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Evaluation of Induced Genetic Variability for Yield and Yield Contributing Traits in M_4 Generation of Mungbean (*Vigna radiata* (L.) Wilczek)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The goal of the current study was to determine how much genetic variability there was for yield and traits that contributed to yield in two different mungbean varieties, WGG-42 and LGG-460, following the induction of mutations through chemicals (ethyl methane sulphonate and sodium azide) and physical (gamma rays) mutagens. In Rabi, 2018-19, in RBD with three replications in M4generation, fifty-five mutant lines selected from M3 progenies (36 in WGG-42 and 19 in LGG-460) were assessed alongside the two parents. Number of primary branches per plant, number of

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clusters per plant and number of pods per plant all showed high GCV and PCV. All the characters under study have high heritability. High heritability coupled with high genetic advance as per cent of mean was recorded for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length and seed yield per plant indicating that the genetic variances for these characters are probably owing to their high additive gene effects. Our study indicates promising avenues for future mungbean breeding programs to enhance these characteristics.

Keywords: EMS; gamma rays; mungbean; M_4; SA; variability.

1. INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] (2n=22) is one of the most important pulse crops in the world, especially in Asia. It belongs to the family *Fabaceae* and genus *Vigna*. It occupies the third position after chickpea and redgram among legume crops [1]. It is a short duration pulse crop grown mainly in *kharif* as well as in summer seasons. It is widely cultivated in the tropics and subtropics for human consumption and animal feed [2,3].

Improvement of cultivated plants largely depends on the extent of genetic variability available within the species [4].

Researchers are interested in the genetic underpinnings of mungbean in order to comprehend the complex systems that control its growth, yield, and adaptability. Creation of variability through hybridization is difficult in this crop as the flowers are cleistogamous and delicate to handle for emasculation andpollination. But, artificial induction of variability by mutation breeding can be effectively utilized to generate new variability and it has been recognized as a valuable supplement to conventional breeding in crop improvement [5]. Gamma rays, ethyl methane sulphonate (EMS) and sodium azide (SA) are the commonly used mutagens in mungbean for inducing genetic variability [6]. However, the assessment of the extent of induced variability in different traits is highly useful for further utilization in breeding programmes. The estimation of coefficient of variation shows the extent of variation for different traits but the estimate of heritability gives the magnitude of heritable variationin the experimental material. Estimation of genetic advance will give idea regarding the actual worth of the selected plants.

In light of this, the purpose of this study was to use ethyl methane sulphonate, sodium azide and gamma radiation to produce data on the amount of induced genetic variability for yield and yield components.

2. MATERIALS AND METHODS

The experimental material comprised of two popular mungbean genotypes of Andhra Pradesh and Telangana state*s viz.,* WGG-42 and LGG-460. This material was obtained from the pulses section, Regional Agricultural Research Station, Lam, Guntur. This study was carried out at dry land farm of Sri Venkateswara Agricultural College, Tirupati situated in the Southern Agro-climatic Zone of Andhra Pradesh, India located at an altitude of 182.90 m above mean sea level (MSL), 79.36°E longitude and 32.27°N latitude. The soil is sandy loam with medium fertility. Genetically pure, uniform and dry seeds of two mungbean genotypes *viz*., WGG-42 and LGG-460 were taken for induction of mutation using physical (gamma rays) and chemical mutagens (ethyl methane sulphonate and sodium azide).Dry seeds of mungbean genotypes were irradiated with gamma rays at Bhaba Atomic Research Centre (BARC), Trombay. For chemical treatment, seeds were pre-soaked for 6 h in water initially. Then, the seeds were immersed for 6 h in the requisite concentration of mutagens ethyl methane sulphonate and sodium azide with intermittent shaking. The whole treatment was carried out at a room temperature of 23±1°C for 6 h. Treated seeds were thoroughly washed with running water to bleach out the residual chemicals and then dried on blotting paper after treatment. Treated seeds and their untreated controls were sown in the field to raise the M_1 generation. The recovered mutants were first screened, evaluated and advanced to M_2 and M_3 generations. Finally, fifty five isolated promising lines were advanced to M_4 generation. All these fifty five selected mutant lines along with the parents (WGG-42 and LGG-460) were grown in Randomized Block Design (RBD) with

three replications during *rabi* season, 2018-2019 in M_4 generation. Each progeny was grown in one row with 3 m length with spacing of 30 cm between rows and 10 cm between plants within rows, respectively. The characters *viz,* days to 50% flowering and days to maturity were recorded on per plot basis. For other characters like plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, seed fertility, 100 seed weight and seed yield per plant, observations were recorded on 10 randomly selected competitive plants from each mutant and replication along with their respective controls. Recommended cultural practices and plant protection measures were followed to raise a healthy crop. The variation among 55 mutant lines for different characters was tested for significance by using analysis of variance technique as given by Panse and Sukhatme [7]. Parameters of genetic variability: Genotypic and phenotypic coefficient of (GCV and PCV) were computed using Burton's method from 1952. The formulas or PCV and GCV are as.

$$\text{GCV (\%)} = \frac{\sigma_g}{\overline{X}} \times 100$$

$$\text{PCV (\%)} = \frac{\sigma_p}{\overline{X}} \times 100$$

Where,

σ_g, σ_p and $\overline{X}$ were genotypic standard deviation, phenotypic standard deviation and general mean of the character, respectively.

Heritability (Broad sense): Heritability a measure of genotypic variance in relation to total phenotypic variance. Heritability in broad sense [$h^2_{(b)}$] was calculated by the formula given by Lush [8].

$$\text{Broad sense Heritability} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

Genetic Advance: the expected gain in the next generation by selecting the superior individuals under certain amount of selection pressure and was calculated using the method suggested by Johnson *et al*. [9].

2.1 Statistical Analysis

The mean data of all the characters was subjected to ANOVA and ANCOVA analyses to get the estimates of mean sum of squares and mean sum of products and these were utilized for calculation of the following parameters.

Variance:

The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton [10].

$$\text{Genotypic variance } \left(\sigma^2_g\right) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } \left(\sigma^2_p\right) = \sigma^2_g + \sigma^2_e$$

σ^2_g = Genotypic variance

σ^2_e = Error variance

Genotypic and Phenotypic Coefficient of Variation:

The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton [10].

$$\text{GCV (\%)} = \frac{\sigma_g}{\overline{X}} \times 100$$

$$\text{PCV (\%)} = \frac{\sigma_p}{\overline{X}} \times 100$$

where,

σ_g, σ_p and $\overline{X}$ were genotypic standard deviation, phenotypic standard deviation and general mean of the character, respectively.

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1973).

Less than 10% - Low
10 – 20 % - Moderate
More than 20% - High

Heritability (Broad Sense):

Heritability in broad sense refers to the proportion of genotypic variance to the total variance of the population. Heritability in broad sense [$h^2_{(b)}$] was calculated by the formula given by Lush [8].

$$\text{Broad sense Heritability} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

where,

σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

As suggested by Johnson *et al.* [9] heritability estimates were categorized as

Less than 30% - Low
30 – 60 % - Moderate
More than 60% - High

Genetic Advance:

Genetic advance refers to the expected gain in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates, the genetic advance was estimated by the following formula given by Johnson *et al.* [9].

$$GA = k\ \sigma_p\ H$$

where,

GA = Genetic advance
σ_p = Phenotypic standard deviation
H = Heritability (broad sense)
K =Selection differential at 5% selection intensity (2.06)

Genetic advance as per cent of mean (GA as per cent mean):

Genetic advance as per cent of mean was calculated as per the formula.

$$\text{GA as percent of mean} = \frac{GA}{\overline{X}} \times 100$$

where,

GA = Genetic advance
$\overline{X}$ = Grand mean of the character

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.* [9].

Less than 10% - Low
10 – 20 % - Moderate
More than 20% - High

3. RESULTS AND DISCUSSION

Large differences were found for each of the eleven features in the current study's analysis of variance, suggesting that the 55 mungbean mutant lines contain a large amount of genetic variability (Table 1). The variability among the mutants indicated that there was a lot of room for improvement through selection. Table 2 displays variability, heritability and genetic advance as percentage of mean for eleven characters across 55 mungbean mutant lines. Plant height was shown to have the highest estimate of range, followed by the number of pods per plant, seed fertility, days to maturity, days to 50% flowering, number of clusters per plant, and seed yield per plant.The phenotypic coefficient of variation in the current study was significantly greater than the genotypic coefficient of variation for all the characters indicating the influence of environment in the expression of these traits.

In decreasing order of magnitude, high GCV and PCV values were found for the number of primary branches per plant (GCV: 37.93%; PCV: 41.67%), number of clusters per plant (GCV: 28.44%; PCV: 30.95%), and number of pods per plant (GCV: 27.49%; PCV: 28.33%). For seed yield per plant, moderate GCV and high PCV values were noted (GCV: 19.49%; PCV: 22.11%). Yadav et al. [11]. reported high GCV and PCV estimations for seed yield per plant, Baisakh et al. [12] reported number of pods per plant, and Thusharkumar et al. (2019) reported number of clusters per plant, Sineka *et al*. [1] for number of pods per plant; Sindoora *et al*. [13] for seed yield per plant; Shailendra *et al*. [14] for primary branches per plant and number of pods per plant in mungbean. Conversely, moderate values of GCV and PCV were noted for plant height (GCV: 16.12%; PCV: 17.81%) and pod lentgh (GCV: 12.14%; PCV: 14.15%). Similar kind of moderate variability estimates were reported by Paramesh *et al*. [15] for plant height and Muthuswamy *et al*. [16] for pod length in mungbean.

Table 1. Analysis of variance for eleven quantitative characters in 55 (two parents) mutant lines of mungbean in M_4 generation

S. No.	Characters	Mean sum of squares		
		Replications (df: 2)	Treatments (df: 56)	Error (df: 112)
1.	Days to 50% flowering	0.093	18.749**	1.063
2.	Days to maturity	2.111	20.193**	0.950
3.	Plant height (cm)	5.007	96.324**	6.572
4.	Number of primary branches per plant	0.082	0.699**	0.045
5.	Number of clusters per plant	0.786	10.341**	0.599
6.	Number of pods per plant	0.333	77.059**	1.549
7.	Number of seeds per pod	0.249	2.287**	0.168
8.	Pod length (cm)	1.046	2.825**	0.302
9.	Seed fertility (%)	0.849	10.309**	0.771
10.	100 seed weight (g)	0.030	0.508**	0.046
11.	Seed yield per plant (g)	2.740	5.448**	0.474

*** Significant at 1% level*

For every character under study, there were high heritability estimates found. In decreasing order of their magnitude, the following traits showed the least amount of environmental influence: number of pods per plant (94.19%), days to maturity (87.09%), days to 50% flowering (84.71%), number of clusters per plant (84.42%), number of primary branches per plant (82.85%), plant height (81.98%), number of seeds per pod (80.70%), seed fertility (80.46%), seed yield per plant (77.75%), 100 seed weight (76.66%), and pod length (73.53%). This was consistent with the results of Aparna et al. [17] for the number of pods per plant and seed yield per plant; Devendra [18] for the days to maturity, plant height, seed yield per plant, and 100 seed weight; Aparna *et al.* [17] for number of pods per plant and seed yield per plant; Choudhary *et al*. [19] for number of seeds per pod; Sineka *et al*. [1] for single plant yield, plant height and hundred seed weight; Shraddha *et al*. [20] for number of clusters per plant; Shailendra *et al*. [14] for number of pods per plant, pod length, number of seeds per pod, seed yield per plant, number of primary branches per plant , plant height and days to 50% flowering.

The high heritability suggested that the environment had a minimal impact on the features' manifestation. As a result, early generation selection will be more successful in increasing these features based on these traits' inherent performance. Mass or progeny selection may enhance these features. The high heritability of seed yield per plant indicated that improving it may be achieved through simple selection based on seed yield per plant. The number of primary branches per plant (71.12), pods per plant (54.98), clusters per plant (53.83), seed yield per plant (35.42), plant height (30.08) and pod length (21.44) were shown to have the highest genetic advance as a percentage of mean. Similar results were also reported by Aparna *et al*. [17] for seed yield per plant; Omvir and Singh [21] for number of pods per plant and_Mariyammal *et al*. [4] for number of cluster per plant and single plant yield.

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In the present investigation, high heritability coupled with high genetic advance as per cent of mean was recorded for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length and seed yield per plant indicating the preponderance of additive gene action and hence simple selection would be more effective for improvement of these characters. Similar kind of findings were also reported by Madhuri *et al*. [22] for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length and seed yield per plant; Sheena *et al*. [23] number of primary branches per plant, number of clusters per plant, number of pods per plant and seed yield per hectare and Sindoora *et al*. [13] for seed yield per plant, number of pods per plant, number of clusters per plant, plant height and number of primary branches per plant [24].

Table 2. Mean, coefficient of variability, heritability (broad sense) and genetic advance as per cent of mean for eleven quantitative characters in 55 mutant lines of mungbean in M_4 generation

S. No.	Character	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as per cent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
1.	Days to 50% flowering	34.90	28.00	39.00	5.89	6.95	6.97	7.55	84.71	4.60	13.19
2.	Days to maturity	64.64	58.00	69.00	6.41	7.36	3.91	4.19	87.09	4.86	7.53
3.	Plant height (cm)	33.92	25.18	52.18	29.91	36.48	16.12	17.81	81.98	10.20	30.08
4.	Primary branches per plant (No)	1.23	0.44	2.30	0.21	0.26	37.93	41.67	82.85	0.87	71.12
5.	Clusters per plant (No)	6.33	3.33	10.33	3.24	3.84	28.44	30.95	84.42	3.41	53.83
6.	Pods per plant (No)	18.24	10.17	32.50	25.17	26.71	27.49	28.33	94.19	10.03	54.98
7.	Seeds per pod (No)	11.18	8.60	13.24	0.70	0.87	7.51	8.36	80.70	1.55	13.91
8.	Pod length (cm)	7.55	5.88	9.86	0.84	1.14	12.14	14.15	73.53	1.62	21.44
9.	Seed fertility (%)	95.72	91.33	98.86	3.17	3.95	1.86	2.07	80.46	3.29	3.44
10.	100 seed weight (g)	4.08	3.43	5.16	0.15	0.20	9.60	10.97	76.66	0.71	17.32
11.	Seed yield per plant (g)	6.60	4.22	9.99	1.65	2.13	19.49	22.11	77.75	2.33	35.42

4. CONCLUSION

Significant genetic influences on a range of mungbean properties were found in this extensive study, confirming the crucial role that genetics plays in crop development and output. Metrics such as GCV, PCV, which capture genetic variants, demonstrated the possibility of focused breeding, particularly for traits that show significant genetic advancement relative to their mean and high heritability. Notable characteristics controlled by additive genes that support their potential for focused improvement include days to maturity, seed yield, and hundred seed weight. Our results support earlier studies, highlighting the consistency of these genetic factors in various investigations. Via selective breeding, there are encouraging opportunities to improve the mungbean yield as a result of the population's observed genetic variety. By utilizing this genetic potential, mungbean types that are more hardy and productive can be developed in the future.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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