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GENE ACTION FOR SEED YIELD AND MATURITY TRAITS IN MUNGBEAN (*Vigna radiate* (L.) R.Wilczek)

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ABSTRACT

Generation mean analysis in two crosses, involving four parents (SML-668, BM-2002-1, PKV Green Gold and BPMR-145) was studied to estimate nature of gene action involved in the inheritance of seed yield and maturity related traits. The mean data on six generation (P_1, P_2, F_1, F_2, B_1 and B_2) was subjected to joint scaling test. As per Cvalli's joint scaling test in the presence of epistatic, six parameter model was applied to detect the gene effects. Additive, dominance and epistasis interactions were found important in two crosses for three traits under studied. Dominance gene action was predominant for seed yield plant^{-1} in both crosses. The cross PKV Green Gold x BPMR-145 was found promising for further exploitation through biparental mating followed by selection.

Key words *: Mungbean, additive, dominance, epistasis, gene action.*

Pulses, best known as "poor man's meat", and mung bean or green gram (*Vigna radiate* (L.) R.Wilczek) is one of them and has easily digestible protein rich edible seed, it may be used to replace the expensive animal protein. It is grown in diverse climatic conditions as sole or intercrop with other field crops in different part of the country. However, the productivity of mung bean is very low due to low yield potential and narrow genetic base of existing cultivars. Knowledge of gene action pertaining to inheritance of yield and yield contributing characters through generation mean analysis is of immense use to plant breeders to decide suitable breeding strategy for improvement of these characters. Seed yield is an important trait as it measures the economic productivity of the crop, but its inheritance is extremely complex. The classical breeding systems that make use of additive genetic variance will be effective for improving the seed yield..Hence, the present study was attempted for understanding the nature and magnitude of different genetic components. The information generated will be helpful for designing effective breeding programme for improvement of this crop.

MATERIALS AND METHODS

The experiment was conducted in Randomized Block Design with three replications. Total 12 treatments consisting of two mungbean parents, ($P_1$and P_2) F_1, F_2, B_1 and B_2 generations of two crosses *viz.,* PKV green gold × BPMR-145 and SML-668 x BM 2002-1. Parents SML-668, BM-2002-1 and PKV Green- are early maturity with high yield and BPMR-145- is late maturity.

Among the treatments, each of the parents, F_1, B_1 and B_2 were represented by single row and $F_{2'}$ by four rows of 3.0 mt. length spaced at 30 cm apart with 10 cm distance between plants in a row. All cultural practices were followed to have a satisfactory crop growth. Observations were recorded on randomly selected competitive plants from each treatment in each replication. Five plants in parents and $F_{1's}$,10 plants in B_1 and B_2 and 20 plants in F_2 were selected and observations were recorded on days to 50% flowering, days to maturity and seed yield/plant. Data was subjected for analysis of variance as per (1). Components of generation means were analysed for two crosses using six basic generations *viz.,* P_1, P_2, F_1, F_2, B_1 and B_2. (2) Joint scaling test was applied to test the adequacy of additive-dominance model. Whenever, the model was found inadequate, (3) six parameter model was followed to estimate the different gene effects. In presence of epistasis, the additive (d), dominance (h) and non-allelic interaction components i.e. (I, j and l)of generation means were estimated as per (3).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among different generations for traits under study in two crosses viz.SML-668 x BM 2002-1 and PKV Green Gold × BPMR-145 indicating the presence of variability in the existing material. The significant estimate of Cavalli's (1952) Joint scaling test suggested the influence of epistasis in the inheritance of these traits in two crosses.The scaling tests emphasized that the simple additive-dominance model was inadequate in two crosses studied for different traits. Hence, six parameter model of Hayman (1958) was considered for estimation the gene effects i.e. m, d, h, i, j, l (Table-1).

Significance of gene effects (components) controlling to days to 50 % flowering was not consistent in two crosses. The significance of additive (d) effects in different crosses indicated his importance in expression of

Table-1 : Estimates of individual and joint scaling tests in two crosses of mung bean.

Characters	Crosses	Scaling tests				^{2}
		A	B	C	D	
Days to 50% flowering	C-I	-1.00**	4.13**	2.40*	-0.36	362.01**
	C-II	-2.80**	4.20**	-2.33	-1.87**	371.69**
Days to maturity	C-I	-1.46**	2.76**	0.47	-0.40	206.42**
	C-II	-2.20**	2.93**	-5.80**	-3.26**	231.55**
Seed yield/plant	C-I	-0.35**	-0.05	10.63**	5.52**	75.15**
	C-II	0.57**	0.94**	-0.20	0.86	31.45**

Table-2 : Gene effects for seed yield and other components of two crosses [C-I (SML-668 x BM 2002-1) and C-II (PKV Green Gold x BPMR-145)]

Character	Cross	^{2}	Genetic Components						Type of epistasis
			m	d	h	i	j	l	
Days to 50% flowering	C I	34.45**	34.45**	-4.20**	-1.63	0.73	-2.56	-3.86**	-
	C II	371.69**	34.58**	-5.70**	0.87	3.73**	-3.50**	-5.13**	-
Days to maturity	C I	206.42**	64.18**	-3.76**	-0.93	0.80	-2.10**	-2.06	-
	C II	231.55**	63.50**	-4.46**	3.43**	6.53**	-2.56**	-7.26**	Duplicate
Seed yield plant^{-1}	C I	75.15**	9.96**	-1.73**	-7.93**	-11.04**	-0.15**	11.45**	Duplicate
	C II	31.30**	7.99**	-0.57**	2.37*	1.73	-0.19	-3.26*	Duplicate

*, ** significant at 5% and 1% level, respectively.

days to 50% flowering. In cross I (SML-668 x BM 2002-1) and cross II (PKV Green Gold × BPMR-145), magnitude of additive component was higher than dominance components but among digenic interactions, dominance × dominance (l) component was significant indicating its predominance. The significance of additive x additive (i) type of non allelic interaction in cross II (PKV Green Gold × BPMR-145)for days to 50% flowering revealed its importance in selection programme. (4) also reported the similar interaction for days to 50% flowering (Table 2).

Only the additive gene effect was found important in the expression of days to maturity in the cross I (SML-668 x BM 2002-1), while both the additive and dominance gene effects were found important in the expression of days to maturity in cross II (PKV Green Gold × BPMR-145) having significant values. The magnitude of 'd' was higher than 'h' in both the crosses indicating predominance of additive gene action. These results are in conformity with the earlier findings of (4, 5). The estimates of all the epistasis interactions were significant with duplicate type of epistasis was observed for days to maturity in cross II. Additive x additive component, which is fixable and could be utilized in selection programme. Similar results were also reported (4).

Both the additive (d) and dominance (h) components played a significant role in the expression of seed yield plant^{-1} in both the two crosses with dominance (h) component was much high as compared to additive (d) component in both the crosses i.e. cross I (SML-668 x BM 2002-1) and cross II (PKV Green Gold × BPMR-145). Among digenic interactions, dominance x dominance (l) gene interaction was predominant in both the crosses. Duplicate type of epistasis was also detected in these two crosses for seed yield plant^{-1}. This revealed the complexity of gene action underlying for grain yield per plant. (6) has rightly pointed out that, where the inheritance of quantitative traits becomes more complex, the contribution of dominance gene effect to the inheritance becomes greater important. These results are in conformity with the earlier findings of (7, 8, 9).

On the basis of the limited material and number of generations used in this study the additive, dominance and epistatic gene effects were found to contribute significantly for the inheritance of various characters studied in mung bean. The dominant effects, whether significant or not, exceeded the corresponding additive effects with few exceptions in cross I (SML-668 x BM 2002-1) and cross II (PKV Green Gold × BPMR-145)for important yield and maturity related characters, which indicated the presence of either over dominance or complete dominance. Predominance of non-additive component in the inheritance of seed yield/plant and its components in mung bean has been reported by several workers.

Present study thus divulged that inter allelic interactions at digenic level played a greater role in the inheritance of seed yield and Additive and dominance interactions were found operating for the inheritance of maturity related traits. Thus, breeder should follow such breeding methods which can mop-up the genes to form superior gene constellation interacting in a favourable manner. Only duplicate type of epistasis was detected in both the crosses. Therefore, improvement may be expected by exploiting the additive genetic variance first *i.e*. by mild selection intensity in the earlier and intense in the later generations. The early generation isolates may be inter-mated to break undesirable linkages, so as to accumulate favourable additive genes. The Diallel Selective Mating system (10), which allows the infusion of new germplasm at various stages of breeding seems to be the alternative strategy.

CONCLUSIONS

Dominance (Dominance and dominance x dominance) gene action was found predominant in control of seed yield/plant. Therefore, Biparental Mating, Diallel Selective Mating, transgressive segregation followed by effective selection in subsequent generations may be fruitful for bringing improvement in seed yield/plant i.e., selection should be delayed to minimize the dominance effect until virtual homozygosity is attained. Whereas, in case of days to 50% flowering and maturity where additive and additive x additive gene effects were predominant, one should follow the simple selection in early segregating generations. Duplicate type of epistasis at digenic level was observed in both the crosses and hence selection intensity should be mild in earlier generation and intense in later generation. Restricted recurrent selection by inter-mating most desirable segregants followed by selection.

On the basis of results obtained from the experiment the cross PKV Green Gold x BPMR-145 may be expected the most promising to isolate desirable segregants. Pure line may be developed by adopting Single Seed Descent method. As sustainable variability present in early generations can be maintained up to complete homozygosity, as variability in F_2 generations remains very high and selection in early generations may result in drift of some valuable recombinations. Hence, pure lines may be developed by adopting single seed descent method which can efficiently exploit the genetic variation arising from additive and additive x additive type of epistasis.

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