Original Research Article

Assessment of induced genetic variability for yield and yield contributing traits in M_4 generation of mungbean(*Vigna radiata* (L.) Wilczek)

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 M_3 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 M_4generation. 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. 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.

Key words: Gamma rays, EMS, SA, variability, M_4, mungbean

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).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. 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 (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 variationin 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.

Material and Methods

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 M_1 generation. The recovered mutants were first screened, evaluated and advanced to M_2 and M_3 generations. Finally, fifty fiveisolated 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*, 2018-2019 in M_4 generation. Each progeny was grown in one row with 3 m lengthwith 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). Heritabilityin broad sense was calculated by the formula given by Lush (1940) and genetic advance as given by Johnson *et al*. (1955).

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 mungbeanare 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 co-efficient of variation was of high magnitude than the genotypic coefficient of variation for all the characters indicating the influence of environment in the expression of these traits.

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 Thusharkumar*et 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%; 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.

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; 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.

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). Similar results were also reported byAparna *et al*. (2015) for seed yield per plant and Omvir and Singh (2016) for number of pods per plant.

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.

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 mungbeanmutant lines is useful for crop improvement and further study is needed for the analysis of the mutants.

References

Aparna, R., Singh, S.K., Sharma, V and Pathak, R. 2015. Genetic variability, heritability, genetic advance and path analysis in mungbean (*Vigna radiata* (L.) Wilczek). *Legume Research*. 38(2): 157-163.

Baisakh, B., Swain, S.C., Panigrahi, K.K., Das, T.R and Mohanty, A. 2016. Estimation of genetic variability and character association in micro mutant lines of greengram [*Vigna radiata* (L.) Wilczek] for yield attributes and cold tolerance. *Legume Genomics and Genetics*. 7(2): 1-9.

Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings of 6th Grass Land Congress Journal*. 1: 277-278.

Choudhary, P., Payasi, S.K and Patle, N.K. 2017. Genetic study and selection indices for grain yield of mungbean (*Vigna radiata* (L.) Wilczek). *Legume Research*. 40(5): 836-841.

Devendra, K.P. 2015. Genetic variability analysis for seed yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *International Journal of Plant Breeding and Genetics*. 9: 177-188.

Johnson, H.W., Robinson, J.F and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318.

Lush, J.L. 1940. Intra-series correlation and regression of offspring in rams as a method of estimating heritability of characters. *Proceedings of American Society of Animal Product*. 33: 292-301.

Madhuri, M., Rasal and Sachind, D.P. 2017. Genetic diversity studies in mungbean (*Vigna radiata* (L.) Wilczek) germplasm. *Trends in Biosciences*. 10(2): 868-872.

Muthuswamy, A., Jamunarani, M and Ramakrishnan, P. 2019. Genetic variability, character association and path analysis studies in greengram (*Vigna radiata* (L.) Wilczek). *International Journal of Current Microbiology and Applied Sciences*. 8(4): 1136-1146.

Omvir and Singh, A.K. 2016. Analysis of morphological characters inter- relationships in the germplasm of mungbean(*Vigna radiata* (L.) Wilczek) in the hot arid climate. *Legume Research*. 39(1): 14-19.

Panse, V. G and Sukhatme, P. V. 1961. Statistical Methods for Agricultural Workers, 2nd edition, ICAR, New Delhi. pp.328.

Paramesh, M., Reddy, D.M., Priya, M.S., Sudhakar, P and Narasimhulu, P. 2014. Analysis of genetic parameters for morpho-physiological traits in mungbean (*Vigna radiata* (L.) Wilczek). *Indian Journal of Plant Sciences*. 3(2): 1-6.

Singh, S.K., Singh, I.P., Singh, B.B and Singh, O. 2009. Correlation and path coefficient studies for yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *Legume Research*. 32(3): 180-185.

Tah, P.R. 2006. Studies on gamma rays induced mutations in mungbean [*Vigna radiata* (L.) Wilczek]. *Asian Journal of Plant Sciences*. 5(1): 61-70.

Tusharkumar, A., Patel, B.N., Rumit, P., Patil, G.B and Solanki, C. 2019. Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mungbean(*Vigna radiata* (L.) Wilczek). *International Journal of Chemical Studies*. 7(4): 383-387.

Usharani, K.S and Kumar, C.R.A. 2016. Estimation of variability, heritability and genetic advance in mutant populations of black gram (*Vigna mungo* L. Hepper). *SABRAO Journal of Breeding and Genetics*. 48 (3). 258-265.

Wani, M.R and Kozgar, M.I. 2016. Induction of early flowering and maturing mutants in mungbean(*Vigna radiata* (L.) Wilczek). *International Journal of Agricultural Sciences*. 7(1): 79-88.

Yadav, R., Ram, B.L., Suresh, B.G and Lavanya, G.R. 2017. Studies on genetic variability, character association for yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Journal of Pharmacognosy and Phytochemistry*. 6(4): 1988-1991.

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

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