J. Fac. Agr. Hokkaido Univ., Vol. 63, Pt. 4: 387~396 (1988)

CHARACTERIZATION OF INDUCED POLYGENIC VARIABILITY IN PIGEON PEA (*CAJANUS CAJAN* L.)

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Received June 8, 1988

Introduction

Pigeon pea is a major grain legume of the semi-arid tropics and is included in the diets of a vast number of people in India. This crop, by virtue of its symbiotic nitrogen fixation and deep root system, is known to enrich soil fertility and the plants are also used as green manure[5]. Even though pigeon pea is indigenous to India, due attention has not been paid to its improvement. This crop is beset with long duration, poor plant type, susceptibility to pests and frost, high flower drop and low yield potential[1,11]. Enlargement of genetic variability for these traits is of the utmost importance. Limited work has been done on the induction of micromutations in pigeon pea[7,8]. The present investigation was, therefore, initiated to assess the efficacy of independent and sequential treatments of four mutagens in the induction of genetic variability, and its evaluation in M_2 and M_3 generations.

Materials and Methods

Sets of 150 dry and well developed seeds of pigeon pea, variety T-21, were exposed to 20 kR of gamma rays at a dose rate of 438 rads/minute. Similar lots of seeds were presoaked in distilled water for 8 hrs. and were treated with 100 ml fresh aqueous solutions of 0.05% dES, 0.1% EMS and 0.02% HZ for 3, 4 and 5 hrs., respectively, at a room temperature of 26± 2°C. Identical sets of seeds were also used in sequential treatments of 20 kR gamma rays with 0.05% dES, 0.1% EMS and 0.02% HZ. The seeds were first exposed to gamma rays and were presoaked for 8 hrs. prior to treatment with different chemical mutagens. Another set of presoaked seeds were

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first treated with 0.05% dES and 0.1% EMS for 3 and 4 hrs., respectively, and were treated with 0.02% HZ for 3 hrs. The seeds were then washed under tap water for 30 minutes and kept overnight in distilled water. The treated seeds along with the respective controls were sown in the field to raise M_1 generation.

From each treatment 30 plant progenies were raised in M_2 in a completely randomised design (CRD) with a spacing of 30×45 cm. Data on five quantitative characters; viz., days to maturity, plant height, number of pod-bearing branches, number of pods per plant and seed yield per plant, were recorded on five random normal plants in each progeny.

From each M_2 progeny, seeds of 5 plants were bulked and 30 M_3 progenies were raised in each treatment in a CRD. The data were recorded on the same five attributes.

Results

The range and means along with standard error are depicted in Fig. 1. The estimates of different genetic parameters of the five characters in the M_2 and M_3 generations are given in Tables 1-5.

Days to maturity: In M_2 the range was bi-directional for 20 kR+EMS, whereas for 20 kR, dES, EMS, 20 kR+dES, dES+HZ and EMS+HZ is shifted towards the negative direction. In M_3, the range was bi-directional for HZ, 20 kR+dES, 20 kR+HZ and EMS+HZ. However, for 20 kR and 20 kR+EMS it was in the positive direction. In M_3, the range was bi-directional for HZ, 20 kR+dES, 20 kR+HZ and EMS+HZ. However, for 20 kR, 20 kR+EMS it was in the positive direction, while for dES, EMS and dES+HZ it was in the negative direction. The mean values did not alter significantly in either of the generations. It was observed that genotypic variance and other genetic parameters were increased in both generations. In different mutagenic treatments, except for 20 kR, dES and EMS+HZ, the estimates for various genetic parameters were high in M_2 as compared to M_3 generation (Table 1).

Plant height: The range was bi-directional in M_2 for EMS, HZ, 20 kR+HZ, dES+HZ and EMS+HZ, while it tended towards the positive side for 20 kR and 20 kR+EMS. For dES and 20 kR+dES the range showed a negative shift. In M_3 the range was bi-directional in nature for all the treatments. Significant decreases in mean values were observed for 20 kR+dES in M_2 and for dES and dES+HZ in M_3 generation. All the treatments except dES+HZ showed higher genotypic variance (σ^2g), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance (GA) in M_3 generation

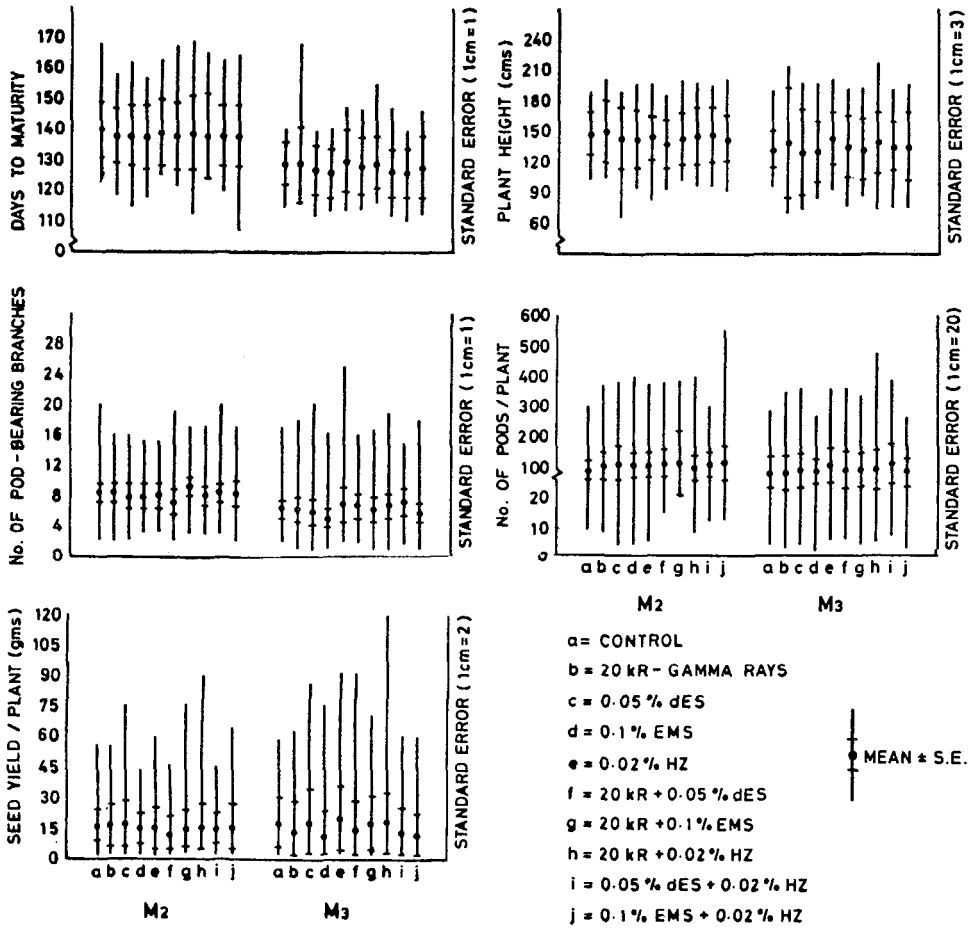

Fig. 1. Range and means of five quantitative characters in T-21 in M_2 and M_3 generations.

when compared to M_2 (Table 2).

Number of pod-bearing branches: The range did not alter significantly in M_2, whereas in M_3 it was bi-directional for 20 kR, dES, 20 kR+HZ and EMS+HZ, while it was in the positive direction for HZ and towards negative side in EMS and 20 kR+EMS. Significant differences in the mean values were not observed in any of the treatments in either of the generations. After mutagenic treatments, the various genetic parameters increased for all the treatments. Estimates of various genetic parameters for this trait, disclosed increased values in M_3 generation when compared to M_2 (Table 3).

TABLE. 1 Estimates of different genetic parameters for days to maturity in T-21 in M_2 and M_3 generations

Treatment	$\sigma^2 g$		GCV		h^2		GA	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
Control	—	—	—	—	—	—	—	—
20 kR	2.34	39.08	0.28	3.03	9.12	33.25	1.04	7.84
0.05% dES	6.94	7.10	0.70	0.82	9.19	15.77	1.64	2.19
0.1% EMS	17.04	5.31	1.44	0.66	23.15	13.40	4.09	1.74
0.02% HZ	18.93	16.15	1.55	1.52	31.94	21.25	5.06	3.95
20 kR+0.05% dES	18.95	11.60	1.58	1.21	25.92	16.02	4.56	2.91
20 kR+0.1% EMS	15.15	3.11	1.28	0.37	10.87	6.44	2.72	0.93
20 kR+0.02% HZ	38.21	4.34	2.66	0.55	46.60	8.41	8.69	1.26
0.05% dES+0.02% HZ	10.71	3.60	1.00	0.47	22.13	13.24	3.20	1.43
0.1% EMS+0.02% HZ	7.84	12.30	0.77	1.26	16.41	12.62	2.36	2.75

TABLE 2. Estimates of different genetic parameters for plant height in T-21 in M_2 and M_3 generations

Treatment	$\sigma^2 g$		GCV		h^2		GA	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
Control	—	—	—	—	—	—	—	—
20 kR	105.22	323.04	2.51	8.32	24.75	34.12	10.56	22.99
0.05% dES	143.66	230.08	3.71	7.17	13.74	25.19	10.12	16.82
0.1% EMS	31.12	108.77	1.02	3.94	9.92	8.64	3.62	7.47
0.02% HZ	4.66	60.39	0.23	1.92	4.66	9.65	1.12	5.26
20 kR+0.05% dES	17.50	136.73	1.10	4.61	1.02	13.46	1.17	9.87
20 kR+0.1% EMS	18.02	142.12	0.74	4.17	9.15	19.08	2.72	11.39
20 kR+0.02% HZ	64.28	167.20	1.83	5.18	12.02	17.82	5.85	12.27
0.05% dES+0.02% HZ	41.88	33.64	1.22	1.74	1.13	7.55	2.46	0.28
0.1% EMS+0.02% HZ	25.60	193.71	1.10	6.06	1.75	20.66	1.74	14.13

TABLE 3. Estimates of different genetic parameters for number of pod-bearing branches in T-21 in M_2 and M_3 generations

Treatment	$\sigma^2 g$		GCV		h^2		GA	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
Control	—	—	—	—	—	—	—	—
20 kR	0.62	2.49	3.78	13.63	11.10	24.58	0.55	1.63
0.05% dES	2.06	2.36	10.89	13.87	27.07	28.34	1.54	1.69
0.1% EMS	1.69	1.56	9.13	13.53	21.48	29.70	1.24	1.40
0.02% HZ	1.80	5.10	9.15	18.58	23.32	42.93	1.34	3.08
20 kR+0.05% dES	1.56	2.16	9.86	10.33	19.00	28.74	1.12	1.63
20 kR+0.1% EMS	1.01	2.36	4.95	13.43	11.66	27.15	0.71	1.66
20 kR+0.02% HZ	1.08	3.39	6.62	15.11	16.95	27.66	0.89	2.03
0.00% dES+0.02% HZ	0.87	3.45	4.75	12.34	9.24	40.23	0.58	2.43
0.1% EMS+0.02% HZ	1.45	4.88	7.69	23.91	15.87	39.67	0.99	2.90

TABLE 4. Estimates of different genetic parameters for number of pods per plant in T-21 in M_2 and M_3 generations

Treatment	$\sigma^2 g$		GCV		h^2		GA	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
Control	—	—	—	—	—	—	—	—
20 kR	938.10	579.89	8.32	10.19	16.75	10.45	26.24	16.16
0.05% dES	1791.89	1685.03	14.44	17.93	23.06	22.33	43.26	40.99
0.1% EMS	1354.31	37.96	11.32	3.84	22.09	18.80	36.30	12.07
0.02% HZ	611.99	1315.44	3.43	1.14	9.73	5.53	16.37	22.79
20 kR+0.05% dES	348.04	1397.14	1.55	7.98	2.47	10.90	7.32	28.21
20 kR+0.1% EMS	880.79	1052.43	4.74	2.73	18.23	12.52	26.31	24.67
20 kR+0.02% HZ	726.25	1707.93	6.13	6.01	14.23	15.04	21.19	35.64
0.05% dES+0.02% HZ	146.34	2276.84	3.42	2.76	1.18	16.09	3.24	43.79
0.1% EMS+0.02% HZ	1090.73	107.09	8.37	5.10	6.76	9.67	20.92	7.96

TABLE 5. Estimates of different genetic parameters for seed yield per plant in T-21 in M_2 and M_3 generations

Treatment	$\sigma^2 g$		GCV		h^2		GA	
	M_2	M_3	M_2	M_3	M_2	M_3	M_2	M_3
Control	—	—	—	—	—	—	—	—
20 kR	22.94	37.97	12.56	25.84	9.85	24.84	3.29	6.33
0.05% dES	13.83	62.27	27.58	20.54	0.73	10.99	1.21	6.08
0.1% EMS	1.56	22.34	1.94	23.08	0.61	13.90	0.11	3.63
0.02% HZ	12.42	43.88	8.55	5.07	4.23	7.74	1.67	4.35
20 kR+0.05% dES	5.90	27.54	7.19	17.35	3.99	10.72	1.03	3.61
20 kR+0.1% EMS	4.06	24.07	5.48	9.61	3.65	6.62	0.79	2.77
20 kR+0.02% HZ	16.73	9.97	13.17	5.32	13.67	15.91	3.12	1.81
0.05% dES+0.02% HZ	1.94	4.52	1.34	13.72	4.21	4.78	0.20	0.99
0.1% EMS+0.02% HZ	16.32	15.89	8.05	24.12	2.82	21.36	1.86	3.99

Number of pods/plant: In M_2, a bi-directional shift in range was observed for 20 kR, dES, EMS, HZ and 20 kR+HZ, while in the rest of the treatments a positive shift was noticed. In M_3, a bi-directional shift was noticed only for 20 kR, while for dES, HZ, 20 kR+dES, 20 kR+EMS, 20 kR+HZ and dES+HZ the range was towards the positive direction. However, for EMS and EMS+HZ the range was towards the negative direction. Significant alterations in the mean values were not observed in either of the generations. HZ and most of the sequential treatments revealed higher values for $\sigma^2 g$ and GA in M_3 than in M_2 generation. Whereas other independent treatments and EMS+HZ showed increased values in M_2 compared to M_3 for genetic parameters (Table 4).

Seed yield/plant: For dES and HZ treatments in M_2 the range was bi-directional in nature, while for 20 kR, 20 kR+EMS, 20 kR+HZ and EMS+HZ the range shifted towards positive direction; whereas for EMS, 20 kR+dES and dES+HZ the shift in range was towards the negative side. However in M_3, a positive shift in the range was observed. No significant alterations were observed for the mean values in both the generations. For various treatments, except 20 kR+HZ, the genetic parameters showed increased values in M_3 generation when compared to M_2 (Table 5).

Discussion

The practical utility of induced mutations for improvement of polygenic characters is well recognised, since most of the economic traits in crop species are quantitatively inherited. It is well established that ionising radiations and chemical mutagens are effective in inducing micromutations in various crops[2,3,4,10,12].

Increases in range, means and estimates of different genetic parameters, viz., $\sigma^2 g$, GCV, h^2 and GA, for five attributes provide ample evidence that mutagenic treatments could create additional genetic variability in polygenic systems.

The range in the mutagenised populations was greater when compared to controls for all the characters in M_2 and M_3 generations, indicating enhanced scope for selection. The mean values for all the characters in M_2 and M_3 did not alter significantly despite the increased variance observed for these characters, suggesting the incidence of plus and minus mutations with equal frequency[9].

Maximum values for $\sigma^2 g$, GCV, h^2 and GA were observed for days to maturity in M_2 when compared to M_3 indicating a fewer number of genes controlling this character. Hence effective selection could be practised for this trait in M_2 itself. On the other hand, increased values for genetic parameters were observed for plant height, number of pod-bearing branches and seed yield per plant in M_3 generation than in M_2 suggesting that these attributes are governed by a relatively greater number of genes. Therefore efficient selection may be practised for these traits in M_3 and/or later generations. Such differences observed in M_2 and M_3 generations are conceivably due to variation in the number of genes governing these characters. Effective use of induced variability through selection would be possible if the generation in which maximum variability is likely to be released is identified. From the present investigation, it is evident that selection of desirable mutant progenies could be made in M_2 for earliness. Whereas, selections may be practised for plant height, increased pod-bearing branches and seed yield per plant in the M_3 generation. For number of pods per plant the independent mutagenic treatments could generate higher levels of genetic variability in M_2, while sequential treatments showed greater genetic variability in M_3. Hence, for this trait, selection may be practised in M_2 after independent treatments and in M_3 after sequential treatments.

The data further indicate that, in general, maximum variance in M_2 was caused by 0.05% dES and 20 kR+0.02% HZ, while in M_3, 20 kR induced

maximum variance. Thus, the extent of induced variation seems to depend on the mutagen used as well as its mode of administration. Increased variability might also arise from enhanced crossovers near the centromere[6,13].

The estimates of h^2 and GA were of higher magnitude for all the characters in both the generations. This may be mainly due to an increase in the genetic component; from the crop improvement stand point, this implies higher response to selection.

Independent mutagenic treatments, in general, when compared to sequential treatments, generated higher levels of $\sigma^2 g$, resulting in higher GCV, h^2 and GA, probably because of more severe diplontic and haplontic selections operating after sequential treatments.

An overview of the results indicates that additional genetic variability could be generated for seed yield and yield components. Hence, genetic improvements may be achieved through judicious selection in the mutagenised populations of pigeon pea.

Summary

The present paper deals with the varietal improvement of the important characters related with the yield potential of pigeon pea, (*Cajanus cayan* L.) by means of mutagenesis.

Dried seeds of the variety, T-21 were irradiated with 20 kR of gamma rays at a dose rate of 438 rads/minute following to various kinds of pre-treatments with aqueous solutions of the chemical mutagens such as dES, EMS and HZ.

Obtained data indicated that increases in range, means and estimats of different genetic parameters, viz., $\sigma^2 g$, GCV, h^2 and GA, for five characters provide ample evidence that mutagenic treatments could create additional genetic variability in polygenic systems. From the present investigation, it is also evident that selection of desirable mutant progenies could be made in M_2 for earliness. Whereas, selections may be practised for plant height, increased pod-bearing branches and seed yield per plant in the M_3 generation. The data further indicated that, in general maximum variance in M_2 was caused by 0.05% dES and 20 kR+0.02% HZ, while in M_3, 20 kR induced maximum variance. Thus the extent of induced variation seems to depend on the mutagens as well as their application modes. It is expected that independent mutagenic treatments, in general, when compared to sequential treatments, generated higher levels of $\sigma^2 g$, resulting in higher GCV, h^2 and GA. Hence, genetic improvements may be achieved through rational selection in the mutagenized populations.

Acknowledgements

The authors are grateful to Prof. G. M. REDDY of Department of Genetics, Osmania University, Hyderabad (India), for his kind help and constant encouragement.

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