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GENERATION MEAN ANALYSIS FOR YIELD AND ITS COMPONENTS IN GREEN GRAM [*VIGNA RADIATA* (L.) WILCZEK]

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Abstract

The analysis of gene effects for some yield characters and detection of epistasis in green gram [*Vigna radiata* (L.) Wilczek] was studied in three crosses, namely, Pusa 0871 × ML 818, Pusa 0672 × IPM 02-14 and ML 818 × RMG 991 involving five parents and evaluated in randomized block design for days to maturity, number of seeds per pod, 100-seed weight and grain yield per plant under timely and late sown conditions through generation mean analysis during *kharif* 2015 at Rajasthan Agriculture Research Institute, Durgapura, Jaipur (Rajasthan), India. Six populations, *viz.* P_1, P_2, F_1, F_2, BC_1 and BC_2 of three crosses were evaluated. The nature and magnitude of gene effects for yield and its components in green gram was studied using six parameter models of generation mean analysis. The presence of epistasis was detected by joint scaling test and inadequacy of additive-dominance model was established. Additive (*d*), dominance (*h*) gene effects along with one or more type of non-allelic interactions (i, j, l) contributed significantly towards the inheritance of all the quantitative characters in majority of the crosses. Duplicate type of epistasis and predominant of dominance effects was also prevalent in most of the cases. Thus, postponement of selection in later generations may be suggested to obtain transgressive segregates for improvement of green gram populations.

Key words : Epistasis, gene effects, joint scaling test, green gram, *Vigna radiata*, yield components.

Introduction

India is the largest producer and consumer of pulses in the world. Green gram [*Vigna radiata* (L.) Wilczek] belongs to the family Leguminaceae, subfamily Papillionaceae, genus Vigna and species radiata with chromosome number 2n = 22 is an important pulse crop of india after chickpea & pigeon pea. Though, there are so many reasons of low yields like marginal land for its cultivation, high seed cost, comparatively more risky, poor condition of Indian farmers etc. but unavailability of quality seed of high yielding and disease resistance varieties is the main constraint in green gram production. Plant breeders have been utilizes the available genetics resources to develop improved genotypes. An understanding of the genetic factors that govern the yield components is necessary, because breeding for yield depends largely upon genetic manipulations of the components along with yield. The choice of appropriate breeding procedure depends on the type of gene action involved in the expression of these characters. Gene action is measured in terms of components of genetic variance. Three type of genetic variance, *viz.* additive, dominance and epistatic variance. In natural plant breeding population, epistatic variance has the lowest magnitude. Breeder cannot oversight 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. The presence and absence of epistasis can be detected by the analysis of generation means using the scaling test. Generation mean analysis provides information about the component of genetic variation and provides the information about the predominant type of gene action for important traits of a crop species. This helps in deciding a suitable breeding procedure for the improvement of the various quantitative traits of the species. In the present studies, the detection

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of epistasis and estimates of additive and dominance components of variation for yield components in three sets of green gram crosses were carried out by using generation mean analysis as per Hayman (1958).

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. In any classical 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 and Singh, 1974a). Moreno (1994) 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 green gram (Khattak e*t al*., 2001b).

Materials and Methods

The experimental materials consisting of three crosses, namely Pusa 0871 × ML 818, Pusa 0672 × IPM 02-14 and ML 818 × RMG 991. 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 RARI, Durgapura, Jaipur (Rajasthan), India. 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 maturity, number of seeds per pod, 100-seed weight and grain yield per plant under timely and late sown conditions. The data were subjected to individual scaling tests (Hayman and Mather, 1955) to detect the presence of epistasis. Further, the data were subjected to joint scaling test of Cavelli (1952). The gene effects of six parameter model were calculated as per Jinks and Jones (1958).

Results and Discussion

The estimates of gene effects and interactions for the best fit model with respect to different traits in three crosses of mungbean revealed that inheritance pattern varied with cross, character and sowing conditions.

The mean (table 1) of F_1s for days to maturity were found to be intermediate or closer to the lower parents (desirable) in all crosses under both the environments, indicating dominance of positive gene for days to maturity. Mean values of F_1s for number of seeds per pod, 100-seed weight & grain yield per plant were found higher the parents suggesting dominance of genes for yield (desirable) in both the environments. BC_1 and BC_2 100-seed weight & grain yield per plant closer to the parents indicating that an extra back cross dose of parent lead to the accumulation of favourable genes in this set of material.

The estimates of joint scaling test and magnitudes of components of genetic mean variation for the yield characters studied during *kharif* 2015 are presented in table 2. The expected mean (m) was significant and positive in all the crosses for all the traits. The scaling tests indicated that the epistatic interaction was responsible for the inheritance of days to maturity for all the crosses in both environments. Both additive (d) and dominance (h) gene effects generally played preponderant role in the inheritance of this trait for all the crosses in both environments. The magnitude of dominance gene effects prevailed over additive gene effects in most of the environments. The signs and magnitude of main effects frequently changed with the change of sowing date and cross. Among the interactions, additive x additive (i) and dominance × dominance (l) were generally high in magnitude and exceeded the additive × dominance (j) effect in most of the crosses under both environments. Additive × dominance and dominance × dominance type of non-allelic gene actions were useful for the inheritance of day to maturity in these populations as indicated by negative and significant magnitude in most of the crosses. Thus, further change in day to maturity could be possible through selection in this population. The parameters (h) and (l) were significant but, different in signs indicated the involvement of duplicate epistasis under different environments reported in 3 cases, whereas, parameters (h) and (l) were significant but, same in signs show the complementary epistasis in one case only. Similar result also reported by Mansuria (1982) and Patel (1983).

Dominance gene effect was more important than additive in most of the crosses for seeds per pod. Among epistasis, dominance × dominance played major role than

Table 1 : *Per se* performance of six generation of three crosses of mungbean for different timely and late sown conditions.

Cross	Envi.	P_1	P_2	F_1	F_2	BC_1	BC_2
1. Days to maturity							
Pusa 0871 × ML 818	Timely	67.167±4.420	70.500±2.603	62.433±1.220	63.000±1.793	67.033±2.447	65.400±2.662
	Late	62.967±3.826	64.967±4.516	57.833±2.833	60.000±2.069	61.800±1.752	61.000±2.483
Pusa 0672 × IPM 02-14	Timely	65.067±3.926	69.900±2.852	62.167±2.144	69.033±2.033	66.967±2.033	70.000±2.414
	Late	58.400±1.972	65.267±2.96	58.067±4.547	59.200±1.890	60.033±1.757	62.000±1.862
ML 818 × RMG 991	Timely	70.333±6.437	69.533±2.533	65.133±1.913	67.100±2.852	68.000±2.345	64.000±2.000
	Late	59.800±4.234	64.033±1.964	59.167±2.626	63.700±2.148	64.033±2.447	61.100±2.231
2. Number of seeds per pod							
Pusa 0871 × ML 818	Timely	10.150±0.104	11.150±0.076	9.683±0.394	9.658±0.124	9.717±0.233	10.467±0.060
	Late	7.933±0.044	8.717±0.136	7.600±0.076	6.867±0.051	8.050±0.029	7.567±0.133
Pusa 0672 × IPM 02-14	Timely	10.367±0.073	11.133±0.145	10.067±0.192	9.967±0.082	10.100±0.076	8.800±0.144
	Late	7.517±0.060	9.067±0.117	7.750±0.104	7.950±0.076	7.883±0.093	7.467±0.088
ML 818 × RMG 991	Timely	9.517±0.120	11.767±0.169	11.233±0.117	10.092±0.096	10.267±0.176	11.100±0.029
	Late	7.283±0.088	8.300±0.104	7.917±0.120	6.417±0.079	8.383±0.088	7.800±0.058
3. 100-Seed weight							
Pusa 0871 × ML 818	Timely	6.977±0.985	6.502±0.605	7.548±0.847	7.116±2.590	6.807±1.182	6.472±1.001
	Late	4.990±0.137	4.423±0.276	5.205±0.121	5.020±0.348	4.930±0.193	4.620±0.495
Pusa 0672 × IPM 02-14	Timely	6.815±0.813	6.812±0.649	7.318±0.576	7.499±1.529	6.508±1.196	7.688±0.840
	Late	4.280±0.157	4.367±0.642	4.255±0.529	4.455±0.189	4.233±0.307	3.588±0.139
ML 818 × RMG 991	Timely	6.405±0.727	7.057±0.767	6.908±0.640	7.418±3.051	7.583±0.947	6.908±1.236
	Late	4.387±0.372	4.205±0.323	4.800±0.550	4.223±0.549	4.480±0.645	3.962±0.543
4. Grain yield per plant							
Pusa 0871 × ML 818	Timely	6.977±0.985	6.502±0.605	7.548±0.847	7.116±2.590	6.807±1.182	6.472±1.001
	Late	4.990±0.137	4.423±0.276	5.205±0.121	5.020±0.348	4.930±0.193	4.620±0.495
Pusa 0672 × IPM 02-14	Timely	6.815±0.813	6.812±0.649	7.318±0.576	7.499±1.529	6.508±1.196	7.688±0.840
	Late	4.280±0.157	4.367±0.642	4.255±0.529	4.455±0.189	4.233±0.307	3.588±0.139
ML 818 × RMG 991	Timely	6.405±0.727	7.057±0.767	6.908±0.640	7.418±3.051	7.583±0.947	6.908±1.236
	Late	4.387±0.372	4.205±0.323	4.800±0.550	4.223±0.549	4.480±0.645	3.962±0.543

Table 2 : Scaling tests, estimates of gene effects and type of epistasis for different characters of three crosses of green gram under normal and late sown conditions.

Scaling Test	Days to maturity					
	Pusa-0871 × M-818		Pusa-0672 × IPM-02-14		ML-818 × RMG-991	
	Timely	Late	Timely	Late	Timely	Late
A	-4.467±0.717**	-2.80±0.675**	-6.7±0.688**	-3.6±0.672**	-0.533±0.769	-9.100±0.745**
B	2.133±0.695**	0.800±0.759	-7.93±0.69**	-0.667±0.706	6.667±0.644**	1.000±0.671
C	10.533±1.163**	3.600±1.326**	-16.83±1.2**	3.000±1.334*	1.733±1.440	-12.633±1.305**
Gene effects in different models: 3-Parameter:						
(m)	68.571±0.202	63.982±0.225	69.399±0.205	61.913±0.816	68.958±0.224	63.194±0.198
(d)	0.898±0.207**	0.346±0.215	2.295±0.201**	3.073±0.175**	0.168±0.213	1.102±0.195**
(h)	-6.481±0.31**	-6.054±0.40**	-4.771±0.35**	-3.262±0.38**	-5.859±0.41**	-4.790±0.324**
X2(3)	166.145**	37.487**	270.452**	53.423**	39.838**	167.277**
6-Parameter:						
(m)	63.000±0.244	60.00±0.263	69.033±0.260	59.200±0.251	67.100±0.308	63.700±0.268
(d)	1.633±0.413**	0.800±0.376	-3.033±0.38**	-1.96±0.347**	4.000±0.381**	2.933±0.395**
(h)	6.467±1.318**	-0.53±1.354	-7.517±1.34**	3.500±1.297**	-9.20±1.496**	-7.283±1.382**
(i)	12.867±1.280**	5.600±1.292	-2.200±1.295	7.267±1.221**	-4.40±1.449**	-4.533±1.330**
(j)	6.600±0.957**	3.600±0.918	-1.233±0.905	2.933±0.804**	7.200±0.937**	10.100±0.911**
(l)	-15.20±2.019**	-7.60±2.004	-12.4±1.992**	-11.5±1.926**	10.533±2.096**	-3.597±2.049
Type of epistasis:	D	-	C	D	D	-
Number of seeds per pod Scaling Test						
A	2.050±0.420**	1.533±0.293**	0.233±0.435	-0.500±0.290	-1.667±0.482**	2.267±0.357**
B	2.283±0.429**	1.117±0.310**	3.600±0.381**	1.883±0.285**	1.900±0.443**	1.183±0.316**
C	4.467±0.735**	0.583±0.405	1.767±0.785*	0.283±0.398	-1.167±0.756	-1.683±0.402**
Gene effects in different models: 3-Parameter:						
(m)	9.807±0.105	7.703±0.072	10.563±0.085	8.260±0.067	9.476±0.090	7.416±0.068
(d)	-0.590±0.106**	-0.702±0.073**	0.189±0.086*	0.606±0.069**	0.423±0.090**	0.437±0.069**
(h)	0.479±0.174**	0.561±0.137**	-0.948±0.158**	-0.661±0.124**	-0.104±0.183	0.333±0.133*
$\chi^2(3)$	66.960**	37.131**	89.848**	50.612**	38.905**	103.588**
6-Parameter:						
(m)	9.400±0.162	8.058±0.071	9.967±0.179	7.950±0.077	9.708±0.162	7.992±0.071
(d)	0.567±0.260*	0.550±0.178**	1.300±0.258**	0.417±0.174**	1.183±0.289**	-0.950±0.210*
(h)	0.700±0.848	-1.342±0.479**	-2.750±0.896**	-1.642±0.481**	-1.567±0.889	-4.808±0.527**
(i)	0.133±0.830	-2.067±0.457**	-2.067±0.881**	-1.100±0.463**	-1.400±0.867	-5.133±0.508*
(j)	0.233±0.572	-0.417±0.391	3.367±0.546**	2.383±0.379**	3.567±0.609**	-1.083±0.445**
(l)	4.200±1.275**	4.717±0.821**	5.900±1.295**	2.483±0.802**	1.633±1.381	8.583±0.930**
Type of epistasis :	-	D	D	D	-	D

Table 2 continued....

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Scaling Test	Pusa-0871 × M-818		Pusa-0672 × IPM-02-14		ML-818 × RMG-991	
	Timely	Late	Timely	Late	Timely	Late
	100-Seed weight					
A	0.293±0.153	0.673±0.156**	0.883±0.150**	1.033±0.164**	0.897±0.120**	-0.587±0.110**
B	0.300±0.127*	0.717±0.155**	0.037±0.115	0.560±0.150**	-0.200±0.153	-0.207±0.125
C	1.780±0.264**	-1.483±0.300*	2.367±0.287**	1.347±0.295**	-1.243±0.18**	1.027±0.208**
Gene effects in different models : **3-Parameter :**						
(m)	4.486±0.040	3.845±0.041	4.574±0.035	3.807±0.043	4.560±0.037	3.908±0.035
(d)	-0.144±0.04**	-0.034±0.041	0.217±0.035**	0.247±0.043**	0.468±0.039**	-0.012±0.034
(h)	0.492±0.063**	0.303±0.074**	0.363±0.064**	0.387±0.076**	0.291±0.058**	0.219±0.059
X2(3)	71.375**	83.997**	93.169**	54.134**	147.745**	93.893
6-Parameter :						
(m)	5.153±0.058	4.420±0.066	4.300±0.064	3.857±0.063	4.937±0.030	4.047±0.063
(d)	0.127±0.083	0.070±0.092	-0.563±0.07**	-0.477±0.09**	0.503±0.085**	0.190±0.075*
(h)	-1.87±0.292**	-2.558±0.33**	1.890±0.306**	0.220±0.320	-0.137±0.220	0.438±0.300
(i)	-2.37±0.285**	-2.873±0.32**	1.447±0.299**	-0.247±0.310	-0.487±0.208*	0.167±0.293
(j)	0.007±0.189	0.043±0.207	-0.847±0.17**	-0.437±0.205*	1.073±0.186**	0.350±0.175*
(l)	2.967±0.423**	4.263±0.476**	-0.527±0.43	1.840±0.467**	1.007±0.386**	-0.317±0.411
Type of epistasis :	D	D	-	-	-	-
Scaling test	**Grain yield per plant**					
A	0.912±0.331**	0.335±0.131**	1.117±0.321**	0.068±0.148	-1.853±0.29**	0.227±0.242
B	1.107±0.302**	0.388±0.199	-1.247±0.27**	1.445±0.170**	0.148±0.325**	1.082±0.225**
C	0.112±0.654	-0.257±0.328	-1.733±0.51**	-0.633±0.35**	-2.392±0.689	1.298±0.441**
(m)	6.640±0.075	4.676±0.038	6.878±0.072	4.095±0.048	6.874±0.073	4.221±0.051
(d)	-0.24±0.075**	-0.278±0.03**	0.172±0.072	-0.266±0.043	0.172±0.073*	-0.144±0.050**
(h)	0.682±0.139**	0.486±0.061**	0.577±0.124	-0.010±0.097	0.287±0.128*	0.329±0.102**
χ^2(3)	19.549**	11.577**	49.739	133.674	48.339**	26.548**
6-Parameter:						
(m)	7.116±0.147	5.020±0.076	7.499±0.113	4.455±0.056	7.418±0.159	4.223±0.096
(d)	0.335±0.191	0.310±0.107**	1.18±0.18**	0.645±0.070**	0.675±0.191**	0.518±0.141**
(h)	-1.098±0.715	-0.482±0.377	-1.098±0.596	-2.245±0.28**	-0.509±0.754	0.494±0.488
(i)	**-1.907±0.70****	**-0.980±0.372**	**-1.603±0.58***	**-2.177±0.26****	**-0.687±0.743**	**-0.010±475**
(j)	**0.195±0.415**	**0.053±0.230****	**2.363±0.4****	**-1.377±0.18****	**2.002±0.413****	**0.855±0.301****
(l)	**3.925±1.005****	**1.703±0.540****	**1.473±0.90**	**3.690±0.421****	**-1.018±1.028**	**1.318±0.715**
Type of epistasis :	**-**	**-**	**-**	**D**	**-**	**-**

*, ** significant at 5 per cent and 1 per cent level, respectively. D= Duplicate gene effect, C= Complementary gene effects.

additive × additive and additive × dominance in the expression of this trait. However, additive gene effects were positive and significant in 2 cases revealed that, this component could be improved through selection in these crosses. Positive and significant heterosis in ML 818 × RMG 991 in timely sown crop for this trait might be due to dominance effect only. Hegde *et al*. (1994) also reported importance of dominance effect in the inheritance of seed per pod.

For 100-seed weight both additive and dominance effects were highly significant in most of the crosses, however, the magnitude of dominance effect was much higher compared to additive in majority of the crosses, which suggested its predominant role in the expression of this trait. All the three types of epistasis were significant in majority of the cases, however, additive × additive and dominance × dominance components contributed maximum in crosses Pusa 0871 × M-818, ML 818 × RMG 991. Duplicate epistasis was present in 2 cases. Kattak *et al.* (2001) and Barad *et al.* (2008) also reported similar result.

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 × additive and dominance × dominance gene interactions.

Among three types of epistasis, sign attached to dominance × dominance effects was of more importance. Gamble (1962) suggested that negative effects of dominance × dominance was undesirable. Duplicate type of epistasis played significant role in the inheritance of grain yield in crosses Pusa 0672 × IPM 02-14 in late sown environment. In 3-parameter model dominant (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 dominant (h) was greater than additive (d) effects. The science and magnitudes of gene effects were influenced by the environments created by altering sowing dates as also reported by Kute *et al*. (1999), Meshram *et al*. (2013).

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 the sowing time (environment) indicating the need of specific breeding strategy for improvement of this trait. However, 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 green gram.

Results of the present study thus, indicated that dominance (h) effect and dominance × 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 bi parental mating in early segregating generations (Joshi and Dhawan, 1966) might prove to be an effective approach.

Conclusion

On the basis of the above observations, it was concluded that non-additive gene effects controlled the expression of most of the characters in both the environments and it is suggested that non-conventional breeding methods such as diallel selective mating, multiple crosses, bi parental mating and mass selection with recurrent random mating etc. are suitable for amelioration of grain yield through its component traits. The duplicate type of epistasis was also observed in most of the traits in generation mean analysis, so the selection intensity should be mild in the earlier and intense in later generations.

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