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Evaluation of Gamma Rays Induced Genetic Variability and Divergence in M_3 Generation of Mungbean

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***Abstract* – Genetic variability and divergence for ten economically important traits in 51 genotypes (50 mutant lines of mungbean variety K 851+ one control) in M_3 generation were studied. Number of pods/plant for high GCV was recorded. While number of primary branches/plant and number of pods/plant showed high PCV. All the traits showed high heritability, whereas, plant height, number of primary branches/plant, number of clusters/plant, number of pods/plant and seed yield/plant showed high genetic advance. On the basis of D^2 values, a total of five cluster were obtained, indicating that induced mutations are effective in creating genetic divergence. Maximum number of mutant lines were included in cluster I, cluster II and cluster III whereas only control was present in cluster IV. The maximum inter-cluster distance was recorded for cluster IV. Cluster V, Cluster I, cluster II and cluster IV were recorded for high plant height and maximum number of seeds/pod, seed index, pod length and number of clusters/plant. The results from the present experiment concluded that MML-26 could be superior mutant line with high number of clusters per plant, number of pods per plant, seed index and seed yield per plant.**

***Keywords* – Variability, GCV, PCV, Heritability, Genetic Advance and Genetic Diversity.**

I. INTRODUCTION

Mungbean is the third most important pulse crop with an average yield of 697 kg/ha and production 3.42 million tonnes in India (FAOSTAT). However, very limited genetic variability is available in cultivated population of mungbean. As an alteration, induced mutation can act as potential generation of variability to be used in entire breeding programmes. Gamma irradiation can induce useful as well as harmful mutation in plants. It is therefore necessary to predict the most beneficial dose of gamma rays for improvement of specific traits of crop plants (Muhammad et al. 2001). Parameters such as genotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding program (Mishra et al. 2008). Therefore, proper evaluation of the extent of genetic variation available for yield components, their variability values and genetic advance could be of great help to the breeder (Tabasum et al. 2010). Study of genetic diversity in genetic resources is a critical factor to better understand the evolutionary and genetic relationships among accession and to select germplasm in a more systemic and effective way (Lavanya et al. 2008). Keeping these points in consideration the present study focused on following objectives (1) To assess induced variability in M_3 generation of mungbean variety K851. (2) To estimate genetic diversity in M_3 generation of mungbean variety K851.

II. MATERIAL AND METHODS

Present investigation was conducted at the Field Experimentation Center, Department of Genetics and Plant Breeding, Allahabad School of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad during Kharif 2010. The material comprised of M_1 and M_2 generations produced from physical mutagen (Gamma rays) on mungbean variety K851. The mutagen namely gamma rays with 10 different concentrations (5, 10, 15, 20, 25, 30, 35, 40, 45, and 50 kR) were applied. During kharif 2010, the M_3 generation of certain M_2 mutant progenies were grown. The M_3 generation was derived individual selection of seed from M_2 plants. These individual M_2 plants were, in turn, selected from high yielding M_2 progenies (those showing statisticaliy significant mean and significantly high CV than their respective parent). Thus, M_3 progenies of 50 M_2 progenies were selected from the mungbean variety K851 and raised. The means of M_3 progenies were analyzed for variance as per the method suggested by Fisher, 1936. The statistical parameters were analyzed as per the method suggested by (1) Genetic variability (Genotypic coefficient of variation, phenotypic coefficient of variation, environmental coefficient of variation (Burton, 1952), Heritability (Broad sense) (Burton and Devane, 1953), Genetic advance (Johnson *et al.* 1955). (2) Genetic diversity (D^2- Statistic (Mahalanobis, 1936). The entire material was divided into 3 groups with 17 M_3 progenies each. Each group of M_3 progenies was accommodated in a separate block. A popular variety K851 was chosen as control in each block. Thus in each block, 17 M_3 progenies and one control were grown in plots of single row after randomization. Each row was 2 m long and spaced 30 cm apart with plant to plant distance of 10 cm. The data was recorded for a total of eleven characters on five plants selected randomly.

III. RESULTS AND DISCUSSION

Due to M_3 progenies, control and due to treatments the mean sum of squares were significant for all ten characters. Both GCV and PCV were closely comparable indicating less influence of environment. Higher magnitude of PCV (30.14) and GCV (29.59) were recorded for the trait number of pods per plant. More

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recently high PCV and GCV was reported for number of pods per plant in mutant lines Momin et al. (2006). In the present investigation, this was also substantiated by the higher values of broad sense heritability observed for all characters in mutants lines in M_3 generation of mungbean (Table 1). Moderate to high heritability estimates in M_3 generation for yield components in mungbean have also been reported by Sahu and Patra (1997). The extreme utility of GCV and heritability in practicing selection in breeding programe has already been demonstrated by Burton (1952). The number of pods per plant and plant height exhibited relatively moderate value of genetic advance. Johnson et al. (1955) suggested that heritability and genetic advance when calculated together would prove more useful predicting the resultant effect of selection on phenotypic expression.

On the basis of significantly higher mean for seed yield per plant, 20 mutant lines of M_3 progenies found better than control K851 (10.77 g/plant). Additionally the mutant lines exhibiting higher yield also showed significant higher number of pods per plant, seeds per pod, clusters per plant. All mutant lines had shown high significance except one mutant line for plant height. The M_3 progenies exhibiting better yield than parents have been reported by Yadav and Singh (1988). Similarly, Khan and Wani (2006) have also reported in M_3 generation mutant of Pusa Baisakhi variety of mungbean.

In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extend to available genetic diversity (Mohammadi, 2003). The fifty mutant lines and one control of variety K851 of mungbean were grouped into five clusters using Non Hierarchical Euclidean cluster analysis. The results of cluster analysis are shown in table 2. As a result cluster I, II and III consisted of 15 mutant lines, cluster IV of 5 mutant lines and only control was present in cluster V. Natarajan et al. (1988) also grouped a total of 45 genotypes in to five clusters by D^2 analysis. The results showed that the cluster I has the highest mean for plant height, pod length, seeds per pod and seed index. Cluster II was recorded high mean values for days to 50% flowering, cluster per plant and pods per plant and cluster IV for primary branches per plant, days to maturity and seed yield per plant. But Cluster V and cluster III were recorded lowest mean values for all eleven characters. Inter-cluster distance (D^2) was found maximum between clusters IV and V (673.79). Dikshit et al. (2002) also grouped 34 mungbean genotypes in to seven clusters and cluster III and IV exhibited maximum inter cluster distance. The intra and inter-cluster average distances among five clusters were variable (Table 4). Percent contribution of ten characters to genetic divergence is presented in table 5. But only two characters are cited namely days to maturity (43.37), number of seeds per pod (19.45) contributed maximum to the manifestation of genetic divergence.

IV. CONCLUSION

In summary, it can be concluded that MML-26 was identified as desirable mutant line with high number of cluster per plant, number of pods per plant, seed index and seed yield per plant. High estimates of GCV, PCV and heritability were observed for characters including number of primary branches per plant, number of cluster per plant, number of pods per plant and seed yield per plant. A total of 5 clusters were observed and among these the present investigation further revealed that cluster II and V were most diverse. Therefore, mutant lines present in these clusters are suggested to provide a broad spectrum of variability in segregating generations and may be used as parents for future hybridization programme to develop desirable types.

Table 1: Coefficient of variation, Heritability and Genetic Advance for 10 yield contributing characters in mungbean mutant population

S. No.	Characters	Coefficient of variation		h2 (bs) %	Genetic advance	Genetic advance as % of mean
		Genotypic	Phenotypic			
1	Days to 50% flowering	2.76	3.20	74.54	2.59	6.26
2	Plant height (cm)	12.74	13.19	93.28	15.99	25.82
3	Primary branches per Plant	18.98	22.54	70.91	1.42	44.11
4	Clusters per Plant	17.68	18.20	94.44	3.70	35.61
5	Pods per Plant	29.59	30.14	96.40	15.05	58.99
6	Days to maturity	7.42	7.48	98.29	9.04	14.65
7	Pod length (cm)	4.92	7.05	48.77	1.19	13.80
8	Seeds per Pod	4.96	9.46	27.47	2.24	18.51
9	Seed index (g)	6.47	8.68	55.54	0.67	16.98
10	Seed yield per Plant (g)	15.73	16.49	91.00	3.25	32.27

Table 2: Distribution of 50 mungbean mutant lines into different clusters

Cluster No.	No. of Mutant Lines	Mutant lines included
I	15	MML2, MML3, MML1, MML5, MML6, MML11, MML7, MML4, MML14, MML8, MML15, MML10, MML13, MML9, MML12,
II	15	MML16, MML23, MML17, MML25, MML18, MML24, MML19, MML27, MML21, MML20, MML26, MML28, MML30. MML-22, MML29,
III	15	MML31, MML39, MML33, MML42, ML34, MML41, MML36, MML37,

		MML38, MML32, MML35, MML41, MML40, MML45. MML42, MML44,
IV	5	MML50, MML48, MML46, MML49, MML47.
V	1	MML51.

Table 3: Cluster mean values for 10 characters in mutant population of mungbean

Characters Clusters	Days to 50% Flowering	Plant Height (cm)	Primary Branches/ Plant	Clusters / Plant	Pods/ Plant	Days to Maturity	Pod Length (cm)	Seeds/ Pod	Seed Index (g)	Seed Yield/ Plant (g)
I	40.933	72.044	3.266	9.048	19.273	63.667	8.980	12.674	4.032	9.271
II	40.333	59.012	2.778	13.125	35.995	63.020	8.601	11.463	3.902	11.250
III	41.844	57.665	3.058	9.396	21.734	61.088	8.640	12.300	3.858	9.171
IV	40.533	56.267	4.836	9.376	24.343	53.045	7.780	11.599	4.028	11.487
V	42.110	46.603	3.467	9.680	24.397	67.543	8.543	11.330	3.367	10.770

Table 4: Intra (Diagonal) and Inter-Cluster Distances (D^2) In Mutant Population of Mungbean

CLUSTERS	I	II	III	IV	V
I	103.347 (10.166)	406.026 (20.150)	179.904 (13.413)	473.031 (21.749)	301.274 (17.357)
II		132.221 (11.499)	354.649 (18.832)	585.410 (24.195)	328.848 (18.134)
III			126.242 (11.236)	308.067 (17.552)	234.281 (15.306)
IV				9.517 (3.085)	673.798 (25.958)
V					0.000 (0.000)

D values represented parenthesis

Table 5: Percent contribution of different characters to genetic divergence in mungbean

S.No.	Characters	Number of appeared times ranked 1st	Percent contribution of characters
1	Days to 50% flowering	3	0.23
2	Plant height (cm)	104	8.15
3	Primary branches per Plant	1	0.07
4	Clusters per Plant	37	2.90
5	Pods per Plant	150	11.76
6	Days to maturity	553	43.37
7	Pod length (cm)	53	4.15
8	Seeds per Pod	62	4.86
9	Seed index (g)	64	5.01
10	Seed yield per Plant (g)	248	19.45

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