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Diallel analysis in mungbean (*Vigna radiata* (L.) Wilczek)

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Abstract
The 8x8 diallel analysis experiment was conducted in 13 quantitative characters in mungbean. The general combining ability and specific combining ability were highly significant for all the characters studied. Better combining parents were Pusa Bold (Vishal), Pusa Baisakhi. Best combination were Pusa Baisakhi x Pusa Bold(Vishal) x Pant Mung-2 x ML-613, Pant M-3 x PS-16 and Pusa Bold (Vishal) x ML-613. Both additive and non additive gene effects were found contributing the inheritance of plant height, number of clusters per plant, number of pods per plant and seed yield per plant. The additive gene effects appeared to be more important for number of seeds per pod and non additive effects for primary branches per plant and protein content in seeds.

Keywords: Mungbean, diallel analysis, combining ability analysis

Introduction
The genetic improvement of field crops for various characters of economic importance is a constant exercise breeders have to pursue to meet their obligations in an ever evolving environment. Information on the relative importance of general and specific combining ability effects are significant in the development of an effective mungbean breeding programme.

Sprague & Tatum (1942) [4] defined general combining ability as the average performance of lines in hybrid combinations. They used specific combining ability to designate deviations of certain crosses from expectations on the basis of average performance of the lines involved. They also stated that general combining ability is due to the genes which are largely additive in their effects and specific combining ability is due to the genes with dominant or epistatic effects. Present investigations were planned to estimate general and specific combining ability in a diallel cross of eight promising mungbean genotypes. So that the desirable parents may be identified for use in conventional breeding programmes.

Materials and Methods
Eight mungbean genotypes *viz.* Pusa Baisakhi, Pant mung-2, Pant M-3, Pusa Bold (Vishal), Pusa-105, ML-613, Narendra Mung-1 and P.S.-16 were crossed in a diallel fashion excluding reciprocals. The parent their 28F$_1$'s were grown in a randomized block design with three replications during Kharif 2017-2018 at the crop Research farm of Post Graduate college Ghazipur, U.P., India. Each plot consisted of single row of ten plant with row to row and plant to plant spacing of 30 cm and 10 cm. Data on days to 50% flowering, days to first picking maturity, plant height (cm), primary branches per plant, number of nodes on main stem, number of clusters per plant, number of pods per cluster, pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), protein content in seed and seed yield per plant (g), were recorded on five randomly selected plants from each plot in each replications. The data were subjected to Method II of combining ability analysis developed and illustrated by Griffing (1956) [1].

Results and Discussion
The genotypes used in the experiment showed considerable variability for the characters under study (Table-1). The analysis of variance showing mean square value for replications genotypes, general combining ability (gca) and specific combining ability (sca) are presented in Table 2. The mean squares of genotypes were significant in respect of all traits. This indicated an adequate amount of variability present in the parental materials. Mean squares due to gca and sca effects were highly significant for all the characters revealed the presence of additive and non additive gene action for the expression of these traits.

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Significant contribution of general and specific combining ability in the expression of these various characters had also been reported in more or less similar pattern by other workers (Malhotra *et al.* (1980), Rao *et al.* (1984), Tiwari *et al.*(1993) [2, 3, 5].

Estimates of general and specific combining ability effects (gca & sca) were made for all the characters are given in Table 3& 4 respectively. The general combining ability effects indicated that the genotypes Pusa bold (Vishal) showed high significant positive effect for five characters and thus prove to be the best general combiner in the group of parents. Pusa Baisakhi was the second best genotype which exhibited high significant positive effects for four characters. Similarly Pant M-3 and Narendra Mung-1 showed high significant positive effect for three characters. These genotypes might contribute significantly the higher yields through their influence an individual yield components. In a hybridization programme crosses involving these varieties should produce segregates with near optimal level yield components consequently expecting a better yield potential.

Estimates of specific combining ability effects revealed that the cross combinations; Pusa Baisakhi x Pusa Bold (Vishal), Pant Mung-1 x ML-613, Pant M-3 x PS-16, Pusa Bold (Vishal) x ML-613 had high significant positive value for plant height, Primary branches per plant, number of pods per cluster, number of pods per plant, proterin content in seed and seed yield per plant. The crosses, Pusa Baisakhi x Pusa-105, Pusa Baisakhi x Narendra Mung-1 and Pusa Baisakhi x PS-16 had high significant positive value for number of nodes on main stem, number of pods per plant, protein content in seeds, seed yield per plant were the best. Similar results have been reported by Tiwari *et al.* (1993) [5].

The higher magnitudes of general combining ability component of variance for plant height, number of pods per cluster, number of pods per plant, number of seeds per pod and seed yield per plant indicated the predominance of additive gene effects for these characters. However, the higher magnitude of specific combining ability component of variance for plant height, primary branches per plant, number of pods per cluster, number of pods per plant, protein content and seed yield per plant indicated the predominance of non additive gene effects for these characters. Both gca and sca variance for plant height, number of pods per cluster and seed yield per plant were highly significant and almost equal in magnitude showing that additive as well as non additive genetic components were involved in determining the inheritance of these traits. It may thus be concluded from the present investigation that maximum yield may be achieved with a system that can manipulate both additive and non additive gene effects in an effective manner.

Table 1: Mean values of 13 quantitative characters of 8 genotypes of mungbean

Character Parents	Days to 50% Flowering	Days to first picking maturity	Plant height	Primary branches/ plant	No. of nodes on main stem	No. of Clusters/ plant	No. of Pods/ cluster	Pod length	No. of Pods/ plant	No. of Seeds/ pod	100 seed weight	Protein content in seed	Seed yield/ plant
Pusa Baisakhi	39.67	72.79	40.12	2.67	7.67	15.56	3.89	7.33	42.55	5.67	3.40	20.57	7.59
Pant Mung-2	42.67	73.22	40.33	2.22	7.55	14.11	3.78	7.56	45.33	7.55	3.60	21.70	8.66
Pant M-3	40.33	73.11	40.44	3.56	7.89	12.89	3.56	8.00	43.00	7.33	4.13	21.27	8.65
Pusa bold (Vishal)	38.89	72.78	41.08	2.45	7.33	13.22	4.22	7.11	46.22	8.11	3.83	20.33	9.53
Pusa-105	39.11	73.00	40.22	2.89	7.22	14.33	3.22	8.01	42.00	7.89	3.47	21.32	8.55
ML-613	38.67	71.22	40.16	3.11	6.33	15.11	3.67	7.12	45.77	5.67	3.17	20.71	8.27
Narendra mung-1	39.55	71.55	41.06	2.89	6.78	13.00	4.11	7.44	45.11	5.44	3.93	22.30	7.27
PS-16	39.44	72.22	40.90	3.11	5.78	11.78	3.33	7.64	46.11	5.78	3.27	21.30	6.93
Gand mean	39.79	72.48	40.54	2.86	7.06	13.75	3.72	7.52	44.50	6.68	3.60	21.18	8.18
SE	0.48	0.35	0.27	0.29	0.35	0.58	0.24	0.24	0.72	0.41	0.21	0.30	0.41

Table 2: Analysis of variance for genotypic difference and general combining ability (gca), spacific combining ability (sca) for 13 chacracter in 8 parant diallel crosses in mung bean.

	D.F.	Days to 50% Flowering	Days to first picking maturity	Plant height	Primary branches/ plant	No. of nodes on main stem	No. of Clusters/ plant	No. of Pods/ cluster	Pod length	No. of Pods/ plant	No. of Seeds/ pod	100 seed weight	Protein content in seed	Seed yield/ plant
Replication	2	0.25	1.48*	0.3	0.17	0.13	0.48	0.15	0.55	0.74	0.016	0.028	0.097	0.49
Genotype	35	9.52**	7.26**	1.24**	.45**	1.12**	3.58**	.91**	.60**	86.26**	1.52**	.23**	.87**	.10**
gca	7	0.680**	0.618**	0.590**	0.368**	0.620**	1.372**	0.291**	0.134	1.573**	0.492**	0.038**	0.217*	1.091**
sca	28	3.799**	2.873*	0.369**	0.096**	0.314**	1.151**	0.310**	0.217**	35.549**	0.512**	0.088**	0.311**	4.049**
Error	70	0.158	0.143	0.910	0.043	0.065	0.140	0.056	0.076	0.315	0.092	0.010	0.098	0.133

* significant at 5% level of significance

** significant at 1% level of significance

Table 3: Estimates of gca effects of different characters in 8 parent diallel crosses in mungbean

Character Parents	Days to 50% Flowering	Days to first picking maturity	Plant height	Primary branches/ plant	No. of nodes on main stem	No. of Clusters/ plant	No. of Pods/ cluster	Pod length	No. of Pods/ plant	No. of Seeds/ pod	100 seed weight	Protein content in seed	Seed yield/ plant
Pusa Baisakhi	-0.25	-0.05	0.22*	0.11	0.34**	0.43**	0.16	0.03	-0.35	-0.06	-0.07	-0.08	0.26*
Pant Mung-2	0.33*	0.22	0.11	-0.26**	-0.06	0.00	0.01	0.04	0.08	0.30*	-0.01	0.20	-0.20
Pant M-3	0.16	0.40**	0.16	0.37**	0.27**	-0.24	0.08	0.16	-0.46*	0.10	0.05	0.07	0.02
Pusa bold (Vishal)	-0.15	-0.15	0.22*	-0.13*	-0.23**	0.00	0.20*	-0.12	0.68**	0.24*	0.04	-0.12	0.62**
Pusa-105	-0.06	-0.01	-0.37**	-0.04	0.26**	0.11	-0.17*	0.07	-0.45*	0.03	-0.04	-0.01	0.03
ML-613	-0.36*	-0.42**	-0.34**	0.10	-0.17*	0.52**	-0.03	-0.08	0.15	-0.40**	-0.08*	-0.12	-0.02
Narendra mung-1	0.35*	0.12	-0.12	-0.02	-0.22*	-0.20	0.06	-0.19*	0.16	-0.11	0.10*	0.22*	-0.25

	Days to 50% Flowering	Days to first picking maturity	Plant height	Primary branches/plant	No. of nodes on main stem	No. of Clusters/plant	No. of Pods/cluster	Pod length	No. of Pods/plant	No. of Seeds/pod	100 seed weight	Protein content in seed	Seed yield/plant
PS-16	-0.04	-0.11	0.11	-0.12	-0.20*	-0.62**	-0.32**	0.09	0.20	-0.10	0.02	-0.16	-0.45**
SE gi	0.117	0.113	0.089	0.054	0.070	0.109	0.063	0.077	0.164	0.090	0.030	0.092	0.108
Se (gi - gj)	0.178	0.170	0.134	0.089	0.114	0.339	0.104	0.122	0.250	0.136	0.045	0.140	0.164
CD gi(5%)	0.276	0.267	0.210	0.127	0.165	0.257	0.148	0.182	0.387	0.212	0.070	0.217	0.255
CD gi (1%)	0.409	0.395	0.311	0.188	0.244	0.381	0.220	0.269	0.573	0.314	0.104	0.321	0.377
CD SE (gi-gj) (5%)	0.365	0.348	0.374	0.182	0.233	0.695	0.213	0.250	0.513	0.279	0.092	0.118	0.336
CD SE (gi-gj) (1%)	0.493	0.471	0.371	0.246	0.315	0.939	0.880	0.338	0.454	0.376	0.124	0.387	0.454

* significant at 5% level of significance

** significant at 1% level of significance

Table 4: Estimates of specific combining ability (sca) effects of different characters in 8 parent diallel crosses in mungbean

S. No.		Days to 50% Flowering	Days to first picking maturity	Plant height	Primary branches/plant	No. of nodes on main stem	No. of Clusters/plant	No. of Pods/cluster	Pod length	No. of Pods/plant	No. of Seeds/pod	100 seed weight	Protein content in seed	Seed yield/plant
1	PusaBaisakhi x Pantmung-2	-2.64**	-1.78**	-0.50	0.66**	-0.10	0.44	0.25	0.12	0.92	0.25	-0.08	0.19	0.38
2	PusaBaisakhi x PantM-3	-0.70	-0.96**	1.00**	0.15	-1.22**	0.35	-0.26	-0.28	1.81**	0.22	-0.15	-0.49	2.38**
3	PusaBaisakhi x Pusabold (Vishal)	-0.28	-1.42**	0.71*	0.43*	-0.60*	0.00	0.62**	-0.35	3.89**	-0.02	-0.30**	1.38**	1.91**
4	PusaBaisakhi x Pusa-105	0.08	-0.11	0.09	0.12	0.58*	-0.67	0.10	0.39	5.35**	-0.48	-0.13	0.53*	1.07**
5	PusaBaisakhi x ML-613	0.05	-1.70**	-0.28	-0.25	0.23	-0.08	-0.04	0.15	3.42**	-0.27	-0.17	-0.30	1.10**
6	PusaBaisakhi x Narendra mung-1	-1.11**	-0.35	-0.06	0.32	0.62*	0.54	0.32	-0.02	2.97**	1.00**	0.01	-0.67*	1.28**
7	PusaBaisakhi x PS-16	-1.94**	0.88*	0.92**	-0.25	0.16	0.51	-0.08	-0.28	3.37**	0.54	0.36**	-0.02	0.45
8	Pant Mung-2 x Pant M-3	1.50**	-0.11	-0.78**	-0.15	0.52*	0.45	0.34	-0.62*	2.71**	-0.13	0.29**	0.21	0.44
9	Pant Mung-2 x Pusabold (Vishal)	-1.96**	-1.90**	0.17	0.35	-0.42	-0.12	-0.01	-0.12	3.56**	-0.27	-0.29**	-0.47	0.58
10	Pant Mung-2 x Pusa-105	-0.94*	-1.26**	0.41	-0.29	-0.47	0.65	0.13	-0.91**	2.47**	0.05	-0.15	0.32	0.31
11	Pant Mung-2 x ML-613	-1.53**	-0.08	0.59	0.34	-0.26	0.02	0.66**	0.87**	2.99**	-0.84**	0.27**	-0.77**	1.28**
12	Pant Mung-2 x Narendra Mung-1	-0.13	-0.39	0.65*	0.02	-0.76**	-0.03	-0.32	-0.66*	3.42**	0.19	-0.23*	-0.08	0.64
13	Pant Mung-2 x PS-16	-1.52**	0.28	0.45	-0.33	-0.22	0.83*	0.17	0.64*	1.82**	-0.38*	0.14	0.04	0.92*
14	Pant M-3 x Pusa bold (Vishal)	0.79*	-0.41	0.46	0.40*	-0.53*	0.68	-0.64**	0.08	0.44	-0.96**	0.28**	0.21	0.05
15	Pant M-3 x Pusa-105	-1.22**	-1.56**	0.16	-0.30	-0.02	0.46	0.95**	-0.19	3.35**	-1.08**	-0.11	-0.22	1.24**
16	Pant M-3 x ML-613	-0.92*	0.09	0.12	0.28	-0.14	0.15	0.93**	0.12	4.75**	-0.20	-0.15	1.16**	0.36
17	Pant M-3 x Narendra mung-1	-0.63	-1.24**	0.25	-0.38	-0.20	0.76*	0.62**	0.07	3.74**	0.06	-0.37**	-0.05	0.37
18	Pant M-3 x PS-16	-0.47	-0.12	0.71*	0.16	0.56*	0.85*	-0.01	-0.13	3.59**	0.60*	-0.12	-0.60*	0.61
19	Pusa bold(Vishal) x Pusa-105	1.02**	0.77*	-0.63*	-0.08	-0.63*	-0.24	0.16	0.08	3.54**	0.00	0.15	0.20	0.49
20	Pusa bold(Vishal) x ML-613	-0.50	-0.15	0.49	-0.12	0.46	0.80*	0.92**	-0.30	2.05**	-0.68*	0.28**	-0.25	0.89*
21	Pusa bold(Vishal) x Narendramung-1	-0.43	-1.24**	-0.19	-0.10	-0.37	1.63**	-0.06	0.02	3.49**	-0.19	-0.22*	0.17	1.29**
22	Pusa bold(Vishal) x PS-16	0.40	-1.46**	-0.13	-0.23	0.17	1.28**	-0.57*	0.34	1.55**	-0.35	-0.22*	0.09	0.89*
23	Pusa-105 x ML613	-0.81*	1.63**	0.19	0.13	0.09	1.47**	0.27	-0.10	1.52**	0.18	0.12	0.13	0.54
24	Pusa-105 x Narendra mung-1	-0.74	0.17	-0.50	0.14	0.48*	0.30	-0.25	-0.15	2.73**	0.54	-0.19*	-0.61*	0.92*
25	Pusa-105 x PS-16	-0.02	-2.06**	-0.43	0.13	0.23	0.27	0.13	-0.59*	3.46**	-1.02**	-0.17	-0.70**	1.12**
26	ML-613 x Narendra mung-1	-0.22	1.25**	-0.71*	0.11	-0.54	-0.11	-1.16**	-0.50	0.91	0.56	-0.21*	0.01	0.78*
27	ML-613x PS-16	-1.05**	-1.55**	-0.84**	-0.24	0.45	0.09	-0.45*	-0.50	1.64**	1.10**	-0.16	0.45	1.13**
28	Narendra mung-1x PS-16	0.65	-0.51	-0.81**	0.11	-0.06	0.59	-0.94**	-0.13	1.40**	0.37	0.36**	-0.45	1.89**
	+ Sij	0.361	0.346	0.273	0.187	0.230	0.339	0.215	0.248	0.508	0.276	0.092	0.284	0.333
	+ Sij - Sik	0.533	0.513	0.404	0.277	0.342	0.501	0.258	0.378	0.753	0.409	0.132	0.421	0.493
	+ Sij - Skl	0.503	0.483	0.382	0.262	0.322	0.473	0.317	0.347	0.710	0.385	0.130	0.397	0.465

* significant at 5% level of significance

** significant at 1% level of significance

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