

Induced Polygenic Mutations in *Vigna marina* (Burm) Merr.*

P. VINDHIYAVARMAN,¹ P. CHANDRASEKARAN² and V. SIVASUBRAMANIAN³

The nature of induced mutations in quantitative characters of *Vigna marina* (Burm) Merr. was studied in M₂ generation obtained by treating dry seeds in gamma rays and pre-soaked seeds in EMS. The mean of the four out of eight characters studied was shifted towards positive direction. The rest of the characters was found to respond differently to the mutagens. The treated populations have released more variability. The GCV and genetic advance were higher in fodder yield at 10 krad of gamma rays.

The practical utility of induced mutations for the improvement of quantitatively inherited characters is well recognised since most of the economic traits in crop species are quantitatively inherited. There are many reports on induction of polygenic variability in various crop plants. In the present study the effect of gamma rays and ethyl methana sulphonate (EMS) on induction of variability in eight quantitative characters in M₂ generation was investigated by utilising dry and water soaked seeds of *vigna marina*.

MATERIAL AND METHODS :

The dry and presoaked seeds of *vigna marina*, were treated with 10, 20, 30, 40, 50, 60 and 70 krad of gamma rays through the gamma cell at the Sugarcane Breeding Institute, Coimbatore, by exposing the seeds to a cobalt-60 gamma source, the dose rate being 0.3×10^6 rads per hour. The pre-soaked seeds

(12 hours) were treated with EMS at room temperature $26 \pm 2^\circ\text{C}$ with intermittent shaking. The treatments were 25, 50, 75, 100, 125 and 150 mM of EMS for four hours. After EMS treatment, the seeds were thoroughly washed with running tap water for half an hour.

The treated and control seeds were sown as M₁. Twenty M₁ plants in each treatment and in control were advanced to M₂ generation and raised as individual progeny in randomised block design replicated twice. In M₂ generation, the analysis was carried out with individual plant measurement as this gave more precise information than that obtained based on mean values. Ten plants were selected at random in each family and control replication wise for recording metric traits, deliberately omitting border plants abnormal and pest damaged plants.

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1. Cashew Research Station, Vridhachalam, and 2 and 3 Department of Agricultural Botany, A.C. & R.I. Coimbatore 641003.

RESULTS AND DISCUSSION

The induction of mutations in polygenes controlling quantitative characters can be detected by the estimation of mean, coefficient of variations, heritability and genetic advance of mutagen treated populations. In the present material it was observed that the mean of treated populations compared to control was shifted towards positive direction in four out of eight characters studied. The mean vine length of the treated populations was shifted towards the positive direction (tallness) (Table I). The number of days to flowering was also found to shift towards the positive direction (lateness). The number of pods per cluster and fodder yield shifted towards the positive direction (tallness). The number of pods per cluster and fodder yield shifted towards higher productivity direction. The mean of the number of clusters was shifted towards the negative direction (Table II). For pod length the mean shifted towards the negative direction in gamma rays treated populations and in a few concentrations of EMS treated lots. The mean number of seeds per pod shifted towards positive direction in low doses of both the mutagens and shifted towards negative direction in high doses. Number of branches was slightly high in most of the doses in gamma rays treatment and was slightly reduced in EMS treatment. The results indicated that induced polygenic mutations do not follow any par-

ticular direction and that they are at random, supporting the views expressed by Gaul (1965) and Goud (1968).

High variance was observed for all the characters in the treated populations than control, a finding that agrees with the reports from Krishnaswami *et al.* (1977) in greengram and chowdhury *et al.* (1975) in guar. Gaul (1964) stated that the radiation induced variability could be determined as early as in M_2 generation. Increase in variability could be explained to be due to mutation of polygenes governing the quantitative characters and their segregation in M_2 generation.

All the eight characters studied were found to respond differently to the mutagens. No linear relationship was observed between the dose and variance. *vigna marina* has recently been introduced at Coimbatore and is now being cultivated for its green fodder. Therefore, for breeding forage improvement, fodder yield and its associated characters like vine length, number of branches and days to flowering should have wider variability for selection of superior lines. The extent of variability and the transmissibility of the traits to the progeny are usually measured on the basis of coefficient of variation, heritability and genetic advance. In the present investigation, the treated populations of gamma rays and EMS have released more variability compared to control populations. A high heritability accom-

panied by high genetic gain is a good indication of variation which is due to high degree of additive effects (Johnson *et al.*, 1955).

Since the GCV, and genetic advance were higher in fodder yield at 10 krad of gamma rays, this character will respond to selection favourably. Besides, at this dose level the GCV, heritability and genetic advance were relatively on the higher side for the associated characters like vine length, number of branches and days of flowering.

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TABLE I Estimates of Mean, Genotypic coefficient of variation (GCV), Heritability (H) and Genetic advance (GA) in M_2 Generation.

Mutagen (Dose/ conc.)	Length of the main vine			Number of primary branches			Days to flowering			Number of clusters on the main vine						
	Mean (cm)	GCV	H	GA	Mean	GCV	H	GA	Mean (days)	GCV	H	GA	Mean	GCV	H	GA
Control	116.1	10.7	29.1	16.8	4.4	14.3	31.2	0.7	72.2	3.3	41.8	3.1	6.4	—	—	—
Gamma rays (Krad)																
10	117.3	20.9	66.3	41.2	4.2	31.1	58.3	2.0	72.1	12.7	86.8	17.6	5.8	—	—	—
20	134.5	13.8	44.3	25.4	4.5	17.3	54.2	1.2	71.4	7.8	71.0	9.7	6.1	23.9	49.7	2.1
30	128.9	13.9	41.3	23.7	4.5	15.1	38.0	0.9	73.9	8.6	77.2	11.4	6.0	25.4	52.1	2.3
40	124.7	16.0	53.7	30.2	4.7	20.0	45.5	1.3	75.4	3.2	7.2	1.3	5.5	30.4	49.7	2.4
50	124.4	14.7	44.6	25.1	4.4	19.9	54.4	1.3	72.5	7.4	30.6	6.1	5.9	31.8	49.3	2.7
60	141.2	10.7	29.1	16.8	4.6	11.9	24.5	0.6	72.8	9.1	73.8	11.7	6.3	15.5	25.8	1.0
70	128.3	24.7	70.5	54.9	4.5	28.3	56.8	1.9	75.5	8.3	75.0	11.1	5.0	43.0	61.8	3.5
EMS (mM)																
25	132.6	31.5	67.2	70.4	4.2	15.7	37.7	0.8	74.4	3.9	61.1	4.7	5.5	27.3	35.6	1.8
50	132.1	38.1	76.1	90.5	4.3	21.9	57.3	1.5	74.4	7.0	86.1	9.9	5.0	26.9	33.0	1.6
75	125.8	23.0	44.1	39.8	4.2	28.0	57.8	1.8	74.4	4.3	18.6	2.8	5.8	31.0	49.3	2.6
100	131.8	19.5	47.9	36.6	4.1	14.3	31.2	0.7	75.3	4.9	77.8	6.8	5.3	26.4	36.6	1.7
125	137.7	27.2	65.8	62.5	4.5	19.3	43.4	1.2	75.8	8.5	85.1	12.3	5.7	22.8	26.9	1.4
150	118.9	31.1	65.7	61.7	4.5	24.6	64.9	1.8	77.6	6.3	90.7	10.0	5.0	—	—	—

TABLE II Estimates of Mean, Genotypic coefficient of variation (GCV), Heritability (H) and Genetic advance (GA) in M₂ Generation

Mutagen (Dose/ conc.)	Pods per cluster			Pod length			Seeds per pod			Fodder yield						
	Mean	GCV	H	GA	Mean (cm)	GCV	H	GA	Mean	GCV	H	GA				
Control	2.1	—	—	—	4.8	9.8	9.9	0.2	5.8	7.6	14.2	0.3	529.7	20.7	52.9	189.6
Gamma rays (krad)																
10	2.8	—	—	—	4.8	14.1	42.2	0.9	6.0	11.8	34.0	0.9	561.3	68.2	80.5	707.3
20	2.9	33.2	41.9	1.3	4.7	29.8	76.3	2.5	5.9	31.9	76.4	3.4	787.6	42.4	64.9	554.4
30	2.6	32.9	55.9	1.3	4.7	18.6	51.5	1.3	5.9	20.4	59.7	1.9	662.9	29.5	53.5	294.6
40	2.6	32.0	41.3	1.0	4.6	22.1	62.4	1.7	5.8	10.6	29.2	0.7	599.7	27.8	49.9	242.8
50	2.7	6.0	2.5	0.1	4.6	14.4	38.0	0.8	5.7	11.9	37.1	0.9	621.9	47.9	70.2	514.2
60	2.7	30.4	36.5	1.0	4.5	19.4	48.2	1.2	5.5	15.4	42.7	1.2	806.4	45.6	95.4	739.3
70	2.9	33.3	44.1	1.3	4.8	14.7	40.3	0.9	5.7	9.6	25.2	0.6	688.9	52.7	64.5	600.6
EMS (mM)																
25	2.1	—	—	—	5.0	18.4	59.9	1.5	6.0	—	—	—	569.5	27.1	66.6	259.2
50	2.2	16.5	13.7	0.3	4.9	15.9	47.5	1.1	6.0	6.3	16.0	0.3	663.1	23.6	51.2	230.9
75	2.3	11.4	7.5	0.2	4.9	17.1	55.2	1.3	5.9	3.5	4.6	0.1	630.1	22.2	54.7	213.3
100	2.2	—	—	—	4.6	16.1	51.7	1.1	5.7	8.8	38.7	0.9	648.3	20.6	61.0	217.3
125	2.2	11.6	8.5	0.2	4.9	6.8	10.0	0.2	5.9	—	—	—	658.9	30.7	73.9	358.0
150	2.2	—	—	—	4.7	12.7	41.8	0.8	5.8	—	—	—	612.9	20.7	52.9	189.6