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# Combining ability analysis for seed yield, its contributing traits and protein content in Mungbean (Vigna radiata (L.) Wilczek)

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#### Abstract

Seven genotypes of mungbean were studies in diallel with fixed effect model (method II). All the parents and crosses showed significant positive as well as negative general combining ability (GCA) and specific combining ability (SCA) effects for the traits. HUM-16 and IPM-410-3 with significant negative GCA estimates for days to maturity were good general combiner and possessed favourable genetic architecture for early maturity. The general combining ability results indicates that the parent LBG-460 is good general combiner for all the traits except seed yield per plant and harvest index. The cross combination, BM-4 x Pusa Vishal with high SCA effects for number of pods per plant, plant height and days to 50 % flowering, while the cross HUM-16 x RMG-1028 showed significant SCA effects for all the traits except for number of branches per plant. The study revealed non additive gene action involved in controlling all the characters namely, days to 50 % flowering, days to maturity, plant height, number of branches per plant, pod length, seeds per pod, protein content, yield per plant etc. These crosses could help in further development of transgressive segregants with superior combinations of alleles for yield and yield contributing traits.

Keywords: mungbean, greengram, combining ability, diallel analysis

# Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is one of the important pulse crop cultivated since prehistoric time in India. It is also known as Greengram or Golden gram. Mungbean is native to the Indian subcontinent. It is a major edible legume seed in Asia (India, South East-Asia and East Asia) and is also consumed in Southern Europe and in the Southern USA (Dahanayake *et al.*, 2015)<sup>[1]</sup>. India is of the major producer and consumer of mungbean, which about 65 % of the world acreage and 54 % of the world production of this crop (Gowda *et al.*, 2015)<sup>[2]</sup>. The mature seeds provide an invaluable source of digestible protein (22-24 %) for humans in places where meat is lacking or where people are mostly vegetarian (AVRDC, 2012)<sup>[3]</sup>. Farmers mostly cultivate the landraces due to unavailability of improved mungbean cultivars causing low productivity. Mungbean is third most important pulse crop in India with total area and production of 3.00 million hectares and 2.13 million tons, respectively with average productivity of 568 kg per hectare (Anonymous, 2017)<sup>[4]</sup>. Most of the diallel analysis in Mungbean indicated presence of variability due to GCA (Kumar *et al.*, 2010)<sup>[5]</sup>. General and specific combining ability study is necessary to study the gene action and genetic components of variation.

As the productivity of mungbean is very low, extensive research efforts for the improvement of yield and its component traits is necessary. The genetic makeup of genotypes for quantitatively inherited traits can be well understood by the study of genetic parameters. Hence, the present study was conducted to estimate the combining ability and gene action in Mungbean genotypes and their hybrid combinations made in diallel fashion.

# Materials and Methods

The experimental material consisted of seven Mungbean varieties (LBG-460, BM-4, Pusa Vishal, HUM-16, IPM-410-3, RMG-1028 and KM-2241) with phenotypic variability and diverse nature. These seven parents were crossed in diallel mating design to generate 21  $F_1$ 's (excluding reciprocals) during *kharif*, 2016-17. The 21 hybrid combinations along with seven

Parents were grown in *Rabi*, 2017 in Randomized Complete Block Design with two replications at Research Farm, College of Agriculture, IGKV, Raipur to study the gene action and combining ability for yield and yield contributing traits. All the recommended agronomic practices for raising a good Mungbean crop stand were followed. The observation for days to 50 % flowering and days to maturity were taken replication wise while observations for plant height, number of branches per plant, pod length, number of seeds per pod, seed yield per plant, harvest index were taken from the individual plant basis. Seed index was recorded by weighing 100 seeds from randomly selected three plants in each replication. The protein was estimated according to the modified Kjeldhal's method (Piper, 1966)<sup>[6]</sup>. The estimates of variance for the GCA, SCA and their effects were calculated according to fixed effect model (Model I) and Method II (parents and crosses, excluding reciprocals) as given by Griffing (1956)<sup>[7]</sup>.

Table 1: Analysis of variance of diallel analysis in Mungbean.
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Source of variation	df	Days to 50% flowering	Days to maturity	Plant height	Number of branches per plant	Number of pods per plant	Pod length	No. of seeds per pod	Seed yield per plant	100 seed weight	Harvest index	Protein content
Treatments	27	73.40**	23.40**	96.03**	1.10*	307.72**	0.56**	2.40**	16.92**	0.33**	43.04**	2.26*
Parents	6	83.24**	32.17**	141.29**	2.48**	509.48**	0.9**	2.07	6.49*	0.94**	63.25**	1.72**
$F_1$	20	73.97**	17.88**	83.73**	0.70	250.56**	0.48*	2.62**	19.47**	0.13**	25.77	2.53**
Parent vs F1	1	3.15	81.48**	70.72**	0.86	240.48	0.21	0.15	28.67**	0.9**	267.42**	0.07
Replication	1	6.45	7.88	11.16	0.29	204.45	0.07	3.02	23.92	0.03	55.04	0.30
Error (±)	27	3.19	2.69	3.01	0.51	62.48	0.19	0.91	2.20	0.01	15.99	0.09
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\*, \*\* Significant at 5% and 1% level of significance, respectively

**Table 2:** Analysis of variance for combining ability and genetic components of variance in Mungbean

df	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Pod length (cm)	No. of seeds pod <sup>-1</sup>	100 seed weight (g)	Seed yield plant <sup>-1</sup>	Harvest index (%)	Protein content (%)
6	107.10**	16.29**	96.06**	1.04**	191.03**	0.42**	2.13**	0.28**	9.06**	20.25*	1.17**
21	16.58**	10.39**	34.29**	0.41	143.24**	0.24**	0.93*	0.13**	7.55**	21.88**	1.11**
27	1.59	1.34	1.5	0.25	31.24	0.09	0.45	0.005	1.09	7.99	0.04
	10.06	0.66	6.86	0.07	5.31	0.02	0.13	0.02	0.17	-0.18	0.01
	14.99	9.05	32.79	0.16	112.00	0.15	0.48	0.13	6.46	13.89	1.07
a	0.67	0.07	0.21	0.44	0.05	0.13	0.28	0.13	0.03	-0.01	0.01
	6 21 27	flowering           6         107.10**           21         16.58**           27         1.59           10.06         14.99	df         flowering         maturity           6         107.10**         16.29**           21         16.58**         10.39**           27         1.59         1.34           10.06         0.66           14.99         9.05	Days to 50%         Days to maturity         height (cm)           6         107.10**         16.29**         96.06**           21         16.58**         10.39**         34.29**           27         1.59         1.34         1.5           10.06         0.66         6.86           14.99         9.05         32.79	Days to 50%         Days to maturity         height (cm)         branches plant <sup>-1</sup> 6         107.10**         16.29**         96.06**         1.04**           21         16.58**         10.39**         34.29**         0.41           27         1.59         1.34         1.5         0.25           10.06         0.66         6.86         0.07           14.99         9.05         32.79         0.16	Days to 50%         Days to maturity         height (cm)         branches plant <sup>-1</sup> Number of pods plant <sup>-1</sup> 6         107.10**         16.29**         96.06**         1.04**         191.03**           21         16.58**         10.39**         34.29**         0.41         143.24**           27         1.59         1.34         1.5         0.25         31.24           10.06         0.66         6.86         0.07         5.31           14.99         9.05         32.79         0.16         112.00	Days to 50%         Days to maturity         height (cm)         branches plant <sup>-1</sup> Number of pods plant <sup>-1</sup> length (cm)           6         107.10**         16.29**         96.06**         1.04**         191.03**         0.42**           21         16.58**         10.39**         34.29**         0.41         143.24**         0.24**           27         1.59         1.34         1.5         0.25         31.24         0.09           10.06         0.66         6.86         0.07         5.31         0.02           14.99         9.05         32.79         0.16         112.00         0.15	$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Days to 50% flowering         Days to maturity         height (cm)         branches plant <sup>-1</sup> Number of pods plant <sup>-1</sup> length (cm)         seeds pod <sup>-1</sup> weight (g)         yield plant <sup>-1</sup> 6         107.10**         16.29**         96.06**         1.04**         191.03**         0.42**         2.13**         0.28**         9.06**           21         16.58**         10.39**         34.29**         0.41         143.24**         0.24**         0.93*         0.13**         7.55**           27         1.59         1.34         1.5         0.25         31.24         0.09         0.45         0.005         1.09           10.06         0.66         6.86         0.07         5.31         0.02         0.13         0.02         0.17           14.99         9.05         32.79         0.16         112.00         0.15         0.48         0.13         6.46	Days to 50% flowering         Days to maturity         height (cm)         branches plant <sup>-1</sup> Number of pods plant <sup>-1</sup> length (cm)         seeds pod <sup>-1</sup> weight (g)         yield plant <sup>-1</sup> Harvest index (%)           6         107.10**         16.29**         96.06**         1.04**         191.03**         0.42**         2.13**         0.28**         9.06**         20.25*           21         16.58**         10.39**         34.29**         0.41         143.24**         0.24**         0.93*         0.13**         7.55**         21.88**           27         1.59         1.34         1.5         0.25         31.24         0.09         0.45         0.005         1.09         7.99           10.06         0.66         6.86         0.07         5.31         0.02         0.13         0.02         0.17         -0.18           14.99         9.05         32.79         0.16         112.00         0.15         0.48         0.13         6.46         13.89

\*, \*\* Significant at 5% and 1% level of significance, respectively

Table 3: General combining ability effects of parents f	s for yield and contributing traits in Mungbean
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GCA Effects	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Pod length (cm)	No. of seeds pod <sup>-1</sup>	100 seed weight (g)	Seed yield plant <sup>-1</sup>	Harvest index (%)	Protein content (%)
LBG 460	7.59 **	2.41 **	4.36 **	0.62 **	4.28 *	0.30 **	0.69 **	-0.09 **	0.39	-0.38	0.19 **
BM 4	-1.30 **	-0.25	4.30 **	-0.38 *	-2.50	0.19	0.02	-0.13 **	0.50	-1.86 *	0.20 **
Pusa Vishal	-2.69 **	0.52	0.08	0.29	6.56 **	0.05	0.41	0.02	1.78 **	1.56	0.58 **
Ham 16	-1.47 **	-1.14 **	-1.03 *	-0.21	-5.06 **	-0.06	-0.81 **	0.26 **	-0.80 *	-0.19	0.01
IPM 410-3	-0.86 *	-1.70 **	-2.87 **	-0.05	2.78	0.05	-0.25	0.23 **	-0.45	2.47 **	-0.52 **
RMG 1028	-1.41 **	-0.42	-0.75	-0.10	-5.06 **	-0.23 *	0.13	-0.15 **	-0.17	-0.97	-0.23 **
KM 2241	0.14	0.58	-4.09 **	-0.16	-1.00	-0.31 **	-0.20	-0.14 **	-1.25 **	-0.62	-0.23 **
S.E (gi)±	0.38	0.35	0.37	0.15	1.72	0.09	0.2	0.02	0.32	0.87	0.06
S.E (gi-gj)±	0.59	0.54	0.57	0.23	2.63	0.14	0.31	0.03	0.49	1.33	0.09

\*, \*\* Significant at 5% and 1% level of significance, respectively

Table 4: Specific combining ability effects of crosses for yield and contributing traits in Mungbean

SCA Effects	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Pod length (cm)	No. of seeds pod <sup>-1</sup>	100 seed weight (g)	Seed yield plant <sup>-1</sup>	Harvest index (%)	Protein content (%)
LBG 460 x BM 4	-1.62 **	-0.07	-10.07 **	0.33	-16.90 **	0.22	0.13	0.23 **	1.80 **	2.09	-1.16 **
LBG 460 x Pusa Vishal	6.26 **	-1.35 **	-2.85 **	-0.33	-19.96 **	-0.14	0.24	-0.38 **	-3.34 **	-6.29 **	1.00 **
LBG 460 x HUM 16	-1.96 **	2.32 **	-8.24 **	-1.33 **	-4.35	-0.03	-1.04 **	0.17 **	-1.50 **	-1.36	-2.09 **
LBG 460 x IPM 410-3	-0.07	-1.62 **	-0.90	0.00	9.82 **	0.11	0.40	0.22 **	1.25 **	-0.97	2.15 **
LBG 460 x RMG 1028	6.49 **	2.60 **	6.49 **	0.56 *	14.65 **	0.39 **	0.51	-0.02	-1.34 **	0.86	-0.07
LBG 460 x KM 2241	-3.07 **	-4.40 **	3.82 **	0.11	-1.90	0.72 **	-0.15	-0.28 **	3.00 **	-0.99	1.02 **
BM 4 x Pusa Vishal	7.15 **	0.32	8.71 **	0.17	19.82 **	-0.03	0.90 **	-0.51 **	0.20	0.38	0.95 **
BM 4 x HUM 16	3.93 **	0.49	0.82	0.67 **	10.43 **	0.08	1.13 **	-0.14 **	3.29 **	0.97	-0.11
BM 4 x IPM 410-3	-6.68 **	-4.46 **	-5.85 **	-0.50 *	0.10	-0.28 *	-1.43 **	-0.16 **	0.29	-0.25	-0.09
BM 4 x RMG 1028	-3.12 **	-3.24 **	7.54 **	0.56 *	-3.57	0.75 **	1.18 **	0.30 **	4.75 **	2.97 *	1.16 **
BM 4 x KM 2241	-1.18 *	-1.24 *	-5.12 **	1.11 **	-9.63 **	0.08	-0.49	0.07 *	-2.71 **	-2.51 *	-0.61 **
Pusa Vishal x HUM 16	-2.18 **	-0.79	4.04 **	0.50 *	-1.63	-1.03 **	-2.26 **	-0.24 **	3.51 **	1.05	-0.33 **
Pusa Vishal x IPM 410-3	-0.79	5.76 **	-1.12 *	-0.17	-6.46 **	0.11	0.18	-0.26 **	4.66 **	-3.78 **	-1.47 **
Pusa Vishal x RMG 1028	-4.24 **	-1.01 *	0.76	0.39	6.88 **	0.14	0.79 **	0.13 **	2.52 **	-1.78	-0.51 **

0.39 ** -0.21 * 0.55 **
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\*, \*\* Significant at 5% and 1% level of significance, respectively

# **Results and Discussion**

The combining ability analysis provides information about i) the nature and amount of genetic parameters and ii) general as well as specific combining ability of parents and their cross combinations. The parent with good performance may not completely transfer its superiority to its progeny. The general combining ability is primarily due to additive gene effects and additive x additive interaction, while specific combining ability is concerned with non-additive genetic effects which may be due to dominance and epistatic interactions. The identification of good general and specific combiners among the parents is the major objective of diallel analysis. It also allows the scientists to select the appropriate breeding method for improvement of yield and its related traits. It also helps in identification of superior cross combinations. In this study, the analysis of variance for seven parents and twenty-one F<sub>1</sub> combinations between them in half diallel fashion revealed significant differences among parents, crosses and parent versus crosses for all the eleven characters studied. This result indicates that there is much scope for selection of parents on the basis of general combining ability (GCA) and specific combining ability (SCA).

Analysis of variance revealed that there is highly significant difference between parents, crosses and parent versus crosses for all characters except number of branches per plant which showed non-significant difference between crosses and parent versus crosses (Table 1). All the traits showed significant difference between parents excluding for number of seeds per pod which is in agreement with Narasimhulu *et al.* (2014) <sup>[8]</sup>, while when compared between parents and crosses the traits namely days to maturity, plant height, seed yield per plant, 100 seed weight and harvest index showed significant difference which was also observed by Swarn Latha *et al.* (2018) <sup>[9]</sup> except for days to maturity. This indicates the existence of adequate variation between the parents and crosses. These results are comparable with the findings of Patil *et al.* (2011) <sup>[10]</sup>.

Analysis of variance analysis for general combining ability (GCA) and specific combining ability (SCA) was significant for all the characters studied except for SCA of number of branches per plant (Table 2). This indicates the presence of sufficient amount of variation for all the traits. A wide range of variation was observed in  $\sigma^2$ gca for most of the traits studied. Variances due to SCA are higher as compared to variances due to GCA for all the characters, which suggests the predominance of non-additive gene action. Similar results were also reported by several researchers like Swarn Latha *et al.* (2018) <sup>[9]</sup>, Narasimhulu *et al.* (2014) <sup>[8]</sup> and Barad *et al.* (2008) <sup>[11]</sup> for different traits. For utilization of non-additive genetic variability, population improvement method such as bi-parental mating followed by recurrent selection will be rewarding.

The estimates of GCA effects further exposed that the parent variety showing high GCA effects for seed yield also showed

significant GCA effects for one or more yield components. These results are comparable with the results obtained by Sujatha and Kajjidoni (2013)<sup>[12]</sup> and Suresh (2014)<sup>[13]</sup>. All the parents showed significant positive and negative GCA effect for different traits (Table 3). The general combining ability results indicates that the parent LBG-460 is good general combiner for all the traits except seed yield per plant and harvest index (Table 3). HUM-16 and IPM-410-3 with significant negative GCA estimates were good general combiner and possessed favourable genetic architecture for early maturity to their progenies. For the trait number of branches per plant only LBG-460 showed significant positive GCA. The genotypes namely, LBG-460 and Pusa Vishal for number of pods per plant, LBG-460 for pod length and number of seeds per pod, HUM-16 and IPM-410-3 for 100 grain weight, Pusa Vishal for seed yield per plant were good general combiners. While, LBG-460, BM-4 and Pusa Vishal were found to be good general combiner for protein content. Specific combining ability results produced wide range of variation for all the characters (Table 4). In case of Mungbean being autogamous nature, specific combining ability is not readily useful. Yet, if SCA effect tis due to additive × additive gene action which is fixable and helpful in selection of superior transgressive segregants. Present investigation identified the cross BM-4 x Pusa vishal recorded high SCA effects for number of pods per plant, plant height and days to 50% flowering, while the cross HUM-16 x RMG-1028 showed significant SCA effects for all the traits except for number of branches per plant. The crosses between LBG-460 x IPM-410-3 and BM-4 x RMG-1028 showed highest significant SCA effects for protein content. The crosses between BM-4 x IPM-410-3 and RMG-1028 x KM-2241 showed significant negative SCA effects for days to maturity which will help in development of early genotypes. BM-4 x RMG-1028 showed highest SCA effect for seed yield per plant. Desirable recombinants can be obtained from the segregating generations for the traits which are showing highest SCA effects and if there is additive x additive gene action. It is also observed that crosses with high SCA effects for seed yield per plant have positive SCA effects for some yield related traits. Similar results were also reported by Narasimhulu et al. (2014)<sup>[8]</sup>. In some cases we found that parents with inferior GCA effects for a particular trait produced significant SCA effects for the trait; which is also reported by Anbu Selvam Y. (2012) <sup>[14]</sup>. This indicates the additive gene action due to accumulation of favourable genes. The cross between BM-4 x RMG-1028 shows similar relation between GCA and SCA effects.

This combining ability study indicated that the genotypes namely LBG-460, IPM-410-3 and BM-4 could be the best source of elite alleles on the basis of their general combining ability effects, specific combining ability effects and *per se* performance. It is normally observed that GCA and SCA both have similar prominence in the improvement of self-

pollinated crops. The findings of present research will be useful in the selection of superior segregants with better combination of different traits for improvement of yield in Mungbean.

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