

## Studies on Heritability and Genetic Advance for Yield and its Contributing Traits in Greengram (*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 area falls in sub-tropical climatic zone. The soil type is sandy loam. The annual rainfall is about 1270 mm. The climate of district Kanpur is semi-arid with hot summer and cold winter. Geographically, Kanpur is located at an altitude of 127 meters above the mean sea level and the latitude and longitude with 26.40° N and 80.10° E respectively. The increase under selection may typically be predicted more accurately with the combination of heritability estimates and genetic advancement than with heritability estimates only. In this study, heritability was reported for days to maturity (23.1%), days to 50 % flowering (21.8%), harvest index (21.5%), no. of pods per plant (21.0%) and pod length (20.4%) in F<sub>1</sub> generation. Heritability was reported for days to maturity (20.9%), days to 50% flowering (20.5%), number of pods per plant (20.2%), protein content (18.6%) and harvest index (14.0%) in F<sub>2</sub> generation. High genetic advance as percent of mean was recorded for number of branches per plant, number of pods per plant, harvest index in F<sub>1</sub> generation while number of branches per plant, plant height and harvest index in F<sub>2</sub> generation.

**Keywords:** Heritability, Genetic advance, 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. Green gram (*Vigna radiata* L. Wilczek) is also known as mungbean belongs to the family Leguminaceae, subfamily Papilionaceae, genus *Vigna* and species *radiata* with chromosome number 2n = 22 (Karpechenko, 1925; Krishnan and De 1965). The average global grain yields of green gram are low at 0.73 ton ha<sup>-1</sup> (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 (1<sup>st</sup> 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) Heritability:** The heritability in narrow sense (h<sup>2</sup>) was calculated as suggested by Crumpacker and Allard (1962)

$$\text{Heritability (ns)} = \frac{2\hat{\sigma}^2_g}{2\hat{\sigma}^2_g + \hat{\sigma}^2_s + \hat{\sigma}^2_e} \times 100$$

Where,

$\hat{\sigma}^2 g$  = Variance due to GCA

$\hat{\sigma}^2 s$  = Variance due to SCA

$\hat{\sigma}^2 e$  = Variance due to error

Verhalen and Murray (1969) proposed the following formula for calculation of heritability narrow sense in F<sub>2</sub> generation –

Heritability (ns) =  $1/4D / (1/4D + 1/16H_1 - 1/8F + E) \times 100$

**(b) Genetic advance:**

The genetic advance was calculated as per formula given by Robinson *et al.* (1949)

$G_s = (K) \times (\sigma_{ph}) \times (h^2)$

where,

$G_s$  = The expectation of genetic advance under selection

$K$  = Selection differential (2.06), a constant at 5 percent selection intensity

$\sigma_{ph}$  = The phenotypic standard deviation

$\hat{h}^2$  = The estimate of heritability coefficient in narrow sense

**Genetic advance as percentage of mean was calculated as follows**

$G_s (\%) = (G_s / \bar{X}) \times 100$

Where,

$G_s$  = Expectation of genetic advance

$\bar{X}$  = Mean of the character

$G_s (\%)$  = Genetic advance in per cent over mean of the character

**RESULT AND DISCUSSION**

Statistics are presented in the Table 1 & 2.

**(a) Heritability (Narrow sense).** Estimates of genotypic coefficient of variation represent the total sum of genotypic variability; heritability reflects the proportion of this genotypic variability that is transmitted from parents to progeny. The heritability in narrow sense requires an estimate of additive genetic variance in a population. Genetic variation along with heritability will give better idea about expected efficiency of selection, according to Burton (1952). Characters with high heritability estimates showed that variation in these traits predominantly governed by heritable factors and can be utilized for genetic improvement as they are least influenced by the environmental effects.

In present study, heritability was reported for days to maturity (23.1%), days to 50 % flowering (21.8%), harvest index (21.5%), no. of pods per plant (21.0%), pod length (20.4%), plant height (19.0%), biological yield per plant (19.0%), seed yield per plant (14.8%), protein content (12.1%), 100 seed weight (10.2%), no. of clusters per plant (05.6%) and no. of branches per plant (04.1%) in F<sub>1</sub> generation. Heritability was reported for days to maturity (20.9%), days to 50% flowering (20.5%), number of pods per plant (20.2%), protein content (18.6%), harvest index (14.0%), number of seeds per pod (13.4%), pod length (13.3%), plant height (12.1%), 100 seed weight (11.9%), biological yield per plant (09.1%), seed yield per plant (07.6%), number of clusters per plant (03.5%) and number of branches per plant (00.2%) in F<sub>2</sub> generation. If, the heritability estimates are low in narrow sense, it shows that there is preponderance of non-additive gene action and heterosis breeding may be useful. Similar results were in accordance with the findings of Singh *et al.* (2014), Anuradha *et al.* (2019), Mohammed *et al.* (2020), Vadivel *et al.* (2020) and Yadav *et al.* (2017).

**(b) Genetic advance as % of mean.** Genetic advance when expressed as percentage of mean is called genetic gain. Johnson *et al.* (1955) classified the genetic advance as percent of mean into three major classes i.e., high (>20%), moderate (10-20%) and low (<10%).

High genetic advance as percent of mean was recorded for number of branches per plant (44.208), number of pods per plant (25.846), harvest index (20.884) in F<sub>1</sub> generation while number of branches per plant (23.383), plant height (21.406), harvest index (20.884) in F<sub>2</sub> generation. The above results were in agreement with the findings of Reddy *et al.* (2011), Majhi *et al.* (2020), Ramachandra *et al.* (2017) and Tamalapakula *et al.* (2021).

Characters showing low heritability coupled with high genetic advance as percent of mean was recorded for number of branches per plant, number of pods per plant, harvest index, plant height. Such results indicate predominantly the presence of additive gene action in the expression of the characters and consequently chance of improving these characters through simple selection procedures.

**Table 1: Estimation of genetic parameters for 13 characters of greengram (*Vigna radiata* L. Wilczek) in F<sub>1</sub> generation.**

Characters/Selection parameters	DFV	DTM	NBPP	NCPP	NPPP	PH	PL	NSPP	100SW	BYPP	HI	SYPP	PC
GCV	6.193	3.250	31.169	10.297	12.987	9.388	7.978	10.961	8.000	8.310	11.416	9.882	3.193
PCV	6.469	3.479	45.272	14.371	13.443	9.879	8.818	13.494	9.119	8.919	12.856	10.948	3.971
<b>h<sup>2</sup> (Narrow sense)</b>	0.218	0.231	0.041	0.056	0.210	0.190	0.204	0.137	0.102	0.190	0.215	0.148	0.121
Genetic advancement 5%	4.692	3.944	0.606	1.096	6.590	6.742	1.372	1.580	0.569	2.954	10.096	1.636	1.193
Gen. adv. as % of mean	12.216	6.256	44.208	15.198	25.846	18.376	14.870	18.342	14.460	15.948	20.884	18.376	5.288

**DFV:** Days to Flowering 50 %, **DM:** Days to maturity, **NBPP:** Number of branches per plant, **NCPP:** Number of clusters per plant, **NPPP:** Number of Pods per plant, **PH:** Plant height, **PL:** Pod length, **NSPP:** Number of seeds per pod, **100SW:** 100 Seed weight, **BYPP:** Biological yield per plant, **HI:** Harvest index, **SYPP:** Seed yield per plant, **PC:** Protein Content %

**GCV:** Genotypic coefficient of variation, **PCV:** Phenotypic coefficient of variation, **h<sup>2</sup>:** Heritability

**Table 2: Estimation of genetic parameters for 13 characters of greengram (*Vignaradiata* L. Wilczek) in F<sub>2</sub> generation.**

Characters/Selection parameters	DFE	DTM	NBPP	NCPP	NPPP	PH	PL	NSPP	100SW	BYPP	HI	SYPP	PC
GCV	6.859	3.370	20.243	11.680	11.716	10.520	8.671	11.862	7.137	8.510	9.862	9.729	2.959
PCV	7.213	3.630	46.045	15.073	12.093	10.650	9.604	14.364	8.251	8.747	10.716	10.411	3.813
h <sup>2</sup> (Narrow sense)	0.205	0.209	0.002	0.035	0.202	0.121	0.133	0.134	0.119	0.091	0.140	0.076	0.186
Genetic advancement 5%	5.235	4.191	0.251	1.320	6.325	7.753	1.496	1.739	0.506	3.279	8.964	1.719	1.066
Gen. adv. as % of mean	13.435	6.446	18.334	18.645	23.383	21.406	16.126	20.178	12.717	17.054	18.699	18.728	4.732

**DFE:** Days to Flowering 50 %, **DM:** Days to maturity, **NBPP:** Number of branches per plant, **NCPP:** Number of clusters per plant, **NPPP:** Number of Pods per plant, **PH:** Plant height, **PL:** Pod length, **NSPP:** Number of seeds per pod, **100SW:** 100 Seed weight, **BYPP:** Biological yield per plant, **HI:** Harvest index, **SYPP:** Seed yield per plant, **PC:** Protein Content %

**GCV:** Genotypic coefficient of variation, **PCV:** Phenotypic coefficient of variation, **h<sup>2</sup>:** Heritability

From the foregoing discussion, it can be concluded that high PCV, GCV, low heritability and high genetic advance as percent of mean were observed for number of branches per plant indicating the prevalence of additive gene action was playing major role for expression of these characters and simple selection may be effective for improvement of these traits. The findings were in agreement with the findings of Yusufzai *et al.* (2017) and Tamalapakula *et al.* (2021).

## CONCLUSIONS

Number of branches per plant, number of pods per plant, harvest index and plant height shows low heritability accompanied with high genetic advance. Characters are determined by additive gene effects when low heritability is combined with strong genetic advancement. High environmental impacts are manifesting as poor heredity. In such circumstances, selection could be useful.

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