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Scaling and Joint Scaling tests for Quantitative Characters in Greengram (*Vigna radiata* (L.) Wilczek.)

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Abstract
In the present study, generation mean analysis and chi-square test were undertaken to estimate the nature and magnitude of gene action for yield and its component traits in four crosses of Greengram. Scaling and joint scaling test revealed the presence of one or more kinds of epistatic effects for almost all the traits except for pod length in MGG 347 X KM 11-564, protein content in WGG 42 X RM 12-13, days to maturity in LGG 543 X KM 11-564 and number of primary branches per plant in MGG 347 X RM 12-13. For remaining traits, significance of either all or the three or any of the individual scaling tests A, B or C and significant Chi-square values confirming the involvement of digenic interaction in inheritance. The non-additive gene effects were more pronounced than additive ones for most of the traits in this study. The selection for the traits controlled by predominant additive component is recommended in early segregating generation while in majority traits selection should be deferred to later generations.

Keywords: Epistasis, gene effects, Joint scaling test, Scaling test, Greengram

Introduction
Greengram like other pulse crops is being grown for hundreds of years under marginal conditions of moisture stress and low soil fertility. Under these conditions of poor crop management, natural selection has had a much greater role in determining the plant type and other characteristics of this crop than human selection. The genes for agronomic characteristics responsible for high yield have been eroded from Greengram like other marginal crops, which had relatively little value under the competitive and stress conditions of a wild habitat or a primitive agriculture.
Seed yield is an important trait as it measures the economic productivity in Greengram, but its inheritance is extremely complex. The classical breeding systems that make use of additive genetic variance will be effective breeding procedures for improving the Greengram seed yield, but very little basic information is available on all types of gene effects/inheritance controlling the seed yield and its components in Greengram (Khattak *et al*., 2004) [7]. To exploit the existing genetic variability in Greengram breeding material for seed yield as efficiently as possible, the breeder would need the basic information regarding the inheritance of grain yield and its closely related components for devising an efficient selection program.
In the present studies, the detection of epistasis, and estimates of additive and dominance components of variation for secondary yield components in four sets of Greengram crosses were carried out by using generation mean analysis.

Materials and methods
The experiment involved the six basic generations (the P_1 and P_2 parent cultivars, the F_1 and F_2 first and second filial generations, and the BC_1 and BC_2 first and second back crosses) of four combinations of the parental cultivars, these combinations being MGG- 347 X KM 11 -564, WGG -42 X RM 12-13, LGG -543 X KM 11 -564 and MGG-347 X RM 12-13. All the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were raised in randomized block design with three replications in College Farm, College of Agriculture, Rajendranagar, Hyderabad during *Kharif* season, 2016.
We used the parents of the respective crosses as the male parent and the F_1 generation as the female parent and effected back crosses to produce the BC_1 (F_1 back crossed to P_1) and BC_2 (F_1 back crossed to P_2) generations and the F_1 hybrids were selfed to obtain F_2 seeds. All these generations were produced during two cropping seasons and, as such, all the six generations had to be grown together during the same cropping season. The row-length was always four meters but the number of rows varied as follows: three rows, for the non-segregating P_1, P_2 and

F_1; 40 rows for the F_2; and 20 rows for the BC_1 and BC_2 generations. Since, the non-segregating generations represent the homogeneous population while the segregating generations represent the heterogeneous population the sample size (i.e., number of plants analyzed) varied as follows: 40 plants for the P_1, P_2 and F_1 generations, 300 plants for the F_2 generations and 100 plants in the BC_1 and BC_2 generations. The recommended agronomic practices were followed to raise healthy crop. The traits assessed were days to 50% flowering, days to maturity, number of primary branches, plant height (cm), number of clusters/plant, number of pods/plant, pod length (cm), number of seeds/pod, weight of 100 seed weight (g), seed yield/plant (g) protein content (%) and harvest index (%).

Scaling test: To predict genetically control of traits in the beginning only additive [d] and dominance [h] effects are assumed to be present. The means of the different generations were utilized for obtaining the various genetic effects. The data were first tested to fit in simple additive-dominance model and presence of epistasis. The adequacy of simple additive-dominance model was tested by using A, B, C and D scales their variances, standard errors and 't' test were calculated by using the following formulae.

Where, P_1, P_2, F_1, F_2, BC_1 and BC_2 are the means of different generations over replications. The variances (VA, VB, VC and VD) of the scales A, B, C and D were obtained as the square root of VA, VB, VC and VD, respectively. The significance of the deviations of the scales from zero was tested using their standard errors. The significance of the scales A, B, C and D were determined by comparing the observed and expected 't' values at 5 and 1% level of significance. When any one of the four scales was found to deviate significantly from zero the additive – dominance model was considered inadequate. In such case, the joint scale test was employed (Cavalli, 1952) [2].

Joint scaling test: Three parameters *viz*., m, d and h defining the additive-dominance model was estimated using weighted least square (Mather and Jinks, 1982) [8]. This model provides χ^2 test for the goodness of fit of the model (Kearsey and Pooni, 1996) [5]. From these estimated parameters, the expected generation means were calculated as follows:

P1 = m - d F2 = m + (1/2)h
P2 = m + [d] B1 = m - (1/2)d + (1/2)h
F1 = m + [h] B2= m + (1/2)d + (1/2)h

All the yield and yield contributing traits were analyzed statistically and tested for significance. The significance of the joint scaling test was determined by the using χ^2 test and compared observed and expected 't' values at 5 and 1% level of significance. In instances where the A, B, C and D values and χ^2 test significantly deviated from zero in the joint scaling test of simple additive-dominance model, digenic interaction was assumed. Statistical analysis for scaling test, joint scaling test and χ^2test were carried out by using advanced biometrical Indostat statistical package, Hyderabad, India.

Results and discussion

The scaling tests were applied to the data to detect the presence or absence of non-allelic interactions. The estimates of genetic parameters m, [d] and [h] were obtained for all the 12 traits in four crosses were presented in Table 2.The results of the scaling tests in four hybrids showed significant values of A, B, C and D scales for all the traits under study were presented in Table 1. Majority of the hybrids coupled with traits showed deviation from zero indicated that simple additive-dominance model was inadequate. The joint scaling test were analyzed and found that mean, additive [d] and dominance [h] gene effects coupled with χ^2 test was highly significant for all the traits, and values deviated from zero. For traits like pod length in cross 1 (MGG 347 X KM 11-564), protein content in cross 2 (WGG 42 X RM 12-13), days to maturity in cross 3 (LGG 543 X KM 11-564) and number of primary branches per plant in cross 4 (MGG 347 X RM 12-13) additive-dominance model were adequate, so data for these traits was not subjected to further analysis.

(i) Cross 1(MGG 347 X KM 11-564)

In this cross, dominance (*h*) and dominance × dominance (*l*) gene effects displayed opposite signs for the traits, namely, days to 50% flowering, days to maturity, number of primary branches per plant, plant height, number of clusters per plant, number of seeds per pod, 100-seed weight and protein content indicating duplicate epistasis. The values of dominance (*h*) and dominance × dominance (*l*) interaction were in the same direction for traits like pods per plant, seed yield per plant and harvest index and the interaction followed the complementary mode of nonallelic gene interaction. Presence of complementary gene action for above mentioned traits indicates that parents selected for crossing are diverse. Therefore, it is possible to realize enhanced genetic gain in breeding programme. In the present investigation, genotypes MGG 347 and KM 11-564 could be identified as the best parents since their respective crosses showed complementary gene action for number of pods per plant, seed yield per plant and harvest index. These findings are in accordance with the results published by Ajay *et al.* 2012 [1].

The classification of gene interaction depends on the magnitude and sign of the estimates of dominance (*h*) and dominance × dominance (*l*) effects, when there are many pairs of interacting genes. The sign associated with the estimates of additive effects (*d*) and dominance effects (*h*) indicates the parent who concentrates the highest number of genes or positive alleles for increasing the traits. Therefore, the significant but positive *d* for harvest index indicates that additive effect of the gene is predominant and selection for this trait can be done by simple selection. The significant negative value of *d* for traits number of clusters per plant, number of seeds per pod, 100 seed weight indicated that the inheritance of these traits is not controlled by additive gene action. Similarly, the significant and positive value of *h* for plant height and 100-seed weight showed that the dominant effect of gene is predominant. Presence of *h* indicates that selection should be delayed until heterozygosity is reduced in population. The earlier findings reported that traits with high magnitude of dominance than additive can be improved through conventional breeding approach such as pedigree or bulk or single seed descent method if selection is delayed until later generation when the dominance effect would have diminished (Khattak *et al.* 2004 [7] and Punia *et al.* 2011 [11]).

On the contrary, the significant but negative values of *h*, *i*, *j* and *l* for some traits showed that negative alleles were also dispersed in the parents involved in the cross. Negative sign of *h* in cross for any trait indicates that dominance effects were contributed by the parents having alleles responsible for low value for the traits, for example, in plant heights of MGG 347 and KM 11-564 in respective crosses. Thus, selection for these traits should also be delayed to later generation when desirable segregants become available. The significant but similar sign of *d* and *h* for primary branches indicated

predominant role of additive and dominant effects for the inheritance of these traits. The type of epistatic interaction additive × additive (*i*) was significant for plant height. Additive × dominance type of epistasis (*j*) was nonsignificant with negative sign for most of the traits in this cross, which indicate that this type of epistasis is not contributing in inheritance of any trait in the crosses. The *d* effect for seed yield per plant, pods per plant and protein content was nonsignificant indicating involvement of several genes with small effects (Ajay *et al.* 2012) [1].

(ii) Cross 2 (WGG 42 X RM 12-13)

In this cross dominance (*h*) and dominance × dominance (*l*) gene effects displayed opposite signs for all the traits except number of clusters per plant and number of pods per plant witnessed duplicate epistasis. The opposite signs of *h* and *l* counterbalance each other, thus leading to reduced heterosis (Suresh *et al.* 2010 [14] and Ajay *et al.* 2012 [1]). The positive sign of additive effects (*d*) for all the traits except 100-seed weight indicates that the additive effect of gene is predominant for all traits, and 100-seed weight exhibited negative value of *d* suggest that these traits are not controlled by additive gene action. In this case as magnitude of *d* was less, we could move for heterosis breeding. The estimates of *h*, *i* and *l* were found significant with negative signs suggesting that selection for the traits, namely, plant height, pods per plant and seed per pod should be delayed to later generation, so that negative alleles are removed. Hence, improvement of these traits could be achieved through recurrent selection procedure. The significant but similar signs of *d* and *h* for primary branches indicated predominant role of additive and dominant effects for the inheritance of this trait. Both additive and nonadditive gene effects were also reported in earlier studies. Nonsignificant *d* effects for harvest index and 100-seed weight indicates that these traits are under the control of several genes (Ajay *et al.* 2012 [1] and Jog *et al.* 2016 [4]).

(iii) Cross 3 (LGG 543 X KM 11-564)

Opposite sign for dominance (*h*) and dominance × dominance (*l*) type of interaction was recorded for all the traits except number of clusters per plant, harvest index and seed yield per plant. It indicates that all the traits depicted duplicate type of epistasis and number of clusters per plant, harvest index and seed yield per plant displayed complementary type of epistatic effect. The complementary type suggested the possibility of considerable amount of heterosis for these three traits in this particular cross (Punia *et al.* 2011 [10]). Duplicate type of nonallelic gene interaction for most of studied traits with few exceptions further confirms the prevalence of dominance effects (Singh and Sharma 2001 [13]). Presence of duplicate epistasis indicates that variability in segregating generations may be reduced which hinder the selection process, hence it is difficult to utilize them in breeding programme (Sameer *et al.* 2009) [12]. The positive sign of additive effect (*d*) for number of clusters per plant, harvest index and seed yield per plant indicated that these traits are governed by additive effect of genes. Significant but negative value of *d* for most of the traits indicted that the inheritance of these traits in this particular cross combination is not controlled by additive genes. The significant but similar sign of *d* and *h* for primary branches and seed yield per plant indicated predominant role of additive and dominant effect for the inheritance of these traits. In this cross protein content and 100-seed weight lacked significant *d* effects indicated that these traits are under the control of complex gene pathway in this cross involving several minor genes with small effect and different expressions (Payasi *et al.* 2010 [10] and Pathak *et al.* 2014 [9]). The estimates of *h* and *l* were found significant with positive sign for some traits indicated predominant role of dominant component in the inheritance of these traits. Significant but positive sign of *i* (additive × additive) for any of the traits portrayed that the inheritance of these traits in a particular cross is controlled by additive gene action. Overall additive gene effects were exhibited by three characters out of twelve characters studied, however, the relative magnitude of these effects to the mean effects (*m*) suggests that they are of minor importance in the explanation of traits variation. The positive sign of additive effects (*d*) for seed yield per plant indicated predominant role of additive gene action for the inheritance of this trait. Hence this cross is desirable for future breeding programmes.

(iv) Cross4 (MGG 347 X RM 12-13)

This cross showed opposite sign for dominance (*h*) and dominance × dominance (*l*) type of interaction for all the traits except number of pods per plant and pod length. It indicates that all the traits depicted duplicate type of epistasis and number of pods per plant and pod length displayed complementary type of epistatic effect. The complementary type suggested the possibility of considerable amount of heterosis for these three traits in this particular cross (Punia *et al.* 2011 [11]). Duplicate type of nonallelic gene interaction for most of studied traits with few exceptions further confirms the prevalence of dominance effects (Singh and Sharma 2001 [13]). Presence of duplicate epistasis indicates that variability in segregating generations may be reduced which hinder the selection process, hence it is difficult to utilize them in breeding programme (Sameer *et al.* 2009 [12] and Jog *et al.* 2016 [4]).

For seed yield per plant, number of seeds per pod both additive (d) and dominant (h) gene action are playing a role in the inheritance of this trait, but predominantly dominant gene action is contributing higher in magnitude than additive effects. Dominant gene action is more important than additive in case of number of clusters per plant, number of pods per plant and harvest index indicating non additive gene effects.

Among the interactions additive x additive (i) and dominant x dominant (l) were generally higher in magnitude and exceeds the additive x dominant (j) effect for all the traits under study. Negative sign of dominant effect (h) for days to flowering and days to maturity shows reducing alleles involving dominant phenotype (Suresh *et al.* 2010 [14] and Jog *et al.* 2016 [4]).

Table 1: Scaling tests and joint scaling test (χ^2) for 12 yield contributing characters in four selected crosses of Greengram.

Character	Cross	Scales				χ^2
		A	B	C	D	
Days to 50 % flowering	I	-0.71±0.10	-2.26±0.17**	1.62±0.15**	0.93±0.05	30.35**
	II	1.06±0.14	-1.16±0.21**	3.75±0.32**	0.6±0.01	31.69**
	III	-1.83±0.20**	-1.01±0.03	2.64±0.27**	0.12±0.01	23.26*
	IV	-0.25±0.11	1.17±0.12**	0.48±0.09	1.19±0.12**	60.89**
Days to maturity	I	-0.58±0.02	-0.69±0.11	1.98±0.17**	0.07±0.01	186.94**
	II	1.55±0.10**	-0.73±0.09	1.01±0.12	-1.98±0.15**	52.55**
	III	-0.33±0.08	-0.25±0.01	1.02±0.02	0.47±0.03	-
	IV	-1.02±0.12	-1.93±0.15**	-0.28±0.11	1.92±0.19**	77.47**
Number of primary branches	I	-0.38±0.09	-0.19±0.01	2.54±0.11**	0.96±0.08**	35.66**
	II	-0.18±0.03	-0.1±0.0	2.02±0.10**	0.31±0.05	63.54**
	III	-0.10±0.01	-0.19±0.05	2.78±0.21**	0.67±0.01	34.52*
	IV	-1.37±0.12	-0.71±0.08	0.38±0.11	0.45±0.02	-
Plant height (cm)	I	4.25±0.13**	-3.37±0.21**	10.04±0.17**	-7.35±0.23**	90.33**
	II	7.51±0.18**	-7.79±0.33**	6.43±0.32**	-13.4±0.34**	38.75**
	III	-8.99±0.54**	-3.56±0.12**	8.86±0.45**	-11.37±0.50**	194.7**
	IV	-14.92±1.01**	-4.86±0.09**	10.55±0.68**	-9.74±0.18**	55.44**
Number of clusters/ plant	I	-2.54±0.10**	-1.99±0.04**	11.76±0.17**	2.23±0.07**	60.82**
	II	-1.92±0.07**	-2.26±0.12**	5.09±0.10**	-0.54±0.01	41.76**
	III	-1.91±0.05**	-0.96±0.01**	5.72±0.11**	-0.93±0.08*	61.74**
	IV	-2.64±0.03**	-1.24±0.02**	8.21±0.20**	0.73±0.04	55.44**
Number of pods/ plant	I	-5.17±0.01	-1.96±0.02	30.17±1.51**	-10.12±0.50**	412.42**
	II	-16.8±0.18**	-1.85±0.01	17.21±0.48**	3.44±0.11	71.89**
	III	-19.38±0.12**	12.18±0.27**	42.36±1.25**	31.122±1.01**	533.15**
	IV	5.33±0.09	3.39±0.11	30.28±0.91**	-13.7±0.95	116.13**
Pod length (cm)	I	-0.55±0.19	-0.43±0.01	1.03±0.11	-0.25±0.02	-
	II	-0.27±0.05	-0.45±0.02*	4.86±0.09**	-0.26±0.01	59.65**
	III	-0.1±0.01	-2.2±0.33**	6.14±0.14**	1.06±0.11**	46.12**
	IV	-0.04±0.0	-0.03±0.01	5.69±0.12**	-0.19±0.05	46.13**
Number of seeds/pod	I	0.42±0.01	0.76±0.05**	2.88±0.03**	0.53±0.05	33.51**
	II	0.06±0.01	0.04±0.01	0.86±0.02	0.12±0.03	45.38**
	III	0.36±0.02	0.01±0.0	1.59±0.19**	0.56±0.09	-
	IV	0.22±0.02	0.33±0.01	2.68±0.12**	0.35±0.01	70.44**
100 Seed weight (g)	I	-0.36±0.02**	-0.19±0.02	0.88±0.02**	0.15±0.01*	32.74**
	II	-0.01±0.0	-0.25±0.10*	0.56±0.01**	0.17±0.01*	34.24**
	III	-0.21±0.01	-0.14±0.01	0.08±0.01	-0.12±0.01*	26.18**
	IV	-0.25±0.01*	-0.07±0.01	0.76±0.02**	0.12±0.01*	24.31**
Protein content (%)	I	-0.19±0.02	1.25±0.09**	2.24±0.01**	-1.16±0.02**	26.38**
	II	0.20±0.11	0.41±0.12	1.06±0.03	-0.56±0.05	-
	III	-0.58±0.01*	-0.02±0.01	1.97±0.05**	-2.17±0.12**	120.35**
	IV	-0.66±0.03*	-0.23±0.01	2.26±0.01**	-1.34±0.11**	32.57**
Harvest index (%)	I	-7.77±0.07**	-3.69±0.11*	6.03±0.17**	2.46±0.01	52.61**
	II	-2.35±0.02	-1.82±0.01	2.58±0.01	-2.64±0.02	25.78*
	III	-8.64±0.12**	-7.35±0.13**	5.16±0.15**	-5.74±0.11**	65.82**
	IV	1.09±0.03	-4.12±0.05*	4.13±0.12*	-4.9±0.12	52.38**
Seed yield/plant (g)	I	-1.06±0.01**	-1.28±0.08**	10.23±1.01**	-0.98±0.02**	70.01**
	II	-1.16±0.10**	0.59±0.05	7.78±0.54**	-2.36±0.32**	43.18**
	III	-0.96±0.05**	-0.13±0.01	11.02±1.12**	-0.56±0.05*	42.58**
	IV	-0.64±0.02	0.67±0.02*	12.18±1.03**	-0.36±0.01	43.18**

*Significance @ P = 0.05, ** Significance @ P = 0.01, CI = MGG 347 X KM 11-564, CII = WGG 42 X RM 11-13, CIII = LGG 543 X KM 11-564, CIV = MGG 347 X RM 11-13

Table 2: Estimates of gene effects for twelve component characters in selected four crosses of Greengram

Characters	Cross	Gene effects							Type of Epistasis
		Main effects			Interaction effects				
		(m)	(d)	(h)	(i)	(j)	(l)		
Days to 50 % flowering	CI	38.15±0.12**	-0.62± 0.21*	21.23±1.75**	-	-1.78±0.62**	-18.26±1.21**		Duplicate
	CII	35.56±0.62**	0.69±0.28*	-	7.62±1.65**	-	-		-
	CIII	36.12±0.15**	-6.50±0.21**	-10.88±0.67**	-	-0.42±0.11*	4.36±0.60**		Duplicate
	CIV	36.75±0.11**	-7.38±0.30**	-12.52±0.72**	-2.20±0.20**	-	1.40±0.45*		Duplicate
Days to Maturity	CI	76.12±0.21**	0.95±0.11**	16.89±0.45**	-	-	-21.39±0.51**		Duplicate
	CII	69.35±0.22**	5.64±0.42**	-11.43±1.21**	3.56±0.26**	1.14±0.18**	-8.38±1.00**		Complimentary
	CIII	71.01±0.24**	-	-12.11±1.20**	-	-	7.48±1.00**		Duplicate
	CIV	78.10±1.01**	-5.01±0.60**	-12.88±0.92**	-	-	4.85±0.45**		Duplicate
No. of primary branches per plant	CI	2.91±0.11**	6.68±0.13**	2.84±0.21**	1.95±0.18**	-	1.38±0.15**		Complimentary
	CII	2.02±0.10**	0.17±0.22*	8.12±*0.95*	0.95±0.20*	-	-6.21±0.72**		Duplicate
	CIII	2.58±0.11**	0.65±0.24*	-15.76±0.45**	-1.50±0.11**	-	9.33±0.35**		Duplicate
	CIV	-	-	-	-	-	-		-
Plant Height (cm)	CI	44.37±0.85**	-1.08±0.69**	54.85±1.65**	12.02±1.50**		-20.58±1.45**		Duplicate
	CII	41.20±0.12**	3.21±0.10**	-9.89±0.21**	-1.25±0.09**	0.58±0.05*	-6.72±0.20**		Complimentary
	CIII	39.81±1.28**	-1.49±0.56**	-13.75±0.89**	12.74±0.45**	0.78±0.36*	20.81±0.72**		Duplicate
	CIV	43.55±3.50**	-7.52±1.00**	-16.48±2.21**	21.40±0.95**	-	28.55±2.20**		Duplicate
No. of clusters per plant	CI	10.28±0.10**	-1.69±0.13**	-20.42±0.62**	-4.41±0.11**	-	-8.95±0.42**		Complimentary
	CII	9.40±0.11**	-	4.75±0.35**	1.82±0.06**	-	3.65±0.10**		Complimentary
	CIII	8.51±0.11**	-	3.36±0.40**	-	-	7.28±0.21**		Duplicate
	CIV	8.95±0.09**	-	5.35±0.14**	-	-	5.42±0.12**		Complimentary
No. of pods per plant	CI	31.78±0.34**	-	90.22±0.71**	31.01±0.34**	-8.85±0.25**	82.20±0.50**		Complimentary
	CII	28.40±3.42**	-	26.22±3.10**	-6.85±0.01**	-	-29.21±1.20**		Duplicate
	CIII	33.21±0.15**	-2.24±0.10**	-54.93±0.25**	-66.44±0.19**	-0.78 ±0.12	67.64±1.01**		Duplicate
	CIV	28.75±1.24**	-3.64±0.15**	45.10±1.75**	57.91±0.20**	-	91.12±1.00**		Complimentary
Pod length (cm)	CI	-	-	-	-	-	-	-	
	CII	6.55±0.10**	-0.62±0.30**	-2.99±0.85**	-	0.18±0.10*	1.30±0.70**	Duplicate	
	CIII	7.11±0.02**	-	1.72±0.18**	-	-	-	-	
	CIV	7.87±0.09**	-0.82±0.12*	0.81±0.01**	-	-	1.35±0.02*	Complimentary	
No. of seeds per pod	CI	11.57±0.21**	16.34±0.98**	8.73±0.25**	7.24±0.75**	-0.66±0.18**	-1.87±0.22**	Duplicate	
	CII	10.55±0.11**	-	-1.01±0.61*	-	-	-0.42±0.42*	Complimentary	
	CIII	-	-	-	-	-	-	-	
	CIV	10.82±0.95**	3.21±0.20**	4.85±0.71**	0.78±0.10*	-	-0.48±0.32*	Duplicate	
100 seed weight	CI	3.72±0.02**	-0.82±0.11**	4.38±0.10**	3.71±0.05*	-	-6.21±0.13**	Duplicate	
	CII	3.45±0.10**	-	-0.35±0.05*	-0.30±0.03*	0.21±0.01*	0.60±0.33*	Duplicate	
	CIII	3.45±0.05**	-0.31±0.22*	2.37±0.40**	-0.83±0.10*	-0.25±0.09*	1.19±0.26*	Complimentary	
	CIV	3.65±0.21**	-0.20±0.15*	-2.15±0.40**	-0.31±0.03*	-	1.55±0.20*	Duplicate	
Protein content (%)	CI	22.67±0.10**	0.78±0.10*	3.35±0.25**	2.32±0.18**	-0.72±0.11**	-3.38±0.15**	Duplicate	
	CII	-	-	-	-	-	-	-	
	CIII	22.26±0.20**	-0.92±0.11*	1.25±0.05*	1.32±0.10*	-	-3.75±0.70**	Duplicate	
	CIV	22.63±0.12**	0.48±0.05*	4.12±0.12**	2.89±0.08**	2.68±0.01**	2.38±0.10**	Complimentary	
Harvest index (%)	CI	31.57±0.30**	7.84±0.65**	-3.72±1.20**	-2.00±0.60**	-	-5.11±0.75**	Complimentary	
	CII	28.78±0.52**	-0.31±0.01*	2.85±0.15**	-	-	-	-	
	CIII	27.30±0.25**	-1.74 ±0.12	1.18±0.23**	0.95±0.01**	0.54±0.05**	0.98±0.18**	Complimentary	
	CIV	29.55±2.50**	2.60±0.74**	14.54±4.20**	7.20±1.01**	-	18.95±2.12**	Duplicate	
Seed yield per plant (g)	CI	11.28±0.34**	-	-4.95±0.75**	-1.52±0.35**	0.95±0.26*	-5.67±1.01**	Complimentary	
	CII	8.45±1.21**	-1.05±0.11*	-26.91±4.45**	-14.50±1.00**	-	18.76±3.20**	Duplicate	
	CIII	10.33±1.35**	1.68±0.42*	8.85±2.21**	12.12±0.15**	-0.41±0.19*	10.03±1.12**	Complimentary	
	CIV	9.53±1.02**	0.69±0.44*	-8.55±0.75**	1.77±0.90*	-	15.75±2.00**	Duplicate	

* Significance @ P = 0.05, ** Significance @ P = 0.01, CI = MGG 347 X KM 11-564, CII = WGG 42 X RM 11-13, CIII = LGG 543 X KM 11-564, CIV = MGG 347 X RM 11-13

Conclusion

All the traits examined in the present study have shown complex genetic behaviour. The simple selection procedure in the early segregating generation may not contribute significantly for the improvement of these traits. The complex genetic behavior particularly additive and dominance components could be successfully exploited in later generation. It is therefore, suggested that the selection for the improvement of all these traits particularly seed yield should be delayed to the latter generation of segregation population in mungbean. The bulk method of selection is recommended in which selection is performed after attaining the homozygosity for maximum heterozygous loci. The biparental hybridization between recombinants in early segregating generation (F_2) would produce better genetic combinations through which the accumulations of desirable genes could be achieved for high yield potential in an individual line.

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