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Study of gene action for yield and its contributing traits in green gram (*Vigna radiata* L. Wilczek)

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Abstract
The present investigation was carried out at Student's Instructional Farm, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur- 2080 02 (U.P.) during 2020-23. This region has a subtropical climate. Sandy loam is the kind of soil. Roughly 1270 mm of rain falls there each year. Kanpur district has a semi-arid climate with scorching summers and chilly winters. Geographically, Kanpur is situated in latitude 26.40^0 N and longitude 80.10^0 E, respectively, with elevation 127 meters above mean sea level. The estimate of additive genetic component ($\hat{D}$) was significant for all the characters except *viz.* no. of branches per plant, no. of clusters per plant, no. of seeds per pod, harvest index (%) and protein content (%) in F_1 generation while days to 50% flowering (days), no. of branches per plant and protein content (%) in F_2 generation. Relatively magnitude of $\hat{H}_1$ component was higher than that of $\hat{D}$ component values for all the characters under study indicating role of both additive and dominance gene action with prevalence of dominant gene action. The significant and positive value of ($\hat{F}$) component for days to 50% flowering (days), no. of pods per plant, plant height (cm), 100 seed weight (g), biological yield per plant (g), seed yield per plant (g) in F_1 generation while days to maturity (days), no. of pods per plant, plant height (cm), no. of seeds per pod, 100 seed weight (g), biological yield per plant (g), seed yield per plant (g) in F_2 generation while positive non-significant for remaining characters.

Keywords: Variance, gene action, green gram and yield

Introduction
India is the largest producer and consumer of pulses in the world. It has 36.8% of global area, 24.2% of global production and 27% of consumption. About 80% of world pigeonpea, 65% of chickpea, 37% of lentil, 65-70% of mungbean/uradbean are produced in India. According to Karpechenko, 1925, and Krishnan and De, 1965 [14, 16], the green gram (*Vigna radiata* L. Wilczek), also known as mungbean, is a member of the family Leguminaceae, subfamily Papillionaceae, genus *Vigna*, and species *radiata* with chromosome number 2n = 22. The average global grain yields of green gram are low at 0.73 ton ha^{-1} (AVRDC). The strategy for increasing green gram productivity involves integrating green gram into local cultivation systems. It is widely planted together with other crops, such as maize, sorghum, peanuts, and sugar cane, either by intercropping or catch cropping between wheat and rice seasons. These cultivation systems require high-yielding mungbean cultivars. India is the major producer of greengram in the world, and it is grown in almost all states. It is grown on about 40.38 lakh hectares with a total production of 31.5 lakh tonnes with a productivity of 783 kg/ha and contributes 11 % to the total pulse production in the year 2021-2022. In *Kharif* 2022, greengram production was 17.5 lakh tonnes (1st advance estimates) in an area of 33.37 lakh hectares (GOI, 2022). Diallel analysis provides a systemic approach for identification of superior parent and crosses which is the basic material on which the success of a breeding programme depends. The advantage of the diallel analysis is that, it gives better picture of genetic information of the material under investigation.

Genetic information regarding gene action, combining ability, heterosis, inbreeding depression, heritability, genetic gain, correlation and path coefficient provides a clue for selecting the most suitable parents and crosses for hybridization.

Materials and Methods

(A) Graphical analysis

Following the guidelines provided by Jink and Hayman (1953) and Hayman (1954a, b) [9, 10, 12, 13] the graphical analysis was carried out using the variance and covariance values

The genetic components of variation that were estimated were as follows Jinks and Hayman (1953), Hayman (1954a), Aksel and Johnson (1963) [1, 9, 10, 12, 13].

The following two approaches were followed for diallel analysis -

1. Hayman's approach
2. Griffing's approach

$\hat{D}$ = Component of variation due to additive effects of genes

$\hat{H}_1$ = Component of variation due to dominance effects of gene

$\hat{H}_2 = H_1 [-(u-v)^2]$

u= Proportion of positive genes in parents

v= Proportion of negative genes in parents

$\hat{F}$ = The mean of F_r over arrays, where F_r is the covariance of additive and dominance gene effects in a single array.

$\hat{E}$ = The expected environmental component of variation which was calculated as with ungrouped randomization as suggested by Aksel and Johnson (1963) [1] as –

$$\frac{\text{Replication SS} + \text{Error SS}}{\text{Replication d.f.} + \text{Error d.f.}} \times \text{number of replications}$$

(B) Estimation of components of variation

The estimates of these components of genetic variation were determined using following formulae as suggested by Hayman (1954a) [9, 10] -

$\hat{D} = V_0L_0 - \hat{E}$

$\hat{F} = 2V_0L_0 - 4W_0L_{01} - \frac{2(n-2)\hat{E}}{n}$

$\hat{H}_1 = V_0L_0 + 4V_0L_1 - 4W_0L_0 - \frac{(3n-2)\hat{E}}{n}$

$\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\hat{E}$

$\hat{h}^2 = 4(ML_1 - ML_0)^2 - \frac{4(n-1)\hat{E}}{n^2}$

The statistics in the above formula may be explained as here under.

V_0L_0 = Variance of parents

V_r = Variance of r^{th} array

V_1L_1 = Mean variance of the array

W_r = the covariance between the parents and their offspring in the r^{th} array

W_0L_1 = Mean of covariance between the parents and their arrays

V_0L_1 = the variance of the means of arrays

Estimates of standard error

To assess the precision of the above parts of change, the conditions of fundamental corner to corner of the grid given by Hayman (1954a) [9, 10] with normal multipliers S^2 was utilized, where -

$S^2 = (1/2)$ [Var (Wr- Vr)]

The formula being -

S.E. $(\hat{D}) = \pm[S^2 (n^5 + n^4)/n^5]^{0.5}$

S.E. $(\hat{F}) = \pm [S^2 (4n^5 + 20n^4 - 16 n^3 + 16 n^2) /n^5)^{0.5}$

S.E. $(\hat{H}_1) = \pm [S^2 (n^5 + 41 n^4 - 12 n^3 + 4n^2)/n^5]^{0.5}$

S.E. $(\hat{H}_2) = \pm [S^2 (36 n^4/n^5)^{0.5}$

S.E. $(\hat{h}^2) = \pm [S^2 (16n^4 + 16n^2 - 32 n + 16)/n^5]^{0.5}$

S.E. $(\hat{E}) = \pm [S^2 (n^4/n^5)]^{0.5}$

After testing the significance of the components of variation $\hat{D}, \hat{F}, \hat{H}_1, \hat{H}_2, \hat{h}^2$ and $\hat{E}$ the mean *degree* of dominance was calculated as $[(\hat{H}_1/\hat{D})]^{0.5}$, the proportion of genes with positive and negative effects as $(\hat{H}_2/4\hat{H}_1)$, the proportion of dominant and recessive genes in the parents as $(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}/(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}$ or K_D/K_R and the number of groups of genes, which control the character that exhibit dominance as $(\hat{h}^2/\hat{H}_2)$.

Experimental Findings

The estimate of all the components of variation namely $\hat{D}, \hat{H}_1, \hat{H}_2$ $\hat{F}$, h^2 and $\hat{E}$ along with their standard errors and related statistics as presented in the Table 1 & 2.

The estimate of additive genetic component $(\hat{D})$ was significant for all the characters except *viz.* no. of branches per plant, no. of clusters per plant, no. of seeds per pod, harvest index (%) and protein content (%) in F_1 generation while days to 50% flowering (days), no. of branches per plant and protein content (%) in F_2 generation.

The dominance component $(\hat{H}_1)$ and $(\hat{H}_2)$ found to be significant for all thirteen characters while the value of $(\hat{H}_1)$ was observed higher than the value of $(\hat{H}_2)$ for all characters.

The significant and positive value of $(\hat{F})$ component for days to 50% flowering (days), no. of pods per plant, plant height (cm), 100 seed weight (g), biological yield per plant (g), seed yield per plant (g) in F_1 generation while days to maturity (days), no. of pods per plant, plant height (cm), no. of seeds per pod, 100 seed weight (g), biological yield per plant (g), seed yield per plant (g) in F_2 generation.

The value of (h^2) was observed positive and significant for days to 50% flowering (days), days to maturity (days), no. of pods per plant in F_1 generation and days to maturity (days), no. of clusters per plant in F_2 generation among thirteen characters which was due to the presence of dominant genes.

The estimates of $\hat{E}$ component were found non-significant for all the characters except no. of branches per plant in F_1 generation and no. of branches per plant, no. of clusters per plant, no. of seeds per pod in F_2 generation.

.The average degree of dominance $(\hat{H}_1/\hat{D})^{0.5}$ was found more than unity for all the characters in F_1 and F_2 generations.

The positive and negative genes ratio of ($\hat{H}_2/4\hat{H}_1$) were found to be less than the theoretical value (0.25) for all the characters in F_1 and F_2 generations.

The proportion of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{0.5}+\hat{F}$ / $(4\hat{D}\hat{H}_1)^{0.5}-\hat{F}$ was more than unity for all characters in F_1 and F_2 generations.

The ratio of h^2/H_2 was lower than unity for all characters in F_1 and F_2 generations.

Results and Discussions

The gene action is prerequisite to formulate an appropriate breeding methodology. The genetic variation can be divided into three components namely -

- Additive or fixable variance which arising from the average effects of genes.
- Dominance variance arising from infra-allelic interaction of the gene and
- Epistatic variance arising from the inter-allelic interaction of genes.

The estimate of additive genetic component ($\hat{D}$) was significant for all the characters except *viz.* no. of branches per plant, no. of clusters per plant, no. of seeds per pod, harvest index (%) and protein content (%) in F_1 generation while days to 50% flowering (days), no. of branches per plant and protein content (%) in F_2 generation.

The dominance component ($\hat{H}_1$) and ($\hat{H}_2$) found to be significant for all thirteen characters while the value of ($\hat{H}_1$) was observed higher than the value of ($\hat{H}_2$) for all characters.

Relatively magnitude of $\hat{H}_1$ component was higher than that of $\hat{D}$ component values for all the characters under study indicating role of both additive and dominance gene action with prevalence of dominant gene action. However, the non-additive component was more prominent than additive component for all the traits based on average degree of dominance (more than unity for almost all characters).

The significant and positive value of ($\hat{F}$) component for days to 50% flowering (days), no. of pods per plant, plant height (cm), 100 seed weight (g), biological yield per plant (g), seed yield per plant (g) in F_1 generation while days to maturity (days), no. of pods per plant, plant height (cm), no. of seeds per pod, 100 seed weight (g), biological yield per plant (g), seed yield per plant (g) in F_2 generation while positive non-significant for for remaining characters. The positive value indicates the frequent involvement of dominant genes for its expression.

The estimates of average degree of dominance expressed ($\hat{H}_1/\hat{D}$) $^{0.5}$ were higher than unity for all the traits. It revealed that there was over dominance effect for these traits.

The value of positive and negative gene proportion ($\hat{H}_2$ / 4 $\hat{H}_1$) was less than 0.25 for all the characters indicating that the distribution of positive and negative alleles was asymmetrical in the parents.

The ratio for dominant and recessive gene was expressed more than unity for all the characters, denotes presence of more frequency of dominant genes. If value is less than one, denotes presence of more frequency of recessive genes.

The ratio of h^2/H_2 was lower than unity for all characters in F_1 and F_2 generations, it indicated the frequent involvement of single gene group for inheritance of traits and it may be due to complementary gene interaction causing depression in the ratio.

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Table 1: Estimates of genetic variance components of 13 characters of green gram using the diallel analysis of the Hayman method in F_1 generation

Characters	Variance component						Related parameter (genetic ratio)			
	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{F}$	h^2	$\hat{E}$	$(\hat{H}_1/\hat{D})^{0.5}$	$(\hat{H}_2/4\hat{H}_1)$	$\frac{(4D\hat{H}_1)^{0.5}+\hat{F}}{(4D\hat{H}_1)^{0.5}-\hat{F}}$	$(h^2/\hat{H}_2)$
Days to 50 % flowering (days)	5.22*	23.04*	19.24*	6.23*	5.31*	0.19	2.10	0.20	1.79	0.27
SE±	1.23	2.63	2.24	2.86	1.50	0.37				
Days to maturity (days)	5.22*	15.76*	13.71*	5.08	3.53*	0.20	1.73	0.21	1.77	0.25
SE±	1.33	2.83	2.40	3.07	1.61	0.40				
No. of branches per plant	0.08	1.03*	0.91*	0.17	0.05	0.06*	3.42	0.22	1.82	0.06
SE±	0.08	0.17	0.15	0.19	0.10	0.02				
No. of clusters per plant	0.32	2.98*	2.61*	0.58	0.43	0.17	3.03	0.21	1.86	0.16
SE±	0.19	0.41	0.35	0.44	0.23	0.05				
No. of pods per plant	14.58*	48.10*	34.48*	23.48*	33.54*	0.26	1.81	0.17	2.59	0.97
SE±	2.41	5.14	4.37	5.58	2.92	0.72				
Plant height (cm)	12.40*	58.23*	42.44*	23.02*	0.26	0.42	2.16	0.18	2.49	0.006
SE±	3.37	7.18	6.10	7.78	4.08	1.01				
Pod length (cm)	0.50*	2.27*	1.92*	0.59	0.19	0.04	2.11	0.21	1.76	0.10
SE±	0.16	0.35	0.29	0.38	0.20	0.04				
No. of seeds per pod	0.47	4.31*	3.70*	0.74	-0.01	0.15	3.00	0.21	1.69	-0.05
SE±	0.26	0.56	0.47	0.60	0.31	0.07				
100 seed weight (g)	0.12*	0.57*	0.39*	0.27*	-0.002	0.009	2.16	0.17	3.12	-0.006
SE±	0.02	0.05	0.04	0.05	0.03	0.007				
Biological yield per plant (g)	3.10*	11.16*	8.18*	5.07*	1.46	0.11	1.89	0.18	2.5	0.17
SE±	0.96	2.06	1.75	2.23	1.17	0.29				

Harvest index (%) SE±	23.41	149.19*	109.40*	46.76	-0.97	2.71	2.52	0.18	2.30	-0.009
	13.70	29.16	24.78	31.61	16.59	4.13				
Seed yield per plant (g) SE±	1.09*	3.67*	2.81*	1.67*	0.39	0.06	1.83	0.19	2.44	0.14
	0.25	0.53	0.45	0.58	0.30	0.07				
Protein content (%) SE±	0.26	2.44*	2.21*	0.31	-0.02	0.09	3.02	0.22	1.49	-0.009
	0.28	0.59	0.50	0.64	0.33	0.08				

*Significant at 5 % level, ** Significant at 1 % level, ***Significant at 0.1 % level

Table 2: Estimates of genetic variance components of 13 characters of green gram using the diallel analysis of the Hayman method in F_2 generation

Characters	Variance component						Related parameter (genetic ratio)			
	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{F}$	h^2	$\hat{E}$	$(\hat{H}_1/\hat{D})^{0.5}$	$(\hat{H}_2/4\hat{H}_1)$	$\frac{(4D\hat{H}_1)^{0.5}+\hat{F}}{(4D\hat{H}_1)^{0.5}-\hat{F}}$	$(h^2/\hat{H}_2)$
Days to 50 % flowering (days) SE±	5.16	34.01*	25.71*	10.02	1.13	0.24	2.56	0.18	2.21	0.04
	3.01	6.42	5.45	6.96	3.65	0.90				
Days to maturity (days) SE±	5.17*	22.26*	16.30*	8.84*	5.89*	0.25	2.07	0.18	2.40	0.36
	1.32	2.81	2.38	3.04	1.59	0.39				
No. of branches per plant SE±	0.04	0.58*	0.55*	0.07	0.04	0.10*	3.45	0.23	1.60	0.07
	0.07	0.14	0.12	0.16	0.08	0.02				
No. of clusters per plant SE±	0.34*	3.5*	3.20*	0.58	0.94*	0.15*	3.19	0.22	1.73	0.29
	0.17	0.36	0.31	0.40	0.21	0.05				
No. of pods per plant SE±	14.62*	49.64*	33.51*	26.40*	5.61	0.21	1.84	0.16	2.92	0.16
	4.78	10.18	8.65	11.04	5.79	1.44				
Plant height (cm) SE±	12.70*	74.32*	56.68*	26.41*	2.78	0.12	2.41	0.19	2.50	0.04
	4.20	8.94	7.60	9.69	5.08	1.26				
Pod length (cm) SE±	0.49*	2.68*	2.55*	0.41	0.10	0.05	2.32	0.23	1.43	0.04
	0.15	0.32	0.27	0.35	0.18	0.04				
No. of seeds per pod SE±	0.46*	5.56*	4.37*	1.37*	-0.02	0.16*	3.45	0.19	2.30	-0.006
	0.21	0.45	0.38	0.49	0.26	0.06				
100 seed weight (g) SE±	0.12*	0.48*	0.30*	0.27*	0.01	0.009	1.98	0.15	3.59	0.05
	0.03	0.07	0.06	0.08	0.04	0.01				
Biological yield per plant (g)	3.17*	14.59*	10.58*	6.64*	0.08	0.05	2.14	0.18	2.90	0.008
	1.18	2.51	2.13	2.72	1.43	0.35				
Harvest index (%) SE±	24.80*	105.69*	85.24*	37.85	0.27	1.32	2.06	0.20	2.17	0.003
	11.02	23.46	19.94	25.43	13.34	3.32				
Seed yield per plant (g) SE±	1.11*	4.31*	3.18*	2.10*	-0.01	0.03	1.97	0.18	2.84	-0.004
	0.24	0.53	0.45	0.57	0.30	0.07				
Protein content (%) SE±	0.26	2.48*	1.73*	0.77	-0.03	0.09	3.07	0.17	2.84	-0.02
	0.18	0.38	0.33	0.42	0.22	0.05				

*Significant at 5 % level, ** Significant at 1 % level, ***Significant at 0.1 % level

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