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Short Communication

Genetic variability among advanced mutant lines of mungbean

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Mungbean (*Vigna radiata* L.Wilczek) being a self pollinated crop has very limited genetic variability. It occupies an area of 3.53 m ha in India with 1.49 m tonnes production. In Orissa, this crop is grown in 0.74 m ha with production and productivity of 0.29 m tonnes and 396 kg/ha, respectively. The yield potential of this crop is low and plagued with a number of diseases. In order to achieve the goal of increased production by increasing yield potential of genotype, knowledge of variability and inheritance is essential by plant breeders. Mutagens are known to induce genetic variability, thus, producing enough scope for effective selection. In recent years, the role of mutation breeding increasing the genetic variability of polygenic traits in mungbean has been proved beyond doubt (Tickoo and Chandra 1999, Sharma *et al.* 2008). Accordingly, the present study was aimed to assess the genetic variability parameters in Mj generation progenies of mungbean, which were derived from different mutagenic treatments applied on seeds of mungbean (Var. Dhauli).

The experimental material comprised of 47 genotypes of mungbean involving 46 mutant lines and parent Dhauli, a popular mungbean variety grown in Orissa. The mutant lines were derived from 18 mutagenic treatments of three chemicals mutagens each at two different concentrations and their different combination (Table 1). Seeds of M_j plants were bulked treatment wise and M_1 generation was raised. After eliminating the macro-mutants, 120 plants in each treatment were observed and 15 plants per treatment were selected imposing 12.5% selection intensity on the basis of higher yield to raise MS generation. Again 20% selection intensity was imposed and 3 progenies per treatment were selected on the basis of higher yield. Thus, the selected 46 mutant cultures were evaluated along with parent in a Randomised Block Design with 3 replications in M4 generation for estimating genetic variability parameters at College of Agriculture, Bhubaneswar following recommended agronomic practices. Observations on days to 50% flowering and maturity were on plot basis, while for other quantitative characters like plant height, number of branches per plant, pods per plant, seeds per pod, 100-seed weight and yield per plant were taken from 10 randomly selected plant from each progeny. Analysis of variance and genetic parameters were computed by following standard statistical methods.

Analysis of variance exhibited significant differences among 47 genotypes for all 8 characters, indicating presence of genetic variability among the genotypes. The differences between estimates of PCV and GCV were low for all characters (Table 2) indicating low influence of genotype x environment reaction in the expression of these characters which was in close agreement with earlier findings (Nagaral and Kajjdoni 2008) for 100-seed weight, days to maturity, pod length and number of seeds per pod. Verma and Garg (2003) for number of pods per plant and Reddy (1997) for plant height. Results of the per cent investigation indicated existence of good amount of variability in M4 generation and scope for selection for pods per plant and seeds per pod traits.

High estimates of genetic advance as per cent of mean was recorded for pods per plant, plant height and branches per plant while moderate for seeds per pod, 50% flowering and plant yield. This indicates good scope for effective

Table 1. Details of mutagenic treatments in mungbean

Treatment code	Chemical and concentration	Period of treatment (hours)
E1	EMS (0.4%)	6
E2	EMS (0.2%)	6
S1	SA 200 PPM	6
S2	SA 100 PPM	6
N1	NG 200 PPM	6
N2	NG 100 PPM	6
E1S1	EMS (0.4%)+SA200	First mutagen 3 hours & Second one for 3 hours
E1N1	EMS(0.4%)+NG 200ppm	First mutagen 3 hours & Second one for 3 hours
S1N1	SA200 PPM+ NG 200ppm	First mutagen 3 hours & Second one for 3 hours
E2S2	EMS(0.2%)+SA 100ppm	First mutagen 3 hours & Second one for 3 hours
E2N2	EMS(0.2%)+NG100ppm	First mutagen 3 hours & Second one for 3 hours
S2N2	SA100 PPM+ NG 100ppm	First mutagen 3 hours & Second one for 3 hours
E1S2	EMS (0.4%)+SA 100ppm	First mutagen 3 hours & Second one for 3 hours
E1N2	EMS(0.4%)+NG100 ppm	First mutagen 3 hours & Second one for 3 hours
S1N2	SA200 PPM+ NG 100ppm	First mutagen 3 hours & Second one for 3 hours
E2S1	EMS (0.2%)+AS200ppm	First mutagen 3 hours & Second one for 3 hours
E2N1	EMS (0.2%)+jNG200ppm	First mutagen 3 hours & Second one for 3 hours
S2N1	AS 100PPM+NG200ppm	First mutagen 3 hours & Second one for 3 hours 6 hours
Control	Distilled water	6 hours

Table 2. Mean, range and genetic variability parameters for seed<field and it's component trait progenies of mungbean

Character	Mean	Range	$CV_{(E)}$	PCV	GCV	h2 (%)	G.A (5%)	Gain
50% flowering (days)	38.77	32.40-47.67	2.24	10.38	10.13	95.30	7.90	20.30
Maturity (days)	55.75	48.00-65.00	2 .33	8.27	7.93	92.00	8.74	15.84
Plant height (cm)	41.11	29.37-61.23	2.84	19.13	18.92	97 80	15.85	38.55
Branches / plant	1.43	1.13-1.83	5.16	15.82	14.95	89.40	0.42	37.17
Pods / plant	30.44	21.67-48.94	1.91	21.69	21.61	99.20	13.50	44.35
Seeds / pod	4.36	3.02-5.11	0.85	12.19	12.16	99.50	1.04	25.00
100-seed weight (g)	3.66	3.02-4.96	11.52	15.10	9.75	41.71	0.47	12.84
Plant yield (g)	4.59	3.55-5.29	1.54	9.60	9.47	97.41	0.88	19.17

selection based of these characters. In spite of high heritability, seeds per pod, plant yield, maturity and 50% flowering had low genetic advance, thus heritability alone does not necessarily mean an increase in genetic advance. The high inheritability along with high genetic advance for a character suggests that phenotypic selection is likely to be more efficient. In present study, high genetic advance as per cent of mean together with high heritability and GCV for pods per plant, branches per plant, plant height and seeds per indicating simple directional selection could be effective for improving these characters.

High heritability with low genetic advance was observed for 50% flowering, maturity, 100-seed weight, plant yield indicating that section in later generation would be more elective. These results are in confirmation for 100-seed weight with Nagaral and Kajjidoni (2008).

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