Research Paper

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Genetic Parameters for Yellow Mosaic Virus Resistance in Greengram (*Vigna Radiata* (L).Wilczek)

Biotechnology

KEYWORDS : Heritability, Mungbean, Genetic advance

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ABSTRACT

*A study was carried out in mungbean (Vigna radiata (L.) Wilczek) with 123 F2 plants of cross PM 115 * LGG 460 to estimate mean, range, genotypic and phenotypic coefficients of variation, heritability and genetic advance for 8 trait viz. height of the plant, number of branches, number of clusters, days to 50 per cent flowering, number of pods per plant, length of the pod, number of seeds per pod, single plant yield without any replication. Heritability in broad sense and genetic advance as percent of mean was high for number of pods per plant, single plant yield, plant height, number of branches per plant, pod length indicating that these traits were controlled by additive genes indicating the availability of sufficient heritable variation that could be made use in the selection programme and can easily be transferred to succeeding generations*

INTRODUCTION

Mungbean (Vigna radiata (L.) Wilczek) is an important pulse crop in developing countries of Asia, Africa and Latin America, where it is consumed as dry seeds, fresh green pods (Karuppanapandian). It is also known as mungbean, green bean, mash bean, golden gram, greensoy is an excellent source of easily digestible proteins with low flatulence which complements the staple rice diet in Asia. It is a self-pollinating diploid grain legume (2n=2x=22) crop belonging to the Leguminaceae family and has genome size of 560 mb (Arumuganath and Earle).

It is native of India-Burma and is cultivated extensively in Asia (Khattak). India is the leading mungbean cultivator, covers up to 55% of the total world acreage and 45% of total production next to pigeon pea and blackgram. In India, major greengram producing states are Andhra Pradesh, Orissa, Maharastra, Madhya Pradesh, Rajasthan, Bihar and Tamil Nadu. In Andhra Pradesh the area covered under greengram is about 4.38 L. ha with an average production and productivity of 1.92 lakh tons and 597 kg per hectare respectively (Department of Economics & Statistics).

A field experiment was conducted during rabi, 2014 at College farm, Acharya N.G Ranga Agricultural University campus, Rajendranagar, Hyderabad, Andhra Pradesh. The two parents LGG 460 as resistant and PM 115 as susceptible was selected to raise the F_2 population. A total of 123 plants were raised without any replication. All the 123 plants in the F_2 generation were evaluated for the following morphological traits viz., height of the plant, number of branches, number of clusters, days to 50 per cent flowering, number of pods per plant, length of the pod, number of seeds per pod, single plant yield.

The range observed was wider for number of pods per plant, number of seeds per plant, pod length, number of branches per plant, plant height, number of clusters, days to 50% flowering and single plant yield in F_2 population. In the present study high variance was observed for number of pods per plant, plant height and days to 50% flowering. Less variance was observed for the remaining traits. The lowest variation was observed for the trait pod length.

In general, phenotypic coefficient of variation and genotypic coefficient of variation showed a wide spectrum of variability in most of the characters studied. The GCV depends on the heritable part of variability and therefore it is regarded to be more useful for the assessment of inherent or real variability. High PCV and GCV estimate were observed in number of pods per plant, single plant yield, number of branches per plant, plant height. Moderate PCV and GCV estimate were observed in number of clusters, number of seeds per pod, pod length. Days to 50% flowering had low PCV and GCV values. The PCV value was found higher than the GCV for most of the characters and the differences between them were very less indicating less environmental influence on those characters. These results are in accordance with the finding of Rahim, Singh, Konda who also reported similar effects of environment.

Heritability in broad sense and genetic advance as percent of mean was high for number of pods per plant, single plant yield, plant height, number of branches per plant, pod length indicating that these traits were controlled by additive genes indicating the availability of sufficient heritable variation that could be made use in the selection programme and can easily be transferred to succeeding generations. Similar results were found with Rahim, Arulbalachandran, Singh and Konda. Moderate genetic advance as percent of mean values and moderate heritability in broad sense was observed in number of seeds per pod which indicate that the greater role of non-additive genetic variance and epistatic and dominant environmental factors controlling the inheritance of these traits. Similar results were found with Ghafoor and Ahmad. High heritability and moderate genetic advance as percent of mean was observed in days to 50% flowering indicating that these traits were controlled by dominant epistasis which was similar to Muhammad Siddique.

CONCLUSIONS

The material generated from this cross can be forwarded by single seed-descent method to develop RILS and can be used for mapping YMV resistance gene and validation of identified markers. High heritability, variability, genetic advance as percent mean in the segregating population can be handled under different selection schemes for improving productivity.

Table 1: Estimates of genetic parameters for different characersof F_2 population in greengram

Character	M	R	PCV	GCV	h^2%	GAM
Plant height (cm)	31.5	8-46	22.3	20.2	72.5	35.5
Number of branches per plant	4.2	3-7	23.92	20.1	68	33.5

Character	M	R	PCV	GCV	h^2%	GAM
Number of clusters (cm)	9.4	6-14	20.5	15.4	56.8	23.4
Pod length (cm)	4.2	2.9-6.3	13.8	12.5	82.4	21.2
Number of pods per plant	33.9	13-47	25.95	24.5	83.8	44.38
No of seeds per pod	4.2	3-8	18.7	12.6	45.8	16.94
Days to 50% flowering	43.1	37-56	10	8.2	67.7	14.1
Single plant yield (g)	2.6	1.7-7.9	24.6	24.0	70.9	38.5

M= Mean, R= Range, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2%= heritability (broad sense) GAM= Genetic advance as percent mean.

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