RESEARCH PAPER

Inheritance of quantitative traits and yellow mosaic virus in mungbean [*Vigna radiata* (L.) Wilczek]

M.B. PATEL*, J.H. VACHHANI, L.L. JIVANI, B.N. PATEL AND D.S. KELAIYA
Main Oilseeds Research Station, Junagadh Agricultural University, JUNAGADH (GUJARAT) INDIA

Abstract : This study comprised of five families to study gene action. For days to flowering, all three types of gene effects were observed in five families, this indicated that both additive as well as non-additive gene effects had a major contribution in inheritance of this trait. In plant height, all the type of gene effect were registered in five significant crosses but the magnitude of non-additive gene effect was much higher than additive component except in PDM 14 x GM 4, this cross expressed additive x additive (i) type of gene action. In seed yield, it was concluded that epistatic components additive x additive (i) and dominance x dominance (l) effect was significant in cross GM 4 x GM 3 and PDM 143 x GM9918, PDM 11 x K 851 and PDM 87 x GM 3, respectively. In general, the magnitude of dominance x dominance type of gene action was very higher magnitude for yield per plant. In this trait, none of the family observed significant in desire direction for intra- allelic interaction gene action for YMV incidence. For improvement of such crosses, *inter-se* mating, multiple crossing and recurrent selection would be more fruitful as dominance could be diluted due to inbreeding and additive gene could be fixed.

Key Words : Inheritance, Mungbean, Quantitative traits, YMV

INTRODUCTION

India has done remarkable progress in enhancing the productivity of cereals but the production of pulses to the level of self-sufficiency has been a cause of worry in the past and even today. Every year country suffers from gross deficit of pulses and shortfall in requirement is to meet through import from various countries. The yield levels of this crop could be increase by way of genetic improvement. However, very scanty information is available on this aspect of yellow mosaic virus in mungbean (MYMV). Identification of suitable parents for hybridization is an important means to meet the objectives of breeding programme. It not only helps to identify parents and crosses which are likely to give the maximum improvement for the trait under consideration but also provide means of understanding regarding gene action involved in it. An attempt was made to identity specific cross combinations for YMV incidence, seed yield and its components in mungbean.

The analysis of generation means (Hayman and Mather, 1995 and Hayman, 1958) is useful in testing the adequacy of different types genetic models and then estimating the genetic parameters in the form of components of means. The parameters obtained are useful to the breeder in understanding the genetic structure of populations, their variation and response to various breeding approaches. The grain yield is a very complex trait controlled by polygene with small effects. The information of genetic architecture of yield and its various components is therefore, the prerequisite for adopting a sound breeding programmme with the above in view, the present investigation was conducted to study genetic parameters for yield components, including resistance to yellow mosaic virus(YMV).

MATERIALS AND METHODS

This study comprised of five families to study gene action. Five families were *viz.*, PDM 143 x GM 9918, PDM 11 x K 851, PDM 14 x GM 4, PDM 87 x GM 3 and GM 4 x GM 3. From

---

* **Author for correspondence.**

these crosses were selfed and back cross to obtain their F_2, B_1 and B_2 generation. The crosses were affected in such way that, resistant x resistant, resistant x susceptible and susceptible x susceptible crosses for yellow mosaic virus can be derived. The experiment material comprised of parents (P_1, P_2), F_1, F_2, B_1 (F_1 x P_1) and B_2 (F_2 x P_2). Generations of all these five crosses were studied during summer season of 2004 at Main Pulses Research Station, Gujarat Agricultural University, Sardarkrushinagar. Each genotype consisted of single row of two meter length. The infector row of GM 3 variety (susceptible to YMV) was grown in alternate rows, so as to increase the incidence of yellow mosaic virus. The hybrid cotton and okra were also sown around the plot for increasing the incidence of the whitefly (*Bamisia tabaci*), which acts as a vector of the YMV. Five random plants were selected from each parents and crosses in each replication. The observations were recorded for eight important characters. The important character YMV incidence recorded prior to leaf senession on standard scale 0-5. International mungbean breeding nursery follows 5 point scale system for YMV incidence.

0 = No plant infection
1 = Up to 5 per cent plant infection
2 = Up to 6-15 per cent plant infection
3 = Up to 16-25 per cent plant infection
4= Up to 26-40 per cent plant infection
5= Up to 41 per cent or more plant infection

RESULTS AND DISCUSSION

The analysis of variance due to generation means was significant for most of the characters in all the crosses. The scaling (A, B, C, D) indicated an appreciable amount of epistasis

Table 1 : Estimate of genetic parameters for different quantitative traits in five crosses of mungbean

Crosses	Scale				Genetic components					
	A	B	C	D	m	d	h	i	j	l
Days to flowering										
PDM 143 x GM 9918	5.92	-1.53**	12.30	3.95	41.68**	-1.95	-10.09	-7.90**	3.72	3.51
PDM 11 x K 851	0.50	1.80	0.83	-0.73**	42.00**	-1.26**	-0.11	1.46**	-0.65	-3.76**
PDM 14 x GM 4	-1.46**	-0.98**	-1.81**	-0.66**	40.00**	2.33	-2.75**	-1.33**	1.22	0.85
PDM 87 x GM 3	-1.29**	-4.89	-8.35	-1.08**	38.83**	-0.08	1.19**	2.17**	1.80	4.01**
GM 4 x GM 3	-3.91	-6.22	-11.02	0.44	36.83**	-0.73	1.25	0.88	1.15	9.26
Plant height (cm)										
PDM 143 x GM 9918	3.58**	6.08**	4.39**	2.54**	71.24**	-10.66	4.48**	-5.09**	-3.24	5.79**
PDM 11 x K 851	4.51**	-5.87	4.71**	3.03	64.76**	-1.56**	-4.13**	6.07	5.19	7.43**
PDM 14 x GM 4	3.77**	-2.27**	-3.35**	-2.43**	61.13**	-5.67	5.87	4.86**	3.02	-6.36
PDM 87 x GM 3	-0.74	2.45**	7.10	2.69	60.71**	-4.93	6.19	-5.38	-1.60	3.67**
GM 4 x GM 3	-0.26**	2.58**	5.24**	2.45	71.71**	2.77	4.46**	-4.91	-2.42	4.58**
Pods per plant										
PDM 143 x GM 9918	-1.45**	-0.12	-0.43	0.57**	18.16**	-1.17**	0.69	-1.14**	-0.66	2.72**
PDM 11 x K 851	2.00	-1.17**	4.42	2.06	17.36**	3.34	-2.04**	-4.13	-1.85	3.84**
PDM 14 x GM 4	0.38	0.87	1.86	0.30	18.10**	-1.17	0.11**	-0.60	-0.24	-0.66**
PDM 87 x GM 3	055**	0.14	1.42	0.36**	17.22**	-1.08	-0.22	-0.73**	0.20	0.04
GM 4 x GM 3	1.03**	0.60**	2.07	0.21**	18.31**	1.32	-1.28	-0.43**	0.21	-1.20**
Seed yield per plant (g.)										
PDM 143 x GM 9918	1.03	-0.58**	2.15	0.85	8.08**	-0.14**	-0.76**	-1.71	0.80	1.27**
PDM 11 x K 851	-0.06	0.61**	3.36	1.41	7.28**	-0.29	-1.68**	-2.82	-0.33	2.27**
PDM 14 x GM 4	0.01	0.26**	2.21	0.96	7.16**	-0.84	-0.92	-1.93	-0.12**	-1.65
PDM 87 x GM 3	-0.40**	0.60	0.93**	0.36	5.83**	-0.76	0.02	-0.73	-0.50	0.53**
GM 4 x GM 3	0.85	0.40**	0.96	-0.14**	6.10**	1.98	-0.53**	0.28**	0.22	-1.54
YMV incidence (%)										
PDM 143 x GM 9918	1.33**	0.33	-2.33**	-2.00	10.86**	-0.50	4.83	9.24	2.51	-6.27**
PDM 11 x K 851	0.33	-0.66	-2.33**	-1.00**	-1.66**	0.33	1.50**	2.00**	0.50	-1.66
PDM 14 x GM 4	2.00	0.01	-6.00	2.00	2.00**	-2.66	5.00	4.00	-1.00	-2.00**
PDM 87 x GM 3	-0.66*	-5.33**	-2.33**	0.01	2.00**	1.00**	4.00	4.66	-0.33	-4.07**
GM 4 x GM 3	-1.66	-0.66**	-8.33	-1.00	-1.66**	1.00	7.16	6.00	-0.50	-3.66**

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

present in different traits of five crosses under study. Similar results haven reported by Ram (1997). For days to flowering all three types of gene effect *i.e.* additive, dominance and epistasis were involved in significant cross *viz.*, PDM 143 x GM 9918, PDM 14 x GM 4, PDM 87 x GM 3 and GM 4 x GM 3. This indicated that both additive as well as non-additive gene effects had a major contribution in inheritance of this trait. In epistasis, additive x dominance gene action did not participate in days to flowering. The additive (d) gene effect in negative direction was observed in PDM 11 x K 851, while dominance (h) gene effect was observed in cross PDM 14 x GM 4. Among the epistatic components, additive x additive (i) and dominance x dominance (l) was significant in cross PDM 143 x GM 9918 and PDM 11 x K 851, respectively. Among digenic epistasis, major role in inheritance of days to flowering was observed by additive x additive and dominance x dominance gene interactions. The presence of additive x additive gene action in the expression of the trait in crosses PDM 14 x GM 4 indicated that the desired improvement for this trait in this cross is expected through selection and isolation of desired homozygous recombination by employing pedigree method of selection, while remaining crosses *viz.*, PDM 143 x GM 9918, PDM 87 x GM 3 and GM 4 x GM 3 exhibited dominance type of gene action so these crosses improve by multiple crossing and bi-parental mating. The importance of dominance x dominance gene effect was reported by Ram (1997) and Godhani *et al.* (1978) reported the importance of additive x additive gene effect also. In plant height, all the type of gene effect were registered in five significant crosses but the magnitude of non-additive gene effect was much higher than additive component except in PDM 14 x GM 4, this cross expressed additive x additive (i) type of gene action. In general predominance of non-additive gene effect was depicted. For improvement of plant height, *inter-se* mating and reciprocal recurrent selection would the more effective to break undesirable linkage. Selection in later generation would be more fruitful as dominance could be diluted due to inbreeding and additive genes could be fixed. The presence of complementary epistasis was found in majority of the crosses. In pod per plant traits observed desire direction of significant was dominance (h) and dominance x dominance x dominance (l) type gene action play preponderance for governed this trait. In dominance (h) and dominance x dominance (l) gene effect was observed significant in PDM 14 x GM 4 and PDM 143 x GM 9918, PDM 11 x K 851, respectively. Additive component did not significant role in pod per plant. The results of the present study are in agreement with the finding of Khattak *et al.* (2002). In seed yield, it was concluded that epistatic components additive x additive (i) and dominance x dominance (l) effect was significant in cross GM 4 x GM 3 and PDM 143 x GM 9918, PDM 11 x K 851 and PDM 87 x GM 3, respectively. In general, the magnitude of dominance x dominance type of gene action was very higher magnitude

for yield per plant. In seed yield preponderance of non-additive gene effect was evident. For improvement of such trait *inter se* mating and multiple crossing would be more effective to break undesirable linkage. Preponderance of non-additive gene effect has been reported by Kute *et al.* (1995) and Khattak *et al.* (2001). The finding is also in agreement with result of Ram (1997) and Hegde *et al.* (1994), as they reported importance of both additive and non-additive gene effect for the inheritance for this trait.

The gene effects for YMV disease in crosses involving resistance x resistance, resistance x susceptible are presented in Table 1. The perusal of results on gene effect in PDM 143 x GM 9918, PDM 14 x GM 4, PDM 87 x GM 3 and GM 4 x GM 3 revealed significant dominance x dominance (l) gene effect. In this trait, none of the family observed significant in desire direction for intra- allelic interaction gene action. Under such situation this YMV resistance trait could be improved by multiple crossing and bi-parental crossing. Khattak *et al.* (1999) reported dominance gene effect in YMV with results reported here are in close agreement. It is difficult to go for reciprocal recurrent selection due to cleistogamous nature of mungbean. Hence, bi-parental mating, *inter se* mating and multiple crossing are the most desired breeding method to be used for the improvement of this crop.

REFERENCES

Godhani, P.R., Jaisani, B.G. and Patel, G.J. *(1978). Epistatic and other genetic variances in greengram varieties. *GAU Res. J.,* **4**:1-6

Hayman, B.I (1958). The separation of epistatic from additive and dominance. Variation in generation means. *Heredity.,***12** : 371-390.

Hayman, B.I. and Mather, K. (1955). The descriptions of genetic interaction in continuous variation. *Biometrics.*, **11**: 69-82

Hegde, V.S., Parameshwarappa, R. and Goud, J.V. *(1994). Genetics of some quantitative characters in mungbean [*Vigna radiata* (L.) Wilczek]. *Mysore. J. Agril. Sci.,* **28**:204-208

Khattak, G.S.S., Haq, M.A., Rana, S.A., Srineves, P. and Ashraf, M. (1999). Inheritance of resistance to mungbean yellow mosaic virus (MYMV) in mungbean [*Vigna radiata* (L.) Wilczek], *Thialand J. Agrcl. Sc.*, **32** :49-54.

Khattak, G.S.S., Haq, M.A. Ashraf, M. and Srinives, P.(2001). Combining ability in mungbean [*Vigna radiata* (L.) Wilczek]. *Korean J. Crop Sci.,* **46** : 420-423.

Khattak, G.S.S., Ashraf, M., Haq, M.A., Srinives, P. (2002). Genetic architecture of seed yield components in mungbean [*Vigna radiata* (L.) Wilczek]. *Trop. Agric.,***79** :260-264.

Kute, N.S., Deshmukh, R.B., Saroda, N.D. and Mamjae, M.K. (1995). Combining ability for yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. *Madras Agric. J.*, **86**:210-212.

Ram, T. (1997). Gene action for quantitative characters in greengram [*Vigna radiata* (L.) Wilczek]. *Indian J. Genet.*, **57**:143-148.

✽_✽_✽_✽_✽_✽