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GENERATION MEAN AND PATH ANALYSES OF REACTION TO MUNGBEAN YELLOW MOSAIC VIRUS (MYMV) AND YIELD-RELATED TRAITS IN MUNGBEAN (*Vigna radiata* (L.) Wilczek)

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SUMMARY

A study was conducted to determine types of gene action governing the resistance to mungbean yellow mosaic virus (MYMV) disease, yield components and effect of MYMV on yield-related traits. Two populations each composed of the generations P_1, P_2, F_1, F_2, P_1F_1 and P_2F_1 were developed from two crosses involving two susceptible ('BM1' and 'KPS1') and one resistant ('BM6') mungbean genotypes. Additive and dominant gene effects were found important in both crosses for all the traits examined. Additive gene effect contributed more to the resistance, while dominance and epitasis gene effect were found significant in most of the traits. For MYMV resistance, segregating populations were classified into four reactions, viz. susceptible (S), moderately susceptible (MS), moderately resistant (MR), and resistant (R). Segregation of the responses in F_2 populations agreed with a ratio of 9 S : 3 MS : 3MR : 1 R, suggested that the resistance was governed by two recessive genes. The mean number of major genes or effective factors controlling MYMV resistance in the crosses was estimated at 1.63 to 1.75 loci. The correlation estimates revealed that MYMV had negative correlation with number of pods per plant, seeds per pod, and 100-seed weight. Path coefficient analysis indicated that MYMV significantly and negatively affects yield-related traits, and thus suggested that breeder can use yield as a target selection trait for development of MYMV-resistant cultivar(s).

Keywords: Yellow mosaic disease, MYMIV, disease resistance, green gram

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INTRODUCTION

Mungbean (*Vigna radiata* (L.) Wilczek) is a self-pollinated grain legume and the third most important annual pulse crop of Asia. Mungbean can be grown in marginal soils with low inputs and is well suited to a large number of cropping systems due to its nitrogen-fixing ability. It can also improve soil fertility and texture (Graham and Vance 2003). Mungbean is an important source of easily digestible protein (up to 24%) and iron (40–70 ppm) for nutritionally balanced cereal-based diets in South and Southeast Asia (Bains *et al*., 2003; Weinberger, 2005). Sprouts and green pods of mungbean are also rich in vitamins and minerals, thus are good sources of dietary protein for poor people. Owing to its high demand, mungbean is incorporated into various cropping systems, especially as a summer crop in rice–wheat cropping system in Indo–Gangetic plains of India and Bangladesh. The mungbean cultivars released for spring/summer season in the past are generally of long duration (75-80 days), thus did not fit well with the cultivation in rice-wheat cropping system. Extensive cultivation year-round leads

to heavy disease and pest infestation, causing low productivity. Among various diseases, mungbean yellow mosaic virus (MYMV) is the most destructive and widely distributed, causing 10–100% yield loss depending on crop growth stage at the infection time (Marimuthu *et al*., 1981). MYMV is the major threat to mungbean production in Bangladesh, India, Pakistan, Philippines, Sri Lanka and Thailand (Malik and Bashir 1992). The use of resistant genotypes is the best way to reduce yield loss by MYMV disease.

Yield is a complex trait associated with various contributing characters which are interrelated. Knowing the magnitude and type of association between yield and its components would greatly help evaluating the contribution of different components upon yield as well as determining the suitable traits in indirect selection for seed yield. The correlation simply measures the association between yield and other traits. The path coefficient analysis allows further partitioning of correlation coefficients of yield-related traits into direct and indirect effects. The importance of correlation and path coefficient analysis is particularly appreciable when highly heritable characters associated with a complex trait like yield are identified, and successfully used as criteria for effective selection to achieve high yield. To accumulate yield contributing characters together with MYMV resistance, it is essential to know the association among various characters along with path coefficients between the major contributors and the target trait. The knowledge on nature and magnitude of genetic variation with respect to quantitative characters like yield and its components is also essential for crop improvement. Varietal resistance/tolerance to MYMV in mungbean was reported by Srinives (1996). Inheritance of the resistance has been reported as conferred by a single recessive gene (Basak *et al*., 2004; Reddy, 2009), a dominant gene (Sandhu *et al*., 1985), two recessive genes (Pal *et al*., 1991; Ammavasai *et al*., 2004). Understanding the reaction of each resistance gene to MYMV could lead to identification and pyramiding of the genes with different mechanisms that can complement each other.

There are reports on generation mean analysis (Khattak *et al*., 2002, 2004; Vinod and Kandali, 2012), and also on path coefficient analysis (Srivastava and Singh, 2012; Khajudparn and Tantasawat, 2011; Sriphadet *et al*., 2010) on yield-related traits in mungbean but none of them considered together with reaction to MYMV. Thus, the present study was conducted to investigate the inheritance of gene-specific resistance to MYMV and to examine the association between yield-related traits with MYMV resistance in mungbean.

MATERIALS AND METHODS

Plant material

Plant materials used in the present study are 2 mungbean populations developed from 3 mungbean genotypes, viz. MYMV susceptible 'BARImung1' (BM1) and 'Kamphaeng Saen1' (KPS1), and MYMV resistant 'BARImung6' (BM6). BM6 is selected from NM94 in which the latter is a derivative of NM36 (MYMV resistance) x VC2768A (MYMV susceptible). Each population comprises 6 generations, viz. P_1, P_2, F_1, F_2, P_1F_1 and P_2F_1 derived from BM1× BM6 and KPS1× BM6. The populations were developed at the field laboratory of the Department of Agronomy, Kasetsart University, Kamphaeng Saen, Nokhon Pathom, Thailand. To ensure infestation of MYMV, the field evaluation was performed at Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh. The tested site was characterized as having a clay soil having pH 5.7-6. The location is situated at 23^o 94' E and 90^o 42' N with the altitude of 33 m above mean sea level.

Field experiment

Two experiments were conducted; each consisted of 6 basic generations (P_1, P_2, F_1, F_2, P_1F_1 and P_2F_1) as mentioned above. Each generation was treated as a treatment and sown in a randomized complete block design with two replications at Bangladesh Agricultural Research Institute (BARI), Gazipur during March to May in 2012. Spacings used were 10 cm between plants in the same row, 40 cm between rows and 100 cm between the adjacent plots. Each row was 2 m long. The row length was always the

same while number of rows in the segregating generations (F_2, P_1F_1 and P_2F_1) were more than those in the non-segregating generations (P_1, P_2 and F_1), i.e. four rows for P_1, P_2 and F_1 and eight rows for F_2, P_1F_1 and P_2F_1. The highly susceptible BARImung1 was sown as 2 border rows around the plot. Fertilizers were applied at 40 kg/ha urea, 90 kg/ha triple super phosphate, 60 kg/ha muriate of potash and 40 kg/ha gypsum prior to soil preparation as per a fertilizer recommendation guide of Bangladesh. No insecticide was sprayed in order to maintain the natural white fly population. Weeds were controlled manually. The traits assessed were days to flowering, days to maturity, number of pods per plant, number of seeds per pod, 100-seed weight and MYMV disease score. Disease scoring was done when over 80% of the spreader plants (BM1) showed MYMV symptoms. For MYMV evaluation, number of MYMV infected plants in each generation and disease scoring scale were considered together. The scoring system was based on 1 to 9 rating scale as suggested by Singh *et al*., (1995). At maturity, the mature pods were harvested by hands.

Data analysis

The analysis of variance was done by an R program. Mean value, standard error and variance of different generations were subjected to analysis using a scaling test (Cavalli, 1952). Significance of the scales and gene effects were tested by using t-test (Singh and Chaudhury, 1985). Genetic effects were estimated using a model suggested by Mather and Jinks (1982). The A, B and C scaling tests were carried out for the traits indicated non-allelic interaction. The A and B tests provided the evidence for the presence of additive × additive (*i*), additive × dominance (*j*), and dominance × dominance (*l*) types of gene interactions. The C scaling provided a test for type-I epistasis. The type of epistasis was determined only when dominance (*h*) and dominance × dominance (*l*) effects were significant. The effects showing the same sign were complimentary to each other, while those with different signs indicated duplicated epistasis (Kearsey and Pooni 1996). The number of effective factors controlling resistance was estimated by five methods.

Method 1 was proposed by Wright (1968); $EF_1 = (P_2 - P_1)^2[1.5 - 2h\,(1 - h)]/8[\sigma^2_{F2} - 0.25(\sigma^2_{P1} + \sigma^2_{P2} + 2\sigma^2_{F1})]$. Where F_1, P_1 and P_2 are average, σ^2_{P1}, σ^2_{P2}, σ^2_{F1} and σ^2_{F2} are variance of the respective generations and $h = F_1 - P_1/P_2 - P_1$.

Method 2 was proposed by Mather and Jinks (1982); $EF_2 = [0.5(P_2 - P_1)]^2/[2\sigma^2_{F2} - (\sigma^2_{B1} + \sigma^2_{B2})]$. Where P_1 and P_2 are average and σ^2_{F2}, σ^2_{BC1}, and σ^2_{BC2} are variances of the respective generations.

Methods 3 to 5 were proposed by Lande (1981); $EF_3 = (P_2 - P_1)^2/8[\sigma^2_{F2} - 0.25(\sigma^2_{P1} + \sigma^2_{P2} + 2\sigma^2_{F1})]$, $EF_4 = (P_2 - P_1)^2/8[2\sigma^2_{F2} - (\sigma^2_{BC1} + \sigma^2_{BC2})]$, and $EF_5 = (P_2 - P_1)^2/8[\sigma^2_{BC1} + \sigma^2_{BC2} - (\sigma^2_{F1} + 0.5\sigma^2_{P1} + 0.5\sigma^2_{P2})]$. Where P_1 and P_2 are average, σ^2_{P1}, σ^2_{P2}, σ^2_{F1}, σ^2_{F2}, σ^2_{BC1}, and σ^2_{BC2} are variances of the respective generations.

All formulas are based on the assumption that genes segregating for MYMV resistance are located in the resistant parent, not linked, having equal effects on the resistance, and absent of epistatic effect, dominance effect, and genotype × environment effects (Wright 1968).

Correlation and path coefficient analyses were estimated adopting the procedure suggested by Dewey and Lu (1959).

RESULTS

Generation Mean Analysis

The mean values and standard errors of the analyzed traits are presented in Table 1. Significant differences were detected between the parental lines for all traits in both crosses except for seeds per pod and 100-seed weight in cross KPS1 × BM6. The hybrids seemed to be longer than mid-parent in days to flowering and days to maturity and larger in number of pods/plant, seeds/pod, 100-seed weight and MYMV disease reaction in both crosses. In general, the trait mean values for F_1 and F_2 generations were higher than the corresponding values of P_1F_1 and P_2F_1 generations. The values of the F_2 generation were lower than those of the F_1 generation in cross BM1 × BM6.

Table 1. Mean and standard error of the observed traits in 6 generations of 2 mungbean crosses derived from MYMV susceptible and resistant parents.

Traits Generations	Days to 1st flowering	Days to 50% flowering	Days to 1st pod maturity	Days to 50% pod maturity	Pods/plant	Seeds/pod	100 seed weight (g)	MYMV disease score
BM 1 X BM 6								
P_1	$41.69^{b} \pm 0.30$	$57.17^{a} \pm 0.30$	$66.00^{a} \pm 0.36$	$77.06^{a} \pm 0.35$	$20.19^{a} \pm 0.32$	$7.92^{c} \pm 0.32$	$2.95^{d} \pm 0.03$	$7.50^{a} \pm 0.20$
P_2	$29.44^{e} \pm 0.37$	$35.38^{d} \pm 0.23$	$50.50^{e} \pm 0.40$	$57.13^{d} \pm 0.30$	$15.63^{c} \pm 0.34$	$11.50^{a} \pm 0.28$	$4.87^{a} \pm 0.07$	$1.75^{c} \pm 0.18$
F_1	$38.27^{c} \pm 0.22$	$49.19^{b} \pm 0.22$	$62.60^{ab} \pm 0.23$	$68.31^{b} \pm 0.23$	$21.13^{a} \pm 0.41$	$11.89^{a} \pm 0.22$	$5.01^{a} \pm 0.22$	$5.00^{b} \pm 0.41$
F_2	$35.81^{d} \pm 0.78$	$44.25^{c} \pm 0.90$	$56.00^{c} \pm 1.05$	$63.00^{bc} \pm 1.02$	$17.75^{b} \pm 0.56$	$10.47^{b} \pm 0.45$	$4.45^{ab} \pm 0.19$	$4.25^{b} \pm 0.22$
P_1F_1	$45.19^{a} \pm 0.43$	$47.38^{b} \pm 0.56$	$65.38^{a} \pm 0.49$	$74.13^{a} \pm 0.59$	$19.06^{ab} \pm 0.39$	$9.59^{b} \pm 0.25$	$3.94^{bc} \pm 0.08$	$6.38^{a} \pm 0.50$
P_2F_1	$31.25^{e} \pm 0.36$	$36.00^{d} \pm 0.39$	$53.28^{cd} \pm 0.67$	$60.59^{c} \pm 0.70$	$16.25^{bc} \pm 0.38$	$10.88^{ab} \pm 0.34$	$4.25^{b} \pm 0.06$	$3.50^{b} \pm 0.37$
KPS 1 X BM6								
P_1	$44.12^{a} \pm 0.30$	$55.38^{a} \pm 0.28$	$67.31^{a} \pm 0.29$	$81.06^{a} \pm 0.19$	$17.00^{b} \pm 0.27$	12.69 ± 0.23	6.03 ± 0.04	$7.88^{a} \pm 0.25$
P_2	$30.00^{d} \pm 0.17$	$36.95^{d} \pm 0.19$	$49.90^{d} \pm 0.22$	$58.88^{d} \pm 0.20$	$15.18^{c} \pm 0.32$	11.80 ± 0.19	4.75 ± 0.03	$1.7^{c} \pm 0.20$
F_1	$36.63^{b} \pm 0.22$	$46.79^{c} \pm 0.22$	$56.83^{c} \pm 0.35$	$65.69^{bc} \pm 0.22$	$18.69^{a} \pm 0.25$	12.19 ± 0.25	6.23 ± 0.22	$7.00^{a} \pm 0.46$
F_2	$37.16^{b} \pm 0.78$	$45.88^{c} \pm 1.17$	$60.23^{b} \pm 0.95$	$69.00^{b} \pm 1.11$	$16.50^{b} \pm 0.48$	11.50 ± 0.35	5.08 ± 0.20	$5.13^{b} \pm 0.22$
P_1F_1	$44.69^{a} \pm 0.54$	$51.00^{b} \pm 0.52$	$65.33^{a} \pm 0.46$	$72.50^{b} \pm 0.76$	$17.94^{a} \pm 0.34$	12.30 ± 0.33	5.94 ± 0.08	$6.00^{b} \pm 0.40$
P_2F_1	$34.80^{bc} \pm 0.41$	$39.63^{d} \pm 0.43$	$54.25^{c} \pm 0.39$	$65.59^{bc} \pm 0.60$	$15.00^{c} \pm 0.38$	11.25 ± 0.36	5.22 ± 0.06	$4.13^{c} \pm 0.43$

Means in the same column with the same letter are not significantly different (at $P \leq 0.05$) by DMRT.

The values of P_1F_1 and P_2F_1 progenies resembled their respective recurrent parents with respect to their characteristics, while the F_2 individuals varied considerably for the yield-related traits examined. In the field, the resistant plants did not show any yellow mosaic symptoms on leaves or pods during the entire growth period, while the susceptible plants showed various grades of yellowish symptom. For disease incidence in resistant × susceptible crosses, F_1 from the cross KPS1 × BM6 showed similar symptoms to that of the susceptible parent, while F_1 from the other cross BM1 × BM6 was near to mid-parent value. Segregating populations were classified into four reactions, susceptible (S), moderately susceptible (MS), moderately resistant (MR) and highly resistant (R). The pattern of segregation ratio in the F_2 was 9S:3MS:3MR:1R. The segregation ratio of both crosses also suggested a possible 3:1 (Table 2), given that susceptible and moderately susceptible are considered as susceptible and moderately resistant and resistant as resistant.

Gene action

The estimates of gene effect in the individual cross clearly illustrate high variation in the observed traits (Table 3). Mean and additive components for days to first flowering, days to 50% flowering, days to first maturity, days to 50% maturity, pods/plant, seeds/pod, 100-seed weight and MYMV disease score were highly significant. The additive, dominance and epistatic gene actions in each cross were found significant in days to flowering and maturity. Days to first flowering and days to first maturity of both crosses showed a significant additive (*d*), dominance (*h*), additive × additive (*i*), and additive × dominance (*j*) types of gene action. For days to 50% flowering, both crosses showed significant additive and dominance gene action, but only BM1 × BM6 showed additive × additive (*i*) and dominance × dominance (*l*) interaction. In case of days to 50% maturity, both crosses showed significant additive and non-allelic additive × dominance interaction. For number of pods per plant and 100 seed weight, additive gene showed more important action than the other gene actions in both crosses. Additive effect was the only significant portion of gene controlling seeds per pod of these mungbean. Finally, additive and dominance gene effects were found important in controlling MYMV disease reaction. The plus sign in the additive gene effect implies that P_1 contributes positively to the trait as compared to P_2, and vice versa. The estimates of effective factors/minimum number of genes controlling MYMV resistance are presented in Table 4. The number of effective factors ranged between 1.35 to 2.09 in BM1× BM6 and between 1.29 to 1.98 in KPS1 × BM6.

Table 2. Segregation of MYMV reaction in F_2 generation from the cross between MYMV susceptible and resistance parents.

Crosses	Total number of F_2 plants	MYMV reaction of F_2 plants				Chi-square	P-value
		S	MS	MR	R	expected values	
		Susceptible		Resistant		9:3:3:1 or 3:1	
BM 1 X BM 6	138	76	23	28	11	1.17	0.90-0.75
		99		39		0.78	0.50-0.25
KPS 1 X BM6	117	64	19	25	9	0.894	0.90-0.75
		83		34		1.02	0.50-0.25

Table 3. Estimates of gene effects for maturity, 100 seed weight and MYMV reaction in two mungbean crosses.

Character	Cross	*m*	*d*	*h*	*i*	*j*	*l*
Days to 1st	BM 1 X BM 6	35.38±0.78**	14.62±0.66**	13.03±3.43**	11.24±3.41**	7.92±0.70**	-16.50±4.14**
flowering	KPS 1X BM 6	36.75±0.97**	7.81±0.72***	12.62±4.15**	15.62±4.13**	1.31±0.74*	-35.57±4.88**
Days to 50%	BM 1 X BM 6	44.26±0.94**	10.25±0.75**	-9.05±4.08*	-11.98±4.06**	-0.63±0.78	37.86±4.89**
flowering	KPS 1X BM 6	47.25±0.64**	10.35±0.63**	-2.21±1.26*	-	-	-
Days to 1st pod	BM 1 X BM 6	53.75±0.94**	11.94±0.81**	18.48±4.46**	13.64±4.60**	3.59±0.85**	-8.21±5.54
maturity	KPS 1X BM 6	56.50±1.07**	12.23±0.50**	4.97±3.93*	10.50±3.92**	3.28±0.57**	-14.42±4.33*
Days to 50% pod	BM 1 X BM 6	67.94±1.02**	13.82±0.44**	-2.66±4.21	-2.88±4.19	3.85±0.50**	2.81±4.53*
maturity	KPS 1X BM 6	66.96±1.10**	6.00±0.96**	-3.10±4.83	4.24±4.821	-5.08±0.96**	-11.04±5.91
Pods/plant	BM 1 X BM 6	17.88±0.48**	2.32±0.42**	7.35±2.22**	4.10±2.19*	0.06±0.54*	-1.70±2.89*
	KPS 1X BM 6	16.16±0.34**	2.13±0.44**	2.22±1.70	-0.38±1.64	1.22±0.49*	5.68±2.42*
Seeds/ pod	BM 1 X BM 6	10.47±0.36**	-1.29±0.41**	1.24±1.69	-0.94±1.66	-0.50±0.45	-3.20±2.27
	KPS 1X BM 6	11.25±0.26**	1.25±0.30**	2.05±1.25	1.74±1.23	0.43±0.33	-0.35±1.70
100 seed weight	BM 1 X BM 6	3.85±0.05**	-0.93±0.04**	1.10±0.11	-	-	-
	KPS 1X BM 6	5.08±0.20**	0.53±0.14**	2.46±0.84**	1.62±0.82*	-0.11-±0.14	-0.32±0.97
MYMV disease	BM 1 X BM 6	6.38±0.42**	1.88±0.53**	3.69±2.03**	-	-	-
score	KPS 1X BM 6	6.50±0.47**	2.87±0.61**	3.73±2.34**			

* and ** indicate significant difference at 5% and 1% probability levels, respectively.

Table 4. Estimates of minimum number of genes or effective factors (EF) controlling MYMV resistance in mungbean.

Cross	EF1	EF2	EF3	EF4	EF5	Mean
BM 1 X BM 6	1.93	1.87	1.49	1.35	2.09	1.75
KPS 1X BM 6	1.98	1.46	1.92	1.29	1.53	1.63

Table 5. Correlation coefficients among MYMV reaction and yield-related traits in mungbean.

	100-seed weight	Seeds/ pod	Pods/ plant	Days to first flowering	Days to 50% flowering	Days to first maturity	Days to 50% maturity
MYMV	-0.869**	-0.873**	-0.817**	0.348	0.396	0.297	0.162
100 seed weight.		0.792**	0.764**	-0.360	-0.422	-0.091	-0.123
Seeds/ pod			0.741*	-0.256	-0.287	-0.195	-0.018
Pods/ plant				-0.456	-0.450	-0.209	-0.084
Days to first flowering					0.964**	0.661**	0.721**
Days to 50% flowering						0.637**	0.797**
Days to first maturity							0.528*

* and ** indicate significant difference at 5% and 1% probability levels, respectively.

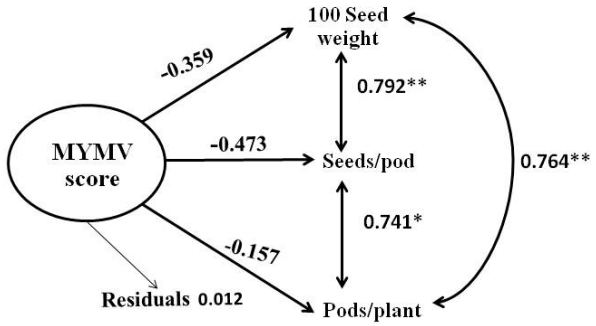

Figure 1. Path coefficients between MYMV score and yield-related traits in mungbean.

Correlation and path coefficient analysis

Correlations among MYMV score and seed yield-related traits are presented in Table 5. MYMV showed negative correlation with 100-seed weight, seeds per pod, and pods per plant while 100-seed weight was positively correlated with seeds per pod and pods per plant. Mathur and Jinks (1994) reported that the magnitude of correlation among attributes depends on development of the relationship between them, and genetic linkage or pleiotropic effect of genes. MYMV scores showed no correlation with days to flowering and days to maturity, while the latter two traits showed positive correlation with each other. The association between MYMV and yield related traits were partitioned into direct and indirect effects through path coefficient analysis (Figure 1). For positively related characters, improvement of one character will result in a simultaneous improvement of the others. This relationship caused indirect effects among the yield components upon seed yield, giving a combined R^2 for the three yield-related traits of 0.988. The low residual effect (0.012) revealed that the yield components chosen in this study are suitable to explain the variation in MYMV score.

DISCUSSION

A similar variation in gene action were observed from the same characters in both crosses showing the presence of similar gene loci and frequencies opposing and reinforcing the traits involved in the crosses (Mather and Jinks 1982). Positive dominance gene effect implies its enhancing effect on the performance of different traits. For days to 50% flowering and 50% pod maturity, both crosses showed the important role of additive and dominance gene effects. The negative dominance effect indicated that it promotes early maturity. Khattak *et al*. (2002) reported that all types of gene action controlled days to flowering and maturity in mungbean. Selection for early maturity should be deferred to later generations after genes controlling the other desirable traits have been fixed. For seeds/pod in BM1 × BM6 cross, *h* and *l* values with opposite sign indicate the duplicate type of non-allelic gene interaction. The involvement of non-allelic interactions along with additive and dominance gene effects in inheritance of mungbean traits were reported earlier by Singh & Singh (1996), Ram (1997) and Khattak *et al*. (2002). The additive, dominance and additive × additive gene effect were involved in 100-seed weight in the cross BM1 × BM6. The additive × additive gene action suggests the possibilities in obtaining transgressive segregants in later generations. The magnitude of significant genetic components varied depending on parents and traits chosen. In chickpea and mungbean, varying magnitudes of additive and non-additive gene effects were reported earlier in different traits (Singh *et al*., 1993; Ram, 1997; Khattak *et al*., 2002). Simultaneous occurrence of significant estimates of different types of gene action in most traits revealed action of the same genes contributing towards each genetic component. The complementary types of gene interaction, particularly *i* and *l* reinforce, but the duplicate type of gene action (*j*) opposes the effect of dominance component. The segregation ratio in the F_2 populations from both crosses supports 9 S : 3 MS : 3 MR : 1 R, revealed two recessive genes controlling the resistance to MYMV disease. This finding agrees with the earlier reports by Pal *et al*. (1991) and Ammavasai *et al*. (2004). Each F_2 population was grouped into four classes on the basis of a disease rating scale together with phenotypic observation of the infected plants at different growth stages. The susceptibility of the F_1 plants in both crosses to MYMV revealed that the resistance is recessive. Our result shows a digenic inheritance of this trait similar to the report of Verma and Singh (1988) and Ammavasai *et al*. (2004). The segregation ratio of 15:1 was detected in the F_2, probably due to different rating scales used (Verma and Singh, 1988; Pal *et al*., 1991; Ammavasai *et al*., 2004). Vinod and Kandali (2012) also reported a resistance response in their F_2 mungbean populations being governed by 2 recessive genes each with incomplete dominance action. The work of Vinod and Kandali, (1012) and the present study showed

that when one resistance locus is present in the homozygous recessive condition it conferred MR reaction to the plant, while homozygous recessive in the other locus conferred MS. When both resistance genes jointly present in the homozygous recessive state, the plants show resistant reaction (R). The estimates of number of genes/effective factors in Table 4 also indicated that 2 genes were involved in the inheritance of resistance to MYMV.

In order to understand significance of the correlations between traits studied, the data were subjected to path coefficient analysis which showed that mean seed weight is the most important yield component and directly proportional to seed yield per plant. Among the traits, number of pods per plant is the major yield component and thus should be given high priority in selection strategy for yield improvement in mungbean. Sriphadet *et al*. (2010) and Idress *et al*. (2006) showed high direct effect of pods per plant and seeds per pod on yield in mungbean, while Kutty *et al*. (2003) reported a similar result in cowpea. The correlation between seeds per pod with seed weight was positive, indicated that high yielding mungbean genotypes derived from these materials can be obtained by selecting high number of seeds per pod and pods per plant which will increase seed weight and ultimately seed yield. In the present study, MYMV incident was negatively correlated with 100 seed weight, seeds/pod and pods/plant. Although MYMV caused small negative effect to 100 seed weight, seeds/pod and pods/ plant, the combined effects of the yield components were high due to high positive correlations among them. Low chlorophyll concentration from MYMV infection directly limits photosynthetic potential and hence reduces primary products of photosynthesis and also the yield-related traits.

This study gives useful information for plant breeders to develop new mungbean cultivars resistant to MYMV with desirable yield components.

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