

Original Research Article

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Generation Mean Analysis using Six Parameters Genetic Model for Quantitative Traits in Cowpea [(*Vigna unguiculata* (L.) Walp.)]

Pallavi^{1*}, Alankar Singh² and Sumit Chaudhary²

¹Department of Agriculture, Dolphin (PG) Institute of Biomedical & Natural Sciences, Dehradun, India

²College of Forestry, VCSGUUHF, Ranichauri, Uttarakhand, India

*Corresponding author

ABSTRACT

Keywords

Generation mean analysis, Epistasis, Cowpea and Micronutrients

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Generation mean analysis study in cowpea was undertaken to estimate the gene action operating in the inheritance of yield and its components using six basic generations *viz.* P₁, P₂, F₁, F₂, BC₁ and BC₂ of two different crosses namely PGCP-63 X Pant Lobia-1 and Pant Lobia-3 x Pant Lobia-1 were studied. For most of the studied traits, additive, dominant, additive x additive, additive x dominance and dominance x dominance were significant. Additive effect significantly contributed for number of pods per plant and 100 seed weight. Dominance effect was significant for the pod length in both the families. Additive x dominance type of interaction contributed significantly for days to flowering, days to pod maturity and seed yield per hectare. Duplicate type of epistasis was observed for days to flowering, and pod length in family1 and also in family 2. The findings suggested that the recurrent selection could be followed in cowpea improvement.

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is the most important grain legume of subfamily Faoideae (Papilionideae) of family Fabaceae (Leguminosae). Cowpea production has been increasing at an average rate of 5% annually, with 3.5% annual growth in area and 1.5% growth in yields. Cowpea (*Vigna unguiculata* (L.) Walp.) is an herbaceous, warm-season annual plant requiring temperatures of at least 18°C throughout all stages of its development and having an optimal growing temperature of about 28°C (Craufurd *et al.*, 1997).

Generation mean analysis has proved to be an important technique to estimate different genetic parameters. The concept of generation mean analysis was developed by Hayman (1958) for the estimation of genetic components of variation. Analysis of this technique is based on six different generations of a cross, *viz.*, parents (P₁, P₂), their F₁, F₂ and backcrosses (BC₁ and BC₂). This method provides information about the different genetic parameters and epistatic interactions. The precise knowledge of nature and magnitude of gene action for characters related to productivity is helpful in the choice

of effective breeding methods to accelerate the pace of genetic improvement of seed yield and other economically important characters. However, epistasis is important in the inheritance of quantitative traits besides additive and non-additive effects.

Materials and Methods

The experiment comprising six generation of each of two families viz. P₁, P₂, F₁, F₂, BC₁ and BC₂ were sown in family block design with three replications *i.e.* PGCP-63 X Pant Lobia-1 and Pant Lobia-3 X Pant Lobia-1, respectively, at G. B. Pant University of Agriculture & Technology, Pantnagar during 2015/16 cropping season. The plot size consisted of variable number of rows of 4m length each for different generation P₁, P₂ (One row for each parent), whereas F₁ was raised in three row, BC₁ and BC₂ generations in two row each and F₂ was raised in seven rows. Depending on the variability different numbers of plants (P₁, P₂, F₁, BC₁ and BC₂ ten plant selected and F₂ are 50 plant selected) were randomly selected from each plot in each replication. The traits included in this experiment were Days to 1st flowering, Pod length (cm), Days to pod maturity, 100-seed weight (g), and Seed yield/ha (quintals).

Results and Discussion

The result of simple scaling test for days to first flowering, days to pod maturity, and pod length is presented in Table 1. The results showed that in family 1, scale A, B and C were highly significant and the family 2, scale A, B and D were significant for days to first flowering. For pod length with family 1, scale A and C and with family 2, scale A, and B exhibited highly significant scaling test. In family 1 scaling tool A, B and C were significant while with family 2 all the scaling tests were significant for number of seeds per pod. Scaling tool A and D in family 1, and

scale A and C in family 2, were highly significant for days to pod maturity. Results of scaling test for 100-seed weight, showed that in family 1, scale B and C were highly significant, while in family 2, scale B, C and D were significant. Both the families had highly significant estimate of all the scales in seed yield.

The results of scaling test for days to 1st flowering has been provided in Table 2. In family 1, non-significant chi-square suggested adequacy of digenic interaction (5-parameter) model. Highly significant estimates of mean [m], additive x dominance [j], additive x additive [i] and dominance x dominance [l] whereas, significant estimates of dominance [h], effect was observed. The significant effect of dominance [h] effect and highly significant additive x dominance [j] and additive x additive [i] effect indicated preponderance of additive type of gene action in inheritance of days to flowering. Based on scaling test additive-dominance (6-parameter) model for this trait in family 2, highly significant estimates of mean [m], significant estimates of additive [d], dominance [h], additive x dominance [j] and dominance x dominance [l] were observed under digenic interaction (6-parameter) model. The results obtained for this trait are in agreement with Subbiah *et al.*, (2013) and Pal *et al.*, (2007). The results obtained from scaling test for pod length indicated the importance of epistatic gene action for this trait (Table 4). Highly significant estimates of additive [d], dominance [h] additive x dominance [j] and dominance x dominance [l] effect were observed in family 1 under 5-parameter model and opposite sign of [h] and [l] indicated the presence of duplicate epistasis. Non-significant chi-square and highly significant estimates of additive [d], dominance [h], additive x additive [i], and dominance x dominance [l] effect were observed in family 2 under (5-parameter)

model. The opposite signs of [h] and [l] confirmed the predominance of duplicate epistasis in family 1 and 2. The results obtained in this study are in agreement with Umaharan *et al.*, (1997), Romanus *et al.* (2008), Subbiah *et al.*, (2013) who reported the importance of additive and dominance effects in controlling the inheritance of pod length.

The presence of non-allelic interaction was detected by scaling test for number of seeds per pod in all the families. The estimates of gene effects for this trait are given in Table 5. Highly significant estimates of dominance [d] and additive x dominance [j] effects were observed in family 1 under (6-parameter) model. In family 2 significant estimates of dominance [h] while, additive x additive [i] and additive x dominance [j] highly significant effects were found under (6-parameter) model. The results showed additives x dominance effect were important in controlling the expression of number of seeds per pod. The similar results have been reported by Romanus *et al.*, (2008), Rashwan (2010) and Singh (2014).

The estimates of gene effect for days to maturity are given in Table 8. In family 1, non-significant chi-square was indicative of the adequacy for digenic (3-parameter) model. Highly significant mean [m] and dominance [h] with significant additive x additive [i] effect indicated that the dominance [h] effect was more important for this character. In family 2, non-significant chi-square was indicative of the adequacy for digenic (3-parameter) model.

Highly significant mean [m] along with, additive x dominance [j] and dominance x dominance [l] were observed in family 2 for days to maturity. These results are in agreement with the findings of Patil and Bhapkar (1986), and Upreti (2011), who observed the significant contribution of

additive and dominance effects in inheritance of this trait.

The estimates of gene effect for 100-seed weight are presented in Table 10. The results obtained from different scaling tests for 100-seed weight revealed that epistasis effect were present in all the families. In family 1, 6-parameter model was most adequate with significant chi-square and highly significant estimate of additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] effects were observed for 100 seed weight.

In family 2, significant chi-square and highly significant estimates of the genetic parameters confirmed adequacy of (6-parameter) model. Highly significant estimate of additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] effect were observed for 100 seed weight. The results showed additive [d], additive x dominance [j] and dominance x dominance [l] effects controlling the 100-seed weight, and this gene interaction indicated the possibilities of manipulating this trait by selection in subsequent generations. This result is in agreement with Jatasra *et al.*, (1980), Umaharan *et al.*, (1997), Francisco *et al.*, (2003) and Romanus *et al.*, (2008).

The estimates of gene effect for seed yield per hectare are given in Table 12. The presence of epistasis was detected by scaling tests for seed yield per hectare in family 1 and 2. In family 1, the estimate of chi-square was found significant in digenic interaction which indicates adequacy of 6-parameter model was found most adequate. Highly significant mean [m], additive x dominance [j], additive x additive [i] and dominance x dominance [l] effects with significant additive [d] and dominance [h] effect were revealed under (6-parameter) model in family 1.

Table.1 Estimates of different scales for various quantitative traits and their significance

Families	Days to 1st flowering				Pod length (cm)				Number of seeds per pod				Days to pod maturity			
	A	B	C	D	A	B	C	D	A	B	C	D	A	B	C	D
Family 1	3.33**	2.81**	2.27*	1.15	13.98**	1.41	4.81**	0.97	5.41**	11.64**	4.67**	0.78	2.61**	0.16	0.38	2.03**
Family 2	4.60**	2.79**	0.57	2.36*	10.13**	6.45**	4.48	0.79	2.46*	11.39**	5.45**	4.79**	8.54**	0.36	4.13**	0.93

Families	100-Seed weight (g)				Plant height (cm)				Seed yield (q/ha)			
	A	B	C	D	A	B	C	D	A	B	C	D
Family 1	1.13	8.10**	2.02*	1.66	14.25**	27.22**	39.49**	13.24**	14.25**	27.22**	39.49**	13.24**
Family 2	0.58	15.55**	34.11**	2.49*	26.79**	2.26*	4.03	12.95**	26.79**	2.18*	4.03**	12.95**

** Significant at 1% probability level
 * Significant at 5% probability level

Family 1=PGCP-63 X PantLobia-1
 Family 2 =Pant Lobia-3 X Pant Lobia-1

Table.2 The estimates of gene effects for days to 1st flowering

Families	Models	Gene effects							Epistasis	Chi-square
		m	d	h	i	j	l			
Family 1	DI (5 PM)	30.18± 0.18**	---	20.32±0.67**	7.06±0.32**	-3.73±1.54**	9.37±0.22**	---	0.77	
Family 2	DI (6 PM)	46.12±3.48**	2.05± 0.23**	-19.46± 7.87**	-7.00±4.23	-1.50±0.75*	-14.87±3.69*	---	---	

Table3 The estimates of gene effects for pod length (cm)

Families	Models	Gene effects							Epistasis	Chi-square
		M	d	h	i	j	l			
Family 1	DI (5PM)	12.78± 0.13**	0.73± 0.13**	-1.57±0. 48**	---	4.51±0.30**	3.65± 0.50**	D	0.69	
Family 2	DI (5 PM)	63.87± 2.34**	-0.43±0.12**	-46.46±7.16**	-18.90±3.33**	---	20.94±6.10**	D	0.94	

Table.4 The estimates of gene effects for number of seeds per pod

Families	Gene effects								
	Models	M	d	h	i	j	L	Epistasis	Chi-square
Family 1	DI (6 PM)	23.67±1.36**	0.50±0.12*	-21.71±2.95**	-8.86±1.36**	3.66±0.54**	-6.61±1.63**	---	---
Family 2	DI (6 PM)	22.16± 0.42**	0.16±.20*	7.08±2.26*	-6.57±0.61**	-0.36±0.23**	2.29±1.31**	---	---

Table.5 The estimates of gene effects for days to pod maturity

Families	Gene effects								
	Models	m	d	h	i	j	l	Epistasis	Chi-square
Family 1	DI (3PM)	55.46±0. 34**	---	27.99± 0.91**	7.33± 0.34**	---	---	---	1.42
Family 2	DI (3 PM)	65.18±0.52**	---	---	---	-4.73±1.28*	1.84± 0.96**	---	1.62

Table.6 The estimates of gene effects for 100-seed weight (g)

Families	Gene effects								
	Models	m	d	h	I	j	l	Epistasis	Chi-square
Family 1	DI (5 PM)	11.76± 0.11**	-0.65± 0.13**	---	5.75± 0.52**	7.49±0. 95**	2.18±0. 39**	---	2.71
Family 2	DI (5 PM)	15.12± 0.81**	-2.51± 0.14**	---	2.06±0. 16**	11.01± 0.93**	9.90± 0.14**	---	0.08

Table.7 The estimates of gene effects for seed yield per hectare (q/ha)

Families	Gene effects								
	Models	m	d	h	i	j	l	Epistasis	Chi-square
Family 1	DI (5 PM)	35.68± 1.18**	0.56± 0.20*	-7.64± 2.88*	-18.14± 1.17**	17.47±0.63**	- 10.50±1.81**	---	0.09
Family 2	DI (6 PM)	51.20± 2.38**	3.49±0. 15**	- 76.59±7.12**	- 30.79±2.37**	- 14.33±2.37**	56.13±4.89**	D	---

Highly significant estimates of additive [d], dominance [h], additive x dominance [j] additive x additive [i] and dominance x dominance [l] effects were observed in family 2 under (6-parameter) model with significant additive x dominance [j] effects. Opposite sign of [h] and [l] indicated the presence of duplicate epistasis in family 2. The results showed importance of additive [d], dominance [h], additive x additive [i] and dominance x dominance [l] effects important for this trait. Similar result was reported by Chaudhari *et al.*, (2013). The importance of both additive and non-additive gene effects in the inheritance of seed yield per hectare has been reported by Mote *et al.*, (2007), Romanus (2008) and Upreti (2011). Preponderance of dominance effect and significant contribution of epistasis effects for seed yield suggested that recurrent selection may be used to exploit these effects for the improvement of seed yield per hectare.

References

- Chaudhari , S.B. Naik , M.R. Patil, S.S. And Patel, J.D. 2013. Combining Ability for Pod Yield and Seed Protein in Cowpea (*Vigna unguiculata* (L.) Walp.) over Environments. *Trends in Biosciences* pp 6 (4): 395-98.
- Craufurd, P.Q. Aiming, Q. Summerfield, R.J. Ellis, R.H. and. Roberts, E.H. 1997. Development in cowpea (*Vigna unguiculata* (L.)Walp.). Effects of temperature and photoperiod on time to flowering in photoperiod-sensitive genotypes and screening for photothermal responses. *Expl. Agric.* pp.32: 29 40.
- Francisco Cláudio da Conceição Lopes, Regina Lúcia Ferreira Gomes; Francisco Rodrigues Freire Filho. 2003. Genetic control of cowpea seed sizes *Print version* ISSN-0103-9016.
- Hayman, B.I. 1958. The separation of epistatic from additive and dominance variation in generation means. *Heredity.* pp. 12 : 371-390.
- Jatasara. 1980. Combining ability for grain weight in cowpea. *Indian J. Geneti.*, pp. 40: 330-333.
- Mote, M.S. Bendale, V.W, Bhawe, S.G and Swant, S.S. 2007. Biomass partitioning studies in cowpea. *J. Arid legume.* pp. 5 (2) 105-109.
- Pal, A.K., Kumar, S., and Maurya, A.N. 2007. Genetic study for earliness in cowpea (*Vigna unguiculata* (L.) Walp.) *Indian J. Hort.* pp. 64(1): 63-66
- Patil, R.B. and Bhapkar, B.G. 1986. Combining ability in cowpea, *J. maharashtra Agri Uni.* 11: 303-306.
- Rashwan, A. M. A. 2010. Estimation of some Gentic Parameters using Six Populations of two Cowpea Hybrids. *Asian J. of Crop Science*; 2(4), p.261.
- Romanus, K.G. Hussein, S. and Mashela, W.P. 2008. Combining ability analysis and association of yield and yield components among selected cowpea lines. *Euphytica.* pp 162: 205-210.
- Singh, A. 2014. Determining Heterotic Response, Combining Ability and Gene Action for Yield and Yield Contributing Traits in Cowpea (*Vigna unguiculata* (L.) Walp.). Thesis, Ph.D.. G.B. P.U.A and T, Pantnagar.
- Singh, A. Singh, Y.V. Sharma, A. and Singh, S. 2017. Genetic analysis of quantitative traits in cowpea (*Vigna unguiculata* (L.) Walp.).using six parameter genetic model. *Legume Res.*, pp. 45-49.
- Subhiah, A. Prabhu, M. Rajangam, J. and Jagadeesan, R. 2013. Genetics analysis of vegetable cowpea (*Vigna unguiculata* (L.) Walp.).
- Umaharan, P. Ariyanayagam, R.P. and Haque, S.Q. 1997 Identification of resistance to cowpea severe mosaic

- virus (Trinidad isolate) in cowpea (*Vigna unguiculata* (L.) Walp.). *Trop Agric.* 74:324–328.
- Uperati, M. 2011. Estimation of gene effects, heterosis and inbreeding depression for yield contributing traits in different Cowpea crosses. Thesis, M.Sc. G.B. P.U.A and T, Pantnagar.

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