I J T A
© Serials Publications
National Academy of Agricultural Science (NAAS)
Rating : 3. 03

Genetic Analysis of Various Yield Components in Cowpea. [*Vigna unguiculata* (L.) Walp.]

D.S. Thakare, M.S. Bhailume*, R.C. Rokade*, S.C. Pulate* and V.P. Chimote**

Abstract: *An investigation to study the genetics of seed related attributes in cowpea [*Vigna unguiculata *(L.) Walp.]" was undertaken at Mahatma Phule Krishi Vidyapeeth, Rahuri. Three crosses (VCM-8 X PHULE CP-629, PHULE CP-629 X PCP-12-11 and PCP-12-11 X CAZC-13-1) along with complete set of six generations (P_1, P_2, F_1, F_2, B_1 and B_2) for genetic analysis. Analysis of variance for eleven characters for three crosses studied revealed the substantial variability among the treatments. The scaling tests indicated appreciable amount of epistasis present in different characters of three crosses under the study, indicated the failure of a simple genetic model to explain the genetic system controlling traits in the three crosses studied. Additive, dominance and epistatic components were found operating in the inheritance of almost all the characters studied. Predominance of additive gene action was prevailed in the expression of seed yield per plant and yield components with duplicate type of epistasis in majority of the crosses. Hence, selection should be useful to achieve the improvement in these traits. In the improvement of these characters reciprocal recurrent selection may also prove fruitful. Single seed descent method may be adopted to develop pure lines.*

Keywords*: Additive gene effects, Bi-parental mating, Complementary epistasis, Gene action, Cowpea.*

INTRODUCTION

Cowpea (*Vigna unguiculata* (L) walp.) is one of the most important leguminous crop native to central Africa. Cowpea commonly known as Lobia is also known by different vernacular names *viz.*, Rawan (Hindi), Chavali (Marathi), Barbati (Bengali) and Lobia (Orissa), southern pea or black eye pea, that is adopted to warm condition and cultivated in the tropics and sub-tropics for dry grains, green edible pods for vegetable as well as fodder. The cultivars grown for their immature pods (vegetable purpose) are known as asparagus bean, snake bean, yard long bean and when grown for dry seeds, it is known as black eye pea, kaffir pea and southern pea. Vavilov (1951) recognized India and Africa as the centres of origin, while china is considered as secondary centre of origin of cowpea.

Pulses are economically cheaper and vital source of protein in Indian diet. India has a distinction of growing over a dozen of pulses and first in acreage, production and consumption. Despite per capita availability of pulses is dismally as low as 28 g/ capita/day as against the optimum and minimum stipulation of 104 and 60 g/capita/day, respectively, as per WHO standards. The situation is dicey and often lead to malnutrition. The predicament still assumes volume, as the predominant Indians are vegetarians. Therefore, pulses may simply be termed as health line of the country and needs all out concerted efforts for enhancing their production. Cowpea is an important multi utility crop Cowpea fits well in a variety of cropping system and is grown as cover crop, mixed crop, catch crop and green manure crop. It can be capable of restoring soil fertility and therefore, remain an integral part of subsistence and sustainable production system.

In a self-pollinating crop like cowpea, variability is often created through hybridization

* Department of Genetics and Plant Breeding, MPKV, Rahuri 413 722, Maharashtra India Part of Ph.D. thesis, Corresponding author: *Email: dsthakare8@gmail.com*

between carefully chosen parents. The scope of exploitation of hybrid vigour will depend on the direction and magnitude of heterosis, biological feasibilities and the type of gene action involved. The information of such estimates is essential to plan efficient breeding programme for the improvement of the crop. One of the common approaches followed to understand the nature of gene effects by growing different generations and carrying out the generation mean analysis, using first-degree statistics was employed in the present study.

MATERIALS AND METHODS

The present investigation to study the genetics effect of various morphological characters in cowpea [*Vigna unguiculata* (L.)Walp.]" was undertaken at the Pulses Improvement project Mahatma Phule Krishi Vidyapeeth, Rahuri during kharif 2014. Three crosses (VCM-8 X PHULE CP-629, PHULE CP-629 X PCP-12-11 and PCP-12-11 X CAZC-13-1) made at the centre during *kharif* 2013 were grown along with its 4 parents to make the F_2, B_1 and B_2 generations during *summer 2014* by hand pollination. Therefore, the material for the present investigation consisting complete set of six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of for generation mean analysis. The experiment was laid out in a randomized Block Design with three replications.Among treatments single row of parents and hybrids, two rows of backcrosses and four rows of F_2's were planted with of 3.0 m row length spaced at 45 cm apart with 10 cm distance between hills in a row.

Recommended agronomic practices and necessary plant protection measures were timely adopted for successful raising of the crop. The observations recorded for the characters viz., days to 50% flowering, plant height, number of branches per plant, number of cluster per plant, days to maturity, number of pods per plant, number of seeds per pod, seed yield per plant, 100 seed weight, pod length and harvest index on five randomly selected plants for all the generations in each replications. The data were subjected to analysis of variance for Randomized Block Design following Panse and Sukhatme (1967). The crosses showing significant differences among the entries (progenies) for the character were subjected to generation mean analysis for the estimation of gene effects using six parameter model as suggested by Hayman (1958). The scaling test as described by Hayman and Mather (1955) was used to check the adequacy of the additive dominance model for different characters in each cross.

RESULTS AND DISCUSSION

Analysis of variance for eleven characters for three crosses studied revealed the substantial variability among the treatments which is evident from significant difference among the generations at 5% and 1% level of significance. The crosses that showed significant differences among their respective generations for various characters were considered for studying gene action. The character expression is the manifestation of gene action and its interactions with the environment. The breeding methodology to be adopted for the genetic improvement of the characters primarily hinges on the type of gene action *viz.,* additive, dominance and epistasis with their relative magnitude. Simple selection procedure would be more rewarding for the character governed by the additive type of gene effects. However, for the characters under the influence of inter-allelic interactions (complimentary or duplicate epistasis), exploitation of heterosis or development of composite and synthetics would precisely be more effective.

Production of hybrids as opposed to open pollinated varieties depends largely on the level of dominance or epistasis (dominance × dominance) or both (Cockerham, 1961). A gain level of dominance and forms of epistasis is influenced by the selection of the parental materials to develop open pollinated varieties. Thus, estimation of additive, dominance and epistasis components of genetic variances are of paramount significance in planning and execution of any plant improvement programme. Empirically estimation of gene action is done on certain assumptions like absence of multiple alleles, lethal genes and linkage, constant viability of all the genotypes and additivity of environmental effects on genotypic value that are rarely fulfilled.

A number of genetic models assuming basic requirements have been suggested for the estimation of the gene effects. Hayman (1958), and Hayman and Mather (1955) have developed models for estimating the relative importance of additive and dominance gene effects. Epistasis gene effects were assumed to be negligible. However, significant epistasis gene effects have been reported for quantitative traits in many crops. However, partitioning of total heritable variance in to additive and dominant components ignoring the presence of inter-allelic gene action does not give a correct picture of the gene action involved. If the epistatic gene actions are not separated, they tend to inflate dominance variance and lower the additive variance culminating in reduced efficiency of the breeding programme. The six-generations model involving P_1, P_2, F_1, F_2, B_1 and B_2 generations in three crosses of cowpea was utilized to ascertain epistasis (additive × additive, additive × dominance and dominance × dominance) in addition to additive and dominance gene effects for seed yield per plant and its attributing characters. The scaling tests (A, B, C and D) indicated blatant and conspicuous epistasis present in the three crosses for different characters studied. This clearly suggested the failure of a simple genetic model to explain the genetic system controlling the traits in the three crosses studied and need for consideration of epistasis in all traits while planning breeding programmes in cowpea.

Individual scaling test *i.e.* A, B, C and D of Mather (1949) and Joint scaling test of Cavalli (1952) were used to detect presence of epistasis by using the data of various generations in all three crosses. Results of Individual scaling test and Joint scaling test for eleven yield and yield contributing characters studied for six generations of the crosses are presented in Tables (1, 2 and 3)

1. Days to 50% flowering: Estimates of scales A, C and D were significant for all three crosses indicating presence of non-allelic interactions and estimates of scale B was non-significant for the cross Phule CP-629 x PCP-12-11. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Both additive and dominance gene effects were significant with relative greater magnitude of dominance component for days for 50 per cent flowering in all the three crosses. In all crosses significant dominance and dominance x dominance components with opposite sign indicated the presence of duplicate epistatic in the expression of this trait. Among the epistatic interactions significant additive x dominance (j) and dominance x dominance (l) gene effects were observed for this character in cross VCM-8 × PHULE CP-629 and Phule CP-629 x PCP-12-11, while additive x dominance (j) gene interaction was non-significant in the cross PCP-12-11 X CAZC-13-1. These findings are in conformity with findings of Rashwan (2010) and Patel *et al*. (2013).

2. Days for maturity: Estimates of scales A, B and D were significant for all three crosses indicating presence of non-allelic interactions and estimates of scale C was non-significant for the cross PCP-12-11 x CAZC-13-1. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Dominance gene effects were significant in all the three crosses for this trait, while the significant additive gene effect was observed in cross III. Epistatic gene interactions were also observed to be significant in crosses VCM-8 × PHULE CP-629 and PCP-12-11 × CAZC-13-1 with duplicate type of epistasis. Additive x Dominance type of interactions were non-significant in cross Phule CP-629 x PCP-12-11, having duplicate type of epistasis. Similar results were also obtained in the studies of Patel *et al.* (2013).

3. Plant height (cm): Estimates of scales A and B were significant for all three crosses indicating presence of non-allelic interactions and estimates of both scale C and D were non-significant for the cross Phule CP-629 x PCP-12-11. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Additive gene effects were significant in all the three crosses for this trait, while the significant dominance gene effects were observed in crosses VCM-8 × PHULE CP-629 and PCP-12-11 × CAZC-13-1. Among the epistatic gene interactions, dominance × dominance (l) was highly significant

Table 1
Estimates of individual and joint scaling test (x^2) for detecting non-allelic interaction for yield and yield contributing characters in Cowpea.

	Characters	*Crosses*	*Scaling tests*				x^2
			A	*B*	*C*	*D*	
1	Days to 50% flowering	VCM-8 × PHULE CP-629	2.73**	2.86**	-6.93**	-6.26**	104.82**
		PHULE CP-629 X PCP-12-11	2.40**	0.4	-3.86**	-3.33**	38.82**
		PCP-12-11 X CAZC-13-1	3.00**	2.86**	-4.80**	-5.33**	95.88**
2	Days to maturity	VCM-8 × PHULE CP-629	2.00*	1.33*	-7.40**	-5.36**	83.18**
		PHULE CP-629 X PCP-12-11	3.06**	1.86*	-6.73**	-5.83**	83.93**
		PCP-12-11 X CAZC-13-1	4.13**	2.06**	-2.46	-4.33**	63.36**
3	Plant height (cm)	VCM-8 × PHULE CP-629	-3.86**	-5.60**	-16.73**	-3.63**	74.73**
		PHULE CP-629 X PCP-12-11	-3.60**	1.66*	-2.6	-0.33	34.14**
		PCP-12-11 X CAZC-13-1	4.06**	2.86**	-9.46**	-8.20**	187.34**
4	No. of primary branches/plant	VCM-8 × PHULE CP-629	-1.40**	-1.00*	-1.80*	0.3	13.79**
		PHULE CP-629 X PCP-12-11	-2.20**	-1.86**	-2.06*	1.00**	26.06**
		PCP-12-11 X CAZC-13-1	2.06**	0.80*	-1.20*	-2.03**	53.20**
5	No. of clusters per plant	VCM-8 × PHULE CP-629	-0.93**	-1.60**	-2.13**	0.2	18.86**
		PHULE CP-629 X PCP-12-11	1.80**	1.00**	-0.66	-1.73**	37.22**
		PCP-12-11 X CAZC-13-1	1.40**	1.06*	-0.66	-1.56**	17.36**
6	No. of pod per plant	VCM-8 × PHULE CP-629	-1.60*	-1.80*	-5.06**	-0.83	22.86**
		PHULE CP-629 X PCP-12-11	-1.73*	-1.80**	-3.13**	0.2	15.81**
		PCP-12-11 X CAZC-13-1	-2.26**	-1.86**	-4.26**	-0.06	35.14**
7	Pod length (cm)	VCM-8 × PHULE CP-629	-1.66**	-3.40**	-3.93**	0.56	46.36**
		PHULE CP-629 X PCP-12-11	1.73**	2.06**	-1	-2.40**	29.26**
		PCP-12-11 X CAZC-13-1	1.93**	2.13**	-2.20*	-3.13**	58.44**
8	No. of seeds per pod	VCM-8 × PHULE CP-629	-1.80**	-3.00**	-3.13**	0.83	31.01**
		PHULE CP-629 X PCP-12-11	-2.66**	-3.20**	-2.00*	1.93**	44.32**
		PCP-12-11 X CAZC-13-1	-2.26**	2.20**	-2.26	-1.10*	49.05**
9	100 seed weight (g)	VCM-8 × PHULE CP-629	-1.95**	-2.19**	-1.35	1.39**	25.76**
		PHULE CP-629 X PCP-12-11	2.17**	-0.82**	-1.08**	-1.22**	216.08**
		PCP-12-11 X CAZC-13-1	2.76**	0.82*	-2.92**	-3.25**	262.31**
10	Yield per plant (g)	VCM-8 × PHULE CP-629	-1.21**	-0.57*	-0.94*	0.42	23.52**
		PHULE CP-629 X PCP-12-11	-1.60**	-1.44**	-7.53**	-2.24**	295.47**
		PCP-12-11 X CAZC-13-1	-1.89**	-2.08**	-5.66**	-0.84**	161.04**
11	Harvest index	VCM-8 × PHULE CP-629	8.32**	9.57**	14.64**	-1.62	86.88**
		PHULE CP-629 X PCP-12-11	4.34**	5.88**	-7.31**	-8.77**	56.80**
		PCP-12-11 X CAZC-13-1	3.45*	2.58*	-2.05	-4.04**	13.68**

*, ** significant at 5 & 1 % respectively.

Table 2
Estimates of gene effects in three crosses for Days to 50% flowering, Days to maturity, Plant height (cm), No of primary branches per plant, No. of clusters per plant and No. of pod per plant in Cowpea.

Characters	*Crosses*	*Genetic parameters*						*Type of epistasis*
		m	*d*	*h*	*i*	*j*	*l*	
1 Days to 50% flowering	VCM-8 × PHULE CP-629	48.65**(0.23)	-1.16** (0.41)	12.03** (1.43)	12.53**(1.26)	-0.06**(0.52)	-18.13**(2.35)	Duplicate
	PHULE CP-629 X PCP-12-11	50.63** (0.21)	1.66**(0.42)	6.66**(1.27)	6.66**(1.19)	1.00* (0.49)	-9.46**(2.09)	Duplicate
	PCP-12-11 X CAZC-13-1	49.26**(0.21)	0.73*(0.35)	10.53**(1.19)	10.66**(1.10)	0.06 (0.44)	-16.53**(1.89)	Duplicate
2 Days to maturity	VCM-8 × PHULE CP-629	70.25** (0.21)	0.73 (0.42)	9.46**(1.27)	10.73**(1.21)	0.33**(0.51)	-14.06**(2.04)	Duplicate
	PHULE CP-629 X PCP-12-11	71.96**(0.20)	-0.36 (0.50)	11.70*(1.41)	11.66**(1.30)	0.60 (0.55)	-16.60**(2.42)	Duplicate
	PCP-12-11 X CAZC-13-1	74.61**(0.23)	2.70**(0.33)	8.20**(1.29)	8.66**(1.15)	1.03**(0.47)	-14.86**(1.99)	Duplicate
3 Plant height (cm)	VCM-8 × PHULE CP-629	41.65**(0.30)	1.66** (0.53)	12.13**(1.79)	7.26**(1.62)	0.86**(0.64)	2.20 (2.91)	—-
	PHULE CP-629 X PCP-12-11	45.95**(0.29)	-3.56**(0.37)	2.13 (1.47)	0.66 (1.38)	-2.63*(0.46)	1.26 (2.15)	—-
	PCP-12-11 X CAZC-13-1	41.70**(0.18)	1.06*(0.49)	18.00**(1.34)	16.40**(1.23)	0.60 (0.56)	-23.33**(2.35)	Duplicate
4 No. of primary branches per plant	VCM-8 × PHULE CP-629	4.20**(0.13)	-0.76**(0.21)	0.10 (0.75)	-0.60 (0.69)	-0.20 (0.27)	3.00**(1.17)	— —
	PHULE CP-629 X PCP-12-11	4.20**(0.14)	0.20 (0.22)	-1.56*(0.80)	-2.00**(0.71)	-0.16 (0.27)	6.06**(1.28)	Duplicate
	PCP-12-11 X CAZC-13-1	3.65**(0.08)	0.26 (0.22)	4.30**(0.62)	4.06**(0.56)	0.63**(0.27)	-6.93**(1.09)	Duplicate
5 No. of clusters per plant	VCM-8 × PHULE CP-629	4.05**(0.13)	0.50**(0.20)	0.83 (0.71)	-0.40 (0.67)	0.33 (0.26)	2.93**(1.07)	— —
	PHULE CP-629 X PCP-12-11	3.43**(0.11)	0.73**(0.20)	3.46**(0.67)	3.46**(0.61)	0.40 (0.27)	-6.26**(1.08)	Duplicate
	PCP-12-11 X CAZC-13-1	3.40**(0.14)	-0.30 (0.29)	3.06**(0.83)	3.13**(0.81)	0.16 (0.33)	-5.60**(1.36)	Duplicate
6 No. of pod per plant	VCM-8 × PHULE CP-629	5.80**(0.21)	0.50 (0.41)	2.86*(1.26)	1.66 (1.21)	0.10 (0.48)	1.73 (2.01)	— —
	PHULE CP-629 X PCP-12-11	6.18**(0.21)	-0.36 (0.39)	0.73 (1.20)	-0.40 (1.16)	0.03 (0.45)	3.93*(1.89)	— —
	PCP-12-11 X CAZC-13-1	5.50**(0.18)	0.13 (0.35)	2.20*(1.04)	0.13 (1.01)	-0.20 (0.42)	4.00**(1.68)	Complimentary

*, ** significant at 5 & 1 % respectively. Figure in Parentheses indicates Standard Error.

Table 3

Estimates of gene effects in three crosses for Pod length (cm), No. of seeds per pod, 100 seed weight (g), Yield per plant (g) and Harvest index in Cowpea.

Characters	*Crosses*	*Genetic parameters*						*Type of epistasis*
		m	*d*	*h*	*i*	*j*	*l*	
7 Pod length (cm)	VCM-8 × PHULE CP-629	11.88** (0.17)	1.53** (0.32)	1.40 (0.99)	-1.13 (0.95)	0.86** (0.36)	6.20** (1.57)	– –
	PHULE CP-629 X PCP-12-11	11.66** (0.18)	0.80** (0.30)	5.10** (1.03)	4.80** (0.96)	-0.16 (0.36)	-8.60** (1.63)	Duplicate
	PCP-12-11 X CAZC-13-1	11.15** (0.18)	-0.50* (0.24)	8.46** (0.94)	6.26** (0.87)	-0.10 (0.31)	-10.33** (1.39)	Duplicate
8 No. of seeds per pod	VCM-8 × PHULE CP-629	11.66** (0.20)	0.96** (0.36)	0.76 (1.12)	-1.66 (1.08)	0.60 (0.42)	6.46** (1.75)	– –
	PHULE CP-629 X PCP-12-11	11.88** (0.17)	0.96** (0.30)	-1.83 (0.97)	-3.86** (0.91)	0.26 (0.38)	9.73** (1.54)	– –
	PCP-12-11 X CAZC-13-1	11.08** (0.23)	-2.66** (0.25)	3.43** (1.13)	2.20* (1.07)	-2.23** (0.35)	-2.13 (1.57)	– –
9 100 seed weight (g)	VCM-8 × PHULE CP-629	9.92** (0.12)	0.64* (0.31)	-1.05 (0.84)	-2.79** (0.79)	0.12 (0.32)	6.94** (1.46)	– –
	PHULE CP-629 X PCP-12-11	8.14** (0.08)	1.99** (0.13)	3.06** (0.45)	2.44** (0.44)	1.49** (0.14)	-3.79** (0.65)	Duplicate
	PCP-12-11 X CAZC-13-1	9.21** (0.11)	-0.57** (0.18)	7.93** (0.59)	6.50** (0.58)	0.97** (0.20)	-10.09** (0.90)	Duplicate
10 Yield per plant (g)	VCM-8 × PHULE CP-629	5.45** (0.09)	0.01 (0.16)	-0.35 (0.50)	-0.84 (0.49)	-0.31 (0.18)	2.62** (0.80)	– –
	PHULE CP-629 X PCP-12-11	5.00** (0.09)	-0.31* (0.16)	6.38** (0.50)	4.48** (0.49)	-0.08 (0.19)	-1.43 (0.79)	– –
	PCP-12-11 X CAZC-13-1	5.38** (0.09)	0.39** (0.16)	3.09** (0.50)	1.67** (0.48)	0.09 (0.17)	2.30** (0.79)	Complimentary
11 Harvest index	VCM-8 × PHULE CP-629	25.86** (0.57)	-0.69 (1.10)	3.76 (3.21)	3.25 (3.19)	-0.62 (1.14)	-21.15** (5.05)	– –
	PHULE CP-629 X PCP-12-11	21.33** (0.32)	-1.33 (1.01)	18.96** (2.52)	17.54**(2.40)	-0.77 (1.05)	-27.76**(4.52)	Duplicate
	PCP-12-11 X CAZC-13-1	22.37**(0.32)	1.20 (0.95)	9.06**(2.33)	8.08**(2.30)	0.43 (0.98)	-14.11**(4.10)	Duplicate

*, ** significant at 5 & 1 % respectively. Figure in Parentheses indicates Standard Error.

for cross PCP-12-11 x CAZC-13-1 while, additive x additive (i) was highly significant in cross VCM-8 × PHULE CP-629 and PCP-12-11 x CAZC-13-1. However, additive x dominance interaction (j) was significant in the crosses VCM-8 × PHULE CP-629 and Phule CP-629 x PCP-12-11. The dominance gene effect (h) was significantly positive and dominance x dominance (l) type of interaction was significantly negative in cross PCP-12-11 x CAZC-13-1, indicating duplicate type of epistasis. Similar results were also reported by Adeyanjul *et al.* (2012).

4. Number of primary branches/plant: Estimates of scales A, B and C were significant for all three crosses indicating presence of non-allelic interactions and an estimate of scale D was non-significant for the cross VCM-8 x Phule CP-629. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Additive (d) genetic effects were highly significant for cross VCM-8 × PHULE CP-629 while, significant dominant effect were observed in two crosses *viz.*, crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1 for the number of primary branches. Among the epistatic gene interactions, dominance x dominance (l) was highly significant for all three crosses while, additive x additive (i) was highly significant in crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. However, additive x dominance interaction (j) was significant in the cross PCP-12-11 x CAZC-13-1. The crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1 showed significant dominance and dominance x dominance components with opposite sign indicated the presence of duplicate epistasis in the expression of this trait. Similar results were also obtained in the studies of Patel *et al.* (2013).

5. Number of clusters/plant: Estimates of scales A and B were significant for all three crosses indicating presence of non-allelic interactions and estimates of scale C was non-significant for the cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1, where as scale D was non-significant for the cross VCM-8 x Phule CP-629. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Additive (d) genetic effects were highly significant for crosses VCM-8 × PHULE CP-629 and Phule CP-629 x PCP-12-11 while, significant dominant effect were observed in two crosses *viz.*, cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1 for the number of clusters per plant. As regards the epistatic gene interactions, additive x additive type of gene interaction (i) was highly significant in two crosses *viz.*, cross Phule CP-629 x PCP-12-11and PCP-12-11 x CAZC-13-1, whereas, dominance x dominance (l) gene interaction was significant in all the crosses. The crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1 showed significant dominance and dominance x dominance components with opposite sign indicated the presence of duplicate epistasis in the expression of this trait. These results are in conformity with the results of Deepak kumar *et al.* (2005).

6. Number of pod/plant: Estimates of scales A, B and C were significant for all three crosses indicating presence of non-allelic interactions and an estimate of scale D was non-significant for all the three crosses. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

The significant dominant effect (h) was observed in two crosses *viz.*, cross VCM-8 × PHULE CP-629 and PCP-12-11 x CAZC-13-1 for the number of pods per plant. Among the epistatic gene interactions, dominance x dominance (l) was highly significant for crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. The dominance gene effect (h) and dominance x dominance (l) type of interaction was significant in positive direction in cross PCP-12-11 x CAZC-13-1, revealing epistasis was predominantly of complimentary type. Similar results were also reported by Rashwan (2010) and Patel *et al.* (2013).

7. Pod length (cm): Estimates of scales A and B were significant for all three crosses indicating presence of non-allelic interactions and estimates of scale C and D were non-significant for the cross Phule CP-629 x PCP-12-11 and VCM-8 x Phule CP-629 respectively. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Additive (d) genetic effects were highly significant for all the three crosses however, the dominant gene effect was highly significant in the two crosses *viz*., cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. Among the epistatic gene interactions, dominance x dominance (l) was highly significant for all three crosses while, additive x additive (i) was highly significant in cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. However, additive x dominance interaction (j) was significant in the cross VCM-8 × PHULE CP-629. The dominance gene effect (h) was significant in positive direction, while dominance x dominance (l) type of interaction was significant in negative direction in cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1, revealing epistasis was predominantly of duplicate type. Rashwan (2010) also found similar type of interactions for this trait.

8. Number of seed/pod: Estimates of scales A and B were significant for all three crosses indicating presence of non-allelic interactions and estimates of scale C and D were non-significant for the cross PCP-12-11 x CAZC-13-1 and VCM-8 x Phule CP-629, respectively. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Additive (d) genetic effects were highly significant for all the three crosses however, the dominant gene effect was highly significant in the cross PCP-12-11 x CAZC-13-1. Among the epistatic gene interactions, dominance x dominance (l) was highly significant for crosses VCM-8 × PHULE CP-629 and Phule CP-629 x PCP-12-11 while, additive x additive (i) was significant in cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. However, additive x dominance interaction (j) was significant in the cross PCP-12-11 x CAZC-13-1. Similar results were also reported by Rashwan (2010) and Patel *et al*. (2013).

9. 100 seed weight (g): Estimates of scales A, B and D were significant for all three crosses indicating presence of non-allelic interactions and estimates of scale C was non-significant for the cross VCM-8 x Phule CP-629. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

Additive (d) genetic effects were highly significant for all the three crosses however; the dominant gene effect was highly significant in the cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. The digenic gene interactions *viz*., additive x additive and dominance x dominance were highly significant for this trait in all the three crosses, whereas additive x dominance was significant for cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. The dominance gene effect (h) was significant in positive direction, while dominance x dominance (l) type of interaction was significant in negative direction in cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1, revealing epistasis was predominantly of duplicate type. These results are in conformity with the results of Deepak kumar *et al.* (2005), Rashwan (2010), Adeyanju *et al.* (2012), Patel *et al.* (2013).

10. Seed yield/plant: Estimates of scales A, B and C were significant for all three crosses indicating presence of non-allelic interactions and an estimate of scale D was non-significant for the cross VCM-8 x Phule CP-629. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses. Additive (d) and dominant gene effects were significant for the crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. Among the epistasis gene interactions, dominance x dominance (l) was highly significant for cross VCM-8 × PHULE CP-629 and PCP-12-11 x CAZC-13-1 while, additive x additive (i) was significant in cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1.

The dominance gene effect (h) and dominance x dominance (l) type of interaction was significant in positive direction in cross PCP-12-11 x CAZC-13-1, revealing epistasis was predominantly of complimentary type. Similar results correlated with the result of Rashwan (2010) and Patel *et al*. (2013).

11. Harvest index (%): Estimates of scales A and B were significant for all three crosses indicating presence of non-allelic interactions and estimates of scale C and D were non-significant for the cross PCP-12-11 x CAZC-13-1 and VCM-8 x Phule CP-629 respectively. The Joint scaling test was also resulted into highly significant *chi square* values for all the crosses.

The dominant gene effect was highly significant in the crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. The digenic gene interactions dominance x dominance was highly significant for this trait in all the three crosses, whereas additive x additive was highly significant for cross Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1. The opposite signs of h (+ve) and l (-ve) in crosses Phule CP-629 x PCP-12-11 and PCP-12-11 x CAZC-13-1, revealed duplicate type of gene effect for this trait which is in conformity with the results of Patel *et al*. (2013).

Generation mean analysis using six parameter model of Hayman (1958) was worked out for those characters, where either of scales found significant in both crosses for estimation of inter-allelic interaction effects. Additive, dominance and epistatic components were found operating in the inheritance of almost all the characters studied. Predominance of additive gene action was prevailed in the expression of seed yield per plant and yield components with duplicate type of epistasis in majority of the crosses. Hence, selection should be useful to achieve the improvement in these traits. In the improvement of these characters reciprocal recurrent selection may also prove fruitful. Single seed descent method may be adopted to develop pure lines.

Based on findings, it may be suggested that in those characters, additive and additive x additive gene effects were predominant, one should follow the simple selection in early segregating generations, whereas in those characters where dominance and dominance x dominance gene effects indicated that these traits are predominantly under the control of non-additive gene action. The multiple crosses, biparental mating, disruptive mating, transgressive segregation followed by effective selection in subsequent generations may be fruitful for bringing improvement in these traits.

Literature Cited

Adeyanju1 A. O., M. F. Ishiyaku, C. A. Echekwu and J. D. Olarewaju. (2012), Generation mean analysis of dual purpose traits in cowpea (Vigna unguiculata [L.] walp) *African Journal of Biotechnology* Vol. 11(46), pp. 10473-10483.

Cavalli, L L. (1952), An analysis of linkage in quantitative inheritance. Quantitative Inheritance, H.M.S.O., London, pp. 135–144.

Cockerham, C.C. (1961), Implications of genetic variance in a hybrid breeding programme. Crop Sci., **1**: 47-52.

Deepak Kumar, Sangwan, V.P. and Arora, R.N. (2005), Genetic components of variation in cowpea. *Forage Res.*, **31** (2) : 138-139.

Hayman, B I, and Mather, K. (1955), The description of genie interaction in continuous variation. *Biometrics*, **11:** 69–82.

Hayman, B.I. (1958), The theory and analysis of diallel crosses III. Genetics, **43** : 65-85.

Mather, K. (1949), Biometrical Genetics. Methuen and Co. Ltd., London.

Panse, V. G. and Sukhatmate, P. V. (1995), Statistical method for Agricultural worker. ICAR, New Delhi 4th Edn. pp. 145-150.

Patel, M. D., Y. Ravindrababu, A. M. Patel and S. C. Sharma. (2013), Heterosis studies for seed yield and its contributing traits in cowpea (*Vigna unguiculata* (L.) Walp). *Environment and Ecology.*, **31**(2C):1051-1053.

Rashwan, A. M. A., (2010), Estimation of some genetic parameters using six population of two cowpea hybrids. *Asian J. of Crop Sci.*, **2** (4): 261-267.

Vavilov, N. I. (1951), The origin, variation, immunity and plant breeding of cultivated plants (Traslated by K. S. Cheaster). *Cron. Bot.*, **13** : 364.