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## Genetic analysis for yield and its components in Cowpea (*Vigna unguiculata* (L.) Walp.)

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#### Abstract

Generation mean analysis was carried out by in two cross NCK-13-07 x NCK-15-09 and NCK-13-07 x GC-3 of cowpea. The mean is partition in to additive, dominance and epistasis by using six parameter models. Magnitude of dominance or dominance x dominance gene effect was higher than the additive gene effect for most of traits in both the crosses. Among epistasis, additive x additive gene interaction was found significant in cross NCK-13-07 x NCK-15-09 for branches per plant and clusters per plant and in cross NCK-13-07 x GC-3 for plant height, branches per plant and harvest index. Dominance x dominance component contributed significantly in cross NCK-13-07 x NCK-15-09 for days to maturity, branches per plant, clusters per plant and grain yield per plant and in cross NCK-13-07 x GC-3 for days flowering, days to maturity and harvest index. Hence selection should be carried out in later generation and it would be desirable to follow population improvement approaches involving inter mating of selected plant in advance generation like biparental mating and diallel selective mating design that take care of both additive and non-additive gene actions are more promising for the improvement of various characters studied.

**Keywords:** Generation mean analysis, scaling tests, black gram, generations, gene actions

#### 1. Introduction

Pulses are extremely important source of plant protein (20 to 30%) for the poorest of the world's poor and play a significant role in restoring and enriching soil fertility by fixing atmospheric nitrogen. Pulses contain in their grains nearly about three times the amount of storage proteins found in cereals.

Cowpea [*Vigna unguiculata* (L.) Walp.] is diploid with chromosome number of  $2n=22$  is one of the oldest source of human food. It belongs to the order *Fabales*, family *Fabaceae*, subfamily *Faboideae*, tribe *Phaseoleae*, subtribe *Phaseolinae* and genus *Vigna*. All cultivated cowpeas are grouped under *V. unguiculata* subspecies *unguiculata*, which is subdivided into four major group, i.e. *Unguiculata*, *Biflora*, *Sesquipedalis* and *Textilis*. (Westphal (1974) [20]; Marechal *et al.* (1978) [9]; Ng and Marechal (1985) [12]. Cowpea is a highly self pollinated because of cleistogamous nature of flower. Significant out crossing can occur in some environment, possibly associated with pollen transfer by bumblebees.

It is consumed in form of green pods as well as grains. Cowpea is known by number of common names *viz.*, crowdel pea, black-eyed pea, southern pea and internationally as lobia, coupe or frijole is well adapted to the tropics. Cowpea is comparatively a cheaper source of quality protein, phosphorus, iron, vitamins and an excellent substitute for meat, eggs and other protein rich foods. Dry cowpea seeds are an important source of affordable protein (~25%), fiber (6.3%), low fat (1.9%), carbohydrate (63.6%), thiamine (0.00074%), riboflavin (0.00042%) and niacin (0.00281%). The protein found in cowpea seed is rich in the amino acids like lysine and tryptophan compared to cereal grains however; it is deficient in methionine and cystine when compared to animal proteins. Therefore, cowpea seed is being valued as a nutritional supplement to cereals and an extender of animal proteins (Stanton, 1966) [16].

About two-thirds of the production and more than three-fourths of the area of production is spread over the vast Sudan Savannah and Sahelian zones of Sub-saharan Africa. The major cowpea growing countries are Nigeria, Burkina Faso, Ghana, Kenya, Uganda, Malawi, Tanzania, India, Sri Lanka, Burma, Bangladesh, Philippines, Indonesia, Thailand *etc.* In India it is mainly grown in Rajasthan, Gujarat, Maharashtra, Central India and some region of Southern India.

Yield is the complex quantitative character and it depends on contributing yield components. For crop improvement, genetics of the yield and its components needs to be thoroughly understood. Predominant role of either additive or non-additive gene actions have been reported in the inheritance of seed yield and its related traits in cowpea by number of workers. Epistatic gene action also plays an important role in the inheritance of quantitative traits in various crops (Hayman, 1958; Brim and Cockerham, 1961; Gamble, 1962; Stuber and Moll, 1974) [7, 2, 4, 17]. The present work was therefore, undertaken to obtain more information on epistasis in addition to additive and dominance gene effects for seed yield and its component traits in cowpea by using generation means analysis.

**2. Materials and Methods**

The research experiment was carried out during *kharif*-2020 at Pulses and Castor Research Station, Navsari Agricultural University, Navsari by taking six generation (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) of each of the two crosses *viz.*, NCK-13-07 x NCK-15-09 and NCK-13-07 x GC-3 in Compact Family Block Design with three replications. Observations were recorded on single plant basis for days to flowering, days to maturity, plant height, branches per plant, clusters per plant, grain yield per plant and harvest index. Mean values obtained from the observations recorded on representative plants and samples for quantitative characters for each entry in each family were used for statistical computation. The scaling tests (A, B, C, and D) as described by Hayman and Mather (1955) [7] were used to check the adequacy of the additive-dominance model for different characters in each cross, the significance of any one of these scales is taken to indicate the presence of non-allelic interaction. Various gene effects were estimated using six parameter model as suggested by Hayman (1958) [9].

**3. Results and Discussion**

Predominant role of either additive or non-additive gene actions have been reported in the inheritance of grain yield and its related traits in cowpea by number of workers. The information pertaining to gene action controlling various quantitative characters in any crop helps in selection of appropriate breeding procedure. To partition mean in to

various genetic components a first order biometrical technique *i.e.* generation means analysis was adopted. The results of scaling test and gene action were depicted in table 1 and 2.

**3.1 Days to flowering**

In cross NCK-13-07 x NCK-15-09 non-significant mean square indicated no mean difference was present between generations for this trait. However, scaling tests A, B and C registered significant value in cross NCK-13-07 x GC-3. The result of six parameter model reported additive (d) component and dominance x dominance (l) interaction were found significant, indicated role of this component in governance of this trait in cross NCK-13-07 x GC-3. Similar result was found by S Thakare *et al.* (2016) [16], Gupta *et al.* (2017) [5] and Pallavi *et al.* (2019) [13].

**3.2 Days to maturity**

The scaling tests A, B and C were significant in cross NCK-13-07 x NCK-15-09 while, scaling test A in cross NCK-13-07 x GC-3.  $\chi^2$  value of joint scaling test was also significant in both the cross, which suggested inadequacy of additive and dominance model for this trait. Estimation of genetic parameters based on six parameter model revealed that the significant value of mean (m) and dominance x dominance (l) type of interaction in cross NCK-13-07 x NCK-15-09 as well as cross NCK-13-07 x GC-3. The result indicated that dominance x dominance gene interaction play major role in governance of this trait in both the crosses. Simmilar results also reported by Deshmukh and Gawande (2015) [3], Gupta *et al.* (2017) [5] and Victoria *et al.* (2021) [19].

**3.3 Plant height (cm)**

The significance of A, B and C in cross NCK-13-07 x NCK-15-09 and all scaling test (A, B, C, D) for plant height were found in cross NCK-13-07 x GC-3, indicated the presence of substantial amount of epistasis and inadequacy of additive-dominance model. Additive x additive (i) was only interaction which found significant in cross NCK-13-07 x GC-3 indicated role of this interaction in governance of this trait in this cross. Similar result were also found by Mehta and Zaveri (1997) [11] and Bhor and Dumbre (1998) [1].

**Table 1:** Estimates of scaling test and gene effects for various characters in cowpea of cross NCK-13-07 x NCK-15-09

Characters	Scale				Parameters						$\chi^2$ Joint scaling test	
	A	B	C	D	m	d	h	i	j	l		
Days to flowering	-	-	-	-	-	-	-	-	-	-	-	-
Days to maturity	-6.17**	-3.90**	-7.90**	1.08	75.50**	-0.38	0.08	-2.17	-1.13	12.23**		4.62
Plant height	-25.30**	17.23**	-11.90*	-1.92	71.63**	1.37	-2.77	3.83	-21.27	4.23		0.24
Branches per plant	0.77*	0.47	-1.90**	-1.57**	3.27**	-0.57**	3.78**	3.13**	0.15	-4.37**		0.66
Clusters per plant	-0.37	-0.73	3.73**	2.42**	6.81**	-1.77**	-5.32**	-4.83**	0.18	5.93**		0.36
Grain yield per plant	-17.73**	-19.69**	-32.68**	2.37	23.98**	-6.64**	4.87	-4.74	0.98	42.16**		2.93
Harvest index	-0.04	0.25	-0.28	-0.25	-	-	-	-	-	-		-

**Table 2:** Estimates of scaling test and gene effects for various characters in cowpea of cross NCK-13-07 x GC-3

Characters	Scale				Parameters						$\chi^2$ Joint scaling test	
	A	B	C	D	m	d	h	i	j	l		
Days to flowering	-2.40**	-3.63**	-5.47**	0.28	36.17**	0.98*	-1.43	-0.57	0.62	6.60**		1.85
Days to maturity	7.17**	2.07	3.37	-2.93	78.14**	1.38	3.93	5.87	2.55	-15.10*		12.02*
Plant height	-8.00*	12.20**	28.70**	12.25**	92.37**	2.85	-1.95	-24.50**	-10.1	20.3		1.66
Branches per plant	0.2	-0.53	-1.57**	-0.62*	3.05**	-0.05	1.68**	1.23*	0.37	-0.9		4.18
Clusters per plant	1.00*	-1.57**	-0.13	0.22	4.92**	-0.35	-0.4	-0.43	1.28	1		0.72
Grain yield per plant	9.31**	3.16	10.65*	-0.91	27.74**	-2.63	4.62	1.82	3.07	-14.29		3.34
Harvest index	1.17	-1.93	4.71**	2.74**	38.31**	-1.43*	-3.35	-5.47**	1.55	6.23*		4.04*

### 3.4 Branches per plant

The significance of A, C and D for branches per plant was found in cross NCK-13-07 x NCK-15-09, while C and D in cross NCK-13-07 x GC-3 indicated the presence of substantial amount of epistasis and inadequacy of additive-dominance model. To calculate various non-allelic gene effects, six parameter model was used for estimation of genetic components and reported that all the parameters except additive x dominance (j) were found significant in cross NCK-13-07 x NCK-15-09. While in cross NCK-13-07 x GC-3 only dominance (h) and additive x additive (i) interaction were found significant. This result is in accordance with the finding of Deshmukh and Gawande (2015) [3], Marenavar *et al.* (2015) [10], Singh and Singh (2016) [15] and Thakare *et al.* (2016) [16].

### 3.5 Clusters per plant

The significance of C and D in cross NCK-13-07 x NCK-15-09 and A and B in cross NCK-13-07 x GC-3 indicated the presence of substantial amount of epistasis and inadequacy of additive-dominance model. Genetic parameters *viz.*, additive (d), dominance (h) and additive x additive (i) and dominance x dominance (l) had highly significant values in cross NCK-13-07 x NCK-15-09 indicated role of additive, dominance and two type of epistasis in inheritance of this trait. Similar result were also found by Bhor and Dumbre (1998) [1], Singh *et al.* (2006) [14], Khodambashi *et al.* (2012) [8] and Thakare *et al.* (2016) [16].

### 3.6 Grain yield per plant

The significance of A, B and C for grain yield per plant was found in cross NCK-13-07 x NCK-15-09, while A and C in cross NCK-13-07 x GC-3 indicated the presence of substantial amount of epistasis and inadequacy of additive-dominance model. To calculate various non-allelic gene effects, six parameter model was used for estimation of genetic components and reported that additive (d) and dominance x dominance (l) had highly significant values in cross NCK-13-07 x NCK-15-09 indicated role of this interaction in governance of this trait in this cross. This result is in accordance with the finding of Marenavar *et al.* (2015) [10], Thakare *et al.* (2016) [16], Gupta *et al.* (2017) [5] and Victoria *et al.* (2021) [19].

### 3.7 Harvest index

Non-significance estimates of all the four simple scaling test as well as  $\chi^2$  value showed absence of epistasis for harvest index and additive-dominance model was found adequate in cross NCK-13-07 x NCK-15-09. While, scaling tests C and D were found significant in cross NCK-13-07 x GC-3 indicated the presence of substantial amount of epistasis and inadequacy of additive-dominance model. In six parameter model of cross NCK-13-07 x GC-3 additive (d) parameter and additive x additive (i) and dominance x dominance (l) gene interaction were found significant, indicates predominant role of these parameters in governance of this trait. This result is in accordance with the finding of Singh and Singh (2016) [15] and Thakare *et al.* (2016) [16].

### 4. Conclusions

Simple additive-dominance model was appropriate in cross NCK-13-07 x NCK-15-09 for harvest index. Hence, selection in early generation itself improves mean performance in the

progenies for these traits. Additive gene effects were found significant for branches per plant, clusters per plant and grain yield per plant and additive x additive (i) type epistasis found significant for branches per plant and clusters per plant. Such traits are improved by selection in later generation. Traits like branches per plant and clusters per plant were governed by dominance and days to maturity, branches per plant, clusters per plant and grain yield per plant by dominance x dominance type of gene action. For the exploitation of dominance effect reciprocal recurrent selection for SCA procedure or other methods which take care of dominance gene effects might be adopted.

In case of cross NCK-13-07 x GC-3 additive gene effect observed significant for days to flowering and harvest index indicated simple selection effectively improve these traits in at early stage of breeding program. Additive x additive (i) gene interaction was found significant in this cross for plant height, branches per plant and harvest index. The additive component of variation can be exploited by simple pedigree selection. Dominance x dominance gene interaction was found significant in this cross for days flowering, days to maturity and harvest index. For the exploitation of dominance effect non-conventional breeding procedure might be adopted, but due to strictly self pollination it is hard to exploitation of heterosis so, in that case methods like biparental mating or diallel selective mating design or reciprocal recurrent selection for SCA might be useful.

Overall, involvement of both additive and non-additive gene effects, for most of the characters suggested that it would be desirable to follow cyclic method of breeding involving conventional breeding approach of selection of superior recombinants and their inter-mating for the development of elite homozygous recombinants having high quality and high yielding potentiality. Thus, population improvement approaches involving inter mating of selected plant in advance generation like biparental mating and diallel selective mating design that take care of both additive and non-additive gene actions.

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