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Gene action of yield and its contributing characters in mungbean [*Vigna radiata* (L.) Wilczek] under different environments

SM Yadav, Ved Prakash and OP Khedar

Abstract
Generation mean analysis was carried out on six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of three crosses namely Pusa-0871 x M-818, Pusa-0871 x RMG-991 and ML-818 x RMG-991 and evaluated in randomized block design for days to flowering, number of pods per plant, pod length, number of seeds per pod and grain yield per plant under timely and late sown conditions. The data of six generations were subjected to individual scaling tests and joint scaling test to detect epistasis. The individual scaling tests indicated the presence of epistatic interactions in all the traits under the both sowing environments. The analysis of joint scaling test indicated the additive-dominance model was inadequate in all the cases indicating the role of epistatic interactions to control the inheritance of the traits studied under both conditions. On the basis of six parameter model, both the main effects and their epistatic interactions involved in inheritance of all traits with the preponderance of non-additive effects. Complementary gene action was found in cross Pusa 0871 x RMG 991 for days to flowering in timely sown condition whereas duplicate type of epistasis was prevalent in other cases under all the environments. Reciprocal recurrent selection or bi-parental mating between the selected plants in early segregating generation could be helpful for the improvement of these traits.

Keywords: Epistasis, Generation mean analysis, Gene effects, Joint scaling, Mungbean, *Vigna radiata*, Yield components

1. Introduction
India is the largest producer and consumer of pulses in the world. Greengram [*Vigna radiata* (L.) Wilczek] belongs to the family Leguminaceae, subfamily Papillionaceae, genus Vigna and species radiata with chromosome number 2n = 22. It is thought to be native of India and Central Asia and is most important legume (Pulse) crop in India after chickpea and pigeonpea. Greengram is a low yielder, to develop high yielding variety, we should know the genetic makeup of a plant, which govern the inheritance of grain yield and the contributing traits under different varying environmental conditions. For any crop improvement programme, selection of superior parents is an essential prerequisite especially for the traits showing higher heritability and genetic advance for various traits (Khan *et al*., 2005). Therefore, present investigation carried out to achieve the higher yield in both optimum and sub optimum environments, attempts should be made to explore and exploit the novel genes of desirable traits through systematic breeding programme by involving diverse cultivars. Selection procedure is more difficult in a trait, where heritability is low or is not precisely measurable. Indirect selection in such a situation is more effective and study of correlation among different economic traits are therefore, essential for an effective selection programme because selection for one or more trait results in correlated response for several other traits (Searle, 1965) [17]. Development of a superior genotype depends upon the contribution of heritable (genetic) and non-heritable (environmental) source of variation and the interaction between them. Therefore, it becomes imperative to estimate the nature and magnitude of genetic variations. The choice of plant breeding methodology of upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects present in the population. A number of methods in quantitative genetics are available to estimate different genetic parameters viz. additive, dominance and epistatic interactions. Mehandi *et.al.* (2013) [15] observed both additive and non-additive type gene action. In any systematic breeding programme, breeder cannot overlook the role of epistasis; otherwise, he would obtain biased estimates of additive and dominance components of genetic variation, which would lead to faulty breeding procedure (Singh & Singh, 1974a). Moreno (1994) [16] suggested that interaction between genes is an important source of genetic variability.

In literature, very limited information is available on all types of gene effects/inheritance controlling the seed yield and its components in mungbean (Khattak *et al*. 2001b) [9] and prepondence of additive gene action indicated by Kumar *et. al*. (2013) [11].

Therefore, study was undertaken with the following objectives:

1. To determine the relative magnitude of different types of gene effects and their interactions for yield and its components in different generations of Greengram under different environments.
2. To suggest a suitable breeding methodology on the basis of results achieved for further improvement in Greengram

Materials and Mathods

The experimental materials consisting of six generations of each cross (P_1, P_2, F_1, F_2, BC_1 and BC_2) were grown in a randomized block design with three replications under timely and late sown conditions during *Kharif* 2015 at Rajasthan Agriculture Research Institute Durgapura- Jaipur. Each plot was consisting of 3.0 m long with two rows of each plot of P_1, P_2, F_1, BC_1 and BC_2 generation and four rows of segregating material F_2. Row to row and plant to plant distance was 30 cm and 10 cm respectively under both the environments. In each replication, parents and their generations were sown by dibbling the seed in a plot in each environment. Boarder rows were plated at the beginning as well as at the end of experimental rows in each block to eliminate the boarder effects. Recommended agronomical practices for each environment were followed for raising the good crop in both the environments. Twenty competitive plants in P_1, P_2, F_1, BC_1 and BC_2 generation and 40 plants in F_2's progenies were randomly selected and tagged after leaving the boarder plants to eliminate boarder effects for recording all observations under both environments (created by different dates of sowing) separately. Data were recorded for days to flowering, number of pods per plant, pod length, number of seeds per pod and grain yield per plant under timely and late sown conditions. The data were subjected to individual scaling tests (Hayman and Mather, 1955) [5] to detect the presence of epistasis. Further, the data were subjected to joint scaling test of Cavelli (1952) [2]. The gene effects of six parameter model were calculated as per Jinks and Jones (1958) [7].

Result and Discussion

The estimates of individual and joint scaling tests and magnitude of components of genetic variation for the yield and contributing characters studied during *kharif* 2015 and presented in Table-1. The results revealed that the individual and joint scaling tests both confirmed the presence of epistatic interaction for the crosses for all the traits in both environments. Non-additive gene action was predominant over additive for days to flowering in both the environments. Among epistasis the magnitude of dominance x dominance effect was comparatively more important than the additive x additive and additive x dominance for all the crosses for both the environments showed the importance of (l) for the inheritance of this character. The parameters (h) and (l) were significant but different in signs indicated the involvement of duplicate epistasis under different environments reported in eight cases, whereas, parameters (h) and (l) were significant but same in signs show the complementary epistasis only in one case. Similar results was also reported by Deshmukh and Majare (1980) [3].

Among the main effects, both are important for inheritance of pods per plant. Varying with the change of crosses and environments. All the three epistatic interaction effects were equally important for the inheritance of this trait. However the relative magnitude of gene effects changed frequently with the change of parental material and environment. The genotypes can also be improved by selection for this trait since two crosses had significant magnitude of additive effect but, improvement will be very slow and require progeny testing. Duplicate epistasis was present for the character in ten cases. Among epistasis contribution of additive x additive (i) and additive x dominance (j) effects have been reported by Ram (1997) [12] while dominance x dominance (l) by Barad *et al*. (2008) [8] for this trait. These are in agreement with the present findings. Non-additive genes played major role in the expression of pod length trait in all the environments. Among epistasis additive x additive epistasis and dominance x dominance are equally important for the inheritance of pod length as compare to additive x dominance. Presence of duplicate epistasis was observed predominantly for the expression of the character. The finding of Singh and Dikshit (2003) [18] is in confirmity with the present findings.

Dominance gene effect was more important than additive in most of the crosses for seeds per pod. Among epistasis, dominance x dominance played major role than additive x additive and additive x dominance in the expression of this trait. However, additive gene effects were positive and significant in five cases which revealed that this component could be improved through selection in these crosses. Similar results also observed in the expression of this trait by Khattak *et al*. (2002) [10] & Singh *et al*. (2006) [19]. The yield is a complex character, yet attempts have been made in the past to explain the nature of gene action on the basis of direct and indirect components. The importance of both additive and dominance gene action have been established by various workers through experimental approaches. Digenic epistatic model, based on six generations, showed that on an average dominance gene effect contributed maximum towards grain yield. Additive gene effects were small in relation to dominance for grain yield in most of the crosses. Results also indicated that magnitude of additive effect was generally dependent upon the magnitude of differences between the two parental lines while signs depend on the magnitude of P_1 and P_2 parents.

Among digenic epistasis, major role in the inheritance of grain yield was showed by additive x additive and dominance x dominance gene interactions. The additive x additive gene effects were Positive and significant in ML 818 X RMG 991in timely sown condition. Among three types of epistasis, sign attached to dominance x dominance effects was of more importance. Gamble (1962) suggested that negative effects of dominance x dominance was undesirable. In 3-parameter model dominance (h) effect was generally greater in magnitude than additive (d) gene effects. In digenic model, both main effects additive (d) and dominance (h) were frequently contributed for this trait under both the environments, however, the relative magnitude of dominance (h) was greater than additive (d) effects. The nature and magnitudes of gene effects were influenced by the environments created by altering sowing dates.

The digenic interaction [(i), (j) and (l)] were equally important for most of the cases under both the environments. The relative magnitude and nature changed with process and environmentindicating the need of specific breeding strategy for improvement of this trait. Moreover, presence of duplicate

type of epistasis put the challenge for the breeder in accomplishing higher productivity. Both additive and non-additive gene action were important in the inheritance of grain yield in mung bean as reported by Malik and Singh (1986) [14] & Rehman *et al*. (2009) [13]. Results of the present study thus, indicated that dominance (h) effect and dominance x dominance (l) epistatic effect were relatively more for inheritance of all the traits studied under both conditions. This indicated the major role of non-allelic gene effects. Therefore, the successful breeding methods would be some forms of recurrent selection and hence, diallel selective mating given by Jensen (1970) or biparental mating in early segregating generations given by Joshi and Dhawan, 1966 [8] might prove to be an effective approach.

Table 1: Scaling tests, estimates of gene effects and type of epistasis for different characters of three crosses of mung bean under normal and late sown conditions.

1. Days to flowering						
Scaling Test	**Pusa 0871 X M 818**		**Pusa 0871 X RMG 991**		**ML 818 X RMG 991**	
	Timely	**Late**	**Timely**	**Late**	**Timely**	**Late**
A	-1.70±0.618**	-2.133±0.88*	3.80±0638**	2.000±0.676**	2.867±0.678**	-4.433±0.787**
B	1.433±0.638**	1.533±0.808	-3.63±0.64**	-1.633±0.747*	5.667±0.721**	4.233±0.860**
C	8.933±1.195**	6.533±1.504**	-9.83±1.45**	-2.633±1.613	-1.33±1.165	-8.867±1.493**
Gene effects in different models:						
3-Parameter:						
(m)	48.460±0.164	44.774±0.178	48.959±0.180	45.541±0.179	48.267±0.123	44.284±0.208
(d)	-0.39±0.162*	0.978±0.178**	0.951±0.17**	0.843±0.173**	-1.655±0.12**	-0.721±0.200**
(h)	2.85±0.298**	-4.915±0.36**	4.104±0.35**	4.677±0.363**	-2.116±0.28**	-0.290±0.410
$\chi 2(3)$	80.833**	32.621**	72.063**	21.691**	84.791**	131.569**
6-Parameter:						
(m)	45.133±0.257	41.000±0.318	48.133±0.310	43.867±0.351	48.033±0.242	46.033±0.301
(d)	1.667±0.367**	0.633±0.512	1.000±1.339**	2.300±0.397**	2.900±0.429**	4.067±0.419**
(h)	6.600±1.299**	2.533±1.682	-7.617±1.46**	7.683±1.662**	-11.10±1.333**	-9.633±1.533**
(i)	9.200±1.263**	7.133±1.633**	-2.400±1.412	-3.000±1.614	-9.667±1.293**	-8.667±1.468**
(j)	3.133±0.819**	3.667±1.092**	0.167±0.785	3.633±0.882**	2.800±0.896**	8.667±0.956**
(l)	-9.467±1.89**	-7.73±2.541**	-5.033±1.985*	3.367±2.262	18.200±2.074**	8.467±2.245**
Type of epistasis :	D	-	C	-	D	D
Scaling Test						
2. Number of pods per plant						
A	2.600±0.620**	3.700±0.576	-0.433±0.559	1.600±0.696*	-4.783±0.55**	-3.533±0.542**
B	1.733±0.611*	4.167±0.532	5.150±0.617**	4.367±0.487**	5.000±0.615**	3.283±0.493**
C	-0.867±0.779	-4.333±0.659	2.717±0.764**	3.367±1.080**	-6.550±1.01**	-0.550±0.944
Gene effects in different models:						
3-Parameter:						
(m)	19.827±0.152	11.836±0.123	20.673±0.144	12.115±0.121	20.591±0.142	12.578±0.131
(d)	0.349±0.161*	-0.914±0.13**	-0.083±0.15	0.732±0.120**	0.023±0.141	-1.192±0.129**
(h)	3.287±0.248**	3.169±0.196**	2.977±0.236**	1.543±0.251**	0.669±0.265*	0.669±0.254**
$\chi 2(3)$	33.452**	192.934**	77.801**	118.448**	201.008**	108.329**
6-Parameter:						
(m)	21.850±0.150	14.508±0.132	21.850±0.150	14.183±0.233	22.075±0.214	13.050±0.194
(d)	0.067±0.376	1.083±0.353**	2.533±0.362**	1.800±0.367**	4.000±0.349**	3.950±0.296**
(h)	-1.967±0.99*	-9.017±0.904**	1.108±0.968	-7.283±1.217**	-6.142±1.13**	0.442±1.013
(i)	-5.20±0.962**	-12.20±0.882**	-2.00±0.938**	-9.333±1.185**	-6.767±1.10**	-0.300±0.977
(j)	-0.867±0.836	0.467±0.760	5.583±0.799**	2.767±0.777**	9.783±0.765**	6.817±0.658**
(l)	9.533±1.695**	20.067±1.557**	6.717±1.635**	15.300±1.822**	6.983±1.725**	0.050±1.515
Type of epistasis :	D	D	D	D	D	-
3. Pod length						
	Pusa 0871 X ML 818		**Pusa 0871 X RMG 991**		**ML 818 X RMG 991**	
	Timely	**Late**	**Timely**	**Late**	**Timely**	**Late**
A	0.183±0.394	0.600±0.296*	0.350±0.380	1.750±0.248**	-1.117±0.40**	-0.100±0.291
B	-0.200±0.311	1.233±0.324**	-0.200±0.366	0.467±0.347	0.867±0.312**	-0.000±0.312
C	2.383±0.487**	-0.800±0.456	1.917±0.465**	0.750±0.443	2.017±0.443**	2.067±0.460**
Gene effects in different models:						
3-Parameter:						
(m)	7.753±086	7.172±0.076	7.958±0.084	7.281±0.071	7.778±0.078	7.119±0.080
(d)	-0.25±.086**	-0.28±0.08**	0.094±0.087	0.128±0.071	0.094±0.081	0.192±0.082*
(h)	0.228±0.164	-0.079±0.135	-0.130±0.155	-0.050±0.133	-0.47±0.139**	0.097±0.136
$\chi 2(3)$	33.078**	28.066**	20.330**	50.898**	38.104**	24.089**
6-Parameter:						
(m)	7.475±0.086	7.392±0.091	7.600±0.085	7.325±0.087	7.217±0.085	6.775±0.093
(d)	0.117±0.209	0.567±0.187**	-0.317±0.23**	-0.583±0.181**	0.767±0.226**	-0.167±0.179
(h)	2.792±0.568**	-2.683±0.54**	1.742±0.592**	-1.358±0.521**	1.858±0.584**	2.283±0.533**
(i)	2.400±0.541**	-2.63±0.522**	1.767±0.570	-1.467±0.503**	2.267±0.567**	2.167±0.515**
(j)	0.383±0.459	0.633±0.412	-0.550±0.495	-1.283±0.395**	1.983±0.485**	0.100±0.402
(l)	-2.417±0.966*	4.467±0.876**	-1.617±1.027	3.683±0.851**	-2.517±1.006*	-2.267±0.850**

Type of epistasis :	D	D	-	D	D	D
4. Number of seeds per pod						
Scaling Test						
A	2.050±0.420**	1.533±0.293**	0.683±0.422	0.967±0.267**	-1.667±0.482**	2.267±0.357**
B	2.283±0.429**	1.117±0.310**	0.100±0.511	1.950±0.315**	1.900±0.443**	1.183±0.316**
C	4.467±0.735**	0.583±0.405	1.917±0.624**	0.550±0.386	-1.167±0.756	-1.683±0.402**
Gene effects in different models :						
3-Parameter:						
(m)	9.807±0.105	7.703±0.072	10.162±0.092	7.947±0.066	9.476±0.090	7.416±0.068
(d)	-0.590±0.106**	-0.702±0.073**	-0.154±0.093	-0.184±0.068**	0.423±0.090**	0.437±0.069**
(h)	0.479±0.174**	0.561±0.137**	-0.071±0.182	-0.011±0.116	-0.104±0.183	0.333±0.133*
$\chi 2(3)$	66.960**	37.131**	10.451**	47.973**	38.905**	103.588**
6-Parameter:						
(m)	9.400±0.162	8.058±0.071	9.842±0.122	7.992±0.076	9.708±0.162	7.992±0.071
(d)	0.567±0.260*	0.550±0.178**	-0.117±0.293	0.633±0.182**	1.183±0.289**	-0.950±0.210*
(h)	0.700±0.848	-1.342±0.479**	1.258±0.787	-2.292±0.489**	-1.567±0.889	-4.808±0.527**
(i)	0.133±0.830	-2.067±0.457**	1.133±0.763	-2.367±0.474*	-1.400±0.867	-5.133±0.508*
(j)	0.233±0.572	-0.417±0.391	-0.583±0.619	0.983±0.392**	3.567±0.609**	-1.083±0.445**
(l)	4.200±1.275**	4.717±0.821**	-0.350±1.329	5.283±0.822**	1.633±1.381	8.583±0.930**
Type of epistasis :	-	D	-	D	-	D
	Pusa 0871 X ML 818		**Pusa 0871 X RMG 991**		**ML 818 X RMG 99**	
	Timely	**Late**	**Timely**	**Late**	**Timely**	**Late**
5.Grain yield per plant						
Scaling Test						
A	0.912±0.331**	0.335±0.131**	-0.437±0.273	0.398±0.127**	-1.853±0.29**	0.227±0.242
B	1.107±0.302**	0.388±0.199	1.542±0.275**	0.658±0.192**	0.148±0.325**	1.082±0.225**
C	0.112±0.654	-0.257±0.328	0.592±0.667	0.637±0.251*	-2.392±0.689	1.298±0.441**
Gene effects in different models:						
3-Parameter:						
(m)	6.640±0.075	4.676±0.038	6.976±0.072	4.633±0.046	6.874±0.073	4.221±0.051
(d)	-0.24±0.075**	-0.278±0.03**	-0.177±0.071*	0.249±0.047**	0.172±0.073*	-0.144±0.050**
(h)	0.682±0.139**	0.486±0.061**	0.462±0.128**	0.249±0.072**	0.287±0.128*	0.329±0.102**
$\chi 2(3)$	19.549**	11.577**	37.442**	20.798**	48.339**	26.548**
6-Parameter:						
(m)	7.116±0.147	5.020±0.076	7.148±0.154	4.712±0.051	7.418±0.159	4.223±0.096
(d)	0.335±0.191	0.310±0.107**	0.997±0.161**	0.347±0.096**	0.675±0.191**	0.518±0.141**
(h)	-1.098±0.715	-0.482±0.377	0.061±0.706	-0.195±0.290	-0.509±0.754	0.494±0.488
(i)	-1.907±0.70**	-0.980±0.372	-0.513±0.694	-0.420±0.281	-0.687±0.743	-0.010±475
(j)	0.195±0.415	0.053±0.230**	1.978±0.359**	0.260±0.220	2.002±0.413**	0.855±0.301**
(l)	3.925±1.005**	1.703±0.540**	1.618±0.928	1.477±0.458**	-1.018±1.028	1.318±0.715
Type of epistasis :	-	-	-	-	-	-

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