



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2019; 7(1): 2078-2082

© 2019 IJCS

Received: 19-11-2018

Accepted: 23-12-2018

**Sujatha K**

Ph.D., Scholar, Department of Genetics and Plant breeding, University of Agricultural Science, Dharwad, Karnataka, India

**Kajjidoni ST**

Senior Scientist, Sorghum Scheme, Department of Genetics and Plant breeding, University of Agricultural Science, Dharwad, Karnataka, India

**Srinivasa N**

Scientist, Division of Plant Pathology, ICAR-IARI, New Delhi, India

## Gene action studies for yield and yield attributing traits in selected powdery mildew resistant lines of mungbean (*Vigna radiata* (L.) Wilczek)

Sujatha K, Kajjidoni ST and Srinivasa N

**Abstract**

The present investigation on genetic analysis involving 12 parents and 20 crosses in mung bean indicated that VC-1, TARM-18, TARM-1 and Vaibhav were the good general combiners based on the overall score across the traits in desirable direction. The cross combination Chinamung x VC-1 exhibited significant sca effects for traits viz., seed yield per plant, seed yield per plot, number of pod bearing cluster per plant, number of pods per plant, hundred weight and harvest index. Gene action study revealed that days to 50 flowering, days to maturity, number of pods per plant, hundred seed weight (g), total dry matter at harvest (g), harvest index (%), seed yield per plant (g) and seed yield per plot (g) in the present study were governed predominantly by additive genetic variation. Since all these characters were also under significant influence of epistatic variation, it appears that additive x additive epistatic variation may be playing a decisive role in the inheritance of these characters.

**Keywords:** Additive, combining ability, dominance, epistatic genetic variation and mungbean

**Introduction**

Green gram (*Vigna radiata* L. Wilczek) is an ancient and well known leguminous crop of Asia, on account of its nutritional quality and the suitability to cropping system. Green gram is the third most important pulse crop in India covering an area of 3.53 million hectare with a total production of 1.49 million tonnes and the average productivity of 532 kg/ha<sup>-1</sup> (Iranna and Kajjidoni, 2008). Important green gram growing states in India are Orissa, Andhra Pradesh, Maharashtra, Karnataka and Bihar. The lower productivity in green gram is mainly attributed to low genetic yield potentiality, indeterminate growth habit, canopy architecture, low partitioning efficiency, cultivation in marginal land and due to biotic and abiotic stresses. Among biotic stresses powdery mildew and mung bean yellow mosaic virus (MYMV) are the major diseases of green gram. Among these two diseases, the powdery mildew is more severe and symptoms of disease are usually observed on 35-40 days old crop (Khare *et al.*, 1998) i.e. during flowering and pod formation stage (Arjunan *et al.*, 1976). The disease usually covers host leaf surface area reducing photosynthetic activity and disease occurs severe form in *kharif* season which is also the main season for green gram cultivation, particularly when temperature is low (20-25<sup>o</sup>c) and humidity is high (80-90 per cent) and yield reduction can range from 20 to 40 percent.

There is not much progress achieved in varietal development of mung bean against powdery mildew and yellow mosaic virus diseases although few varieties developed at national level are also found to be most susceptible. Hence there is an urgent need to develop improved genotypes with early maturity or a variety superior to these genotypes in terms of yield, major diseases and other characters. For the development of an effective breeding programme one needs to elucidate the nature of gene action controlling economic characters. Combining ability studies utilizing line x tester analysis provides information in this direction particularly for initial screening of large number of genotypes for combining ability. Study of gca effects helps in selection of superior parents and sca effects for superior hybrids. The information generated in the process can be used to understand the magnitude of heterosis.

Identification of suitable parents for hybridization programme is an important step to meet the objective of breeding programme. Among several methods available for this purpose, combining ability analysis on the basis of line x tester system found to be most appropriate method to identify the best combiner that can be utilized for hybridization.

**Correspondence****Sujatha K**

Ph.D., Scholar, Department of Genetics and Plant breeding, University of Agricultural Science, Dharwad, Karnataka, India

The knowledge of various gene effects for the expression of yield and its component traits is prerequisite for deciding suitable breeding procedure for the development of superior and desirable genotypes. Hence an investigation was done to identify the best combiner and elucidate gene action for the expression of seed yield and other related attributes for improvement in green gram (*Vigna radiata* (L.) Wilczek).

### Material and Methods

Two adopted varieties namely Chinamung and Pusa baisaki were crossed with ten selected diverse testers for powdery mildew *viz.*, Vaibhav, TARM-1, TARM-2 and TARM-18 (resistant to powdery mildew from BARC, Mumbai) DMG-1030 (resistant) and Meha (susceptible from IIPR, Kanpur), KGS-83 (advance breeding line), BPMR-1 (tolerant) and VC-

1 (resistant exotic line, AVRDC Taiwan) and BPMR-145 in a line x tester fashion and resulting 20 F<sub>1</sub>-s along with their parents were grown in randomised block design with three replications at Main Agriculture Research Station, College of Agriculture, University of Agricultural Science, Dharwad. Five competitive plants were randomly selected from each replication for recording the observations for seed yield and its 11 component traits (Table 1). The parents were also screened for powdery mildew disease by growing them separately without any protection the data were subjected to analysis of variance (Panse and Sukhateme, 1976) [9] and combining ability analysis (Kempthorne, 1957) [6] and nature of gene action was detected as additive, dominance and epistatic component as method suggested by Kersay and Jinks, (1968) [5] and Jinks *et al.* (1969) [4].

**Table 1:** List of parents which exhibited significant gca effects with their per se performance

Sl no	Characters	Parents	Per se performance	gca effects
1	Plant height (cm)	Nil		
2	Days to 50 % flowering	Vaibhav	51.00	-2.67**
		BPMR-145	46.00	-2.33**
3	Day to maturity	BPMR-145	70.00	-5.77**
		Pusa baisaki	78.00	1.13**
4	Number of clusters per plant	TAM-18	6.47	1.94**
		TARM-1	8.03	1.47**
		Vaibhav	7.40	1.29**
		TARM-2	4.87	0.99**
		Chinamung	3.47	0.78
5	Number of pods per cluster	TARM-1	3.05	1.07**
		DMG-1030	3.27	0.93**
		Meha	2.82	0.36*
		Pusa baisaki	3.10	0.25**
6	Number of pods per plant	TARM-1	24.50	8.12**
		TARM-18	22.20	6.48**
		Vaibhav	24.00	2.93*
		DMG-1030	28.40	2.42**
		Chinamung	8.53	1.10**
7	Pod length (cm)	Pusa baisaki	8.89	0.67**
8	Hundred seed weight (g)	VC-1	3.33	0.53*
9	Total dry matter at harvest (g)	TARM-18	17.57	4.69**
		TARM-1	19.57	4.22**
		TARM-2	22.83	1.32**
		Chinamung	8.13	2.09**
10	Harvest index (%)	VC-1	21.59	24.81**
11	Seed yield per plant (g)	VC-1	4.63	4.98**
		BPMR-1	3.57	0.48**
		Chinamung	2.60	0.44**
12	Seed yield per plot (g)	VC-1	121.67	141.00**
		BPMR-1	93.00	15.33**
		TARM-1	131.67	9.67*
		TARM-18	110.33	14.67**
		Chinamung	72.33	10.77**

\* and \*\* indicates significance at 5 % and 1 % probability levels respectively.

### Results and Discussion

The analysis of variance for combining ability showed significant variation for parents and hybrids for most of the characters studied except for pod length in parents, indicating the presence of genetic diversity among parents and hybrids. The partitioning of hybrids mean sum of squares revealed that variance due to male, females and their interaction were significant for all traits except for days to 50 % flowering indicating the manifestation of considerable genetic variability among parents and the hybrids. These findings are in accordance with Ayyangouda Patil *et al.* (2003) [10], Singh *et al.* (2007) [12], Khan *et al.* (2007) [7], Gawande *et al.* (2005) [3].

General combinability effect of the parents indicated that none of parents was good different parents found to be good combiner for all traits, among which TARM-1 ranked as top by exhibiting significant gca effects for five traits *viz.*, number of pod bearing clusters per plant, number of pods per cluster, number pods per plant, total dry matter at harvest and seed yield per plot. This was followed by TARM-18 which was a good combiner for four traits *viz.*, number pods per plant, number of pod bearing clusters per plant, total dry matter at harvest and seed yield per plot. The VC-1 was also a good general combiner with good mean performance for four traits *viz.*, hundred seed weight, harvest index, seed yield per plant and seed yield per plot and all the three testers (TARM-18,

TARM-1 and VC-1) were also resistant to powdery mildew disease (Fig. 1)



(a) TARM-18



(b) TARM-1



(c) VC-1

**Fig 1:** (a), (b) and (c) are the resistant genotype for powdery mildew disease.

Female parent Chinamung was good general combiner for five traits namely number pods per plant, number of pod bearing cluster per plant, total dry matter at harvest and seed yield per plant seed yield per plot with good per se performance than Pusa baisaki.

The study of sca effects across hybrids revealed that none of the hybrids showed significant positive specific combining ability effects for all the characters (Table 2). The cross, Chinamung xVC-1 exhibited significant sca effect for as many as five traits viz., Seed yield per plot (g), seed yield per plant (g), number of pod bearing clusters per plant, number or pods per plant and harvest index (%).

**Table 2:** Top ranking hybrids which exhibited significant sca effects, with their mean performance for different characters

Sl no.	Character	Crosses	Mean	sca effects
1	Plant height	Nil		
2	Days to 50 % flowering	PB X MEHA	46.67	-2.37**
		PB X KGS-83	46.00	-2.20*
3	Day to maturity	PB X TARM-1	73.33	-4.47**
		CM X MEHA	76.67	-3.53**
4	Number of cluster per plant	CM X BPMR-1	73.33	-3.37**
		CM X TARM-1	11.83	3.07**
		CM X TRM-18	11.10	1.87**
		PB X KGS 83	5.60	1.41**
		PB X MEHA	6.33	1.18**
5	Number of pods per cluster	CM X VC-1	5.30	1.06*
		PB X TARM-1	5.74	1.17**
		CM-VC-1	2.99	0.64*
6	Number of pods per plant	PB X DMG-1030	5.11	0.63*
		CM X TARM-18	33.05	4.53**
		PB X MEHA	26.00	4.25*
		CM XTARM-1	34.40	4.24*
7	Pod length (cm)	PB X DMG-1030	25.00	3.73*
		NIL		
8	Hundred seed weight (g)	NIL		
9	Total dry matter at harvest (g)	CM X TARM-18	32.40	6.26**
		CM XMEHA	15.53	6.14**
		CM X TARM-1	30.35	4.68**
		PB X BPMR-1	18.00	4.29**
10	Harvest index (%)	CM X VC-1	36.46	9.67**
		CM X TARM-1	17.79	6.20**
11	Seed yield per plant (g)	CM X VC-1	9.87	3.24**
		PB X MEHA	5.00	0.84**
12	Seed yield per plot (g)	CM XVC-1	287.67	93.07**
		PB X TARM-1	162.33	20.60**
		CM X TARM-2	133.33	16.93**
		CM X TARM-18	123.00	16.10**
		CM X BPMR-1	165	15.73**

CM – Chinamung and PB – Pusa baisaki

\* and \*\* indicates significance at 5 % and 1 % probability levels respectively

The other two crosses, Chinamung x TARM-1 and Chinamung x TARM-18 exhibited significant sca effects for number of pod bearing clusters per plant, number of pods per cluster, number of pods per plant, seed yield per plot (g), total dry matter at harvest and harvest index (%).

These crosses which exhibited significant sca effects for six to eight attributing traits can be further advanced through conventional breeding methods such as bi parental mating, and or diallele selective mating, there after followed by pedigree method of selection for improvement of productivity. For traits like plant height, pod length and hundred seed weight none of the crosses exhibited any significant sca effects.

The best crosses mainly Chinamung x VC-1, Pusa baisaki x TARM-1, Chinamung x TARM-2 and Chinamung x TARM-18 (Table 2) had desirable and significant sca effects with high per se performance for seed yield per plot. The present study clearly indicated that breeder must give proper attention to a systematic breeding approach by using selected promising crosses having significant high sca value as well as high per se performance for seed yield. Such promising combinations are expected to produce desirable transgressive sergeants to achieve higher seed yield.

On the other hand an attempt was made to obtain a generalized picture of the type of gene action involved in the inheritance of the 12 characters by using two methods of

analysis, viz., line x tester analysis providing estimates of variance of general combining ability (additive gene action) and specific combining ability (non-additive gene action) and estimation of D (additive) and  $H_1$  (dominance) components of genetic variation by the method of Jinks *et al.* (1969) [4].

The analysis revealed that the absence for epistasis in plant height, pod length and hundred seed weight traits (Table 3) but further analysis indicated that the characters viz., days to 50 % flowering, days to maturity, number of pods per plant, hundred seed weight (g), total dry matter at harvest (g), harvest index (%), seed yield per plant (g) and seed yield per plot (g) were predominantly governed by additive genetic component than dominant component of variation (Table4,5). Since all these characters were also under significant influence of epistatic variation role of additive x additive epistatic variation in the inheritance of these characters. Significance of  $H_1$  (dominant genetic variation) and non-significant correlation co-efficient between sum and difference for plant height(cm) and number of clusters per plant traits (Table 4) suggested that there was greater dominant contribution to the variation but dominance was bidirectional, i.e. increasing and decreasing alleles being dominant and recessive to the some extent for these traits. Similar observations were also made by Ayyagouda Patil and Kajjidoni (2005) [11], Sing *et al.* (2007), Barad *et al.* (2008) [1], Deth *et al.* (2008) [2].

**Table 3:** Mean sum of squares for detecting epistatic gene action for 12 characters in greengram (*Vigna radiata* (L.)Wilczek)

Source	D.F	Plant height (cm)	Days to 50% flowering	Days To maturity	No. of pod bearing Cluster per plant	No. of pods per clusters	No. of pods per plant	Pod length (cm)	100-seed weight (g)	Total dry matter at harvest (g)	Harvest index (%)	Seed yield per plant (g)	Seed yield per plot (g)
$L_{1i} + L_{2i} - P_{-i}$	9	95.16	33.14**	71.17**	17.26**	6.20**	244.12**	34.87	0.64	177.19**	957.51**	42.18**	35208.44**

**Table 4:** Analysis of variance for sums and differences in respect of 12 characters in greengram (*Vigna radiata* (L.)Wilczek)

Source	D.F	Plant height (cm)	Days to 50% flowering	Days To maturity	No. of pod bearing cluster per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	100-seed weight (g)	Total dry matter at harvest (g)	Harvest index (%)	Seed yield per plant (g)	Seed yield per plot (g)
sum	9	19.36	15.77**	57.52**	9.66**	2.82	195.22**	0.78	0.49	15.37**	493.30**	22.27**	18302.81**
Differences	9	22.93	5.33	20.27	17.45**	1.90	42.48**	1.03	0.37	38227.0**	76.68**	12.57**	11560.06**
Error	62	21.39	2.67	14.08	0.15	3.24	0.14	0.61	0.25	4.33	17.53	0.33	92.69
$\sigma^2 M$	-	-0.33	2.18	7.24	1.58	-0.06	31.99	0.028	0.04	11.77	79.29	3.68	3035.02
$\sigma^2 M_L$	-	0.25	0.44	1.11	2.88	-0.22	6.54	0.06	0.02	9.87	9.85	2.07	1911.22
$E_2$	-	21.39	2.67	14.08	0.15	3.24	3.23	0.61	0.25	4.33	17.53	0.14	92.69

\*and\*\* indicates significance at 5% and 1% probability levels respectively.

**Table 5:** Estimates of genetic parameters, dominance ratio and correlation co-efficient of sums and differences of 12 characters in greengram *Vigna radiata* (L.)Wilczek)

Source of variability	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of pod bearing Cluster per plant	No. of pods per cluster	No. of pods per plant	Pod length (cm)	100-seed weight (g)	Total dry matter at harvest (g)	Harvest index (%)	Seed yield per plant (g)	Seed yield per plot(g)
D	-1.35	8.7	28.96	6.34	-0.27	127.99	0.11	0.16	47.10	317.18	14.75	12140.0
$H_1$	1.02	1.77	4.45	11.53	-0.88	26.54	0.27	0.08	39.51	39.48	8.29	7644.91
F	-68.145	-45.33	-244.26	-269.34	-39.36	-1912.77	-6.92	-6.53	-1416.32	-39260.00	-399.57	-344720.0
$E_2$	21.39	2.67	14.08	0.15	3.24	3.23	0.61	0.25	4.53	17.52	0.14	92.69
$\sqrt{H_1/D}$	@	0.45	0.39	1.32	1.78	0.45	1.57	0.70	0.91	0.35	0.74	0.793
r/sumdiff.	0.004	0.0149	0.005	0.04	0.20	0.006	0.23	0.99	0.008	0.028	0.039	0.000

@ - The estimates of  $\sigma^2 M_L$  was either zero or negative.

On the basis of present study, additive, dominance and epistatic gene effects contributing significantly in the inheritance of the characters, it can be suggested that improvement may be expected by exploiting the additive genetic variance first through pedigree method of selection and at the same time retaining the non additive genetic

variance in population. It is suggested to give enough weightage to individual yield components while selecting by pedigree method. The use of recurrent selection method and diallele selective mating can help in utilizing the all the three type of gene effects (additive, dominant and epistatic).

## References

1. Barad HR, Pithia MS, Vachhani JH. Heterosis and combining ability studies for economic traits in genetically diverse lines of mungbean (*Vigna radiata* (L.) Wilczek). Legume Res. 2008; 31(1):68-71.
2. Dethe AM, Patil JV, Misal AM. Combining ability analysis in mungbean, J Food Legumes. 2008; 21(3):200-201.
3. Gawande VL, Patil JV. Gene action for seed yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. J Maharashtra Agric. Univ. 2005; 30(3):285-288.
4. Jinks JL, Perkins JM, Breese ELA. General method of detecting additive, dominance epistatic variation for metrical traits. II. Application to inbred lines. Heredity. 1969, 24:45-57.
5. Kearsey MJ, Jinks JLA. General method of detecting additive, dominance and epistatic variation for metric traits I Theory. Heredity. 1968; 23:403-409.
6. Kempthorne O. An introduction to genetic statistics. The IOWA State University Press (Eds.). John Wiley and Sons, Inc. New York, 1957, 545.
7. Khan MG, Ahmad W, Khattak GS, Sirajud Din, Ahmad H. Studies on detection of epistasis and estimates of gene effects for secondary yield characters in *Vigna radiata* (L.) Wilczek. Sarhad J Agric. 2007; 23(4):1013-1017.
8. Mansuria CA, Joshi BC. Combining ability analysis for polygenic traits in greengram. Gujarat Agric. Univ. Res. J. 1994; 19:78-81.
9. Panse VG, Sukhatme PV. Statistical methods for agricultural work. Indian Council of Agric. Res. New Delhi, 1967, 167-174.
10. Patil A, Kajjidi ST, Salimath PM Genetic analysis of morpho-physiological traits in green gram. Karnataka J Agric. Sci. 2003; 16:542-547.
11. Patil A, Kajjidi ST. Gene action for morpho – physiological traits in green gram [*Vigna radiata* (L.) Wilczek]. National J Pl. Improv. 2005; 7(1):15-17.
12. Singh VK, Tyagi K, Tomer AK, Singh MN, Nandan R. Gene action for yield and yield attributing traits in mungbean (*Vigna radiata* (L.) Wilczek}. Legume Res. 2007; 30(1):29-32.