GENETICS OF PRODUCTIVE PEDUNCLES ON MAIN STEM AND BRANCHES IN MUNGBEAN (VIGNA RADIATA (L.) WILCZEK)

G.S.S. KHATTAK^{*} AND I. SAEED

¹Nuclear Institute for Food and Agriculture (NIFA), P. O. Box 446, Peshawar, Pakistan ^{*}Corresponding author E-mail: gssktt@yahoo.com

Abstract

Components of genetic variation for productive peduncles on main stem and branches in mungbean were estimated using triple test cross procedure. Treatments used for estimation of genetic variation for both traits exhibited highly significant differences which indicate the existence of considerable genetic variation among inbred lines, testers and developed recombinants. Epistatic effect showed significant role in the inheritance of both traits. Productive peduncles on main stem exhibited almost equal values for both i type, and j + 1 type non-allelic interaction whereas i type interactions value was more compared to j + 1 type interactions in productive peduncles on branches. This indicated that additive x additive type non-allelic interaction plays an important role in the inheritance of productive peduncles on branches. The complex inheritance of both traits can be exploited for improvement by delay in selection until the material is advanced through bulk procedure.

Introduction

The economic productivity in mungbean is measured through its yield. The inheritance of seed yield is very complex as it is controlled by large number of genes. The complex inheritance of seed yield in rice has also been reported by Saleem *et al.*, (2009b). Information about genetics of yield and its components may help to explore yield through combining suitable parents and effective selection procedures but the genetic basis of all yield components are meager in mungbean (Khattak, 2004a). Estimation of genetic components of the traits under improvement provides information which can be utilized to exploit heterosis or the accumulation of desired fixable genes to evolve cultivar (Khattak, 2004b; Saleem *et al.*, 2009a).

In the current study, genetic components of variation of the important yield components in mungbean i.e. number of productive peduncles on main stem and branches was estimated through a biometrical procedure called Triple Test Cross (TTC) as suggested by Khattak *et al.*, (2002) in mungbean and Saleem *et al.*, (2009b).

Materials and Methods

Two extreme high and low mungbean genotypes viz., ML-5 and Ramzan were used as testers. They were crossed in a combination of ML-5 x Ramzan during kharif (July-October) 2006. The resulting F_1 was the third tester designated. Ten true breeding genotypes viz., 6601, NM 20-21, Chakwal 97, Mung-88, NM 93, AEM 96, NFM 8-1, NM 13-1, NM 92 and NM 28 were crossed with the earlier mentioned three testers during summer (March-July) 2007. Testers were used as female in hybridization. The developed experimental material i.e., F_1 (ML-5 x Ramzan), 12 inbred lines (2 testers and 10 inbred lines), 20 single crosses, and 10 three-way crosses was planted in a randomized complete block design with three replications at the research station of Nuclear Institute for Food and Agriculture (NIFA), Peshawar, Pakistan, during kharif 2007. A plot size of 0.6 m² (single row plot of 2-meter length) was assigned to each entry in each replication. The plant-to-plant spacing between and within rows was kept 30cm and 10cm, respectively. The experimental material was bordered by standard mungbean variety NM 92 to avoid border effect. The experimental field soil was clay loam. Fertilizer was applied at the sowing @ 20N: 60P Kg/ha (one bag of DAP per acre). Weeds were removed manually. In summer season experimental crop was irrigated three times (First irrigation after third week of sowing, 2nd at the initiation of flowering and 3rd at the pod filling stage). In kharif no irrigation was required due to rainy season. The data were collected from 10 randomly selected plants per replication for the following traits:

- i. Number of productive peduncles (peduncles with pods) on main stem of plant (Average of productive peduncles of 10 randomly selected plants).
- ii. Number of productive peduncles on branches of plant (Average of productive peduncles of 10 randomly selected plants).TTC analyses were performed as described by Singh & Chaudhary (1985).

Results

Mean squares values calculated through analysis of variance for productive peduncles on main stem and branches of plant in mungbean are presented in Table 1. Highly significant differences were observed among treatments for both traits and between first parent (P_1) and second parent (P_2) for productive peduncles on main stem. The difference between first parent (P_1) and second parent (P_2) was significant for productive peduncles on branches. Analysis of variance results for the test of epistasis are presented in Table 2. Total epistasis (i, and j + 1 types) was highly significant both for productive peduncles on main stem and branches. The additive x additive (i type) interaction (homozygous x homozygous) was significant whereas additive x dominance and dominance x dominance (j and l types) interactions (homozygous x heterozygous and heterozygous x heterozygous) were highly significant. The epistatic effect contributed by an individual line for productive peduncles on main stem and branches is presented in Table 3. All lines contributed significantly to total non-allelic interactions in both traits except non-significant contribution of Chakwal 97 and AEM 98 to the total epistasis of productive peduncles on branches. Inbred line NFM 8-1 and NM 92 imparted major portion of positive and negative non-allelic interaction, respectively to productive peduncles on main stem. All inbred lines contributed positively to total epistasis of the productive peduncles on branches. The line NFM-13-1 was the highest non-allelic contributor to total epistasis in this trait.

Discussion

Significant variation among treatments (F_1 (ML-5 x Ramzan), 12 inbred lines (2 testers and 10 inbred lines), 20 single crosses, and 10 three-way crosses) indicated the existence of considerable genetic variation in inbred lines, testers and hybrids included in current study. The significant differences between first and second parent indicated that they were extremely high vs. low as reported by Saleem *et al.*, (2009b) in rice.

		Mean squares			
Source of variation	df	Productive peduncles on main stem	Productive peduncles on branches		
Replications	2	0.33	0.04		
Treatments	42	3.40***	3.50**		
Hybrids	29	2.92^{**}	3.83**		
Parents	12	4.29**	0.72^{*}		
Lines	9	4.88^{**}	0.81^{**}		
Testers	2	2.32**	0.57^{**}		
$P_1 + P_2$ vs. F_1	1	4.60**	1.08^{**}		
P_1 vs. P_2	1	4.04**	0.06^{**}		
Lines vs. tester	1	2.95**	0.19^{**}		
Hybrids vs. parents	1	6.70^{**}	27.44**		
Error	84	0.14	0.05		

 Table 1. Analysis of variance (mean squares values) of productive peduncles on main stem and branches in mungbean during Kharif 2007.

*, ** = Significant at 0.05 and 0.01 levels, respectively

Table 2. Analysis of variance (mean squares values) for the test of epistasis for productiv	ve
peduncles on main stem and branches in mungbean during Kharif 2007.	

		Mean squares	
Source	df	Productive peduncles	Productive peduncles
		on main stem	on branches
Total epistasis	10	13.34**	31.78**
Epistasis (i type)	1	12.16^{*}	227.42^{*}
Epistasis (j and l type)	9	13.48**	10.04**
Epistasis (i type) x blocks	2	0.05	0.33
Epistasis (j and l type) x blocks	18	0.20	0.18
Total epistasis x blocks	20	0.19	0.19

*, ** = Significant at 0.05 and 0.01 levels, respectively

Table 3. Epistatic deviations of individual mungbean genotypes for productive peduncles on main stem and branches exhibiting significant differences among genotypes tested in Kharif 2007.

Constynes	Productive peduncles on	Productive peduncles on			
Genotypes	main stem	branches			
Var. 6601	-2.63**	4.67**			
NM 20-21	-1.33**	1.50^{**}			
Chakwal 97	-1.50**	0.13			
Mung 88	-1.10**	3.07**			
NM 93	0.80^{**}	1.57**			
AEM 96	1.33**	0.13			
NFM 8-1	3.30**	3.90**			
NFM 13-1	0.60^{*}	4.90^{**}			
NM 92	-3.70***	4.67**			
NM 28	-2.30**	3.00**			
SE	0.25	0.25			

*, ** = Significant at 0.05 and 0.01 levels, respectively

The presence of epistatic effect for productive peduncles on main stem with almost equal values of i and j + l types interactions shows the complex inheritance of this trait. Similar yield components to productive peduncles on main stem i.e. nodes and clusters on main stem in mungbean are also reported with complex inheritance of dominance x dominance interactions (Khattak *et al.*, 2000, 2001 and 2004b). Productive peduncles on main stem are an important yield component in mungbean as contribution in yield through branches is uncertain due to their high sensitivity to environmental fluctuation (Khattak *et al.*, 2002). Thus more productive peduncles on main stem may be given more attention during breeding for high yield in mungbean. The plant type having more height and thick stem with more nodes on main stem exhibiting productive peduncles from the bottom nodes need to be selected to overcome yield losses in fluctuating environments of a genotype due to no or less number of branches.

The inheritance of productive peduncles on branches indicated significant non allelic interaction but compared to productive peduncles on main stem, it showed high value for additive x additive interaction than j + l type of interaction. Contribution of dominance effect in the inheritance of branches per plant has also been reported by Khattak *et al.*, (2004b). Branches per plant are an important yield contributing component if they exhibit more number of productive peduncles. There are genotypes which exhibit branches with less or no pods. Thus branches with more productive peduncles should be the main criterion of selection when seed yield is desired to be improved through number of branches per plant in mungbean. The significant epistatic effect contributed by an individual line for productive peduncles on main stem and branches indicated that lines used in this study had diverse genetic background (Pooni *et al.*, 1980). Non-allelic interactions detected in the inheritance of productive peduncles on main stem and branches in mungbean can be exploited through bi-parental approach and selection in advanced generations where trait is almost homozygous.

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References

- Khattak, G.S.S., M.A. Haq, M. Ashraf and G.R. Tahir. 2000. Heterosis for some morphological traits in mungbean (*Vigna radiata* (L.) Wilczek). *Kasetsart J. Nat. Sci.*, 34(4): 439-442.
- Khattak, G.S.S., M.A. Haq, M. Ashraf and G.R. Tahir. 2002. Triple test cross analysis for some morphological traits in mungbean (*Vigna radiata* (L.) Wilczek). *Euphytica*, 126(3): 413-420.
- Khattak, G.S.S., M.A. Haq, M. Ashraf, A. Jabbar and R. Zamir. 2001. Inheritance of some important agronomic traits in mungbean (*Vigna radiata* (L.) Wilczek). *Breeding Science*, 51(3): 157-161.
- Khattak, G.S.S., M. Ashraf and M.S. Khan. 2004a. Assessment of genetic variation for yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek) using generation mean analysis. *Pak. J. Bot.*, 36(3): 583-588.
- Khattak, G.S.S., M. Ashraf and R. Zamir. 2004b. Gene action for synchrony in pod maturity and indeterminate growth habit in mungbean (*Vigna radiata* (L.) Wilczek). *Pak. J. Bot.*, 36(3): 589-594.

- Pooni, D.P., J.L. Jinks and G.S. Pooni. 1980. A general method for the detection and estimation of additive, dominance and epistatic variation for metrical traits. IV. Trple test cross and analysis for normal families and their self. *Heredity*, 44: 177-192.
- Saleem, M.Y., J.I. Mirza and M.A. Haq. 2009b. Triple test cross analysis of some physiological traits in Basmati Rice (*Oryza sativa* L.). *Pak. J. Bot.*, 41(5): 2411-2418.
- Saleem, M.Y., M. Asghar, M.A. Haq, T. Rafique, A. Kamran and A.A. Khan. 2009a. Genetic analysis to identify suitable parents for hybrid seed production in Tomato (*Lycopersicon esculentum* Mill.). *Pak. J. Bot.*, 41(3): 1107-1116.
- Singh, R.K. and B.D. Chaudhary. 1985. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Pub. Ludhiana, New Delhi, Revised Ed. p. 318.

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