RESEARCH ARTICLE Legume Research- An International Journal, Volume 46 Issue 11: 1541-1546 (November 2023)

Generation Mean Analysis for Yield, its Components and MYMV Disease Resistance in Greengram [*Vigna radiata* (L.) Wilczek]

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10.18805/LR-4829

ABSTRACT

Background: Greengram or mungbean is a diploid (2n=22) autogamous leguminous crop. The average global yield is low and stagnant over years in the entire tropical and subtropical Asia. Any improvement in the yield is hard, predominantly because of pest infestation and diseases. Viral diseases result in significant financial losses due to drop in seed yield and quality in many important crops including greengram. Mungbean yellow mosaic disease (MYMD) can lead to yield loss up to 85% in greengram in epidemic conditions.

Methods: The present study was conducted at Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University during the period August-October 2020 in three crosses of greengram *viz*., PLM 506 × IC 76417, PLM 506 × IC 76381 and IC 398746 × IC 76417. The mean data of five basic generations *viz*., P_1, P_2, F_1, F_2 and F_3 of three crosses were evaluated. Populations were screened for MYMV disease resistance by employing infector row method. Scaling test was done using the mean values of various generations for the characters. Significance of scale C suggested dominance × dominance (l) type of gene interaction, whereas the significance of scale D showed additive × additive (i) type of gene interaction. The significance of any of the scaling tests proposes inefficacy of simple additive-dominance model. Five genetic effects *viz*., mean effect (m), additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) was estimated.

Result: Hundred-seed weight showed additive-dominance model in the cross PLM 506 × IC 76417. The additive as well as additive × additive type of gene action were in control of number(s) of clusters per plant, percentage of disease infection and most of yield components in the cross PLM 506 × IC 76417. Hence, selection at a later generation is effective to improve these traits. Pod length was controlled by additive gene action in the cross PLM 506 × IC 76381, whereas percentage of disease infection showed additive-dominance model. The additive as well as additive × additive type of gene action were in control of plant height and most of yield components in the cross PLM 506 × IC 76381. In the case of other traits, epistatic model was evidenced. Hence, selection needs to be postponed to a later generation. Based on gene action, these crosses may be employed to evolve high yielding plants with MYMV disease resistance.

Key words: Crosses, Gene action, GMA, Greengram, MYMV.

INTRODUCTION

Pulses are highly nutritious possessing crops and are one of the most extensively consumed foods across the world. Apart from being rich in proteins, pulses also provide carbohydrates, vitamins, and minerals. Pulses are a prime protein source in India, the country that has the largest population of vegetarians in the world. Legume crops are susceptible to several pests and seed borne diseases. The major concern is that if these challenges are not addressed appropriately, they could result in destruction of the crop. Deficiency of high yielding genotypes, low harvest index, high vulnerability to diseases and insect pests, dearth of short duration varieties, flower drops, indeterminate growth habits, poor response to inputs and variabilities in performances are some of the varietal constraints that need instant attention in the case of pulse cropping (Singh *et al*., 2013).

Mungbean or greengram is a diploid (2n=22) autogamous leguminous crop of genome size 494 to 579Mb. Genus *Vigna* is among the most significant Asiatic species that belongs to the subgenus *Ceratotropis*. Greengram, a member of the family Fabaceae, is a short-term pulse crop of Indian origin. The average global yield of greengram has been low and stagnant over the years in the entire tropical and subtropical Asia (Rishi, 2009). Any improvement in the

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How to cite this article: Nainu, A.J., Vadivel, K., Murugan, S. and Kumar, N.S. (2023). Generation Mean Analysis for Yield, its Components and MYMV Disease Resistance in Greengram [*Vigna radiata* (L.) Wilczek]. Legume Research. 46(11): 1541-1546. doi: 10.18805/LR-4829.

Submitted: 02-11-2021 **Accepted:** 26-03-2022 **Online:** 09-05-2022

yield of greengram is hard, predominantly because of pest infestation and diseases (Karthikeyan *et al.,* 2014). Viral diseases result in significant financial losses due to drop in seed yield and quality in many important crops (Kang *et al.,* 2005). Mungbean yellow mosaic disease (MYMD) can lead to yield loss up to 85% in greengram and hence it is considered to be the most devastating viral disease infecting the crop (Dharajiy *et al*., 2018).

A more effective, environment friendly, and permanent solution is to develop greengram cultivars resistant to both virus and its vector, *Bemisia tabaci*. But, due to rapid burst of new isolates of Mungbean yellow mosaic virus and the complexity of mechanism for achieving MYMV resistance, conventional breeding methods have not been successful in developing Mungbean Yellow Mosaic Virus (MYMV) resistant greengram varieties. The best means to attain MYMV resistance is through genetic manipulation of the crop, and this could be achieved by exploiting the variability through artificial hybridization and selection (Mishra *et al*., 2020).

Generation mean analysis (Hayman, 1958) is an excellent method for assessing the different components of genetic variance and finding the presence or absence of epistasis via scaling test, would be helpful to formulate a suitable breeding programme and to find the ideal generation for the development of traits.

MATERIALS AND METHODS

The present study was conducted at Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University in Cuddalore district of Tamil Nadu during the August - October 2020 in three crosses *viz*., PLM 506 × IC 76417, PLM 506 × IC 76381 and IC 398746 × IC 76417.The experimental material consisted of two resistant doners including IC 76417 and IC 76381 along with two susceptible doners viz., PLM 506 and IC 398746. The mean data of five basic generations *viz.,* P_1, P_2, F_1, F_2 and F_3 of three crosses were evaluated. Populations were screened for MYMV disease resistance through infector row method. To allow the whitefly population to widen and spread the disease, no insect repellents were used. Data were recorded on individual plants in respect to days to fifty percent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, single plant yield and percentage of yellow mosaic disease infection. The percentage of disease infection was calculated from the ratio of the number of infected plants in a row to the total number of plants. The genotypes were classified using 0-5 arbitrary scale suggested by Bashir *et al*. (2005) and were categorized into separate groupings on the basis of the disease score that ranges from highly resistant to highly susceptible. (Table 1) Scaling test was done using the mean values of various generations for the characters studied as suggested by Mather (1949). Significance of scale C suggested dominance × dominance (1) type of gene interaction, whereas the significance of scale D showed additive × additive (i) type of gene interaction. The significance of any of the scaling tests proposes inefficacy of simple additive - dominance model. Five genetic effects *viz*., mean effect (m), additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) was estimated following Hayman (1958).

RESULTS AND DISCUSSION

Partitioning of non-additive gene action into dominance and epistatic interaction effects on the inheritance of characters could be congregated through generation mean analysis. Mather and Jinks (1982) endorsed that generation mean analysis evaluates the extent of dominance and epistatic gene effects in addition to additive gene effects. The individual scaling tests C and D and the genetic parameters *viz.,* 'd', 'h', 'i' and 'l' of additive, dominance, additive × additive, additive × dominance and dominance × dominance respectively was estimated. The scales and their parameters of three crosses *viz.,* PLM 506 × IC 76417, PLM 506 × IC 76381 and IC 398746 × IC 76417 are presented in Table 2 to 4.

Days to fifty percent flowering

In cross PLM 506 × IC 76381 the significance of both the scales were evidenced, whereas the other two crosses observed significance for scale D alone which indicated the presence of epistatic effects in all the three crosses. Additive (d), additive × additive (i) and dominance × dominance (l) effects were significant for the cross PLM 506 × IC 76417 which indicated the presence of additive-dominance and epistatic gene action for this trait. In cross PLM 506 × IC 76381, dominance (h) and dominance × dominance (l) effects were found significant which suggested the presence of dominance and epistatic component of dominance × dominance type of gene action. Similar findings were also recorded by Yadav *et al.* (2017). In the case of cross combination IC 398746 × IC 76417, all the effects *viz.,* additive (d), dominance (h), additive × additive (i) and

Table 1: Scale used for MYMV reaction (Bashir *et al*., 2005).

Severity	% Infection	Infection category	Reaction group
0	All plants free of virus symptoms	Highly resistant	HR
1	1-10% infection	Resistant	R
2	11-20% infection	Moderately resistant	MR
3	21-30% infection	Moderately susceptible	MS
4	30-50% infection	Susceptible	S
5	More than 50%	Highly susceptible	HS

Table 2: Scaling test and estimates of genetic parameters for various characters in cross PLM 506 × IC 76417.

Character	Scales		Parameters				
	C	D	m	d	h	i	l
DFF	0.88±1.37	-3.17**±1.17	36.55**±0.25	-3.62**±0.27	-0.80±0.83	-4.97**±0.94	-5.41*±2.57
PH	-5.90*±-2.00	3.41±1.40	41.41**±0.66	0.71*±0.29	-2.62±1.90	-1.83±2.01	12.41*±6.11
NBPP	-2.41**±0.52	0.37±0.48	2.66**±0.12	-0.08*±0.04	0.18±0.37	-0.81*±0.36	3.70**±1.13
NCPP	0.93±1.83	3.53*±1.64	10.39**±0.44	-1.84**±0.05	0.93±1.28	-5.87**±1.27	3.47±4.01
NPPC	-0.75*±0.32	1.82**±0.27	3.85**±0.07	-0.06±0.04	0.01±0.21	-1.46**±0.22	3.42**±0.65
NPPP	2.09±5.69	34.66**±5.78	38.27**±1.31	-6.01**±0.27	-1.85±4.37	-34.77**±4.12	43.42**±12.84
PL	-2.52**±0.35	-1.22**±0.35	7.29**±0.08	0.11*±0.05	0.99**±0.26	0.61*±0.26	1.73*±0.77
NSPP	-1.57*±0.64	1.05±0.55	9.80**±0.11	0.03±0.12	0.28±0.39	-0.90*±0.45	3.49**±1.19
100-SW	0.15±0.20	0.34±0.20	4.62**±0.04	0.48**±0.04	0.75**±0.14	-	-
SPSY	-2.90±1.54	3.85**±1.39	9.57**±0.33	0.07±0.09	-0.56±1.07	-2.90**±1.04	9.00**±3.25
PDI	-63.79**±3.13	-66.63**±3.33	10.90**±0.75	37.88**±0.27	-3.51±2.47	109.55**±2.38	-3.78±7.22

DFF- Days to 50% flowering, PH- Plant height (cm), NBPP- Number of branches per plant, NCPP- Number of clusters per plant, NPPC- Number of pods per cluster, NPPP- Number of pods per plant, PL- Pod length (cm), NSPP- Number of seeds per pod, 100 SW- Hundred seed weight (g), SPY- Single plant yield(g), PDI- Percentage of disease infection.

Table 3: Scaling test and estimates of genetic parameters for various characters in cross PLM 506 × IC 76381.

Character	Scales		Parameters				
	C	D	m	d	h	i	l
DFF	9.88**±3.11	6.07*±2.35	36.40**±0.56	0.35±0.26	-2.18*±0.90	-1.68±0.92	-5.09**±1.80
PH	15.70**±3.26	20.91**±2.89	45.42**±0.66	5.09**±0.43	-4.72*±2.16	-1.15±2.18	6.95±6.58
NBPP	-0.92**±0.20	0.17±0.19	3.03**±0.04	-0.17**±0.03	0.39**±0.14	-0.60**±0.14	1.46**±0.41
NCPP	-3.26**±0.72	3.18**±0.76	9.16**±0.15	-1.47**±0.08	0.83±0.56	-5.59**±0.52	8.58**±1.59
NPPC	0.65±0.24	0.78**±0.20	3.86**±0.05	0.13*±0.04	1.82**±0.15	-0.75**±0.17	4.94**±0.46
NPPP	-50.89**±4.65	15.92**±3.21	35.34**±0.73	-5.73**±0.32	23.00**±2.64	-30.56**±2.63	89.07**±8.39
PL	-2.95**±0.46	-1.92**±0.44	7.53**±0.10	-0.67**±0.06	0.53±0.33	-0.55±0.33	1.38±0.99
NSPP	-3.13**±0.96	1.61**±0.29	9.73**±0.12	0.03±0.12	0.28±0.46	-1.54**±0.53	6.32**±1.56
100-SW	-0.51*±0.25	-0.75**±0.15	4.33**±0.04	0.12**±0.03	0.38**±0.13	0.65**±0.14	-0.33±0.42
SPY	-13.77**±1.15	-2.96**±1.06	6.67**±0.24	-0.04±0.08	1.58*±0.81	-0.40±0.78	14.42**±2.43
PDI	-1.94±7.38	4.91±9.36	27.17**±1.81	37.87**±0.26	-39.30**±6.80	-	-

DFF- Days to 50% flowering, PH- Plant height (cm), NBPP- Number of branches per plant, NCPP- Number of clusters per plant, NPPC- Number of pods per cluster, NPPP- Number of pods per plant, PL- Pod length (cm), NSPP- Number of seeds per pod, 100 SW- Hundred seed weight (g), SPY- Single plant yield (g), PDI- Percentage of disease infection.

dominance × dominance (l) effects were found significant. The results suggested that additive along with epistatic gene action plays key role in this cross for the trait. This was also suggested by Latha *et al.* (2018), Panigrahi *et al.* (2020) and Ragul *et al.* (2021).

Plant height

The cross PLM 506 × IC 76381 showed significance in both scales for plant height. while the two other crosses showed significance for scale C alone which explains the inadequacy of simple additive-dominance model. The additive (d) gene effect and dominance × dominance (l) effects were found significant for the cross PLM 506 × IC 76417 which suggested additive and epistatic component of dominance × dominance gene action were involved in controlling this trait. The cross PLM 506 × IC 76381 showed significance for additive (d) and dominance (h) effects, which suggests that the character plant height was controlled by both additive and dominance gene actions in this cross. Similar observations were also reported by Singh *et al.* (2007). The dominance (h) and dominance × dominance (l) interaction effect were significant for cross IC 398746 × IC 76417. Sudhakar *et al.* (2020) and Ragul *et al.* (2021) also reported similar findings for this character. Here dominance component and epistatic component of dominance × dominance were important. Hence, selection can be postponed to later generations after the dominance effects would have diminished.

Number of branches per plant

All the three crosses showed significance for the scale C. PLM 506 × IC 76417 showed significance for additive (d) effect, additive × additive (i) and dominance × dominance (l) effects. It showed the presence of additive and epistatic type of gene actions in the hybrid. PLM 506 × IC 76381 and IC 398746 × IC 76417 recorded significance for additive

Table 4: Scaling test and estimates of genetic parameters for various characters in cross IC 398746 × IC 76417.

Character	Scales		Parameters				
	C	D	m	d	h	i	l
DFF	-2.58±2.45	-22.10**±1.57	39.87**±0.48	-0.54*±0.21	13.48**±1.33	13.22**±1.44	-26.02**±4.57
PH	28.30**±5.83	2.50±4.15	53.72**±1.01	0.36±0.24	11.89**±3.43	3.78±3.41	-34.41**±10.91
NBPP	1.64**±0.21	-0.27±0.14	3.83**±0.04	0.36**±0.04	0.73**±0.10	1.17**±0.13	-2.55**±0.37
NCPP	-3.29**±0.52	-5.35**±0.33	9.07**±0.08	-0.80**±0.11	3.55**±0.24	1.42**±0.33	-2.75**±0.83
NPPC	3.84**±0.31	1.77**±0.29	5.47**±0.07	0.01±0.03	1.58**±0.22	-0.51*±0.22	-2.76**±0.67
NPPP	-5.00±3.00	6.49*±2.67	44.02**±0.68	-0.78**±0.29	20.33**±2.05	-6.71**±2.07	15.32**±6.38
PL	4.15**±0.44	-0.68*±0.29	9.07**±0.08	0.10±0.06	2.00**±0.23	1.34**±0.26	-6.44**±0.79
NSPP	8.94**±0.49	-0.22±0.31	12.58**±0.08	0.46**±0.07	2.34**±0.25	2.54**±0.28	-12.21**±0.86
100-SW	3.57**±0.21	0.48*±0.19	4.96**±0.05	-0.05±0.03	1.27**±0.14	0.17±0.15	-4.11**±0.44
SPY	13.91**±1.02	4.04**±0.8	13.65**±0.21	0.10±0.11	1.82**±0.65	-0.18±0.67	-13.16**±2.05
PDI	-49.92**±1.22	31.75**±5.90	13.65**±0.21	32.83**±0.33	-58.12**±3.93	36.18**±2.90	108.89**±8.02

DFF- Days to 50% flowering, PH- Plant height (cm), NBPP- Number of branches per plant, NCPP- Number of clusters per plant, NPPC- Number of pods per cluster, NPPP- Number of pods per plant, PL- Pod length (cm), NSPP- Number of seeds per pod, 100 SW- Hundred seed weight (g), SPY- Single plant yield (g), PDI- Percentage of disease infection.

(d), dominance (h) effects, additive × additive (i) and dominance × dominance (l) components. The results specified that additive and epistatic gene action are predominant in these two crosses. These two crosses indicated complicated nature of inheritance for branches per plant while the third cross observed non-significant dominance (h) effects. Singh *et al.* (2007) and Narasimhulu *et al.* (2018) also reported similar observations for this trait.

Number of clusters per plant

Two crosses *viz*., PLM 506 × IC 76381 and IC 398746 × IC 76417 exhibited significance for both the scales and the cross PLM 506 × IC 76417 showed significance for scale D only. In cross PLM 506 × IC 76417 additive (d) and additive × additive (i) effects were significant which indicated the existence of additive and additive × additive gene action. In the case of PLM 506 × IC 76381 additive (d), additive × additive (i) and dominance × dominance (l) effects were significant. It indicated the presence of additive and epistatic type of gene actions in the hybrid. Narasimhulu *et al.* (2018) also documented parallel findings in them study for this trait. The cross IC 398746 × IC 76417 exhibited significance for additive (d), dominance (h) effects, additive × additive (i) and dominance × dominance (l) components which advised that the additive and epistatic gene action has a significant role in this cross.

Number of pods per cluster

Inefficacy of simple additive-dominance model to describe the genetic control of this trait was observed due to the significances of both scales in all the three crosses. PLM506 × IC 76417 recorded significant additive × additive (i) and dominance × dominance (l) interaction effects which implies the influence of epistatic gene action in the hybrid. The cross PLM 506 × IC 76381 recorded significant additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) components. The observations showed the existence of additive together with epistatic gene action in the hybrid for the trait. Similarly, additive and non-additive gene action was reported by Zubair *et al.* (2007) and Latha *et al.* (2018) in their studies. In cross IC 398746 × IC 76417, dominance (h), additive × additive (i) and dominance × dominance (l) components were significant which indicated the predominant role of dominance coupled with epistatic gene action. This trait limits the scope of further improvement via direct selection. These findings were in congruence with the reports of Narasimhulu *et al.* (2018).

Number of pods per plant

Significance of one or more scaling tests suggests the inadequacy of simple additive-dominance model for the crosses. The scaling test showed that the scale D was significant in all three crosses *viz*., PLM 506 × IC 76417, PLM 506 × IC 76381 and IC 398746 × IC 76417. In the cross PLM 506 × IC 76417 additive (d) gene effect, additive × additive (i) and dominance × dominance (l) components were found significant. It indicated the presence of additive along with epistatic type of gene actions for the character in this cross. In the case of crosses PLM 506 × IC 76381 and IC 398746 × IC 76417 the components additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) were significant for the trait. It revealed the existence of additive and epistatic type of gene actions. Similar findings were observed by Yadav *et al.* (2017), Vadivel *et al.* (2019) and Ragul *et al.* (2021).

Pod length (cm)

Both the scales reported significance for all the three crosses which indicated the epistatic model in crosses. In the cross PLM 506 × IC 76417 additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) components were significant. It revealed the existence of additive, along with epistatic type of gene actions in this cross. The cross PLM 506 × IC 76381 showed significance for additive (d) gene

effect alone suggests the presence of additive gene action in the hybrid. In the case of cross IC 398746 × IC 76417 dominance (h), additive × additive (i) and dominance × dominance (l) components were significant which denotes the presence of dominance and epistatic type of gene actions. Similar results such as the presence of additive and non-additive gene actions for the trait pod length were recorded by Yadav *et al.* (2017) and Latha *et al.* (2018).

Number of seeds per pod

In scaling test, scale C was significant for all the three crosses whereas for scale D, cross PLM 506 × IC 76381 alone showed significance. Here, in crosses PLM 506 × IC 76417 and PLM 506 × IC 76381, additive × additive (i) gene effect and dominance × dominance (l) gene interaction effect were significant. The results implied that epistatic gene action plays an important role in these two crosses for this trait. Whereas in the case of cross IC 398746 × IC 76417, additive (d), dominance (h), additive × additive (i) and dominance × dominance (l) components were significant. The results revealed that additive and epistatic gene action plays a major role in the hybrid. Similar findings about additive and non-additive gene action were reported by Zubair *et al.* (2007) and Latha *et al.* (2018) respectively.

Hundred seed weight (g)

Simple additive-dominance model was adequate in the cross PLM 506 × IC 76417, whereas the other two crosses were proved significant for both C and D scale. In cross PLM 506 × IC 76417 additive (d) and dominance (h) effects showed high significance which indicated the additive-dominance gene action. In the cross PLM 506 × IC 76381, additive and dominance components along with epistatic component of additive × additive (i) was also important. Sudhakar *et al.* (2020) also reported similar findings for this trait. The cross IC 398746 × IC 76417 showed significance for dominance (h) and dominance × dominance (l) components which indicated that dominance and epistatic component dominance × dominance was prominent for the trait. Similar observations were recorded by Narasimhulu *et al.* (2018) for this trait.

Single plant yield (g)

The scaling test revealed significance for scale C and scale D in the two crosses PLM 506 × IC 76381 and IC 398746 × IC 76417. Among the main effects, the (d) additive gene effects were non-significant in all the three hybrids. In the case of PLM 506 × IC 76381 and IC 398746 × IC 76417 dominance effects (h) and dominance × dominance (l) effects showed significance, which indicated the existence of dominance and epistatic gene action for the trait. Sudhakar *et al.* (2020) also reported similar findings for this trait. In the case of PLM 506 × IC 76417 additive × additive (i) and dominance × dominance (l) components were proved highly significant. This indicated that epistatic gene action plays a major role in this cross. Similar findings were also addressed by Yadav *et al.* (2017) and Latha *et al.* (2018).

Percentage of disease infection

The scaling test showed significance for both scale C and D for the crosses PLM 506 × IC 76417 and IC 398746 × IC 76417. Whereas in the hybrid PLM 506 × IC 76381, both C and D scales had no significance which indicated the adequacy of simple additive-dominance model for this cross. The additive and additive × additive components were found significant in the cross PLM 506 × IC 76417 which indicated the existence of additive and epistatic gene action for the character. This cross can be fixed for later generation. Additive and dominance components in cross PLM 506 × IC 76381 showed significance which indicated additive-dominance gene action model. In the case of cross IC 398746 × IC 76417, additive, dominance, additive × additive, dominance × dominance components were found significant. The results indicated that additive-dominance and epistatic gene action plays a major role in this cross.

CONCLUSION

In the cross-combination PLM 506 × IC 76417, the trait 100-seed weight was controlled by additive-dominance gene action, whereas number of clusters per plant, percentage of disease infection and most of yield components were controlled by additive as well as additive × additive type of gene action. Hence, it is advisable to postpone selection to a later generation to improve these traits. In the cross PLM 506 × IC 76381 the trait pod length was controlled by additive gene action whereas plant height and most of yield components were controlled by additive as well as additive × additive type of gene action. The trait percentage of disease infection showed additive-dominance gene action model. Epistatic model was observed for all the other traits in these two crosses. Hence, based on gene action, these two crosses may be utilized to develop high yielding and MYMV disease resistant genotypes.

Conflict of interest: None.

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