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Generation mean analysis for yield and yield components in mungbean (*Vigna radiata* L.Wilczek)

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SUMMARY

Using the means of P_1, P_2, F_1, F_2 and F_3 generations in each cross, estimates of various gene effects were obtained by partioning method of weighted least square analysis of three parameter model fitted to the five generation means of each cross for twelve characters. Additive-dominance model failed in all the cases, hence five parameter model was applied which gave the information about digenic interactions between genes at different loci. The nature of gene action for seed yield and yield attributing traits were assessed in four sets of crosses involving four oarents through generation mean analysis . An experiment was conducted to fulfill the objective of estimation of heterosis and to understand the genetic nature of seed yield and its contributing traits have been carried out by growing the parents, P_1 and P_2 along with F_1, F_2 and F_3 during *Kharif*, 2006 on July 10th, 2006 in Randomized Complete Block Design (RCBD) replicated four times. A total of 4 populations (4 crosses) and 5 generations of each cross were grown. The mean data of population were subjected to joint scaling test. The results of generation mean analysis indicated varying nature of genes under different genetic backgrounds. Significant inbreeding depression also gave an indication of prevalence of dominance genetic variance along with duplicate type of epistasis for most of the characters under study. Intermating or recurrent selection would be followed for genetic enhancement of grain yield in mungbean

Key words : Generation mean analysis, Five parameter model, Yield, Mungbean

Vigna, a pantropical genus comprises about 150 species, most of which are found in Asia and Africa. Only seven species of *Vigna* are cultivated as pulse crop, of which two are African and five are of Asiatic origin, in which Mungbean (*Vigna radiata* L. Wilczek) is an ancient and well known crop in Asia particularly in the Indian subcontinent and now becoming popular in other continents (Rahman *et al.*, 2003).

Likewise other pulse crops mungbean is a short duration grain legume crops with wide adoptability, low input requirements and helps in increasing soil fertility through its nitrogen fixation and deep root system, and proved an ideal for different crop rotations, intercropping, relay cropping and as catch crop. Virtually green gram and black gram being short duration and photo-thermo insensitive can help in increasing pulse production in India. Besides, it is widely grown as food legume, over a wide range of Agro-climatic conditions like rainy, winter and summer seasons but maximum area is under *Kharif* crop. India is the largest producer of mungbean, contributing 65 per cent by area and 54 per cent by production towards global mungbean production. In India, it is cultivated in about 2.75 million hectares with the production of 0.98 million tonnes. However, the national productivity remains low 425 kg ha^{-1} (Pandiyan *et al.*, 2006). Low yield and poor stability remains one of the most important constraints facing in its expansion.

In Chhattisgarh, mungbean occupies approximately an area of 46.42 thousand hectares, with total production of 16.30 thousand tonnes and productivity of 351 kg ha^{-1} (Anonymous, 2006). The low yield levels are due to several biotic and abiotic factors.The primary yield components in mungbean are pod $plant^{-1}$, seed pod^{-1} and 100 seed weight. The importance of these components mainly depends on the suitable breeding method and proper generation in the segregating population. The estimates of genetic components of variation would be very useful to adopt suitable breeding method and to find the best selection stage (generation) for the improvement of these traits (Khattak *et al.*, 2001).

MATERIALS AND METHODS

Genetics of yield and its component traits:

To understand the genetic nature of seed yield and its contributing traits have been carried out by growing the parents, P_1 and P_2 along with F_1, F_2 and F_3 during *Kharif*, 2006 on July 10th, 2006 in Randomized Complete Block Design (RCBD) replicated four times. A total of 4 population (4 crosses) and 5 generations of each cross were grown. Within each replicate, cross populations were

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first randomized and separate randomization was followed for all the replications. Generations within crosses/ populations were also randomized separately. Single row of 4 m length and 30 cm apart were planted for generations *i.e.*, P_1, P_2 and F_1 were grown in two rows each where as F_2 in 15 rows each and F_3 generation were grown in 8 rows. The plant to plant distance was maintained at 10 cm. Each cross and its generations were surrounded by border rows of mungbean variety Pusa vishal with same plant to plant and row to row spacing. A basal dose of fertilizer was applied at the rate of 20 kg N and 40 kg P_2O_5 and potash 20 kg ha^{-1}. Irrigation at sowing was given to ensure complete seed germination. Thereafter, irrigation was given after 20 days of sowing for adequate manifestation of various traits. Weeding and other agronomical operation were adopted for normal growth of the plant.

Observations recorded:

Observations on metric traits were recorded on single plant basis for each and every character mentioned below in all the crosses under study. Five single competitive plants were observed for each genotype in P_1, P_2 and F_1 but in F_2 all the single plants and in F_3, 25 plants were observed for the following observations:

Days to 50 per cent flowering:

This was noted on plot basis in terms of days taken from date of sowing to 50 per cent plants had initiated flowering.

Days to Maturity:

This was recorded in days taken from sowing to 90 per cent pods matured on each plant.

Plant height (cm):

Plant height was recorded in centimeter at maturity from the base of the plant at ground level to the tip of the main stem.

Number of primary branches $plant^{-1}$:

Number of primary branches $plant^{-1}$ were counted at the time of harvesting and averaged.

Number of clusters $plant^{-1}$:

Number of clusters $plant^{-1}$ were counted on five plants and averaged.

Number of pods $cluster^{-1}$:

Number of pods on each cluster of five plants were counted and averaged.

Pod length (cm):

The length of five fully developed healthy pods was measured in centimeter and averaged.

Number of pods $plant^{-1}$:

Total number of effective pods on individual plants was counted at maturity and averaged.

Number of seeds pod^{-1}:

This was recorded on individual plant by taking 10 pods randomly from each of the five plants at maturity and counting of the total number of seeds and averaged.

Grain filling per cent:

Grain filling per cent was recorded by dividing the number of seeds developed by the total number of ovules within the pod.

$$\text{Grain filling (\%)} = \frac{\text{Number of seeds}}{\text{Number of ovules}} \times 100$$

100 seed weight (g):

The test weight of 100 dried seeds was recorded in gram for each genotype.

Seed yield $plant^{-1}$ (g):

The weight of sun-dried seeds was recorded with the help of electronic balance for each individual plant and averaged.

RESULTS AND DISCUSSION

Using the means of P_1, P_2, F_1, F_2 and F_3 generations in each cross, estimates of various gene effects were obtained by partioning method of weighted least square analysis of three parameter model fitted to the five generation means of each cross for twelve characters. Additive-dominance model failed in all the cases, hence five parameter model was applied which gave the information about digenic interactions between genes at different loci. In absence of backcross generations 'd' and 'j' parameters could not be estimated separately and a combined estimates of (d-j) symbolized, as 'd' was estimated for each character separately. The two interaction effects namely, 'i' explaining sum of additive x additive effects of genes and 'l' *i.e.* sum of dominance x dominance effects of genes were estimated in five parameter model along with m, d and h. It will therefore, be convenient to present the results of this analysis separately for each cross combination for all the twelve characters of four crosses. The estimates are presented in Table 1, 2, 3, 4 and 5.

Breeding method for any crop improvement programme is largely depends on the nature of gene action prevailed. Study of gene effects controlling different characters is therefore, a pre-requisite for launching a systematic and meaningful crop improvement programme.

Quantitative characters, which are of great interest, are governed by large number of genes having their minor but own effects. These are too modified by several environmental factors (Johansen, 1926). Thus, analysis at the level of individual genes become impractical and whole genome analysis over the totality of the gene should be undertaken (Wright, 1956). The genetic variability, thus, should be partitioned into its broad components.

Most valuable genetic analysis of quantitative characters can be said to have initiated with the work of Fisher (1918). He showed that these characters measure continuous variation and follow the Mendelian laws. He partitioned hereditary variance into three components, (i) an additive portion resulting from average effects of genes, (ii) a portion resulting from dominance effects (intra allelic interaction) of genes, and (iii) a portion resulting from epistatic effects (non-allelic interaction) of genes.

Wright (1921, 1935) giving details division and designation defined the above three types of genetic variances namely, additive genetic variance, dominance variance and epistatic variance. Cockerham (1954) and Kempthrone (1954) further demonstrated that epistatic variance can be partitioned into two or higher order interactions designated as additive x additive, additive x dominance and dominance x dominance. Hayman and Mather (1955) described the digenic interactions in continuous variation. Such partitioning of variability into its components requires growing of large number of related generations under an appropriate design.

Hayman (1958) and Jink and Jones (1958) have developed independently the method of estimation of five genetic parameters using generation means. These

Table 1: Analysis of variance for yield and its components in mungbean

Source of variation	df	Mean sum of squares											
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of clusters plant^{-1}	No. of pods cluster^{-1}	Pod length (cm)	No. of seeds pod^{-1}	No. of pods plant^{-1}	Grain filling (%)	100 seed weight (g)	Seed yield plant^{-1}
Malviya Jyoti x TM 99-2 (C-1)													
Replication	3	4.65	4.04	41.48	0.13	5.71	0.20	1.56	0.55	10.23	20.84	0.10	0.12
Genotypes	4	7.75*	13.57*	73.43*	0.57*	9.39*	0.47*	7.16*	0.81	32.57*	62.42*	0.40*	4.34**
Error	12	2.14	3.67	20.83	0.15	2.84	0.14	1.75	0.66	8.91	10.39	0.11	0.39
Malviya Jyoti x TM 2000-2 (C-2)													
Replication	3	2.53	2.73	20.79	4.15	0.20	0.31	1.06	1.42	11.93	23.91	2.27	0.51
Genotypes	4	11.07*	8.69*	50.70*	13.30*	2.58**	1.50*	2.28*	3.19*	37.71**	119.17*	7.00*	3.65**
Error	12	3.40	2.23	12.58	03.00	0.36	0.40	0.65	0.66	6.13	34.37	1.35	0.83
Pusa Vishal x TM 99-2 (C-3)													
Replication	3	2.98	1.38	23.38	0.04	0.75	0.13	0.14	0.32	10.92	10.33	0.11	0.43
Genotypes	4	6.42*	5.67*	10.65*	0.08*	2.93*	0.27*	0.94*	20.36*	29.45*	24.32*	0.63*	4.97**
Error	12	1.70	1.70	2.55	0.02	0.83	0.07	0.29	1.71	08.77	6.29	0.8	1.37
Pusa Vishal x TM 2000-2 (C-4)													
Replication	3	2.33	1.23	15.03	0.08	0.64	0.07	0.13	0.12	21.78	3.13	0.20	2.14
Genotypes	4	8.67*	8.57*	64.96*	0.35*	2.94*	0.37*	0.42*	0.63*	61.13*	14.92**	0.80*	8.91**
Error	12	2.54	2.60	15.79	0.09	0.68	0.10	0.12	0.15	17.50	3.95	0.19	1.81

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 2: Estimates of gene effects for different characters in Malviya Jyoti x TM 99-2

Sr. No.	Characters	m	d	h	i	l	χ^2	Type of epistasis
1.	Days to flower initiation	32.25 ±1.03**	-1.37±0.49**	2.33±0.47**	4.70±1.95**	-10.66±11.61	693.97	Duplicate
2.	Days to maturity	72.25±1.03**	-1.87±0.82**	-0.83±3.51	-1.45±3.55	-3.33±10.20	355.12	Complementary
3.	Plant height	48.90±1.06**	4.61±2.20**	-3.71±5.21	9.99±3.00**	14.73±4.88**	199.75	Duplicate
4.	Primary branches plant^{-1}	2.05±1.14	-6.25±0.83**	-0.03±0.39	-0.97±0.45**	0.13±1.31	2.83	Duplicate
5.	Clusters plant^{-1}	5.52±0.49**	1.51±0.33**	-2.68±2.01	-3.72±1.89**	3.26±1.12**	15.72	Duplicate
6.	Pods cluster^{-1}	3.30±0.16**	-0.33±0.12**	1.60±0.48**	2.53±0.50**	-1.20±1.55	8.49	Duplicate
7.	Pod length	7.45±0.16**	-016±0.10	0.22±0.51	1.47±0.53**	-3.23±1.58	31.64	Duplicate
8.	Seeds pod^{-1}	10.97±0.22**	1.42±0.54**	-0.79±0.78	2.24±1.10**	-0.00±2.58	77.46	Complementary
9.	Pods plant^{-1}	19.70±0.69**	3.58±1.27**	-17.50±4.10**	11.66±3.37**	16.79±5.21**	86.10	Duplicate
10.	Grain filling per cent	93.50±1.84**	3.62±1.02**	12.83±4.11**	9.95±6.99	16.66±19.37	602.36	Complementary
11.	100 seed weight	3.55±0.25**	-0.32±0.10**	1.39±0.61**	0.34±0.18**	-1.59±2.13	8.26	Duplicate
12.	Seed yield plant^{-1}	7.13±0.67**	0.92±0.44**	2.85±0.75**	1.83±0.52**	-4.70±1.38**	14.97	Complementary

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 3 : Estimates of gene effects for different characters in Malviya Jyoti x TM 2000-2

Sr. No.	Characters	m	d	h	i	l	χ^2	Type of epistasis
1.	Days to flower initiation	32.00 ±0.81**	-0.37±0.62	-6.50±3.35	-3.37±3.35	6.00±2.00**	583.60	Duplicate
2.	Days to maturity	72.00±0.81**	3.50±0.56**	-13.00±7.16	0.25±7.71	-20.00±26.87	216.82	Complementary
3.	Plant height	61.07±2.30**	4.29±1.62**	5.53±2.48**	14.55±8.81	-31.46±23.55	212.22	Duplicate
4.	Primary branches plant^{-1}	2.40±0.14**	0.32±0.11**	-0.13±0.41	-0.15±0.46	3.26±1.38**	4.15	Duplicate
5.	No. of clusters plant^{-1}	5.62±0.37**	1.14±0.60**	3.55±1.12**	4.75±1.49**	-5.00±3.44	20.66	Duplicate
6.	No. of pods cluster^{-1}	3.85±0.15**	0.47±0.15**	2.38±0.60**	1.98±0.58**	-2.06±1.64	13.50	Duplicate
7.	Pod length	7.67±0.09**	-0.22±0.12	0.66±0.45	1.19±0.49**	-1.09±1.49	48.49	Duplicate
8.	No. of seeds pod^{-1}	10.52±0.33**	0.91±0.19**	-0.56±0.83	-2.39±0.95**	6.53±2.86**	74.70	Duplicate
9.	No. of pods plant^{-1}	22.50+1.91**	3.96+1.97**	5.56+2.65**	11.17+4.00**	-26.93+2.01**	284.81	Duplicate
10.	Grain filling per cent	89.00±3.34**	-1.62±1.47	2.33±7.49	-2.54±8.88	5.33±2.64**	614.39	Complementary
11.	100 seed weight	3.17±0.17**	-0.36±0.12**	-0.14±0.38	-0.38±0.55	-1.79±1.45	9.41	Complementary
12.	Seed yield plant^{-1}	7.12±1.01**	2.39±0.91**	3.21±1.31**	6.38±2.62**	-0.66±9.66	55.51	Duplicate

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 4: Estimates of gene effects for different characters in Pusa Vishal x TM 99-2

Sr. No.	Characters	m	d	h	i	l	χ^2	Type of epistasis
1.	Days to flower initiation	33.75 ±1.43**	2.25±0.77**	4.83±1.41**	6.08±2.51**	-12.66±3.37**	826.55	Duplicate
2.	Days to maturity	73.75±1.54**	3.87±0.83**	3.66±5.69	4.54±5.24	-13.33±15.76	376.83	Duplicate
3.	Plant height	48.70±2.98**	0.29±2.10	9.91±3.72**	-8.14±9.64	12.73±27.94	142.66	Complementary
4.	Primary branches plant^{-1}	2.15±0.17**	0.28±0.11**	-0.91±1.07	-0.96±0.87	1.53±2.51	2.55	Duplicate
5.	No. of clusters plant^{-1}	5.77±0.81**	1.11±0.51**	-1.19±4.37**	-0.96±3.67	0.40±10.80	23.60	Duplicate
6.	No. of pods cluster^{-1}	2.90±0.07**	-0.48±0.18**	-0.23±0.53	-0.33±0.54	2.66±1.22**	9.06	Duplicate
7.	Pod length	7.46±0.15**	0.33±0.12**	0.83±0.68	0.65±0.63	-0.64±1.87	45.13	Duplicate
8.	No. of seeds pod^{-1}	9.85±0.33**	0.95±0.31**	-0.36±0.14**	-1.26±0.99	2.53±2.99	76.53	Duplicate
9.	No. of pods plant^{-1}	17.40±1.41**	2.58±0.92**	0.96±5.55	0.45±5.11	9.46±15.21	341.30	Complementary
10.	Grain filling per cent	86.25±1.31**	0.37±1.17	-10.16±7.25	-10.79±4.99**	27.33±17.19	535.10	Duplicate
11.	100 seed weight	3.05±0.17**	-0.22±0.06**	-0.96±0.40**	1.41±0.50**	1.93±0.58**	7.74	Duplicate
12.	Seed yield plant^{-1}	5.19±0.29**	0.76±0.24**	-0.62±0.25**	-1.63±0.44**	5.98±2.28**	31.32	Duplicate

* and ** indicate significance of values at P=0.05 and 0.01, respectively

Table 5: Estimates of gene effects for different characters in Pusa Vishal x TM 2000-2

Sr. No.	Characters	m	d	h	i	l	χ^2	Type of epistasis
1.	Days to flower initiation	32.00 ±0.91**	1.87±0.80**	1.50±.24**	4.12±1.98**	-2.00±11.79	787.19	Duplicate
2.	Days to maturity	70.75±1.10**	2.25±1.07**	-1.33±3.95	-1.08±4.09	6.66±1.35**	367.79	Duplicate
3.	Plant height	51.75±1.25*	-0.29±1.68**	-6.94±2.37**	-1.82±7.54	-9.40±21.13	132.90	Complementary
4.	Primary branches plant^{-1}	2.35±0.22	0.34±0.17**	1.61±0.47**	0.49±0.63	-1.53±1.85	4.04	Duplicate
5.	No. of clusters plant^{-1}	4.72±0.42**	-0.02±0.87	-3.35±1.12**	0.77±1.77	-0.19±3.83	13.67	Complementary
6.	No. of pods cluster^{-1}	3.77±0.37**	0.42±0.17**	2.31±1.03**	1.09±1.19	-1.13±3.83	14.87	Duplicate
7.	Pod length	7.80±0.21**	0.99±0.41**	-2.81±0.85**	0.97±0.93	-2.56±2.47	31.49	Complementary
8.	No. of seeds pod^{-1}	10.95±0.34**	0.02±0.27	-2.25±1.20**	1.89±1.28	-7.39±3.24**	51.10	Complementary
9.	No. of pods plant^{-1}	18.25±1.78**	1.83±2.19	-0.88±5.52	5.22±2.79**	-1.53±17.04	234.41	Complementary
10.	Grain filling per cent	77.25±4.44**	-2.25±2.32	-12.16±11.72	-22.66±9.62**	59.33±29.10	535.21	Duplicate
11.	100 seed weight	3.60±0.18**	-0.75±0.22 **	2.01±0.65**	0.54±0.22**	-2.53±1.91**	11.35	Duplicate
12.	Seed yield plant^{-1}	7.33±0.97**	1.41±0.44**	2.90±0.36**	4.83±2.21**	-9.81±2.36**	33.67	Duplicate

* and ** indicate significance of values at P=0.05 and 0.01, respectively

models are based on certain assumptions such as (i) diploid inheritance, (ii) multiple allelism is absent, (iii) linkage is absent, (iv) absence of lethal genes, (v) constant variability for all genotypes and (vi) environmental effects are additive with the genotypic value.

Some of these assumptions like diploid inheritance, random distribution of environmental effects and constant variability of all genotypes can be satisfied. However, some of them like the absence of multiple allelism and epistasis are hardly realistic assumption, though unavoidable, if any analysis is at all to be possible.

Mather (1949) suggested three parameter model measuring a constant mean (m), additive gene effects (d) and dominance gene effects (h). These can be estimated by partitioning of generation means. Powers (1951), working on tomato used partitioning method based on certain assumptions such as (i) frequency distribution of any segregating or heterogeneous population is composed of several genotypes, (ii) the individuals possessing identical genotypes fluctuate about a common mean due to environmental variation. The validity of model can be judged by Chi-square test, while Hayman's (1958) method using generation means allows accommodation of epistasis.

In predominantly self pollinated crops like mungbean only additive component of genetic variation can be utilized. Among the interaction effects additive x additive type of interaction effects are more useful for the breeders. Complementary epistasis can also be successful exploited in the selection programme.

The present study was planned to estimate the nature and magnitude of allelic and non allelic interactions in mungbean. Four elite genotypes differing in many quantitative characters were chosen to generate variability in four cross combinations. The five generations of each of these crosses were grown and observations were recorded on twelve characters. The discussions on the results obtained with regard to nature of gene action are reported here cross and character wise.

Malviya Jyoti x TM 99-2:

In this cross both additive and dominance gene effects were found significant for days to flower initiation, number of pods cluster^{-1}, number of pods plant^{-1}, grain filling per cent, 100 seed weight and seed yield plant^{-1}. Plant height, number of clusters plant^{-1}, number of seeds pod^{-1} had significant positive significant additive gene effects whereas, days to maturity, number primary branches plant^{-1}, number of pods cluster^{-1} and 100 seed weight exhibited negative significant additive gene effects. Dominance effects were negative for days to maturity, plant height, number of primary branches plant^{-1}, number of clusters plant^{-1}, number of seeds pod^{-1} and number of pods plant^{-1}.

Epistasis was present in all of the characters under study. Additive x additive gene effects were found greater for most of the characters. Duplicate type of epistasis were found in majority of characters. Both types of interaction *i.e.* additive x additive and dominance x dominance were found significant for plant height, number of clusters plant^{-1}, number of pods plant^{-1} and seed yield plant^{-1}. Additive x additive type of gene interaction was found significant for all the character except days to maturity and grain filling percentage whereas, dominance x dominance type of gene interaction was found significant for plant height, clusters plant^{-1}, pods plant^{-1} and seed yield plant^{-1}. Additive x additive gene interaction was found significant and negative for number of primary branches plant^{-1} and number of clusters plant^{-1} whereas, dominance x dominance gene effect was significantly negative for seed yield. Both type of interactions were non significant for days to maturity and grain filling per cent. For days to flower initiation, number of primary branches plant^{-1}, number of clusters plant^{-1}, number of pods cluster^{-1}, pod length, number of seeds pod^{-1} and 100 seed weight dominance x dominance interaction was found non significant.

Malviya Jyoti x TM 2000-2:

Both additive and dominance gene effects were significant for plant height, number of clusters plant^{-1}, number of pods cluster^{-1}, number of pods plant^{-1} and seed yield plant^{-1}. Significant negative additive gene effects were recorded for 100 seed weight only. Except days to flower initiation, pod length and grain filling percentage all other characters were found having significant positive effects.

Duplicate type of epistasis was recorded in most of the characters except for days to maturity, grain filling per cent and 100 seed weight. Both additive x additive and dominance x dominance type of interactions were significant only for number of seeds pod^{-1} and number of pods plant^{-1}. Number of clusters plant^{-1}, number of pods cluster^{-1}, pod length, number of pods plant^{-1} and seed yield plant^{-1} showed significant positive additive x additive gene interaction, whereas days to flower initiation, number of primary branches, number of seeds pod^{-1} and grain filling per cent exhibited significant positive dominance x dominance gene effects. None of the characters showed negative significance for additive x additive gene effect whereas, only number of pods plant^{-1} exhibited significant negative dominance x dominance gene interaction.

Pusa Vishal X TM 99-2:

In this cross, both additive and dominance gene effects were significant for days to flower initiation, number of clusters palnt^{-1}, number of seeds pod^{-1}, 100 seed weight and seed yield plant^{-1}. Significant positive additive gene effects were recorded for days to flower initiation, days to maturity, number of primary branches plant^{-1}, number of clusters plant^{-1}, pod length, number of seeds pod^{-1}, number of pods plant^{-1} and seed yield plant^{-1} whereas, significant negative additive effects were exhibited for number of pods cluster^{-1} and 100 seed weight. Days to flower initiation and plant height had significant positive effects for dominance gene effects. Significant negative dominance effects were observed for number of seeds pod^{-1}, number of clusters plant^{-1}, 100 seed weight and seed yield.

Duplicate type of epistasis was recorded for most of the characters except plant height and number of pods plant^{-1}. Both additive x additive and dominance x dominance type of interactions were significant for days to flower initiation, 100 seed weight and seed yield plant^{-1}. Significant negative additive x additive interaction was found for grain filling per cent and seed yield plant^{-1}. Days to flower initiation and 100 seed weight showed significant positive additive x additive gene interaction. Significant negative dominance x dominance interaction was obtained only for days to flower initiation whereas, number of pods cluster^{-1}, 100 seed weight and seed yield plant^{-1} showed significant positive dominance x dominance gene interaction.

Pusa Vishal x TM 2000-2:

In this cross both additive and dominance effects were found significant for days to flower initiation, plant height, number of primary branches plant^{-1}, number of pods cluster^{-1}, pod length, 100 seed weight and seed yield plant^{-1}. Significant negative additive effects were observed for plant height and 100 seed weight. Days to flower initiation, days to maturity, plant height, number of primary branches plant^{-1}, number of pods cluster^{-1}, pod length, 100 seed weight and seed yield plant^{-1} exhibited significant positive additive gene effect. Except days to maturity, pods plant^{-1} and grain filling per cent, all other characters showed significant additive effects. Significant negative dominance effects were obtained for plant height, number of clusters plant^{-1} and number of seeds pod^{-1} whereas, days to flower initiation, number of primary branches plant^{-1}, number of pods cluster^{-1}, 100 seed weight and seed yield plant^{-1} showed significant positive dominance effects.

Dominance gene effects were found greater for most of the characters in this cross. Duplicate type of epistasis was recorded in most of the characters except plant height, number of clusters plant^{-1}, pod length, number of seeds pod^{-1} and number of pods plant^{-1}. Both additive x additive and dominance x dominance type of gene interactions were found significant for 100 seed weight and seed yield plant^{-1}. Days to flower initiation, number of pods plant^{-1}, grain filling per cent, 100 seed weight and seed yield plant^{-1} were found significant for additive x additive gene interaction whereas, days to maturity, number of seeds pod^{-1}, 100 seed weight and seed yield plant^{-1} showed significant dominance x dominance gene interaction. Additive x additive gene interaction was significant and negative for grain filling per cent only where as, number of seeds pod^{-1}, 100 seed weight and seed yield plant^{-1} exhibited negative significance for dominance x dominance gene interaction.

Present findings revealed the digenic control of all the characters under study. Similar results have also been reported by Patil *et al*. (1996). Seed yield plant^{-1} being a complex character showed its genetic control under additive, dominance and epistasis in all the four crosses with duplicate type of epistasis in these crosses except Malviya Jyoti x TM 99-2 where it is complementary type of gene action.

In general, dominance and dominance x dominance genetic variance were high showing preponderance of non fixable genetic variance which is further evidenced by high inbreeding depression in seed yield plant^{-1} in most of the cases. Patil *et al*. (1996) and Singh *et al*. (2007) while studying genetics of quantitative characters in mungbean also described the significance of dominance x dominance and additive x additive genetic variance with major role of duplicate type of gene action for seed yield and its contributing traits. Hence, plant breeders must be cautious while exercising selection especially for seed yield however, selection for superior single plants and their rigorous evaluation in successive generations may lead to fixation of desirable genes as evidenced by prevalence of additive and additive x additive genetic variances also.

Seed size and seed colour in mungbean are considered to be the market traits. Bold seed size with lush green colour are fetching higher market premium therefore, breeding strategies should be to evolve varieties with combination of these characters. In the present investigation seed size having significant positive correlation with seed yield had contributed the highest towards seed yield. Moreover, it showed its varying nature in different genetic backgrounds. In cross Malviya Jyoti x TM 99-2 and Pusa Vishal x TM 99-2 all three types of genetic variances were found important while in case of Malviya Jyoti x TM 2000-2 additive and dominance x

dominance were found significant while additive and dominance x dominance were found significant in case of Pusa vishal x TM 2000-2. Hence, careful selection be practiced for bold seed size. In accordance to these findings Ammavasai *et al*. (2005) and Singh *et al*. (2007) had also reported similar results in mungbean.

Important yield contributing characters like number of pods plant^{-1}, number of seeds pod^{-1}, pod length and number of pods cluster^{-1} also showed differential behaviour of genes in different genetic backgrounds. For pods plant^{-1} all additive, dominance, additive x additive and dominance x dominance variances were found important in cross Malviya Jyoti x TM 99-2 and Malviya Jyoti x TM 2000-2 however, in cross Pusa vishal X TM 99-2 and Pusa vishal X TM additive and additive x additive were found prevalent, respectively. Similarly for number of seeds pod^{-1} and pod length additive and additive x additive genetic variance were found more prevalent in all the crosses with significance of dominance and dominance x dominance genetic variance in few crosses. Additive, dominance and dominance x dominance type of gene action with duplicate type of gene action was found more prevalent in Malviya Jyoti x TM 99-2 and Malviya Jyoti x TM 2000-2 while additive and dominance or dominance x dominance gene action was found significant in cross Pusa vishal x TM 99-2 and Pusa vishal x TM 2000-2. Thus, results clearly indicate that yield and its contributing characters showed different type of gene interaction therefore, intermating or recurrent selection can be practiced for accumulating desirable genes. Patil *et al*. (1966) also suggested such types of breeding methodology for combining better genes.

Plant height additive and dominance both are important clusters plant^{-1} showed differential nature of inheritance in different backgrounds. In cross Malviya Jyoti x TM 99-2, additive, additive x additive and additive x dominance in cross Malviya Jyoti x TM 2000-2, additive, dominance and additive x additive; in cross Pusa vishal x TM 99-2 additive and dominance, and in cross Pusa Vishal x TM 2000-2 only dominance found prevalence. The results further showed decreasing effect of dominance with negative value in cross Pusa Vishal x TM 99-2 and Pusa Vishal x TM 2000-2 while additive x additive was decrease with decreasing effect in cross Malviya Jyoti x TM 99-2. The results further revealed that this character is under the control of duplicate type of epistasis in first three crosses and while it was complementary in cross Pusa Vishal x TM 2000-2. Ammavasai *et al*. (2005) also reported duplicate type of epistasis for this character in mungbean. Patil *et al*. (1996) reported both monogenic and digenic control of this character. Out of three, in two crosses they found complementary gene action while another cross had the duplicate type of gene action.

Growth characters like plant height in general exhibited equal importance of additive and dominance in Malviya Jyoti x TM 2000-2, Pusa Vishal x TM 2000-2 while in cross Malviya Jyoti x TM 99-2 dominance, additive x additive and dominance x dominance important. In cross Pusa Vishal x TM 99-2 only dominance was important. In cross Malviya Jyoti x TM 99-2 and Malviya Jyoti x TM 2000-2 duplicate type epsitasis was observed while in cross Pusa Vishal x TM 99-2 and Pusa Vishal x TM 2000-2 complementary gene action was noted. Ammavasai *et al.* (2005) and Singh *et al.* (2007) also observed duplicate types of epistasis for this character.

For primary branches plant^{-1} additive genetic variance was found important in all the crosses of mungbean. Among the digenic epistasis additive x additive in Malviya Jyoti x TM 99-2 and dominance x dominance in Malviya Jyoti x TM 2000-2 was also prevalent while in cross Pusa Vishal x TM 2000-2 dominance was equally important for this character. In all crosses duplicate type of epistasis was noted for this character which was in agreement with the findings of Ammavasai *et al*. (2005).

The trait grain filling per cent showed presence of digenic epistasis in its expression but showed varying nature of genetic control. In cross Malviya Jyoti x TM 99-2 both additive and dominance were found important while in cross Malviya Jyoti x TM 2000-2, dominance x dominance was important. Similarly, in cross Pusa Vishal x TM 99-2 and Pusa Vishal x TM 2000-2, additive x additive was significant with its decreasing effect.

In cross Malviya Jyoti x TM 99-2 and Malviya Jyoti x TM 2000-2 and in cross Pusa Vishal x TM 99-2 and Pusa Vishal x TM 2000-2 duplicate epistasis was important. It is therefore, advisable to the plant breeder that he must be cautious while exercising selection for higher percentage of grain filling particularly in cross Pusa Vishal x TM 99-2 and Pusa Vishal x TM 2000-2.

Mungbean, being short duration and photo insensitive crop is cultivated in all the three seasons of the year. Therefore, phenology of the crop is an important character. The results of the present findings showed prevalence of digenic epistasis for both days to 50 per cent flowering and days to maturity in all the crosses. In cross Malviya Jyoti x TM 99-2 and Pusa Vishal x TM 2000-2 additive, dominance and additive x additive were important for days to flowering. In cross Pusa Vishal x TM 99-2 all the four parameters, and in cross Malviya Jyoti x TM 2000-2 only, dominance x dominance was important for days to flowering. The results for days to maturity were somewhat different. In cross Malviya Jyoti x TM 2000-2 and Pusa

Vishal x TM 99-2 only additive genetic variance was found important while it was significant with decreasing effect in cross Malviya Jyoti x TM 99-2. In cross Pusa Vishal x TM 2000-2, additive and dominance x dominance were predominant with duplicate type of epistasis. In Malviya Jyoti x TM 99-2 and Malviya Jyoti x TM 2000-2 complementary epsitasis was found important, while duplicate type of epistasis was observed in rest of the cross for days to maturity. Similar findings were also reported by Patil *et al*. (1996), Kute and Deshmukh (2003), Ammavasai *et al.* (2005) and Singh *et al*. (2007).

This can be concluded from the present findings that seed yield and its related characters are under the control of duplicate type of epistasis mostly. The results further indicated varying expression of the genes under different genetic background. Significant inbreeding depression also gave indication of prevalence of dominance genetic variance along with duplicate type of epistasis for most of the characters under study. Under such circumstances intermating or recurrent selection should be follow for genetic enhancement of grain yield in mungbean.

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