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Using six parameter genetic model genetic analysis of micronutrients in cowpea [*Vigna unguiculata* (L.) Walp.]

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Abstract
Generation Mean Analysis was carried out using six basic generations in 2 different crosses of cowpea for micronutrients i.e. iron and zinc to determine suitable breeding methods. Considering results of gene action, it is apparent that either of the family were found under the control of both fixable (additive, additive x additive) and non-fixable (dominance and epistatic) gene effects coupled with duplicate type of epistasis. Therefore, selection programme aiming to improve such traits in a population should accumulate the fixable additive genes first in early generations. Simultaneously breeding method like modified recurrent selection *i.e.,* alternating pedigree and recurrent selection cycle, diallel selective mating system may be tried for the effective and efficient exploitation non-fixable gene effects.

Keywords: Cowpea, epistasis, micronutients

Introduction
Cowpea is an important legume of the semi-arid tropics. It contains carbohydrate (50-67%), fats (1.9%), fibre (6.35%) and small percentage of the B-vitamins such as folic acid, thiamine, riboflavin and niacin as well as some micronutrients such as iron and zinc. The crop provides a cheap source of protein to humans and nutritious fodder (Singh and Fery, 1997) [8]. In current perspective of intensive and multiple cropping system inclusion of earliness as one component is imperative. The exact genetics of earliness has not been fully demonstrated. In this backdrop, an attempt was made to decipher the genetics and inheritance of earliness and other economic traits in cowpea. Cowpeas are sources of many valuable genes including those for adaptation (Singh, 1983) [7]. It is, therefore necessary to identify promising lines, land races and involve them in crosses with appropriate mating design. Early generation testing and selection have gained momentum in selfpollinated crops as additive genetic variance is more important. Yield augmentation is the prime objective of any breeding programme to cater to the demand for food for exploding population during short period. To realize this clear-cut knowledge about type of gene effect, its magnitude and composition of genetic variance i.e., additive, dominance and epistasis in selection of parent and designing an effective and sound breeding programme. The concept of generation mean analysis was developed by Hayman (1958) [2] for the estimation of genetic components of variation. One of the approaches for GMA involves six generations of a cross, viz., parents (P1, P2), their F1, F2 and backcrosses (BC1 and BC2).

Materials and Methods
Six generations (P1, P2, F1, F2, BC1 and BC2) of three crosses of cowpea, PGCP-63 x Pant Lobia-1, Pant Lobia-3 x Pant Lobia-1 3 were evaluated in a complete randomized block design (RBD) with three replications at G. B. Pant University of Agriculture & Technology, Pantnagar (Uttarakhand), 2016. Standard agronomic practices were followed to establish a good crop stand. A variable numbers of plants (10 for P1, P2, F1, BC1 and BC2 and 50 for F2) were randomly selected from each plot in all replications for recording the observations on different traits. The traits included in this experiment were iron and zinc content in cowpea. The mean data for different characters under study were analyzed as per Compact Family Block Design. Data were subjected to individual scaling test as given by Mather (1949) [4] and Hayman and Mather (1955) [3] to detect the presence or absence of epistasis.

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Results and Discussion

For iron content both the families showed significant scaling test for one or more parameters shown in Table 1. Results of scaling test for zinc content are presented in Table 1. In family 1, scale B, C and D had significant estimates while in family 2, all the scales were significant.

For iron content, estimates of gene effect along with their standard errors are given in Table 2. The results obtained from A, B, C and D scaling test for this trait revealed presence of duplicate epistatic effect were presented in both the families. Results of gene effect indicated that in family 1 highly significant estimates of mean [m], and dominance x dominance [l] effects were observed under (5-parameter) model with significant additive [d], dominance [h] and additive x additive [i] effect. In family 2, the estimate of chi-square was found non-significant in digenic interaction indicating adequacy of 5-parameter model. Highly significant mean [m], additive [d], dominance [h] additive x additive [i] and dominance x dominance [l] effects were revealed. The results showed 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) [1].

For zinc content, estimates of gene effect along with their standard errors are given in Table 3. In family 1, 5-parameter model was most adequate with its non-significant chi-square and highly significant estimate of mean [m], additive x additive [i] and dominance x dominance [l] effects with significant additive [d] and dominance [h]. Opposite sign of [h] and [l] indicated the presence of duplicate epistasis in family 1. The highly significant estimates of mean [m], dominance [h], additive x additive [i] and dominance x dominance [l] effects were found in family 2 whereas, with significant additive x dominance [j] under (6-parameter) model. The results showed additive x additive [i] and dominance x dominance [l] effects were important for this trait. Similar result was reported by Mote et al., (2007) [5], Romanus (2008) and Chaudhari et al., (2013) [1].

In recent years though there has been an increase in the area and production of cowpea, the productivity in India is quite low in comparison to some of the developed countries. The amount of success of any breeding programme for improving yield depends on the genetic information about yield and its contributing characters. Hence, the present investigation was carried out to gather information about fixable and non-fixable effects, nature and magnitude of different components of epistasis which may help in designing an appropriate breeding programme for genetic improvement of quantitative characters in cowpea (*Vignav unguiculata* (L.) Walp.).

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

Families	Iron Content				Zinc Content			
	A	B	C	D	A	B	C	D
Family 1	3.41**	2.77**	0.92	1.35**	0.46	0.67*	6.68**	6.27**
Family 2	2.56**	1.56*	1.34**	2.85**	1.26*	3.60**	2.62**	10.98**

** Significant at 1% probability level   Family 1=PGCP-63 X Pant Lobia-1
* Significant at 5% probability level   Family 2 =Pant Lobia-3 X Pant Lobia-1

Table 2: The estimates of gene effects for iron content (mg/kg)

Families	Gene effects							
	Models	M	d	h	i	j	l	Epistasis	Chi-square
Family 1	DI (4 PM)	53.67± 0.17**	4.16± 1.32*	-71.64± 2.94*	23.79± 4.17*	---	39.32±4.61**	D	2.54
Family 2	DI (5 PM)	49.34± 0.38**	5.41±0 2.45**	59.22±2.12**	21.79±1.97**	---	-35.97±4.89**	D	6.12

Table 3: The estimates of gene effects for zinc content (mg/kg)

Families	Gene effects							
	Models	m	d	h	i	j	l	Epistasis	Chi-square
Family 1	DI (5 PM)	11.38± .018**	1.94± 0.22*	57.42± 1.38*	25.11± 0.13**	---	-28.39±2.22**	D	5.58
Family 2	DI (6 PM)	7.16± 0.28**	0.44±1.17**	81.24±3.92**	31.91±3.27**	1.48±0.17*	44.47±6.32**	---	---

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