

Original Research Article

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## Genetic Variability Studies in F<sub>2</sub> Generation for Yield and Yield Component Traits in Green Gram [*Vigna radiata* L. Wilczek]

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### ABSTRACT

#### Keywords

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An investigation was undertaken to evaluate thirty five genotypes of green gram from F<sub>2</sub> generation along with ten parents and one local check with a view to study the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. A wide range of variation was observed for all the characters under study. Highest and lowest coefficient of variation was noticed in the traits yield per plant and days to maturity respectively. The traits days to initiation of flowering, days to fifty per cent flowering, days to maturity and hundred seed weight exhibited close differences between PCV and GCV. In general phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters under study which indicates that the expression of genotype is affected by environmental factor. The traits viz; grain yield per plant, plant height, number of pods per plant and number of branches per plant recorded low to moderate magnitude of PCV and GCV along with high to moderate heritability. Plant height recorded high heritability coupled with high genetic advance as per cent mean which indicated that this character is governed by additive genes and selection will be rewarding for its improvement while number of branches per plant, number of pods per plant and grain yield per plant exhibited moderate to high heritability coupled with moderate genetic advance per cent of mean.

### Introduction

Green gram [*Vigna radiata* (L.) Wilczek] 2n=22 belongs to the family leguminosae and sub family papilionaceae. It is one of the important pulse crops in India which is cultivated from humid tropic to arid and semi-arid regions. Green gram is highly nutritive and is favoured for consumption due to its easy digestibility and low production of

flatulence (Shil and Bandopadhyay, 2007). Besides their high nutritional value, they have a unique characteristic of maintaining and restoring soil fertility through biological nitrogen fixation which plays a vital role in sustainable agriculture (Asthana, 1998).

The knowledge about nature and magnitude of genetic variability such as phenotypic coefficient of variation (PCV), genotypic

coefficient of variation (GCV), heritability and genetic advance present in the gene pool is of immense value for starting any systematic breeding programme. It provides basic information regarding the genetic properties of the population, based on which, breeding methods are formulated for further improvement of the crop. Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures. In view of this, the present study was undertaken to estimate the extent of variation for yield and yield contributing traits in F<sub>2</sub> generation of green gram by studying the genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, which will help in formulation of suitable selection indices for crop improvement and to explore high yield potential and quality traits.

## **Materials and Methods**

The present investigation was carried out at Research and Education farm, College of Agriculture, Dapoli, Dist. Ratnagiri during the period of December, 2018 to March, 2019. The material for present studies comprised of thirty five treatments which consist of twenty four crosses of F<sub>2</sub> generation, ten parents and one check of green gram. A field trial was laid out in randomized block design with three replications.

The seed of all the 35 genotypes (24 F<sub>2</sub>'s, 10 parents, and 1 check) were sown at 30 cm distance between row to row and 10 cm distance between plant to plant (30 × 10 cm). Each plot had 1.5 m x 3.0 m area with three rows for each genotype. Each row contains 30 plants thus there was 90 plants population per genotype which constitute 270 plants per cross in three replications. The plants were randomly selected for recording

morphological observations per treatment per replication. All the agronomic practices were followed to maintain a good crop stand. Five plants each from parents and twenty five plants from F<sub>2</sub> generation were selected per treatment per replication to record data for different twelve quantitative traits *viz*:; days to initiation of flowering, days to 50 per cent flowering, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of grains per pod, pod length (cm), plant height (cm), days to maturity, 100 seed weight (g) and grain yield per plant (g).

The data recorded on various traits were statistically analysed using software WINDOSTAT version 9.2. Analysis of variance carried out by the method suggested by Panse and Sukhatme (1985). The variability parameters, phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953). Heritability in broad sense was computed as per Lush (1949). Heritability and genetic advancement were categorized into low, medium and high as per Johnson *et al.*, (1955).

## **Results and Discussion**

Grain yield is the most complicated trait controlled by polygene and hence generally it seems to be very difficult for making selection. So, high variability among the yield components is of vital importance in fruitful selection programme (Fig. 1 and 2).

## **Analysis of variance**

The analysis of variance revealed that, highly significant differences were found among the genotypes (Table 1) for all the traits except days to initiation of flowering, number of clusters per plant and number of pods per cluster suggested presence of sufficient

variability among the genotypes. High significant variability was noticed for number of clusters per plant, number of pods per plant, plant height and grain yield per plant. Thus, presence of variability in present investigation suggested an ample scope of selection for these traits. These results are in conformity with Hemavathy *et al.*, (2015), Aalok Shiv *et al.*, (2017) Himabindu and Roopa Lavanya (2017) and Muthuswamy *et al.*, (2019) in green gram.

### **Components of variation**

Estimates of genetic parameters *viz*; variability, heritability and genetic advance are presented in (Table 2). The magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters under study which indicates that expression of genotype is affected by environmental factors. These results are in accordance with the findings of Siddique *et al.*, (2006) and Makeen *et al.*, (2007). Closeness between PCV to that of GCV was observed for days to initiation of flowering, days to fifty per cent flowering, days to maturity and hundred seed weight indicates least influence of environment on these traits. Moderate magnitude of Phenotypic and genotypic coefficient of variation (%) was observed for the traits *viz*; number of clusters per plant, number of pods per plant, plant height and grain yield per plant and selection will be effective based on the heritable nature of these traits.

While, low magnitude of phenotypic and genotypic coefficient of variation was observed among the rest of the traits which indicates these traits were highly influenced by the environment and selection would be ineffective. This was in agreement with findings of Kumar *et al.*, (2013), Muthuswamy *et al.*, (2019) and Anuradha *et al.*, (2019) in green gram.

### **Heritability and genetic advance**

Genotypic coefficient of variation with heritability estimates would give showed better picture of advance to be expected by selection. High estimates of heritability exhibited by number of branches per plant, number of grains per pod and plant height which indicates that these traits would be controlled by additive gene action. Moderate estimates of heritability was recorded for number of pods per plant, hundred seed weight, grain yield per plant and fifty per cent flowering number of clusters per plant and number of pods per plant suggested scope for selection of these traits for improvement. These results are in accordance with the findings Rahim *et al.*, (2010); Raturi *et al.*, (2015), Sirohi *et al.*, (2018) and Sindhu *et al.*, (2019) in green gram. While, low heritability was recorded for traits days to initiation of flowering Low estimates of heritability for this trait as also in agreement with findings of Chakraborty *et al.*, (2011) in green gram.

Plant height recorded highest genetic advance as per cent mean which indicated that these character is governed by additive genes and selection will be rewarding for its improvement. Moderate genetic advance as per cent mean was noticed for grain yield per plant, number of pods per plant and number of branches per plant which indicated that these characters are governed by non-additive genes action and selection may not be effective. The remaining characters, *viz*; number of grains per pod, number of clusters per plant, pod length, number of pods per cluster, hundred seed weight, days to 50 per cent flowering, days to maturity and days to initiation of flowering had recorded low genetic advance as per cent mean. Thus, presence of additive as well as non additive genes for these characters were also earlier reported by Payasi (2015) and Govardhan *et al.*, (2018) in green gram.

Heritability alone doesn't provide true indication of genetic potentiality of the genotype, due to scope is restricted by interaction between genotype and environment. High heritability estimates coupled with high genetic advance as per cent

of mean was noticed only for the trait plant height (52.9, 20.074). Also this trait had moderate GCV which indicates presence of additive gene action and scope for improvement through simple selection.

**Table.1** Analysis of variance for yield and its components in green gram genotypes

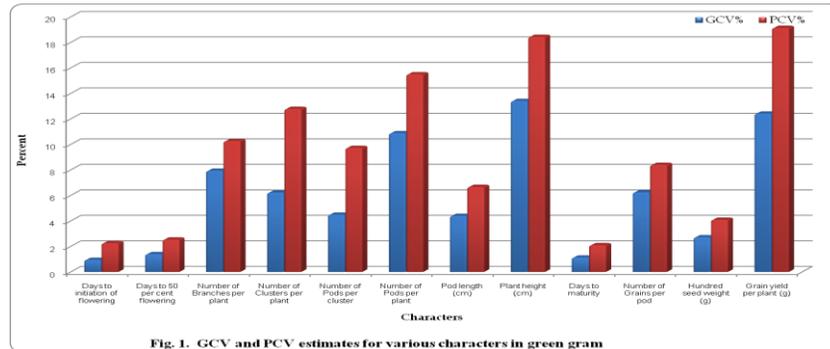
Sr. No.	Characters	Mean Sum of Squares		
		Replications (df=2)	Treatments (df=34)	Error (df=68)
1.	Days to initiation of flowering	1.049	2.041*	1.251
2.	Days to 50 % flowering	4.695	3.551**	1.552
3.	Number of Branches per plant	0.055	0.208**	0.038
4.	Number of Clusters per plant	0.372	0.248*	0.128
5.	Number of Pods per cluster	0.092	0.138*	0.076
6.	Number of Pods per plant	1.140	4.807**	1.230
7.	Pod length (cm)	0.364	0.447**	0.135
8.	Plant height (cm)	10.515	17.377**	3.981
9.	Days to maturity	4.983	3.794**	1.707
10.	Number of Grains per pod	0.543	0.896**	0.191
11.	Hundred seed weight (g)	0.037	0.060**	0.018
12.	Grain yield per plant (g)	1.109	1.128**	0.355

\*\* Significant at 1% level \* Significant at 5% level

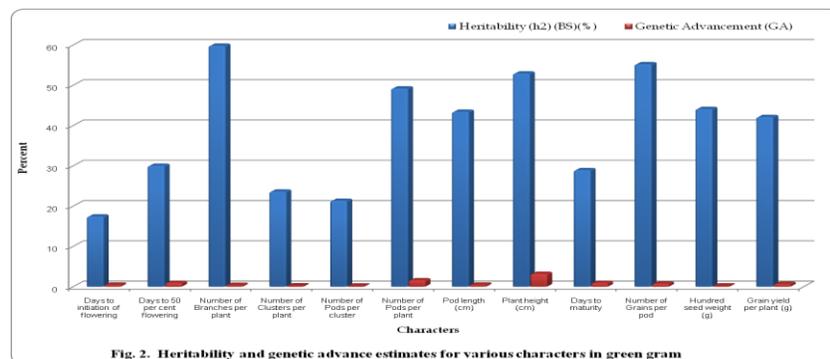
**Table.2** Estimates of genetic parameters for twelve quantitative characters in green gram

Sr. No.	Characters	PCV (%)	GCV (%)	h <sup>2</sup> bs (%)	GA	GAM (%)
1.	Days to initiation of flowering	2.258	0.941	17.4	0.441	0.808
2.	Days to 50 % flowering	2.537	1.391	30.0	0.922	1.570
3.	Number of Branches per plant	10.255	7.931	59.8	0.379	12.636
4.	Number of Clusters per plant	12.782	6.213	23.6	0.200	6.220
5.	Number of Pods per cluster	9.723	4.486	21.3	0.136	4.263
6.	Number of Pods per plant	15.498	10.872	49.2	1.578	15.712
7.	Pod length (cm)	6.663	4.389	43.4	0.437	5.956
8.	Plant height (cm)	18.433	13.402	52.9	3.165	20.074
9.	Days to maturity	2.094	1.127	28.9	0.924	1.249
10.	Number of Grains per pod	8.393	6.235	55.2	0.742	9.542
11.	Hundred seed weight (g)	4.089	2.716	44.1	0.162	3.715
12.	Grain yield per plant (g)	19.132	12.412	42.1	0.678	16.589

**Fig.1** Phenotypic and Genotypic coefficients of variation for twelve characters in green gram



**Fig.2** Heritability (Broad sense) and genetic advance as per cent of mean for twelve characters in green gram



Moderate heritability accompanied with moderate genetic advance as per cent mean was observed for traits number of branches per plant, number of pods per plant and grain yield per plant. While, moderate heritability coupled with low genetic advance as per cent mean was reported for traits pod length, number of grains per pod and hundred seed weight which showed that expression of traits are more likely to be influenced by environmental factors and controlled by non-additive gene action. Similar results were observed by Tabasum *et al.*, (2010); Aalok Shiv *et al.*, (2017); and Himabindu and RoopaLavanya (2017) in green gram.

From present investigation it can be concluded that, significant differences were found among the genotypes for all the characters under study, indicates presence of

sufficient genetic variability for different traits. The parents, PUSA-1472, ML-2056, PKVAKM-04, TARM-2 and DGG-03 while, F<sub>2</sub>crosses ML-2333 x DGG-03, PUSA-1477 x PKVAKM-04, TARM-2 x Karjat local and TARM-2 x PKVAKM-04 showed their superiority for yield based on their mean performance. The characters *viz*; like number of branches per plant, number of pods per plant, plant height and number of grains per pod showed more contribution of genotypic variance to total variance. All the characters under study had moderate to high magnitude of heritability except days to initiation of flowering. Wide variability was observed for number of branches per plant, number of clusters per plant, number of pods per plant, plant height and grain yield per plant. These characters also had higher estimates of heritability coupled with moderate to high

genetic advance as per cent of mean which can be utilized for further improvement through selection.

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