



Gene Action Studies for Yield and its Related Traits by using Generation Mean Analysis in Mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Background: Mungbean is one of the most important legume crop with high nutritional value and is consumed in various forms in different parts of India. In order to meet its growing demand, there is a need to increase the yield through adoption of breeding approaches like heterosis breeding and breeding for high yielding varieties. This demands a critical study of the gene action involved in regulation of yield and yield attributing traits which can be achieved through generation mean analysis.

Methods: In the present study, generation mean analysis was undertaken using five parameter model to estimate the nature and magnitude of gene action of yield and its component traits in six crosses of greengram.

Result: Magnitude of dominance gene effect was reported to be higher than additive gene effect in most of the crosses. Either one or both the interaction components were found significant for all the traits besides number of branches per plant and hundred seed weight. It was evident from the study that the yield components could be improved by exploiting both additive and non-additive gene effects. The transgressive segregants thus produced will prompt the development of desirable high yielding genotypes.

Key words: Gene action, Generation mean analysis, Greengram, Scaling test, Transgressive segregants, Yield attributing traits.

INTRODUCTION

Greengram commonly known as mungbean [*Vigna radiata* (L.) Wilczek] is an important pulse crop of India after chickpea and pigeonpea. India is considered as the primary center of origin of mungbean. During 2017-18, in India mungbean was sown in an area of approximately 4.26 Mha (Kharif and rabi) with a production of 2.01 Mt and productivity of 472 kg/ha. The major contributing states were Rajasthan followed by Madhya Pradesh, Maharashtra, Karnataka, Bihar, Odisha and Tamil Nadu. It is mainly utilized for making dal, soup, sweet, curries and snacks and its seeds sprout are nowadays very popular in vegetarian diet. Despite considerable improvement in the productivity of mungbean, there is still a lot of scope to increase the productivity of this crop. The number of genes controlling the trait, type of gene action and genotype x environment interaction are three major factors that must be considered by plant breeders for improvement of any quantitative trait including seed yield. The choice of a suitable breeding programme depends upon the nature of gene action involved in yield related traits as well as yield *per se* (Kumar *et al.*, 2010).

Generation mean analysis is a simple and efficient technique to elucidate the gene action as it uses first degree statistics for estimation of allelic as well as non-allelic interactions (Mather and Jinks, 1971). It uses basic generations' variance components along with scaling tests (Mather, 1949) to provide accurate information in relation to average dominance ratio and inheritance. In mungbean, both additive (Barad *et al.*, 2008) as well non additive gene action (Bisht *et al.*, 2014; Gupta *et al.*, 2017) was found for seed

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yield. Generation mean analysis was used in several crops including pulses to improve the yield however, in case of mungbean the study of literature revealed that there are very few studies on this aspect (Singh *et al.*, 2016). Therefore, the present investigation was aimed at estimation of various components of gene effects in mungbean by using generation mean analysis.

MATERIALS AND METHODS

Development of genetic population

Generation mean analysis in the present study was conducted for the seed yield and other yield component traits of mungbean using the generations viz. P₁, P₂, F₁, F₂ and F₃ of six different crosses. The plant material for the present

study consisted of seven different genotypes of mungbean (Table 1). From these parents six crosses viz. EC-693369 x NM-94, EC-693369 x ML-818, ML-1299 x EC-693376, LGG-460 x EC-693376, OUM-11-5 x NM-94 and OUM-11-5 x ML-818 were made in *kharif* season of year 2016 at EB-II research farm, Odisha University of Agriculture and Technology, Bhubaneswar. For gene action studies five generations viz. P_1 , P_2 , F_1 , F_2 and F_3 of each of the six crosses were generated in the succeeding seasons. They were then grown in randomized block design (RBD) with two replications during *rabi* 2017 for recording of observations for eight morphological traits. All the recommended agronomical practices were followed to raise a healthy crop.

Observations recorded

The observations were recorded for eight characters viz. plant height (cm), primary branches per plant, clusters per plant, pods per plant, pod length (cm), seeds per pod, hundred seed weight (g) and seed yield per plant (g). Ten randomly selected plants from each parent (P_1 , P_2) and the

F_1 while thirty randomly selected plants from each segregating population (F_2 and F_3) were used for recording the observations.

Statistical analysis

Analysis of variance for each character was carried out by using the method described by Panse and Sukhatme (1985). The generation mean analysis was carried out following the five parameter model proposed by Hayman (1958). The scaling tests 'C' and 'D' was estimated as suggested by Mather (1949). Significance of C scale indicated dominance x dominance epistasis (I) and significance of D scale indicated additive x additive (i) epistasis. The five parameters used in the model are mean effect (m), additive effect (d), dominance effect (h), additive x additive interaction (i) and dominance x dominance interaction (I).

RESULTS AND DISCUSSION

The scaling test was found to be significant for plant height in all the crosses except EC-693369 X ML-818, indicating the presence of non-allelic interactions (Table 2). In all the crosses the presence of both additive and dominance gene action was observed, except in the cross ML-1299 X EC-693376 and OUM-11-5 X NM-94. Singh *et al.* (2007) also reported that plant height was under the control of both additive and dominance gene effects. Duplicate epistasis was present in three crosses EC-693369 X NM-94, ML-1299 X EC-693376 and LGG-460 X EC-693376 whereas complementary epistasis was reported in the cross OUM-11-5 X ML-818. Aher and Dahat (1999) also observed the

Table 1: Details of the mungbean genotypes used

Genotype	Originating center
EC-693369 (TV03980A-G)	AVRDC, Hyderabad
EC-693376 (TV03719A-G)	AVRDC, Hyderabad
LGG-460	LAM, ANGRAU
ML-818	PAU, Ludhiana
ML-1299	PAU, Ludhiana
NM-94	AVRDC, Hyderabad
OUM-11-5 (Kamadeva)	OUAT, Berhampur

Table 2: Scaling test for adequacy of additive-dominance model for different traits in mungbean.

Traits	Scales	Crosses					
		I	II	III	IV	V	VI
		EC-693369 x NM-94	EC-693369 x ML-818	ML-1299 x EC-693376	LGG-460 x EC-693376	OUM-11-5 x NM-94	OUM-11-5 x ML-818
Plant height (cm)	C	-4.6	0.02	-10.38*	-0.9	8.45*	3.35
	D	-7.6*	1.04	-11.36*	-8.3*	10.85*	14.65*
Primary branches / plant	C	1.1	-0.3	-2.3*	-1.5*	0	0
	D	-0.6	0.1	-2.1*	-1.5*	-0.2	-0.8
Clusters / plant	C	1	-2.4*	-6.85*	-8.78*	-1.5	-1.7
	D	-4.0*	0.4	-1.05	-4.96*	-1.1	0.2
Pods / plant	C	17.2*	3.2	3.5	3.2	6.1	8.1*
	D	-1.7	-5.5	11.94*	-3.3	-12.5*	-29.28*
Pod length (cm)	C	2.4*	1.45*	-0.32	-0.2	-4.15*	-3.8*
	D	0.5	-2.55*	0.66	-1.58*	-1.55*	-2.8*
Seeds / pod	C	-4.7*	2.4*	2.2	2.4	-2.5	-7.8*
	D	2.1	-2.28	5.1*	-5.3*	2.8	0.5
Hundred seed weight (g)	C	-0.03	-0.49*	0	0.06	0.47	-0.07
	D	0.19	-0.13	-0.06	-0.12	-0.23	-0.17
Seed yield / plant (g)	C	3.47*	5.15*	4.4*	2.91*	4.13*	4.25*
	D	3.41*	3.27*	5.84*	2.69*	6.49*	4.29*

*indicates significance at 5% level of probability, Scale 'C' indicates dominance x dominance epistasis (I) and Scale 'D' indicates additive x additive (i) epistasis.

Table 3: Estimates of genetic mean and interaction effects for the morphological traits in mungbean crosses.

	Cross	Gene Effects					Type of
Traits	No.	Main effect±SE			Interaction effect±SE		Epistasis
		m	d	h	l	i	
Plant height (cm)	I	35.8*±0.71	-1.6*±0.32	8.4*±2.15	-4.0±6.60	1.1±2.15	Duplicate
	II	8.93*±0.97	-10.05*±0.31	10.46*±3.13	1.36±9.27	-20.79*±3.00	-
	III	53.13*±0.88	0.35±0.25	8.39*±2.98	-1.30±8.64	6.54*±2.79	Duplicate
	IV	5.8*±0.80	-1.85*±0.35	8.93*±2.75	-9.86±7.90	1.68±2.62	Duplicate
	V	44.2*±0.74	2.67*±0.33	0±2.41	3.2±7.11	-0.47±2.33	-
	VI	3.75*±0.76	-5.75*±0.32	1.36±3.27	15.06±8.44	-20.75*±2.82	Complementary
Primary branches / plant	I	1.45*±0.17	-0.15±0.18	0.63±0.53	-2.26±1.70	0.28±0.63	-
	II	1.3*±0.17	-0.05±0.19	0.53±0.58	0.53±1.70	-0.21±0.64	-
	III	1.6*±0.17	-0.65*±0.08	1.86±0.53	0.26±1.68	-0.28±0.54	Complementary
	IV	1.5*±0.14	-0.65*±0.11	1.0*±0.48	0±1.46	-0.55±0.50	-
	V	1.3*±0.14	0±0.19	0.13±0.56	-0.26±1.60	0.13±0.62	-
	VI	1.5*±0.14	0.1±0.20	1.13*±0.47	-1.06±1.38	0.73±0.57	-
Clusters / plant	I	5.0*±0.24	0±0.25	3.53*±0.68	-6.66*±2.24	2.83*±0.83	Duplicate
	II	4.1*±0.17	0.1±0.21	0.13±0.64	3.73±2.03	-0.46±0.75	Complementary
	III	5.3*±0.37	-2.17*±0.15	1.93±1.15	7.73*±3.55	-4.79*±1.15	Complementary
	IV	4.93*±0.28	-0.45*±0.19	0.99±1.10	5.09±3.07	0.94±1.05	Complementary
	V	4.7*±0.22	0.65*±0.19	0.53±0.65	0.53±2.09	1.78*±0.70	-
	VI	4.65*±0.65	0.75*±0.14	-0.16±1.47	2.53±5.45	1.08±1.69	-
Pods / plant	I	23.75*±1.10	-0.6±1.09	12.1*±3.35	-25.2*±10.22	2.8±3.69	Duplicate
	II	18.95*±0.90	-0.6±0.82	9.7*±2.69	-11.6±8.47	3.0±3.11	-
	III	20.7*±0.67	-6.35*±0.51	1.37±3.26	11.25±8.17	-20.07*±2.82	Complementary
	IV	24.25*±0.95	-0.8±0.51	7.63*±3.37	-8.66±9.53	1.13±3.18	-
	V	23.8*±0.93	3.25*±0.90	15.4*±2.83	-24.8*±8.66	15.85*±2.94	Duplicate
	VI	24.65*±0.90	3.25*±0.53	27.62*±3.95	-49.8*±10.21	27.37*±3.44	Duplicate
Pod length (cm)	I	6.6*±0.10	0.05±0.11	-0.63±0.63	3.86*±1.46	-0.63±0.54	Duplicate
	II	7.7*±0.10	-0.07±0.14	2.06*±0.51	-5.33*±1.27	1.79*±0.48	Duplicate
	III	5.22*±0.10	0.35*±0.11	-0.39±0.33	1.30±0.99	0.20±0.36	-
	IV	5.7*±0.10	0.35*±0.11	2.02*±0.42	-1.84±1.11	1.72*±0.40	Complementary
	V	5.9*±0.10	-0.52*±0.11	1.06*±0.34	3.46*±1.03	-0.70±0.39	Complementary
	VI	5.4*±0.10	-0.65±0.14	0.53±0.33	1.33±0.99	-0.06±0.40	Complementary
Seeds / pod	I	7.6*±0.10	0.45*±0.18	-1.73*±0.79	9.06*±1.78	-1.28±0.69	Duplicate
	II	10.8*±0.22	-0.8*±0.25	2.72*±1.01	-6.24*±2.63	0.32±0.94	Duplicate
	III	9.45*±0.34	0.2±0.27	-4.43*±1.03	3.86±3.20	-2.63*±1.10	Duplicate
	IV	11.25±0.30	0.9*±0.26	4.63*±1.37	-10.26*±4.07	5.73*±1.32	Duplicate
	V	10.35*±0.30	1.65*±0.18	0.16±1.07	7.06*±2.99	1.01±1.03	-
	VI	9.45*±0.34	0.4±0.25	-0.83±1.35	11.06*±3.65	-0.83±1.25	Duplicate
Hundred seed weight (g)	I	3.57*±0.03	0.02±0.04	-0.006±0.12	0.29±0.40	-0.08±0.15	-
	II	3.51*±0.04	-0.03±0.03	0.12±0.15	0.48±0.43	-0.06±0.14	Complementary
	III	3.68*±0.03	-0.07±0.04	0.18±0.10	-0.08±0.32	-0.1±0.14	-
	IV	3.64*±0.03	-0.12*±0.03	0.22±0.16	-0.24±0.39	-0.15±0.14	-
	V	3.72*±0.07	-0.03±0.02	0.52*±0.26	-0.93±0.75	0.16±0.24	-
	VI	3.59*±0.04	-0.09±0.07	0.28±0.25	-0.13±0.60	-0.08±0.22	-
Seed yield / plant (g)	I	7.36*±0.14	-0.18±0.17	1.7*±0.48	-0.08±1.41	-2.06*±0.54	Duplicate
	II	7.45*±0.10	-0.56*±0.17	0.65±0.33	-2.50*±0.99	-2.45*±0.44	Duplicate
	III	7.14*±0.10	-1.94*±0.10	-0.52±0.31	1.92±0.96	-7.04*±0.35	Duplicate
	IV	8.6*±0.10	0.11±0.10	0.88*±0.43	-0.29±1.16	-1.07*±0.41	Duplicate
	V	9.2*±0.10	1.33*±0.13	0.06±.51	3.14*±1.30	-0.6*±0.46	Complementary
	VI	9.68*±0.14	0.95*±0.13	1.69*±0.49	0.05±1.48	-0.24±0.50	Complementary

*indicates significance at 5% level of probability.

duplicate and complementary type of epistasis for plant height. Among the interaction components, additive x additive (i) effects was negative and significant for three crosses (Table 3). Hence, selection for the character may be deferred to later generations when desirable recombinants become available (Inderjit *et al.*, 2006) and Patel *et al.*, 2012).

The significance of both the scales for primary branches per plant in two crosses (Table 2) confirmed presence of both dominance x dominance (I) as well as additive x additive (i) type of gene interaction. Significant and negative additive gene effects was observed in these crosses while the crosses LGG-460 X EC-693376 and OUM-11-5 X ML-818 recorded significant and positive dominance gene effect. This shows the complex nature of inheritance of this trait (Gawande and Patil, 2007 and Singh *et al.*, 2007).

In case of clusters per plant, presence of epistatic interaction was observed in all the crosses except two viz. OUM-11-5 X NM-94 and OUM-11-5 X ML-818. Significant additive effect was found in four crosses while significant dominance effect was reported only for the cross EC-693369 X NM-94 (Table 3). Different sign for h and I referred to the presence of duplicate epistasis in EC-693369 X NM-94, which was similar to the results of Malik and Singh (1983). Importance of additive effect for this trait in mungbean has also been reported earlier (Barad *et al.*, 2008, Manivannan, 2002; and Ram, 1997). Also the dominance gene action for this character has been recorded earlier by many researchers.

The presence of inter allelic interactions for pods per plant was observed in four crosses (Table 3). Significant additive gene effects were reported in crosses OUM-11-5 X NM-94, OUM-11-5 X ML-818 and ML-1299 X EC-693376. Five of the crosses recorded dominance effects with higher magnitude. Similar results were recorded by Kute and Deshmukh (2002), Murthy (2000), Gawande and Patil (2007) and Singh *et al.* (2007). Additive x additive interactions were found significant in OUM-11-5 X NM-94 and OUM-11-5 X ML-818 and ML-1299 X EC-693376, while significant dominance x dominance gene effects as well as duplicate gene action was recorded in three crosses (EC-693369 X NM-94, OUM-11-5 X NM-94 and OUM-11-5 X ML-818). Predominant non-additive gene effects may retard the selection process in the earlier generations. Advancing the generations will allow new combination of alleles to arise, which will result in superior lines. Similar results have been reported by Kute and Deshmukh (2002) and Ram (1997).

All the crosses except ML-1299 X EC-693376 recorded significant for one or both the scales for pod length indicating the presence of non-allelic interactions. Duplicate gene interaction was evidenced from the opposite signs of h and I estimates in two crosses (Table 3). Similar results were obtained by Singh *et al.* (2007) and Barad *et al.* (2008).

A critical analysis for seeds per pod (Table 3) revealed the presence of additive effect in EC-693369 X NM-94, LGG-460 X EC-693376, OUM-11-5 X NM-94 and EC-693369 X

ML-818. Dominance effects were found predominant. Ram (1997), Gawande and Patil (2007) and Singh *et al.* (2007) also reported similar results. Additive x additive interaction components were significant for the crosses ML-1299 X EC-693376 and LGG-460 X EC-693376. Ajit and Singh (1996) and Murthy (2000) obtained similar results for this trait. Most of the crosses exhibited duplicate type epistasis for this trait.

Significance of scale C with similar sign of h and I confirmed complementary type of epistasis in the cross EC-693369 X ML-818. Similar kind of result was also obtained for the trait by Rao *et al.* (1984). Significant additive gene effect (d) was noticed only in the cross EC-693376 X ML-818. Significance of additive component for this trait was also reported by Kute and Deshmukh (2002) and Singh *et al.* (2007). Magnitude of dominance effect (h) was higher than additive effect (d) for most of the crosses which was also observed in earlier experiments by Malik and Singh (1983), Seenaiah (1995) and Ajit and Singh (1996). Hence, selection in later generations will be ineffective for this trait.

For seed yield per plant, both the scales were significant in all the crosses. Dominance effects were higher in magnitude in four crosses and levels of magnitude varied between crosses for the same character. Ram (1997) and Gawande and Patil (2007) also reported dominance effect for this character. Among the two epistatic effects, additive x additive (i) component was significant for five crosses and dominance x dominance (I) gene effects were significant in two crosses (Table 3). Similar results were reported by Murthy (2000) and Kute and Deshmukh (2002). Presence of both duplicate and complementary epistasis indicates that improvement of yield mainly depends on the type of cross combinations that are selected for the trait improvement. This study indicates that both duplicate and complementary epistasis are important for the improvement of this character (Aher and Dahat, 1999 and Khattak *et al.*, 2004).

The magnitude of dominance was observed in the traits plant height, primary branches per plant and seeds per pod. Higher dominance gene action suggested that the heterosis breeding will be rewarding in improving these traits in mungbean (Singh *et al.*, 2007). Significance of both the interaction components suggested that selection between families and lines will be promising for the improvement of clusters per plant (Patel *et al.*, 2012).

CONCLUSION

The present study reveals the significant contribution of additive, dominance and epistatic interaction in the inheritance of the yield and its component traits in greengram. The higher magnitude of dominance gene action for most of the traits suggested that heterosis breeding will be effective in improving the yield traits like plant height, primary branches per plant and seeds per pod in greengram. This experiment also indicates that the components of seed yield could be improved by exploiting both additive and non-additive types of gene action. The superior segregants from specific crosses can be identified and intermated followed

by reciprocal recurrent selection. The transgressive segregants produced as a result of this will lead to the development of desirable high yielding genotypes of greengram. However, the gene action identified pertains to the set of experimental genotypes used in this experiment. The gene action need to be validated further by using large number of diverse genotypes and their advanced generations.

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