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Genetic analysis of component of variance in mungbean (*Vigna radiata* (L.) Wilczek)

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Abstract
The 28F_1's were obtained by crossing eight different varieties of mungbean in a diallel fashion and evaluated with parents and F_2 in a randomized block design with 3 replications and components of variance were estimated for yield and yield relative attributes. The estimate of gene effects indicated that significant of both additive and non additive variance and presence of over dominance for all the traits.
The non additive components of variance were significant for all the characters except primary branches per plant, number of nodes on main stem and pod length. The magnitude of non additive components were greater than the additive components. The asymmetrical gene distribution recorded for all the characters.

Keywords: Gene action, genetic component of variance, mungbean, diallel

Introduction
The breeding methods to be adopted for improvement of crops depends primarily upon the nature of gene action involved in the expression of quantitative traits of economic importance. One of the several biometrical techniques available to plant breeders for evaluating and characterizing genetic variability existing in a crop species is diallel analysis.
It is one of the techniques frequently employed to study the nature of genetic variation particular plant traits and to select to potential parents which would produce the best combination (Murty, 1975) [6]. The techniques has been effectively used for such purpose in lentil (Tahir *et al.*, 1995) [11], Chickpea (Singh & Bains 1982; Sarode *et al*., 2001) [10] and cowpea (Sanghwan & Lodhi, 1999) [9]; Munbean (Kattak *et al*. 2002) [5]. Only a few reports are available on the node of inheritance of yield and its components in mungbean. The present study is in this direction.

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 PS-16 were crossed in a diallel fashion (excluding reciprocal). The eight parents 28F_1's and 28F_2's were grown in a randomized block design with three replication during kharif 2018 at the crop-research Farm, Post Graduate College, Ghazipur, U.P., India. Each plot consisted of single row of the plant with row to row and plant to plant spacing of 30 cm. and 10 cm. Data were recorded 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 seeds and seed yield per plant (g) on five randomly selected plant from each plot in each replications. The genetic components of variance analysis by Hayman's approach (1954) [3].

Results and Discussion
The analysis of variance for 13 characters in 8 parents diallel cross in mungbean are presented table 1. The mean squares due to parents were significant for all the character except days to first picking maturity, plant height (cm.), number of clusters per plant and pod length. The mean squares due to F_1's were highly significant for all the characters except primary branches per plant, the parents Vs F_1's were also significant for all the characters except plant height and protein content in seeds. This indicating the genetic variations are presented in the experimental material.
The estimates of genetic components of variance i.e. D, F^ $\hat{H}_1$, $\hat{H}_2$, ĥ 2 and Ê along with their standard error in F_1's generation for all characters are presented in Table-2.

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The non additive components of variance ($\hat{H}_1$ and $\hat{H}_2$) were significant for all the characters except primary branches per plant, number of nodes on main stem and pod length. The magnitude of non additive components were greater than the additive ($D^\wedge$) components which indicated the important role of non additive gene control for the characters. These finding are in agreement with the Azmal *et al.* (2007) [1], Patel *et al.* (2009) [7], Rahman *et al.* (2009) [8]. The significant estimates of additive ($D^\wedge$) component of genetic variance were recorded for number of nodes on main stem, number of clusters per plant, Number of seeds per pod and protein content in seeds.

The main degree of dominant ($\hat{H}_1/D^\wedge$) was greater than the unity for all the characters under study which indicated the over dominance gene action in the expression of these dominant and recessive traits. The gene distribution was found asymmetrical for different traits revealed by the ratio

($\hat{H}_2/4\hat{H}_1$). The KD/KR ratio also indicated the presence of excess of dominant allel are presented in all the characters.

The similarly result have been reported by several worker Gorase *et al.* (2000) [1], Joseph *et al.* (2000) [4], Khattak *et al.* (2002) [5], Azamal *et al.* (2007) [1], Patel *et al.* (2009) [7]. The estimates of heritability narrow sense was high for number of seeds per pod (0.64), followed by number of clusters per plant, 100 seeds weight, number of nodes on main stem and protein content in seeds. From the above discussion for gene action it is clear that both additive and non additive components were involved in the expression at the above mentioned traits. It was further possible to classify the parents on the basis of the type of alleles present in them and this provides useful clues for the selection of parental combination which are likely to give better segregates.

Table 1: Estimates of genetic components of variance and related statistics for different characters in 8 parent diallel cross in mungbean F_1

Component	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 seeds	Seed yield/ plant
$D^\wedge$	1.46	0.41	0.08	0.13*	0.61**	1.44**	0.07	0.05	2.62	1.21**	0.10**	0.31*	0.60
	± 0.73	± 0.32	± 0.15	± 0.05	± 0.11	± 0.24	± 0.14	± 0.12	± 1.92	± 0.18	± 0.02	± 0.11	± 0.41
$F^\wedge$	2.67	0.61	0.13	0.06	0.61	1.49*	-0.02	0.04	3.74	2.11**	0.19*	0.50	0.64
	± 1.73	± 0.76	± 0.36	± 0.13	± 0.27	± 0.57	± 0.33	± 0.29	± 4.53	± 0.44	± 0.06	± 0.26	± 0.96
$\hat{H}_1$	10.28**	7.96**	1.49**	0.31	1.31**	3.12**	1.07**	0.62	82.98**	2.40**	0.34**	1.14**	9.74**
	± 1.68	± 0.74	± 0.35	± 0.13	± 0.26	± 0.55	± 0.32	± 0.28	± 4.41	± 0.43	± 0.05	± 0.25	± 0.94
$\hat{H}_2$	8.86**	7.52**	1.11*	0.24	0.90	2.70**	1.04**	0.59	81.54**	1.37*	0.24**	0.91**	9.26**
	± 1.46	± 0.65	± 0.30	± 0.11	± 0.22	± 0.48	± 0.28	± 0.25	± 3.83	± 0.37	± 0.05	± 0.22	± 0.81
h^2	42.50**	27.21**	-0.01	0.14	0.30	11.08**	0.43	0.73**	467.28**	0.37	0.41**	0.09	50.61**
	± 0.98	± 0.43	± 0.20	± 0.07	± 0.15	± 0.32	± 0.18	± 0.16	± 2.57	± 0.25	± 0.03	± 0.15	± 0.55
$E^\wedge$	0.16	0.15	0.09	0.04	0.07	0.14	0.06	0.08	0.32	0.09	0.01	0.10*	0.14
	± 0.24	± 0.11	± 0.05	± 0.02	± 0.04	± 0.08	± 0.05	± 0.04	± 0.64	± 0.06	± 0.01	± 0.04	± 0.14
$(\hat{H}_1/D^\wedge)^{1/2}$	2.66	4.39	4.43	1.53	1.70	1.47	3.99	3.64	5.63	1.41	1.79	1.90	4.02
$\hat{H}_2/4\hat{H}_1$	0.22	0.24	0.19	0.04	0.17	0.22	0.24	0.24	0.24	0.14	0.18	0.20	0.24
KD/KR	2.05	1.40	1.39	1.35	2.04	2.08	0.92	1.25	1.29	4.27	1.10	2.47	1.30
$h^2/\hat{H}_2$	4.75	3.61	0.009	0.58	0.33	4.10	0.41	1.23	5.73	0.27	1.70	0.98	5.46
t^2	5.98	4.33	3.34	0.27	1.12	3.41	21.41	14.69	40.90	15.98	0.06	1.30	6.27
r	0.980**	0.764*	0.178	-0.457	-0.162	-0.925**	0.134	0.353	-0.991**	0.796*	0.670	0.325	-0.889**
Hns	0.150	0.040	0.040	0.23	0.32	0.39	0.040	0.050	0.030	0.640	0.350	0.230	0.050
* Significant at 5% level of significance ** Significant at 1% level of significance													

Table 2: Analysis of variance (mean square) for 13 characters in 8 parent diallel cross in mungbean

Source of variation	D.F.	Days to 50% flowering	Day 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 seeds	Seed yield/ plant
Replication	2	0.584	1.260	0.139	0.571*	0.413	0.022	0.097	0.184	1.277	0.051	0.075	0.210	1.195
Parents	7	4.841**	1.679	0.501	0.527**	1.564**	4.743**	0.369	0.368	8.800**	3.898**	0.345**	1.236**	2.215**
F_1's	27	1.484**	2.826**	1.473**	0.413	0.982**	0.905**	0.992**	0.513**	4.020**	0.873**	0.123**	0.787**	1.432**
P vs F_1	1	259.452**	166.229**	0.170	0.957**	1.976**	67.912**	2.783**	4.660**	2849.042**	2.505**	2.529**	0.795	308.857**
F_2's	27	6.421**	17.178**	5.513**	0.573	1.335**	2.766**	1.040**	0.395**	5.689**	1.748**	0.638**	1.520**	1.767**
P vs F_2	1	91.321**	240.062**	11.132**	2.881**	1.061*	5.162**	4.731**	3.748**	5254.316**	0.002	6.052**	1.340**	888.49**
Error	126	0.505	0.952	0.471	0.126	0.199	0.506	0.213	0.195	1.019	0.298	0.074	0.255	0.422
* Significant at 5% level of significance ** Significant at 1% level of significance														

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