

Original Research Article

Assessment of induced genetic variability for yield and yield contributing traits in M₄ generation of mungbean (*Vigna radiata* (L.) Wilczek)

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Evaluation of induced genetic diversity in M₄ mungbean (*Vigna radiata* (L.) Wilczek) for yield and attributes that contribute to yield

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ABSTRACT

The present investigation was carried out to study the extent of genetic variability for yield and yield contributing traits existed in two mungbean varieties viz., WGG-42 and LGG-460 after induction of mutations through physical mutagen (gamma rays) and chemical mutagens (ethyl methane sulphonate and sodium azide). Fifty five mutant lines selected from M₃ progenies (36 in WGG-42 and 19 in LGG-460) were evaluated along with the two parents (WGG-42 and LGG-460) during rabi, 2018-19 in RBD with three replications in M₄ generation. High GCV and PCV were observed for number of primary branches per plant, number of clusters per plant and number of pods per plant. High heritability was recorded for all the characters studied.

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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 chemical (sodium azide) and physical (gamma rays) mutagens. In Rabi, 2018-19, in RBD with three replications in M₄ generation, 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 major branches per plant, number of 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

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indicates promising avenues for future mungbean breeding programs to enhance these characteristics.

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Key words: Gamma rays, EMS, SA, variability, M₄, mungbean

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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. 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 (Tah, 2006 and Singh *et al.*, 2009).

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Improvement of cultivated plants largely depends on the extent of genetic variability available within the species. ~~Genetic variability is a prerequisite for any crop improvement programme.~~

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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 and pollination. 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 (Usharani and Kumar, 2016). Gamma rays, ethyl methane sulphonate (EMS) and sodium azide (SA) are the commonly used mutagens in mungbean for inducing genetic variability (Wani and Kozgar, 2016). 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 variation in the experimental material. Estimation of genetic advance will give idea regarding the actual worth of the selected plants. ~~Keeping this in view, the aim of this study was to generate information on the magnitude of induced genetic variability for yield and yield components with the application of gamma rays, ethyl methane sulphonate and sodium azide.~~

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

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Material and Methods

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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). Treated seeds and their untreated controls were sown in the field to raise the M₁ generation. The recovered mutants were first screened, evaluated and advanced to M₂ and M₃ generations. Finally, fifty five isolated promising lines were advanced to M₄ 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*, 2018-2019 in M₄ generation. Each progeny was grown in one row with 3 m length with a 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 (1961). The genotypic and phenotypic coefficient of variation was calculated by the formulae given by Burton (1952). Heritability in broad sense was calculated by the formula given by Lush (1940) and genetic advance as given by Johnson *et al.* (1955).

Comment [h14]: Parameters of genetic variability: Genotypic and phenotypic coefficients of variation (GCV and PCV) were computed using Burton's method from 1952. The formulas for PCV and GCV are as . please explain by formula

Heritability: Heritability, a measure of genotypic variance in relation to total phenotypic variance, is calculated using Hanson et al.'s (1956) formula:

As well as Genetic advance as percent of mean: Genetic Advance, indicating the improvement in mean genotypic value over the parental population, was calculated using the method suggested by Johnson et al. (1955) please again state it well. :

Statistical Analysis

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Results and Discussion

In the present study, the analysis of variance revealed significant differences for all the eleven characters, indicating the presence of substantial genetic variability in the 55 mutant lines of mungbean (Table 1). The variability among the mutants suggested ample scope for improvement through selection. The results of variability, heritability and genetic advance as percentage of mean for eleven characters in 55 mutant lines of mungbean are presented in Table 2. The highest estimate of range was registered for plant height followed by number of pods per plant, seed fertility, days to maturity, days to 50% flowering, number of clusters per plant and seed yield per plant. In the present study, phenotypic coefficient of variation was of high magnitude than the genotypic coefficient of variation for all the

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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 diversity of the mutants indicated that there was a lot of room for improvement through selection. Table 2 displays the genetic progress, heritability, and variability values as a 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 on each plant, seed fertility, days till 50% flowering, number of clusters on each plant, and number of seeds produced 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.

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High GCV and PCV values were observed for primary branches per plant (GCV: 37.93%; PCV: 41.67%) followed by number of clusters per plant (GCV: 28.44%; PCV: 30.95%) and number of pods per plant (GCV: 27.49%; PCV: 28.33%) in the decreasing order of their magnitude. Moderate GCV and high PCV values were observed for seed yield per plant (GCV: 19.49%; PCV: 22.11%). Similar kind of high GCV and PCV estimates were reported by Yadav *et al.* (2017) for seed yield per plant; Baisakh *et al.* (2016) for number of pods per plant and Thusharkumaret *al.* (2019) for number of clusters per plant in mungbean. On contrary, moderate estimates of GCV and PCV were observed for plant height (GCV: 16.12%; PCV: 17.81%) and pod length (GCV: 12.14%;

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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.* (2017) reported high GCV and PCV estimations for seed yield per plant, Baisakh *et al.* (2016) reported pod counts per plant, and Thusharkumaret *al.* (2019) reported cluster counts per plant in mungbean. Conversely, moderate values of GCV and PCV were noted for the height of the plants (GCV: 16.12%; PCV: 17.81%) and the length of the pods (GCV: 12.14%; PCV: 14.15%). Similar kind of moderate variability estimates were reported by Paramesh *et al.* (2014) for plant height and Muthuswamy *et al.* (2019) for pod length in mungbean.

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Table 1. Analysis of variance for eleven quantitative characters in 55 (two parents) mutant lines of mungbean in M₄ generation

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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

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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

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High heritability estimates were recorded for all the characters studied. The highest heritability was registered for 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%) in the decreasing order of their magnitude indicating the least influence of environment on these characters. This was in conformity with the findings of Devendra (2015) for days to maturity, plant height, seed yield per plant and 100 seed weight;

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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. (2015) for the number of pods per plant and seed yield per plant, and Devendra (2015) for the days to maturity, plant height, seed yield per plant, and 100 seed weight. Aparna et al. (2015) for number of pods per plant and seed yield per plant and Choudhary et al. (2017) for number of seeds per pod.

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The high heritability indicated that the influence of environment on expression of the traits is relatively low. Therefore, for improving these traits the selection will be more effective in early generation on the basis of *per se* performance of these traits. These traits may be improved by mass or progeny selection. High heritability for seed yield per plant suggested that straight selection based on seed yield per plant would be effective for its improvement. The maximum genetic advance as per cent of mean was registered for number of primary branches per plant (71.12), number of pods per plant (54.98), number of clusters per plant (53.83), seed yield per plant (35.42), plant height (30.08) and pod length (21.44).

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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 production per plant indicated that improving it may be achieved through simple selection based on seed output per plant. The number of major 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.* (2015) for seed yield per plant and Omvir and Singh (2016) for number of pods per plant.

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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.* (2017) 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.

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 M₄ generation

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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

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Conclusion

From the foregoing discussion, based on genetic parameters it can be concluded that high to moderate GCV estimates and high heritability with high genetic advance as per cent of mean were observed for plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant and seed yield per plant indicating that the variation in the above characters is most likely due to additive gene effects, hence, simple directional selection may be effective to improve these characters. The maximum variation in polygenic traits may show the stable gene mutations in subsequent generation. The results indicated that the variation among mungbean mutant lines is useful for crop improvement and further study is needed for the analysis of the mutants.

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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, and ECV, 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 physiological maturity, grain yield, and the weight of one hundred seeds. 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.

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References

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Comment [h42]: Poor and careless citation and bibliography as well as please need new one.

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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
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** Significant at 1% level

UNDER PEER REVIEW

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 M₄ generation

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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

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