



Short Note

## Estimation of Combining Ability Effects in Mungbean (*Vigna radiata* L. Wilczek) Crosses

Punam Singh Yadav and G. Roopa Lavanya\*

Department of Genetics and Plant Breeding, Allahabad School of Agriculture  
Sam Higginbottom Institute of Agriculture, Technology and Sciences (Formerly  
Allahabad Agricultural Institute), Deemed-to-be-University Allahabad-211007,  
Uttar Pradesh, India

An experiment was conducted to estimate the combining ability in mungbean in order to select good general combining parents and desirable crosses. Analysis of variance revealed that the variances due to GCA and SCA were highly significant, indicating importance of additive and non additive gene action in the inheritance of six different characters such as, plant height, number of clusters/ plant, number of pods/ cluster, number of pods/ plant, pod length and test weight. Genotype SML 382 was found to be the best general combiner for all nine characters under study and PUSA 9871 was found to be desirable parent for seven characters viz., plant height, number of primary branches/ plant, number of pods/ cluster, number of pods/ plant, number of seeds/ pod, 100-seed weight and seed yield/ plant. ML 287 and NARP 1-1 were identified as good general combiners for six characters whereas WGG 37 identified as good general combiner for number of primary branches, number of clusters/ plant, number of pods/ cluster and number of pods/ plant. The crosses SML 382 x WGG 37, PUSA 9871 x WGG 37 and NARP 1 -1 x SML 382 showed significant SCA effects for seed yield/ plant and other yield contributing characters.

**Key words:** Combining ability, mungbean, GCA and SCA effects

Mungbean (*Vigna radiata* (L.) Wilczek) is one of the important pulse crops of India and plays a vital role in meeting the requirements of easily digestible protein. Low productivity of the crop is one of the constraints for large scale production of the crop. In order to break the barriers of stagnant production of pulses, there is a need to evolve high yielding varieties. This issue may be addressed by understanding the nature of inheritance of quantitative characters. In order to accomplish this task, combining ability analysis was performed which furnishes information to identify desirable parents and genetic architecture of the crosses. It also provides an insight into the nature and magnitude of fixable and non fixable genetic variances and thus helps to accomplish proper breeding method. The present study aims to know the nature and magnitude of fixable and non fixable genetic variances and to identify parents and cross combinations that can be used in mungbean improvement programme.

### Materials and Methods

The experimental material of the present study comprised seven diverse mungbean genotypes viz., ML 287, PDM 1, NARP 1 -1, HUM 10, SML 382, PUSA 9871 and WGG 37. These genotypes were crossed

in diallele fashion excluding reciprocals. The resulting 21 hybrids and seven parents (28 entries) were grown in a randomized block design with three replications during *kharif*, 2007. Each entry was grown in two row plot of 2m length with intra- and inter- row spacing of 15 cm and 40 cm, respectively. Recommended crop management and plant protection operations were carried out at different crop growth stages. The observations were recorded on five randomly selected plants on nine characters in each entry. Combining ability analysis was done by following Method 2, Model 1 of Griffing (1956).

### Results and Discussion

The analysis of variance along with GCA and SCA variances and their ratios for different characters is presented in Table 1. The analysis of variance revealed highly significant differences among the parents for plant height, number of pods/ plant, pod length and seed yield/ plant while, the crosses exhibited significant differences for all characters except for plant height, number of seeds/ pod and seed yield/ plant. The variation due to Parents vs Hybrids was significant for all characters except plant height, indicating the presence of substantial heterosis in the crosses. The mean squares due to GCA and SCA were significant for all characters

\*Corresponding author email: lavanya.roopa@gmail.com

**Table 1. Analysis of variance for different characters in mungbean**

Source	df	Plant height	No. of primary branches	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length	No. of seeds per pod	100 seed weight	Seed yield per plant
Replication	2	28.89	0.33	0.35	0.42	22.83	0.03	1.65	0.09	2.43
Parent	6	49.56**	0.14	0.24	0.66	23.25**	0.24*	0.21	0.13	3.52**
Hybrid	20	16.19	0.36**	1.54**	0.60**	12.94**	0.76**	0.28	0.68**	1.47
Parent vs hybrid	1	342.30	12.44**	10.46**	195.10**	820.32**	14.17**	2.11**	2.30**	967.61**
Error	54	11.19	0.15	0.19	0.31	4.43	0.08	0.25	0.12	0.88
$\sigma^2$ GCA	6	16.90**	0.09	0.45**	0.44**	3.73**	0.28**	0.13	0.18**	0.46
$\sigma^2$ SCA	21	10.46**	0.29**	0.55**	3.22**	34.15**	0.41**	0.11	0.12**	16.03**
6 <sup>2</sup> A/6 <sup>2</sup> D	3.23	0.62	1.64	0.27	0.22	1.37	2.36	3.00	0.06	

\*\* Significant at 1% level

except number of seeds/ pod. Combining ability analysis revealed that estimates of SCA variances were highly significant than GCA variances for number of pods/ cluster (3.22\*\*), number of pods/ plant (34.15\*\*) and seed yield/ plant (16.03\*\*), suggesting predominance of non additive gene action for inheritance of these characters. The results are in agreement with Loganathan *et al.* (2001).

Estimates of GCA variances were higher than SCA variances for plant height (16.90\*\*), indicating preponderance of additive gene action in inheritance

of the character. In converse, both GCA and SCA mean squares were equally important for number of primary branches/ plant, number of clusters/ plant, pod length and 100 seed weight, suggesting the relative importance of both additive and non additive effects in the control of these characters. Dethe *et al.* (2008) earlier reported similar results for primary branches/ plant, number of clusters/ plant, 100 seed weight and seed yield per plant in mungbean.

The parents SML 382, ML 287 and PUSA 9871 with significant positive GCA effects were good

**Table 2. Estimation of general combining ability effects for different characters in mungbean**

Parent	Characters								
	Plant height	No. of primary branches	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length	No. of seeds per pod	100 seed weight	Seed yield per plant
ML 287 (P1)	2.958**	-0.042	0.197*	0.192*	1.138*	-0.104*	0.238*	-0.236**	0.343*
PDM 1 (P2)	-1.250*	-0.061	-0.185*	-0.261*	-0.012**	0.055	-0.140	-0.080	-0.369*
NARP 1-1 (P3)	-0.620	0.107	0.248*	0.213*	1.337*	0.158**	0.159*	0.134	0.349*
HUM 10 (P4)	-0.324	-0.143*	-0.159*	-0.305**	-0.580	-0.270**	0.073	0.084	0.005
SML 382 (P5)	1.865*	0.148*	0.200*	0.226*	1.014*	0.260**	0.221*	0.174**	0.397*
PUSA 9871 (P6)	1.772*	0.234*	0.013	0.232*	1.364*	-0.063	0.174*	0.166**	0.371*
WGG 37 (P7)	0.172	0.225*	0.199*	0.255*	1.149*	-0.037	0.065	0.049	-0.140

\* and \*\* significant at 5% and 1% level, respectively

general combiners for many characters (Table 2). SML 382 had significant positive GCA effects for all nine characters under study. The GCA estimates of ML 287 (P1) indicated that it was a good combiner for plant height (2.958\*\*), number of clusters/ plant (0.197\*), number of pods/ cluster (0.192\*), number of pods/ plant (1.138\*), number of seeds/ pod (0.238\*) and seed yield/ plant (0.343\*) and PUSA 9871 was identified as a good combiner for plant height (1.772\*), number of primary branches/ plant (0.234\*), number of pods/ cluster (0.232\*), number of pods/ plant (1.364\*), number of seeds/ pod (0.174\*), 100-seed weight (0.166\*\*) and seed yield/ plant (0.371\*). NARP 1-1 was found to be good general combiner for number of clusters/ plant (0.248\*), number of pods/ cluster (0.213\*), number of pods/ plant (1.337\*), pod length (0.158\*\*), number of seeds/ pod (0.159\*) and seed yield/ plant (0.349\*) and WGG 37 was identified as good general combiner for number of primary branches/ plant (0.225\*), number of clusters/ plant

(0.199\*), number of pods/ cluster (0.255\*) and number of pods/ plant (1.149\*).

However, PDM 1 was also found to be good general combiner for reduced plant height (-1.250\*) and recorded significant negative GCA effects for number of clusters/ plant (-0.185\*), number of pods/ cluster (-0.261\*), number of pods/ plant (-0.012\*\*) and seed yield/ plant (-0.369\*). HUM 10 showed significant negative GCA effects for number of primary branches/ plant (-0.143\*), number of clusters/ plant (-0.159\*), number of pods/ cluster (-0.305\*\*) and pod length (-0.270\*\*). In general, good general combiners for seed yield/ plant had significant GCA effects for two or more yield component characters, suggesting their potential use in further breeding programme to isolate desirable transgressive segregants for seed yield and component characters (Jain *et al.*, 2000 and Dethe *et al.*, 2008).

**Table 3. Estimates of specific combining ability effects of crosses for different characters in mungbean**

Parent	Characters								
	Plant height	No. of primary branches	No. of clusters per plant	No. of pods per cluster	No. of pods per plant	Pod length	No. of seeds per pod	100 seed weight	Seed yield per plant
ML 287 x PDM 1	-0.731	0.484	1.798*	1.867*	2.916**	-0.520	-0.110	1.884*	2.206**
ML 287 x NARP 1 -1	2.027*	0.094	0.475	1.794*	1.304	0.210	0.371	-0.317	1.591
ML 287x HUM 10	-4.323	1.843*	0.660	1.865*	2.927**	-0.138	2.124**	1.939*	2.398**
ML 287 x SML 382	0.484	0.162	0.413	1.871*	2.176**	1.052	0.389	0.812	2.066**
ML 287 x PUSA 9871	6.842**	-1.799*	-0.559	0.218	-3.123**	0.101	0.038	1.825*	0.531
ML 287 x WGG 37	0.574	0.048	1.809*	1.852*	2.535**	0.349	1.931*	0.887	2.209**
PDM 1 x NARP 1 -1	1.814*	0.339	1.796*	1.917*	3.732**	1.971*	1.803*	0.245	2.617**
PDM 1 x HUM 10	-1.782*	1.028	1.801*	1.888*	3.135**	1.023	1.992*	1.964*	2.257**
PDM 1 x SML 382	0.975	2.184**	1.892*	1.915*	3.384**	0.396	1.848*	0.976	2.098**
PDM 1 x PUSA 9871	2.634**	0.033	-0.092	0.348	-0.469	-0.004	-0.341	-0.473	1.224
PDM 1x WGG 37	-3.612	0.194	1.791*	1.961*	3.409**	1.836*	1.996*	1.885*	2.068**
NARP 1 -1x HUM 10	1.255	-0.249	-0.019	0.832	0.966	0.133	-0.220	-0.384	1.209
NARP 1 -1 x SML 382	-3.271**	2.236**	1.908*	1.824*	2.325**	1.846*	1.796*	1.857*	2.383**
NARP 1 -1 x PUSA 9871	0.069	0.309	0.032	0.981	2.469**	2.226**	0.250	1.836*	1.576
NARP 1 -1 x WGG 37	2.242**	0.136	0.069	1.799*	1.904*	0.583	1.811*	0.194	0.887
(HUM 10x SML 382	-1.234	1.899*	1.916*	1.265	2.619**	1.961*	0.516	1.810*	1.891*
(HUM 10 x PUSA 9871	1.440	0.558	1.816*	1.816*	2.376**	0.264	2.213**	0.545	2.150**
(HUM 10 x WGG 37	0.129	-0.278	1.746	1.723	2.311**	1.209	1.660	0.814	1.961
SML 382 x PUSA 9871	0.581	1.844*	1.834*	1.881*	4.121**	1.511	0.907*	1.839*	2.157**
SML 382 x WGG 37	-0.064	2.357**	2.528**	2.452**	5.666**	0.711	1.804*	1.890*	3.669**
PUSA 9871 x WGG 37	-1.723*	2.224**	2.301**	2.079*	5.257**	1.879*	1.844*	1.972*	3.161**

\* and \*\* significant at 5% and 1% level, respectively

Specific combining ability of 21 crosses showed positive significant performance for two or more characters (Table 3). Fourteen crosses out of 21 crosses showed significant positive SCA effects for seed yield/ plant. The crosses showing significant SCA effects for seed yield/ plant also exhibited significant and desirable SCA effects for more than two component characters. This may be because the seed yield is a complex character and is generally dependant upon its component characters. Based on significant SCA effects, NARP 1-1X SML 382 and Pusa 9871X WGG 37 were the best cross combinations for all the traits studied whereas, PDM 1X HUM 10, SML 382 x Pusa 9871 and SML 382 X WGG 37 were recognized as desirable hybrids for seed yield, number of primary branches/ plant, number of clusters/ plant, number of pods/ cluster, number of pods/ plant, number of seeds/ pod and 100-seed weight (Table 3). Crosses, ML 287 x HUM 10, PDM 1 x NARP 1 -1 and HUM 10 x SML 382 exhibited highly significant desirable SCA effects for number of pods/ plant and seed yield/ plant.

The SCA effects represented dominance and epistatic component of variation which are non-fixable in nature. But if the crosses showing significant SCA effects involved both or one high general combining genotypes they could be successfully exploited to throw stable performing transgressive segregants carrying fixable gene

effects (Natarajan and Thiyagarajan, 1989 and Loganathan *et al.*, 2001).

The crosses, SML 382 x PUSA 9871 and NARP 1 -1 x SML 382 with high SCA for seed yield and more than three yield component characters involving parents with high GCA x high GCA combination, indicating that additive and additive x additive gene effects were predominant in the expression of the characters. Therefore, single plant selection could be practiced in segregating generations to isolate transgrants from such combinations due to possibility of fixation (Dethe *et al.*, 2008).

## References

- Dethe, A.M., Patil, J.V. and Misal, A.M. 2008. Combining ability analysis in mungbean. *J. Food Legumes*, **21**: 200-201.
- Griffing, B. 1956. The concept of general and specific combining ability in relation to diallel crossing system. *Australian J. Biol. Sci.*, **9**: 463-493.
- Jain, P.K., Lakhani, J.P. and Singh, C.B. 2000. Combining ability analysis for yield and its components in mungbean. (*Vigna radiata* (L.) Wilczek). *New Agriculturist*, **11**: 5-10.
- Loganathan, P., Saravanan, K. and Ganesan, J. 2001. Combining ability in mungbean (*Vigna radiata* (L.) Wilczek). *Res. Crops*, **2**: 398-403.
- Natarajan, D.C. and Thiyagarajan, K. 1989. Combining ability in mungbean. *Indian J. Pulses Res.*, **2**: 15-19.