ASSESSMENT OF GENETIC VARIATION FOR YIELD AND YIELD COMPONENTS IN MUNGBEAN (*VIGNA RADIATA* (L.) WILCZEK) USING GENERATION MEAN ANALYSIS

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Abstract

The genetic variation for yield and some important yield components was assessed in two sets of crosses involving four parents through generation mean analysis. The mean data of six populations (both parents, F_1, BC_1, BC_2 and F_2) were subjected to joint scaling test. In the presence of epistasis, six-parameter model was used to detect all types of gene actions. Both the crosses had shown complex genetic behaviour for all the traits examined, except branches per plant in cross 6601 x NM 92 and pod cluster per plant in cross ML-5 x NM 54. The additive (d) and dominant (h) components of genetic variation were significant for all the traits in both the crosses, but dominant (h) component was non-significant for branches per plant and 1000 seed weight in cross ML-5 x NM 54, and for pod bearing nodes on main stem in cross 6601 x NM 92. The duplicate type of non-allelic interactions were found for pod cluster per plant and 1000 seed weight in cross 6601 x NM 92, and for 1000 seed weight in cross ML-5 x NM 54. The complementary type of non-allelic interaction for seed yield per plant was found in both crosses. The intercrossing of F_2 plants are recommended to produce best recombinants for the traits having complex genetic behaviour and selection in the latter generations of segregating populations for developing high yielding mungbean genotypes.

Introduction

Mungbean like other pulse crops is being grown for hundreds of years under marginal conditions of moisture stress and low soil fertility. Under these conditions of poor crop management, natural selection has had a much greater role in determining the plant type and other characteristics of this crop than human selection. The genes for agronomic characteristics responsible for high yield have been eroded from mungbean like other marginal crops, which had relatively little value under the competitive and stress conditions of a wild habitat or a primitive agriculture (Tiwari *et al*., 1993; Khattak *et al*., 2001a).

Seed yield is an important trait as it measures the economic productivity in mungbean, but its inheritance is extremely complex. The classical breeding systems that make use of additive genetic variance will be effective breeding procedures for improving the mungbean seed yield, but very little basic information is available on all types of gene effects/inheritance controlling the seed yield and its components in mungbean (Khattak *et al*., 1999 a, b and 2001a, c). To exploit the existing genetic variability in mungbean breeding material for seed yield as efficiently as possible, the breeder would need the basic information regarding the inheritance of grain yield and its closely related components for devising an efficient selection program. In the present study the genetic components of variation was estimated through generation mean analysis to know the magnitude and behaviour of genetic components in the divergent parents for seed yield and its related components in mungbean.

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Materials and Methods

Three local (6601, NM 92 and NM 54) and an exotic Indian (ML-5) mungbean genotypes were hybridized in two sets of combinations according to the crossing technique of Khattak *et al.*, (1998). The basic population of each cross viz., two parents, their F_1, F_2 and back crosses BC_1 (F_1 x male parent) and BC_2 (F_1 x female parent) were developed and planted in a completely randomized block design with three replications on the research farm of Nuclear Institute for Food and Agriculture (NIFA) during kharif 2003. The parents, F_1 and back crosses were sown in two rows each, F_2 in 20 rows with the row length of 4 meter, and the spacing between rows and plants 30 and 10 cm, respectively. Data were recorded on 30 randomly selected plants of each parent and F_1, and on 50 plants of each back cross and 300 plants of each F_2 population. The data recorded were as follows:

Branches per plant: The number of pod bearing branches per plant at 90% pods maturity.

Pod clusters per plant: The number of pod bearing clusters per plant at 90% pods maturity.

Node of the first pod bearing peduncle: The first lower node with a pod bearing peduncle on a plant.

Pod bearing nodes on main stem: The number of nodes on main stem with pod bearing peduncle.

1000 seed weight (g): The weight of 1000 grains in grams.

Seed yield per plant (g): The weight of grains of the plant after threshing.

The joint scaling test (Cavalli, 1952) was used to detect epistasis for the all the traits measured. In the presence of epistasis, the additive (d) and dominance (h) effects, and non-allelic interaction components (i, j and l) of generation means were estimated according to Hayman (1958).

Results and Discussion

The estimates of joint scaling test and the magnitudes of components of genetic variation for the traits examined are presented in Table 1. The non-significant values of χ^2 for branches per plant in cross 6601 x NM 92 and pod bearing clusters per plant in cross ML-5 x NM 54 indicated the adequacy of the additive-dominance model to explain inheritance of these traits, whereas χ^2 values were significant for the remaining traits in both the crosses showing the presence of non-allelic gene interactions in the inheritance of these traits.

The significant values of additive (d), dominance (h) and absence of digenic non-allelic interaction in cross 6601 x NM 92 for branches per plant revealed that selection for this trait would be useful to start from the early segregating generation. Similarly, significant values of additive, and the non-allelic gene interaction, i.e., additive x dominant (j) for branches per plant in cross ML-5 x NM 54 also showed less complexity

Table 1. Estimates of gene effects for some quantitative traits in mungbean crosses.

...cter	Cross	m	d	h	i	j	l	χ^2	Type of non-allelic interaction
...ies per plant	6601 x NM 92	22.63*	3.52*	2.13*	-	-	-	2.45	-
	ML-5 x NM 54	1.46*	0.8*	-0.42	0.56	0.88*	0.07	44.18*	-
...sters per plant	6601 x NM 92	7.80*	5.7*	11.9*	11.0*	6.23*	-12.1*	860.17*	Duplicate
	ML-5 x NM 54	10.08*	0.76*	-2.07*	-	-	-	3.13	
...of the first pod bearing peduncle	6601 x NM 92	6.4*	2.1*	2.55*	2.2*	3.75*	-1.1	49.20*	-
	ML-5 x NM 54	7.23*	3.60*	6.79*	4.69*	1.10*	-2.63	141.07*	-
...aring nodes on main stem	6601 x NM 92	12.59*	4.17*	3.5*	-1.48	6.52*	0.51	77.98*	-
	ML-5 x NM 54	12.61*	5.33*	4.42*	0.77	1.95*	3.66	172.17*	-
...eed weight	6601 x NM 92	42.64*	14.30*	-11.0*	-7.96*	-25.1*	18.58*	149.20*	Duplicate
	ML-5 x NM 54	43.97*	7.01*	-2.33	-3.12	4.20*	9.31*	108.80*	Duplicate
...ield per plant	6601 x NM 92	10.86*	2.3*	11.97*	9.53*	-5.06*	10.7*	355.28*	Complementary
	ML-5 x NM 54	10.82*	0.39*	11.65*	10.24*	0.49*	2.23	492.50*	Complementary

in the inheritance of this trait. The lowest branch on mungbean plant initiated at 2nd or 3rd node of the plant, but the number of branches per plant are very sensitive to environmental fluctuations (Khattak *et al.*, 1999b). The additive and dominance gene action for branches per plant was also reported by some earlier researchers (Tiwari *et al.*, 1993; Khattak *et al.*, 2002c).

The pod clusters per plant had significant values for additive, dominance and non-allelic gene interactions, i.e., additive x additive (i), additive x dominance (j) and dominance x dominance (l) in cross 6601 x NM 92, whereas only d and h were significant for this trait in cross ML-5 x NM 54. The significant but opposite sign values of h and l in cross 6601 x NM 92 indicated duplicate type of non-allelic gene interaction for the pod clusters per plant. Both the additive and dominance gene actions for pod clusters per plant have been reported by Wilson *et al.*, (1985) and only dominance component by Ram (1997) in mungbean. Khattak *et al.*, (2002) have partitioned the pod clusters per plant in to pods cluster on main stem and branches per plant (Khattak *et al.*, 2001b, and 2002a.). They reported additive and dominance components for both pods on main stem and branches per plant.

The estimates of d, h, i and j were found significant for node of the first pod bearing peduncle in both the crosses. The positive and significant values of d and i for the node of the first pod bearing peduncle in both the crosses indicated the predominant role of additive component in the inheritance of this trait. The improvement in the node of the first pod bearing peduncle towards lower node in mungbean could easily be exploited due to predominant gene action of the additive genetic component (Khattak *et al.*, 2000a & 2001b).

The additive, dominance and dominance x dominance type of non-allelic gene interactions played an important role in the inheritance of pod bearing nodes on main stem. The effect of dominant gene action for pod bearing nodes on main stem should be eliminated through bulk selection method through which homozygosity could be achieved prior to the initiation of selection for the trait. The mungbean genotype with maximum number of nodes and less internodal length on main stem is preferred due to lodging resistance. The more number of nodes on main stem in mungbean ensure the provision of more locations for peduncles and thus would produce high seed yield (Khattak *et al.*, 2001a, b).

The estimates of all the genetic components, i.e., d, h, i, j and l were significant for 1000 seed weight in both the crosses. The positive and significant value of d, and negative but significant value of the additive x additive non-allelic gene interaction for 1000 seed weight in both the crosses indicated that negative alleles are dispersed in the parents involved in the crosses for the inheritance of this trait. Thus, the selection for 1000 seed weight should be delayed to latter generation such that the desired recombinants become available in the population. The large seed size is one of the main yield-contributing factors in mungbean. This trait is highly heritable and thus comparatively easy to select large seed size recombinants in mungbean (Khattak *et al.*, 1995, 1997, 1999b, 2002b & 2003). The transgressive segregation for 1000 seed weight has also been reported in mungbean (Waldia 1991, 1996; Khattak *et al.*, 2003). The significant but opposite values of h and l for 1000 seed weight in both the crosses indicated the involvement of duplicate type of non-allelic gene interaction in the inheritance of this trait. Similarly, all the components of genetic variation i.e., d, h, i, j and l were significant for seed yield in both the crosses. The significant and of the same sign values of h and l in both the crosses revealed the involvement of complementary

type of non-allelic gene interaction in the inheritance of seed yield in mungbean. The 1000 seed weight and seed yield showed complex inheritance in the present study. The additive, dominance and non-allelic interaction have also been reported for these traits in mungbean by some earlier researchers (Khattak, 2002d,e; Singh and Singh, 1996; Ram-1997).

All the traits examined in the present study have shown complex genetic behaviour. The simple selection procedure in the early segregating generation may not contribute significantly for the improvement of these traits. The complex genetic behaviour particularly additive and dominance components could be successfully exploited in later generation. It is therefore, suggested that the selection for the improvement of all these traits particularly seed yield should be delayed to the latter generation of segregation population in mungbean. The bulk method of selection is recommended in which selection is performed after attaining the homozygosity for maximum heterozygous loci. The biparental hybridization between recombinants in early segregating generation (F_2) would produce better genetic combinations through which the accumulations of desirable genes could be achieved for high yield potential in an individual line.

Acknowledgement

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