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ASSESSMENT OF GAMMA INDUCED GENETIC DIVERGENCE IN M_2 GENERATION OF SOYBEAN

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ABSTRACT

Genetic diversity in twentyfour M_2 treatments resulted from 10, 20, 30, 40 and 50 kR gamma irradiated soybean varieties was studied. These treatments were grouped into six different clusters. Genetic diversity was independent of varieties and doses of gamma rays. Sufficient amount of variability due to induced mutations for different polygenic characters over the parent variety was observed in M_2 families. It formed basis for restricted desirable selections.

Key words: Soybean, gamma irradiation, induced genetic divergence, M_2.

Genetic diversity and variability play a vital role in framing successful breeding programme. It is evident that genetically diverse parents are likely to produce high heterotic effects and yield desirable segregates [1]. Soybean is the world's most important oilseed crop in terms of total production and trade, and the existing variability in this crop is large [1–3]. Selection in such a population may give better results with creation of additional variability through induced mutations [4, 5]. Since the development of a variety is based on magnitude of genetic variability in base material and extent of variability for desired characters [6], the locked genetic variability in respect of linked genes is not released even by close or distant hybridization, under such situations desired recombinations or variability can be achieved by breaking gene linkages having negligible crossing over by induced mutations, as irradiation enhance chiasma formation, crossing over and induce chromosome structural rearrangements [7] and one or two easily identifiable and desirable characters can be incorporated in an otherwise well adapted variety identified for improvement [8]. The present investigation has been undertaken to induce variability for earliness, dwarfism, nonshattering of pods coupled with high yield in closely related varieties [1] without changing their yield potential and quality status; as well tailoring the genotypes suitable for intercropping in sugarcane and for summer planting and also to assess the variability induced by gamma rays with the help of multivariate analysis. D^2 statistic was used to estimate the degree of induced genetic divergence [9].

MATERIALS AND METHODS

The M_2 generations of 24 treatments in four varieties, i.e. MACS- 57, MACS-124, MACS-346 and Monetta with five doses (10, 20, 30, 40 and 50 kR) of gamma rays were handled as per the procedure described earlier [10].

Salient features of the varieties selected for irradiation are as follows:

Variety	Duration days)	Yield potential (q/ha)	100-grain weight (g)	Improvement target
MACS-57	105–110	25–28	12.5–13	Earliness, development of plant type suitable for intercropping & high yield.
MACS-124	115–120	24–28	11–12	Dwarfism, earliness, summer plantation, high yield
MACS-346	115–120	22–25	12–13	—Do—
Monetta	80–85	20–25	11–13	High yield & nonshattering of pods.

The material was planted along with unirradiated parents in completely randomised block design in two replications in four-row plots of 5.0 m, length keeping the spacing between of 45 x 10 cm.

Observations were recorded on seven morphological characters on each M_2 plants in all the treatments and replications. Analysis of variance was carried out for all individual characters. The multivariate analysis of Mahalanobis was carried out [9] and clustering was done following the Tocher's method [11].

RESULTS AND DISCUSSION

The progenies derived from diverse crosses are expected to show a broad spectrum of variability providing greater scope for isolating high yielding segregates in succeeding generations. The variability can be measured by D^2 statistics.

The analysis of variance for individual character showed highly significant differences among the genotypes for all the seven characters studied. The divergence for character within the lines tested by the Wilk's criterion was significant ($\chi^2 = 541.9$). Hence the analysis of genetic divergences among genotypes used in the study was considered relevant.

The multivariate analysis with D^2 values corresponding to the pairs of comparison between 24 treatments revealed that all these treatments can be grouped into six clusters in

M2 generation. Cluster mean values of different characters (Table 3) helped to select desirable M2 progenies on the basis genetic diversity and variability for different characters.

It was observed that unirradiated treatments were distributed in cluster III (MACS-346); IV (MACS-57 and MACS-124) and V (Monetta) (Table 1) indicating sufficient amount of genetic diversity existing in these treatments.

It was interesting to note that though MACS-346 control was included in cluster III, its treated populations, except 30 kR, were not included in this cluster. This indicates that gamma ray treatments (except 30 kR) induced large genetic divergence in M2 families derived from gamma ray irradiated MACS-346 as compared to unirradiated control.

Table 1. Distribution of 24 treatments resulted from gamma irradiation in M2 generation of soybean in different clusters

Cluster No.	Treatments included	Variety	Doses (kR)
I	12	MACS-57	10, 20, 40 50
		MACS-124	10, 40, 50
		MACS-346	20, 40, 50
		Monetta	20, 30
II	3	MACS-346	10
		Monetta	40, 50
III	5	MACS-346	Control, 30
		MACS-124	20, 30
		MACS-57	30
IV	2	MACS-57	Control
		MACS-124	Control
V	1	Monetta	Control
VI	1	Monetta	10

Table 2. Average intracluster (in bold) and inter-cluster distances (D^2 and D) in different treatments of gamma irradiated soybean varieties in M2 generation

Clusters	I	II	III	IV	V	VI
I	**51.7** **(7.9)**	102.9 (10.1)	135.8 (15.6)	243.0 (15.6)	364.6 (19.1)	187.7 (13.7)
II		**56.1** (7.5)	316.0 (17.8)	376.7 (19.4)	630.9 (25.1)	165.0 (12.8)
III			**49.8** **(7.0)**	195.5 (14.0)	255.5 (16.0)	393.4 (19.8)
IV				**90.6** **(9.5)**	545.5 (23.4)	423.2 (20.6)
V					**0.0** **(0.0)**	667.3 (25.8)
VI						**0.0** **(0.0)**

D values given in parentheses.

The minimum intercluster distance (Table 2) observed between I and III taken together 75% treatments with induced diversity. Maximum distance was recorded between clusters V and VI both together consisted two treatments. Thus the results indicated that all genotypes/ varieties are genetically diverse. All treatments formed different clusters irrespective of doses and varieties. From these studies it is confirmed that, sufficient amount of variability due to induced polygenic variance (genetic variability) for different traits over unirradiated control parents can be induced with the aid of gamma rays.

From the cluster means (Table 3) it appeared that maximum and minimum values for days to 50% flowering varied from 51.5 (V) to 60.5 (II); for days to maturity from 84.8 (V) to 113.5 (VI); for plant height from 27.3 (II) to 63.4 cm (III); for number of branches/plant from 3.0 (V) to 4.9 (II); for pods/plant from 43.6 (IV) to 79.9 (V); for 100-grain weight from 10.00 (VI) to 12.98 g (IV); and for yield/plant from 6.3 (VI) to 16.8 g (II).

Table 3. Cluster means for eight characters in gamma-ray treated soybean varieties in M_2 generation

Character	Cluster means						Overall mean
	I	II	III	IV	V	VI	
Days to 50% flowering	56.88	60.48	52.31	54.1	51.50	59.25	55.75
Days to maturity	100.89	101.52	100.50	105.25	84.75	113.50	101.06
Plant height (cm)	32.30	27.33	34.50	63.38	40.70	33.50	38.60
Pods/plant	65.65	57.52	72.44	43.60	79.90	62.50	63.60
Branches/plant	4.05	4.86	4.23	3.33	3.00	3.50	3.83
100-grain weight (g)	11.23	11.58	11.66	12.98	12.00	10.00	11.59
Grain yield per plant (g)	11.89	14.31	16.75	14.90	7.08	6.25	11.86

From Table 3 it can be seen that there is scope for improvement for earliness (V) dwarfness (II) and tallness (IV); more branches/plant (II); less branches types for intercropping (V); more pods/plant (III); higher seed weight (V); and grain yield/plant (g) (II). The treatments included in the respective clusters would serve as source. On the basis of results it has become possible to select nine diverse M_2 progenies which were further found highly promising as they are early maturing, high yielding and suitable for summer planting as compare to local checks [12]. Without the knowledge of genetic diversity and variability present in M_2 families, such as restricted selections of desirable M_2 families would not have not been possible. Further it has an added advantage in economising time, labour and land.

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