. Pest control was achieved by using insecticides Cypermethrin with application rate of 600 ml/ha and Lara-Force® (Lambda-cyhalothrin) with the application rate of 1000 ml/ha for pre- and post-flowering insect pests control respectively. Vertebrates pest were controlled using scarecrows and wire nettings to cover the experimental plot.

Table 1: Cowpea lines used in the study and their characteristics

S/No.	LINES	SOURCE	SEED COLOUR	FLOWER COLOUR	MATURITY
1	TVu3629	IITA	Brown	White	Medium (75-90 days)
2	TVu14019	IITA	White	White	Medium (75-90 days)
3	TVu1	IITA	Red	Purple	Early (60-70 days)

*IITA= International Institute of Tropical Agriculture, Ibadan, Nigeria.

Data Collection

Data were collected on individual plant basis on the five generations produced from each cross P_1, P_2, F_1, F_2 and F_3. The following data were collected; Days to flowering (days to 1st flower), Pod length (cm), Number of seeds per pod, 100 seed weight (g) and Seed yield per plant (g).

Data Analysis

Data on days to flowering and yield components was analysed on five generations (P_1, P_2, F_1, F_2 and F_3). The genotypic and phenotypic variance, broad sense heritability and genetic advance as percentage of mean was calculated using estimation of variability among generation programme of TNAUSTAT statistical package software (2014).

The mean performances, gene effects and scaling effects on the five generations were analyzed using Generation mean 5 parameter statistical programme of TNAUSTAT statistical package (Manivannan, 2014). The estimation of gene effects determined were computed on mid parental value (m), additive gene effects (d), dominance gene effects (h), additive x additive (epistatic) interaction effect (i) and dominance x dominance (epistatic) interaction effect (l) using the five parameter module developed by Hayman (1958).

The scaling test developed by Hayman (1958) was used to determine C and D

Where $C = 4\bar{F}_2 - \bar{F}_1 - \bar{P}_1 - \bar{P}_2$

$D = 4F_3 - 2F_1 - P_1 - P_2$

Where P_1 = mean of Parent 1

P_2 = mean of parent 2

F_1 = mean of F_1

F_2 = mean of F_2

F_3 = mean of F_3

And where significance of any one of these scales was taken to indicate the presence of epistasis.

The scaling test was estimated in the crosses at the C and D scales to determine if the values were significant to show epistatic interaction in the five characters studied for the crosses in the inheritance of flower pigmentation.

RESULTS AND DISCUSSION
MEAN PERFORMANCE OF PARENTS (P_1, P_2), F_1, F_2 AND F_3 GENERATIONS

The mean performance of different generation consisting parents, F_1, F_2 and F_3 for the days to flowering, yield and its traits on the cross having distinct seed colour in cowpea. The mean performance was evaluated in three crosses as stated below.

Cross I = TVu1 x TVu14019

Cross II = TVu1 x TVu3629

Cross III = TVu3629 x TVu14019

Table 2: Mean performance of P_1, P_2, F_1, F_2 and F_3 generations for five agronomic traits in crosses TVu1 x TVu14019, TVu1 x TVu3629 and TVu3629 x TVu14019.

TRAITS	CROSS	P_1	P_2	F_1	F_2	F_3
DF	I	38.80	47.20	38.30	42.75	42.73
	II	38.80	45.00	39.30	42.55	41.90
	III	45.00	47.20	45.30	45.60	46.60
PL	I	13.12	12.06	14.52	12.71	12.27
	II	13.12	13.50	15.60	14.94	12.89
	III	13.5	12.06	14.85	12.96	12.32
NSP	I	12.00	10.80	14.30	11.45	11.27
	II	12.00	11.80	13.80	13.05	11.43
	III	11.80	10.80	13.70	11.45	11.47
100SW	I	10.12	17.18	14.18	13.83	13.11
	II	10.12	14.50	12.58	10.77	11.15
	III	14.50	17.18	16.52	16.45	14.96
SYP	I	47.47	58.55	61.94	56.21	54.22
	II	47.47	55.59	58.46	52.92	53.40
	III	55.59	58.55	60.80	58.94	53.71

DF=Days to Flowering, PL= Pod Length, NSP=Number of Seeds/Pod, 100SW=100-Seed Weight, SYP= Seed Yield/Plant

Cross I= TVu1 x TVu 14019, Cross II= TVu1 x TVu3629, Cross III= TVu3629 x TVu14019

F_1= First Filial generation, F_2= Second filial generation, F_3= Third filial generation.

Days to flowering

Parents varied from 38.80 days (TVu1) to 47.20 days (TVu14019) for days to flowering. The F_1 cross mean values varied from 38.30 days of cross TVu1 x TVu14019 to 45.30 days of cross TVu3629 x TVu14019. Among the F_2 and F_3

International Journal of Research Available at
https://journals.pen2print.org/index.php/ijr/

e-ISSN: 2348-6848
p-ISSN: 2348-795X
Volume 06 Issue 10
September 2019

(segregating) generation, the F_2 and F_3 of cross TVu3629 x TVu14019 have late days to flowering at 45.60 and 46.60 days respectively whereas the F_2 and F_3 of cross TVu1 x TVu14019 and TVu1 x TVu3629 have a close range of 41.90 to 42.75 days.

Pod Length

Among the parents, TVu3629 recorded the highest length (13.50cm), while TVu14019 had the lowest (12.06cm) pod length. Among the F_1 crosses, highest pod length was registered in cross TVu1 x TVu3629 (15.60cm) and the lowest in cross TVu1 x TVu14019 (14.52cm). Among the segregating generation, all the F_3 and F_2 of the crosses except that of F_2 of cross TVu1 x TVu3629 (14.94cm) does not fall in the range of 12.27 to 12.96cm recorded.

Number of seeds per pod

Parents mean value for number of seeds pod varied from 10.80 (TVu14019) to 12.00 (TVu1). Cross TVu1 x TVu14019 (14.30) produced the highest number of seeds per pod in the F_1 crosses while that of cross TVu1 x TVu3629 and TVu3629 x TVu14019 are 13.80 and 13.70 respectively. Among the F_2 and F_3 (segregating) generation, F_2 of cross TVu1 x TVu3629 had the maximum number of seeds per pod at 13.05 whereas others range at 11.27 to 11.47.

100 Seed weight

Parents mean value varied from 10.72g (TVu1) to 17.18g (TVu14019) fro 100 seed weight. Mean values in the F_1 crosses ranged from 12.58g (cross TVu1 x TVu3629) to 16.52g (cross TVu1 x TVu3629). Among the F_2 and F_3 generation, the F_2 and F_3 of cross TVu3629 x TVu14019 had the maximum 100 seed weight whereas F_2 and F_3 of cross TVu1 x TVu3629 had the minimum 100 seed weight.

Seed yield per plant

Parents mean value varied from 47.47g (TVu1) to 58.55g (TVu14019) for seed yield per plant. The F_1 of cross TVu1 x TVu14019 (61.94) had the highest seed yield among the F_1 generation while the least yield was registered in cross TVu1 x TVu3629 (58.46g). Among the F_2 and F_3 generation, the F_2 of cross TVu3629 x TVu14019 had the maximum seed yield and the minimum by F_2 of cross TVu1 x TVu3629.

HERITABILITY ESTIMATES

The estimates of the genotypic variance, phenotypic variance, broad sense heritability, genetic advance and genetic advance as percentage of mean for the three crosses between morphological different seed colour are presented in Table 3. The character-wise results are presented as under.

Days to flowering

Out of the three crosses for the days to flowering, genotypic variance was highest in cross TVu1 x TVu14019 (5.03) while the least was in cross TVu3629 x TVu14019 (0.30) and for heritability (broad sense) it ranged from 80.59 (cross TVu1 x TVu14019) to 53.95 (cross TVu3629 x TVu14019). For the genetic advance, it also ranged from 9.84 (cross TVu1 x TVu14019) to 1.79 (cross TVu3629 x TVu14019). The present findings are in close agreement with the results obtained by Patil and Bhaviskar (1987), Siddique and Gupta (1991), Sharma and Singhania (1992) and Rocha *et al.* (2003) of high broad sense heritability for days to flowering.

International Journal of Research Available at
https://journals.pen2print.org/index.php/ijr/

e-ISSN: 2348-6848
p-ISSN: 2348-795X
Volume 06 Issue 10
September 2019

Table 4: Estimates of Heritability (%) and Genetic Advance as percent of mean for various characters in crosses TVu1 x TVu14019, TVu1 x TVu3629 and TVu3629 x TVu14019.

TRAITS	CROSS	GV	PV	Herit %	Gen Adv.	Gen Adv. %	Mean
DF	I	5.03	6.24	80.59	4.15	9.84	42.14
	II	2.27	3.03	74.96	2.69	6.44	41.71
	III	0.30	0.55	53.95	0.83	1.79	46.05
PL	I	0.60	0.74	80.84	1.43	11.21	12.76
	II	1.29	1.52	84.81	2.15	15.46	13.92
	III	0.80	0.96	83.74	1.69	13.05	12.93
NSP	I	1.18	1.40	84.21	2.06	17.46	11.77
	II	0.64	1.04	61.72	1.29	10.52	12.30
	III	0.60	0.83	71.82	1.35	11.5	11.76
100SW	I	2.16	2.43	88.98	2.86	21.09	13.54
	II	1.22	1.42	86.03	2.11	18.53	11.41
	III	0.86	0.93	92.14	1.83	11.64	15.73
SYP	I	18.97	22.13	85.71	8.31	14.8	56.11
	II	9.54	12.27	77.73	5.61	10.39	54.00
	III	3.30	10.11	32.62	2.14	3.74	57.20

DF=Days to Flowering, PL= Pod Length, NSP=Number of Seeds/Pod, 100SW=100-Seed Weight, SYP= Seed Yield/Plant

Cross I= TVu1 x TVu 14019, Cross II= TVu1 x TVu3629, Cross III= TVu3629 x TVu14019

GV= Genotypic Variance, PV= Phenotypic Variance, Herit%= Broadsense heritability, Gen Adv.= Genetic Advance, Gen Adv. %= Genetic Advance as percentage of mean

Pod length

The genotypic variance varied from 0.60 (cross TVu1 x TVu14019) to 1.29 (cross TVu1 x TVu3629) for pod length while the broad sense heritability was very high in the three crosses which ranged from 80.84 (cross TVu1 x TVu14019) to 84.81 (cross TVu1 x TVu3629). The genetic advance of 11.21, 15.46 and 13.05 was registered for cross TVu1 x TVu14019, TVu1 x TVu3629 and TVu3629 x TVu14019 respectively. All the crosses that exhibited moderate genetic advance as percentage of mean and can be improved through selection.

Number of seeds per pod

The genotypic variance for number of seeds per pod was highest in cross TVu1 x TVu14019 at 1.18 while it was least in cross TVu1 x TVu3629 and TVu3629 x TVu14019 having 0.64 and 0.60 respectively. The broad sense heritability ranged from 61.72 (cross TVu1 x TVu3629) to 84.21 (cross TVu1 x TVu14019) while the genetic advance was 17.46, 11.50 and 10.52 for cross TVu1 x TVu14019, TVu3629 x TVu14019 and TVu1 x TVu3629 respectively.

All the crosses revealed high broad sense heritability for this trait. The predicted genetic advance as percentage of mean of the crosses exhibited moderate genetic advance. The crosses with moderate genetic advance can be improved through selection while the two with low genetic advance have little possibility of improvement of this trait by straight selection. The high heritability of this trait in cowpea was

reported by Tikka *et al*. (1977), Jana *et al*. (1982), Apte *et al.* (1987), Gowda *et al.* (1991), Siddique and Gupta (1991) and Ram and Singh (1997).

100 Seed weight

The broad sense heritability for 100 seed weight was highest in cross TVu3629 x TVu14019 (92.14) out of the three crosses evaluated and which also have the highest in genotypic variance and genetic advance at 2.16 and 21.09% respectively. The least broad sense heritability of 86.03% was registered in cross TVu1 x TVu3629 while cross TVu3629 x TVu14019 had the least in genotypic variance and genetic advance at 0.86 and 11.64 respectively. The cross TVu1 x TVu14019 have a high broad sense heritability and high genetic advance and this implies that there is close correspondence between genotypic and phenotype values due to relatively smaller contribution of environmental effect on this trait and better opportunity for selection of better genotypes in segregating generations for improvement of the trait the present findings are in close agreement to the findings of Boradia *et al.* (1973), Lakshmi and Goud (1977), Tikka *et al.* (1977), Jana *et al.* (1983), Apte *et al.* (1987), Siddique and Gupta (1991), Pal *et al.* (2003), Kumar and Sangwan (2000) and Rocha *et al.* (2003).

Seed yield per plant

For genetic variance of seed yield per plant, it was highest in cross TVu1 x TVu14019 (18.97) and least in cross TVu3629 x TVu14019 (3.30) while the broad sense heritability followed the same pattern as the genetic variance with cross TVu1 x TVu14019 (85.71) and cross TVu3629 x TVu14019 (32.62). For

the genetic advance, cross TVu3629 x TVu14019 (3.74) had the least while cross TVu1 x TVu14019 (14.80) had the highest genetic advance. All the crosses except TVu3629 x TVu14019 exhibited high broad sense heritability. The high heritability of this trait was reported by Siddique and Gupta (1991), Biradar *et al.* (1993) and Damarany (1994).

GENE EFFECTS AND SCALING TEST

The scaling test (C and D) and gene effects of mid parent (m), gene effects of additive (d), dominance (h) and interaction effect (additive x additive (i) and dominance x dominance (l)) on the five characters in the three crosses of cowpea were studied for the segregation pattern of seed colour. The character-wise results are presented under.

Days to flowering

The scaling test of the three crosses for the estimates of C and D scales for the days to flowering showed that C scale was significant in cross TVu1 x TVu14019 and TVu1 x TVu3629. For the gene effects, all the crosses were significant for the additive (d) gene effects while cross TVu3629 x TVu14019 showed significance in dominance (h) gene effects. In the interaction effects, cross TVu1 x TVu14019 and TVu3629 x TVu14019 showed significance in additive x additive (i) interaction effect.

The significant estimates of scaling tests for all the eight crosses indicated that five of the crosses exhibited the presence on non-allelic interaction for these traits with the exception of TVu3629 x TVu14019. The same signs of dominance (negative) and dominance x dominance (negative) in the other two crosses

indicates that there were complementary epistatic interaction on this traits. The value of h is negative in all the eight crosses indicating that early maturity is completely or particularly dominant to late maturity. This was supported by the report of Ojomo (1971) and Mak and Yap (1980). The complementary epistatic interaction was not in accordance to the report of Ubi *et al.*, (2001), Ishiyaku *et al.* (2005), Rashwan (2010) reporting duplicate epistasis.

Pod length

The scaling test estimates for pod length in the three crosses showed that C scale was significant in cross TVu1 x TVu14019 and TVu3629 x TVu14019 while D scale was significant in cross TVu1 x TVu3629. In the gene effects, dominance (h) gene effects was significant in all the three crosses while cross TVu1 x TVu14019 and TVu1 x TVu3629 also showed significance in additive (d) gene effects. For the interaction effects, cross TVu1 x TVu3629 showed significance in both interaction effects while cross TVu3629 x TVu14019 showed significance in the additive x additive (i) interaction effects. The significant estimates of scaling tests in all the eight crosses exhibited the presence of non-allelic interaction for this trait. The complementary type of epistatic interaction was recorded in TVu3629 x TVu14019 and TVu1 x TVu14019 while it was duplicate type of epistatic interaction in TVu1 x TVu3629. The h estimates is positive in all three crosses thus indicating that long pod length is completely or partially dominant to short pod length. The significance of additive gene effects in all the crosses except in TVu1 x TVu3629 suggests that selection within earlier generations leading to isolation of homozygous lines having

desired pod length could be achieve through selection. This result is in agreement of the reports by Chandhari *et al.* (1998) and Ubi *et al.* (2001).

Number of seeds per pod

The number of seeds per pod scaling test of the three crosses showed that the estimates of (scale was significant in cross TVu1 x TVu14019 and TVu3629 x TVu14019 while the estimates of D scale was significant in cross TVu1 x TVu3629. For the gene effects, additive (d) gene effects was significant in cross TVu1 x TVu14019 and TVu3629 x TVu14019 while dominance (h) gene effects was significant in cross TVu1 x TVu14019 and TVu1 x TVu3629. The interaction effect in the three crosses showed that cross TVu1 x TVu3629 had significance in additive x additive (i) interaction effects. In the number of seeds per pod, the gene effect of the crosses made showed additive, dominance and epistatic interaction. There were significant estimates of the scaling tests in the crosses TVu1 x TVu3629 exhibiting duplicate type of epistatic interaction while complementary epistatic interaction was exhibited in crosses TVu3629 x TVu14019 and TVu1 x TVu14019. The present findings are in conformity to the results of Singh *et al.* (2006); Lal *et al.* (2013) and Thakare *et al.* (2016) who reported that additive, dominance and epistatic effect occurred in the inheritance of seeds per pod in cowpea thereby suggesting that homozygous elite recombinants could be developed following inter-crossing of desirable segregants.

100 Seed Weight

The result obtained in the estimates of the scale tests for the 100 seed weight showed

International Journal of Research Available at
https://journals.pen2print.org/index.php/ijr/

e-ISSN: 2348-6848
p-ISSN: 2348-795X
Volume 06 Issue 10
September 2019

that C scale was significant in cross TVu1 x TVu3629 and TVu1 x TVu14019 while D scale was significant in cross TVu3629 x TVu14019. For the gene effects, additive (d) gene effects was significant in all the three crosses while cross TVu3629 x TVu14019 was also significant in dominance (h) gene effects. In the interaction effects, cross TVu1 x TVu14019 and TVu1 x TVu3629 had significance in additive x additive (i) while cross TVu1 x TVu3629 and TVu3629 x TVu14019 had significance in dominance x dominance (l) interaction effects. The result obtained for this trait in all crosses showed the highly significant values of mid parent values (m) thus implying that the mean of the five generations differed from each other the estimates of the gene effects revealed that additive, additive x additive gene effect were highly significant in all the crosses except in TVu3629 x TVu14019. The significant opposite signs of dominance and dominance x dominance effects indicated the presence of duplicate epistasis in the inheritance of these traits in the cross TVu1 x TVu3629 and TVu3629 x TVu14019. These results of duplicate epistatic inheritance were in agreement to the findings of Sherif and Damarany (1992) and El-Ameen (2008) who have reported both non-allelic gene interactions in their studies. Therefore with additive and non-additive generation involved in this trait breeding methods involving high volume crossing like biparental, recurrent and diallel selective mating designs seemed more promising.

Seed yield per plant

For the scaling test, the estimates of the C and D scale for seed yield per plant showed that there were no significance in all the three crosses at both C and D scale. In the gene effects, there was significance in the additive (d) gene effects in the three crosses while cross TVu3629 x TVu14019 had significance in the dominance (h) gene effects. In the interaction effects, cross TVu1 x TVu14019 and TVu3629 x TVu14019 had significance in additive x additive (i) interaction effects. The seed yield per plant gene effects result obtained showed significant values in the mid parental values (m) thus implying that he five generations (P_1, P_2, F_1, F_2 and F_3) differed from each other. The dominance (h) values were positive in all the crosses thus implying that high seed yield is completely or partially dominant to low seed yield on the crosses. In all the crosses, additive gene effect was significant which is in agreement of the finding of Patel *et al.* (1994) and Mehata and Zaveri (1997) who reported predominance of additive gene interaction.

The duplicate epistatic gene interaction was registered as based on the different sign on dominance and dominance x dominance in the stated crosses as indicated by the significance exhibited in the C and D scaling test. Therefore with the result of the findings, biparental or multiple crossing may be employed for the improvement of this trait in cowpea.

Table 5: Estimates of scaling tests and gene effects for days to flowering, pod length(cm), number of seeds/pod, 100 seed weight(g), seed yield/plant (g) in crosses TVu1 x TVu14019, TVu1 x TVu3629 and TVu3629 x TVu14019.

TRAITS	CROSS	m	d	h	i	l	C	D
DF	I	42.75*	-4.20*	-2.92	-6.22*	-11.96	8.40*	-0.57
	II	42.50*	-3.10*	-0.43	-4.03	-12.13	7.80*	-1.30
	III	45.60*	-1.10*	-2.87*	-4.27*	4.53	-0.40	3.00
PL	I	12.71*	0.53*	2.37*	1.50	2.52	-3.40*	-1.51
	II	14.94*	-0.19	5.91*	3.24*	-9.15*	1.92	-4.94*
	III	12.96*	0.72*	2.98*	2.35*	1.61	-3.42*	-2.21
NSP	I	11.45*	0.60*	2.39*	0.69	6.62	-5.60*	-0.63
	II	13.05*	0.10	4.81*	3.11*	-6.62	0.80	-4.17*
	III	11.45*	0.50*	1.46	0.06	6.09	-4.20*	0.37
100SW	I	13.83*	-3.53*	2.15	-5.44*	-2.87	-0.36	-2.52
	II	10.77*	-2.19*	0.18	-4.46*	6.86*	-6.68*	-1.54
	III	16.45*	-1.34*	4.00*	0.64	-7.70*	1.06	-4.72*
SYP	I	56.21*	-5.54*	9.13	-10.88*	4.67	-5.06	-1.56
	II	52.92*	-4.06*	2.42	-12.62*	17.32	-8.31	4.68
	III	58.94*	-1.48*	15.17*	8.48	-22.88	0.00	-17.16

*= significance at 5% level of probability

DF=Days to Flowering, PL= Pod Length, NSP=Number of Seeds/Pod, 100SW=100-Seed Weight, SYP= Seed Yield/Plant

Cross I= TVu1 x TVu 14019, Cross II= TVu1 x TVu3629 Cross III= TVu3629 x TVu14019

m= mid parent, d= additive gene effects, h= dominance gene effects, i= additive x additive gene effects, l= dominance x dominance gene effects

CONCLUSION

High magnitude of broad sense heritability along with moderate to high genetic advance as percentage of mean recorded for days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant indicated that these characters can be improved through selection in advanced generations.

Since different gene effects were responsible for the inheritance of the same character in different crosses and for the different characters in the same cross specific handling of individual crosses for different characters would be advantageous for the improvement of these characters. The characters controlled by both additive and non-additive gene effects can be successfully improved by utilizing hybrid vigour or biparental mating method of breeding. In addition, the present studies have shown that enough variability, genetic heritability and gene effect exists in the studied morphological and agronomic characters among cowpea lines in the germ plasm for breeders to exploit for further improvement. There is therefore the need for genetic research to be conducted on cowpea for variability and heritability to be for easy selection to improve cowpea production and overcome other constraints such as diseases and insect pests attack.

REFERENCES

[1]. Apte, U. B.; Chavan, S. A. and Jadhav, B. B. (1987). Genetic variability and heritability in Cowpea. *Indian Journal of Agricultural Sciences*. 57: 596-598.

[2]. Biradar, B.D.; Goud, J.V. and Patil, S.S. (1993). Components of variance, heritability and genetic gain in cowpea (*Vigna unguiculata*

(L.) Walp). *Annals of Agricultural Research.* 14(4): 434-437.

[3]. Bordia, P.C.; Yadavendra, J.P. and Kumar, S. (1973). Genetic variability and correlation studies in cowpea (*Vigna sinensis* L. savi ex Hassk.). *Rajasthan Journal of Agricultural Science.* 4(1): 39-44.

[4]. Chaudhari, F.P.; Thaker, D.N.; Tikka, S.B.S. and Patel, I.D. (1998). Genetic architecture of yield and its components in cowpea (*Vigna unguiculata* (L.) Walp). *Gujarat Agricultural University Research Journal*. 24(1): 30-35.

[5]. Damarany, A.M. (1994). Estimates of genotypic and phenotypic correlation, heritability and potence of gene set in cowpea (*Vigna unguiculata* (L.) Walp). *Assiut Journal of Agricultural Sciences*. 25(4): 1-8.

[6]. El-Ameen, T. M. (2008). Genetic components of some economic traits in cowpea *Vigna unguiculata. Journal of Agricultural Science, Mansoura Univ*., 33: 135-149.

[7]. Gowda, T.H.; Hiremath, S.R. and Salimath, P.M. (1991). Estimation of genetic parameters in intervarietal crosses of cowpea (*Vigna unguiculata* (L.) Walp.) and their implication in selection. *Legume Research*. 14(1): 15-19.

[8]. Hayman, B.I. (1958). The separation of epistatic from additive and dominance variation in generation means. *Heredity.* 12: 371-390.

[9]. Ishiyaku, M. F., Singh, B. B. and Craufurd, P. Q. (2005). Inheritance of time to flowering in cowpea. [*Vigna unguiculata (L.)* Walp.]. *Euphytica*, 142: 242-291.

[10]. Jana S, Srivastava JP and Gautam PL. (1983). Evaluation of genetic resources of durum wheat for salt stress tolerance. In Proceedings of Sixth International Wheat Genetics Symposium. Pp137-141, Kyoto University, Japan.

[11]. Jana, S.; Som, M. G. and Das, N. D. (1982). Genetic variability and correlation studies in Cowpea. *Vegetable Science*. 9: 96-106.

[12]. Katiyar, R.P., J. Prasad, A.B. Singh and K. Ram, (1977). Association analysis of grain yield and its components in segregating populations of chickpea. Indian J. Agric. Sci., 47: 325-327.

[13]. Kaur, G., Bansal, P., Kaur, B., and Banga, S. (2007). Genetic diversity and its association with heterosis in *Brassica rapa*. Proceedings, The 12 international rapeseeds congress, Sci. press USA Inc., 1: 144-146.

[14]. Kumar, R. and Sangwan, R.S. (2000). Genetic variability and heritability in cowpea [*Vigna unguiculata* (L.) Walp.]. *Annals of Biology*. 16(2):81-183.

[15]. Lakshmi, P.V. and Goud, J.V. (1977). Variability in cowpea (*Vigna sinensis* L.). *Mysore Journal of Agricultural Sciences*. 11(2): 144-147.

[16]. Lal, J. J., Danghi, K. S., Kumar, S. and Suresh, J. (2013). Scaling and joint scaling test for quantitative traits of generation mean analysis in sesame *(Sesamum indicum* L*.). J. Oilseeds Res.*, 30 (1): 1-5.

[17]. Mak, C. and Yap, T.C. (1980). Inheritance of seed protein content and other agronomic characters in long bean (*Vigna sesquipedalis* Fruw.). *Theoretical and Applied Genetics*. 56(5): 233-239.

[18]. Manivannan, N. (2014). TNAUSTAT-Statistical package. Retrieved from https://sites.google.com/site/tnaustat.

[19]. Mehata, D.R. and Zaveri, P.P. (1997). Variability heritability and expected genetic advance in F2 generation of four cowpea crosses. *Gujarat Agricultural University Research Journal*. 23(1): 98-102.

[20]. Ojomo, O. A. (1971). Inheritance of flowering date in cowpeas [*Vigna unguiculata* (L.) Walp.] *Tropical Agriculture (Trinidad)* 48, 277-282.

[21]. Pal, A.K.; Maurya, A.N.; Singh, B.; Ram, D. and Kumar, S. (2003). Genetic variability, heritability and genetic advance in cowpea *[Vigna unguiculata (L.)* Walp*]. Orissa Journal of Horticulture.* 31(1): 94-97.

[22]. Patel, R.N.; Godhani, P.R. and Fougat, R.S. (1994). Combining ability in cowpea (*Vigna unguiculata* (L.) Walp.). *Gujarat Agricultural University Research Journal.* 20(1): 70-74.

[23]. Patil, R.B. and Bhaviskar, A.P. (1987). Variability studies in cowpea. *Journal of Maharashtra Agricultural Universities*. 12(1): 63-66.

[24]. Ram, D. and Singh, K.P. (1997). Variation and character association studies in cowpea (*Vigna unguiculata* (L.) Walp.). *Horticultural Journal*. 10(2): 93-99.

[25]. Rashwan, A. M. A. (2010). Estimation of some genetic parameters using six populations of two cowpea hybrids. *Asian Journal of Crop Science,* 2: 261-267.

[26]. Rocha de M. M.; Campelo, J.E.G.; Freire Filho, F.R.; Ribeiro, V.Q. and Lopes, A.C. de A. (2003). Estimates of genetic parameters in white coat cowpea genotypes. *Revista Cientifica Rural*. 8(1): 135-141.

[27]. SARI, (1996). Legumes improvements Programme. *Savannah Agricultural Research Institute Annual Report*. Tamale, Ghana. pg. 46-60.

[28]. SARI, (1997). Legumes improvements Programme. *Savannah Agricultural Research Institute Annual Report*. Tamale, Ghana. pp 111-118.

[29]. Sharma, C. D. and Singhania, D. L. (1992). Performance of Cowpea genotypes for fodder traits. *Annals of Arid Zone.* 31: 65-66.

[30]. Sherif, T.H.I. and Damarany, A.M. (1992). Influence of environment on the manifestation of complementary and duplicate gene interaction for quantitative characters in cowpea (*Vigna unguiculata* (L.) Walp.). *Assiut Journal of Agricultural Sciences*. 23(1): 81-103.

[31]. Siddique, A. K. M. A. R. and Gupta, S. N. (1991). Genotypic and phenotypic variability for seed yield and other traits in Cowpea. *International Journal of Tropical Agriculture.* 9: 144-148.

[32]. Singh AK, Singh M, Singh R, Kumar S, Kalloo G. (2005). Genetic diversity within the genus Solanum (Solanaceae) as Revealed by RAPD markers. Curr. Sci. 90: 711-714.

[33]. Singh, A., Arora, R.N., Singh, A., Henry, A., Kumar, D. and Singh, N.B. (2003). Heterosis and inbreeding depression for grain characters in cowpea. Proceedings of the National Symposium on arid legumes, for food nutrition security and promotion of trade, Hisar, India, 15-16 May 2002. *Advances in arid legumes research*. p. 38-41.

[34]. Singh, B. B., Chambliss, O. L. and Sharma, B. (1997). Recent Advances in Cowpea breeding. *In*: Advances in Cowpea Research. B. B. Singh, D. R. Mohan Raj, K. E. Dashiell and L. E. N. Jackai (eds). Joint publication of International Institute of Tropical Agriculture

and Japan International Research Centre for Agricultural Science (JIRCAS) IITA, Ibadan. Pp 30-49.

[35]. Singh, I., Badaya, S.N. and Tikka, S.B.S. (2006). Combining ability for yield over environments in cowpea *Vigna unguiculata (L.)* Walp. *Indian J. Crop Sci*., 1(1-2): 205-206.

[36]. Thakare, D. S., Bhailume, M. S., Rokade, R. C., Pulate, S. C. and Chimote, V. P. (2016). Genetic analysis of various yield components in cowpea. [*Vigna unguiculata (L.)* Walp.]. *International Journal of Tropical Agriculture* 34 (6): 1905-1913.

[37]. Tikka, S. B. S., Jaimini, S. N., Asawa B. M., and Mathur, J .R. (1977). Genetic variability, interrelationships, and discriminant function analysis in cowpea [*V. unguiculata* (L.) Walp.]. *Indian Journal of Heredity* 9, 1-9.

[38]. Ubi, B.E.; Mignouna, H. and Obigbesan, G. (2001). Segregation for seed weight, pod length and days to flowering following a cowpea cross. *African Crop Science Journal*. 9(3): 463-470.