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# Study on EMS Induced Micro-mutational Variability in M<sub>2</sub> Generation in Pigeon Pea(*Cajanus Cajan* L.)

P. P. Poudel<sup>1</sup>, R. S. Singh<sup>2\*</sup>, M. N. Singh<sup>1</sup> and S. K. Saroj<sup>1</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005, UP, India; singhrscoh@gmail.com <sup>2</sup>College of Horticulture Noorsaraj, Nalanda-803113, (BAU Sabour, Bhagalpur) Bihar, India

#### **Abstract**

**Background/Objectives**: To assess the effect of Ethyl Methyl Sulphonate (EMS) on induction of genetic variability in pigeonpea genotypes MA 156 and MAL 13. **Methods/Statistical Analysis**: Healthy, dried, pure line seeds of the crop were pre-soaked in distilled water for 6 hours and treated with 0.01M, 0.015M and 0.02M aqueous solution of EMS in phosphate buffer solution. Treated seeds were thoroughly washed in the running tap water for four hours and sown in rows along with without treated seeds of each variety as control (soaked in distilled water for nine hours). **Results/Findings**: Secondary branches, number of pods and yield per plant were higher variable at 0.015M concentration whereas 50 per cent plant flowered and matured earlier at lower concentration of mutagen. Genotypic coefficient of variation and phenotypic coefficient of variation were significantly higher for most of the traits studied i.e. Plant height, number of branches per plant, number of pods per plant, seed yield per plant and 100-seed weight. **Conclusion/Application**: All the mutagenic treatments were effective in inducing genetic variability in both the genotypes.

**Keywords:** Coefficient of Variation, Mutagen, Mutation, Yield

# 1. Introduction

Pigeon pea *Cajanus Cajan* (L.) Millsp. is the second most important pulse crop of India. In broad spectrum, genetic variability is pre-requisite for any successful breeding program. Being an autogamous nature, natural out-crossing is limited and existing gene pool conserved by nature is insufficient for the improvement of yield attributing traits. Among all sources of variations, mutation breeding offers a great scope and promises for strengthening genetic variability and formulating new gene combinations in crop improvement<sup>1</sup>. This investigation was undertaken to assess the effect of Ethyl MethylSulphonate (EMS) on induction of genetic variability in pigeon pea genotypes MA 156 and MAL 13.

# 2. Materials and Methods

The materials, MA 156 and MAL 13, used for the experiment obtained from the Department of Genetics

and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University Varanasi. These two genotypes of pigeon peawere treated with different concentration of EMS to have M<sub>1</sub> generation. Healthy, dried, pure line seeds of the crop were pre-soakedin distilled water for 6 hours and treated with 0.01M, 0.015M and 0.02M aqueous solution of EMS in phosphate buffer solution. Treated seeds were thoroughly washed in the running tap water for four hours and sown in rows along with without treated seedsof each variety as control (soaked in distilled water for nine hours) in Randomized Block Design (RBD) in three replications during 2009-10. Each row consisted of 4 m length and row to row and plant to plant distances were 75 and 25 cm, respectively. All the recommended agronomical practices were followed to grow a good crop. Total 250 fertile M<sub>1</sub> plants harvested separately from each treatment and sown subsequently during Kharif 2010-11 in progeny rows to have M<sub>2</sub> generation. The observations were recorded on variability parameters namely plant height (cm.), number of branches per plant, Days to 50 percent

<sup>\*</sup>Author for correspondence

flowering, number of pods per plant, number of seed per pod, 100-seed weight and yield per plant.

### 3. Results and Discussion

Mutations being the ultimate source of new genes played an important role in the creation of genetic variation, evolution and improvements of crop plants under scientific guidance. At the current levels of plant breeding research, mutation breeding is highly suitable when natural variation does not provide the gene(s) for the desired traits. On the basis of the data presented in the Tables character wise, wide range of variations recorded for most of the characters indicated great scope of crop improvement. Smaller mean values were observe for days to 50 percent flowering, days to maturity and pod length at lower doses of mutagens<sup>2</sup> due to the cumulative effect of polygenes while higher mean values were at medium dose of 0.015M EMS for number of secondary branches, number of pods per plant and finally yield as well. Fundamentally it is established that there is a non-linear relationship between the dose of mutagen and their effects on organisms. Similar results were also obtained by Arulabalchandran and Mullainathan<sup>3</sup> in mungbean and Singh, et al.4 in lentil.

Increased coefficient of variation were predominant in most of the parameters i.e. plant height, number of branches per plant, number of pods per plant, 100-seed weight and seed yield per plant. The significant deviation of treatment mean values than respective control mean values indicated that used mutagen was most effective to induce polygenic variability for plant height, number of branches per plant, number of pods per plant, seed yield per plant and 100 seed weight in M, generation. The significant positive shift in all concentrations was observed in number of primary and secondary branches, number of pods per plant and seeds yield per plant. However negative shift was recorded in plant height and number of days to maturity. Similar results of increased range, mean and

Table 1. Range, Mean, coefficient of variation, PCV and GCV for plant height and number of primary branches in M, generation

		Plant height					Number of primary branches					
Treatments	Range	Mean	C.V	PCV	GCV	Range	Mean	C.V	PCV	GCV		
T <sub>1</sub> MA 156 (0.01M)	148-191	178.00	5.42	27.64	21.97	7-11	12.32	20.88	1.06	0.57		
T <sub>2</sub> MA 156 (0.015M)	150-199	173.00	7.08	15.43	8.39	9–18	13.23	17.04	1.89	1.36		
T <sub>3</sub> MA 156 (0.02M)	129-176	155.77	20.55	19.77	11.30	7–17	11.69	22.59	1.11	0.68		
T <sub>4</sub> MAL 13( 0.01M)	160-230	193.48	8.28	8.39	5.33	9-21	16.00	18.3	1.44	0.75		
T <sub>5</sub> MAL 13 (0.015M)	186-232	190.00	8.19	12.80	6.96	11-24	16.60	16.63	0.99	0.23		
T <sub>6</sub> MAL 13 (0.02M)	159-213	185.74	6.78	9.86	6.22	9–19	13.64	18.95	0.95	0.29		
T <sub>7</sub> MA 156 (Control)	133-181	179.20	5.3	7.74	4.80	6–9	9.45	15.02	1.06	0.42		
T <sub>8</sub> MAL 13(Control)	168-299	204.56	6.4	7.02	4.72	8-22	13.69	15.54	0.80	0.22		

Table 2. Range, Mean, coefficient of variation, PCV and GCV for number of secondary branches and Days to first flowering in M, generation

	Number of secondary branches					Days to first flowering					
Treatments	Range	Mean	C.V	PCV	GCV	Range	Mean	C.V	PCV	GCV	
T <sub>1</sub> MA 156 (0.01M)	5-13	6.06	65.46	28.55	16.17	180-191	184.85	1.2	8.24	6.23	
T <sub>2</sub> MA 156 (0.015M)	2-14	7.15	50.66	25.03	16.22	182-195	188.62	1.43	8.71	7.05	
T <sub>3</sub> MA 156 (0.02M)	<b>0</b> –11	5.77	81.05	40.03	29.98	181-202	187.31	2.49	12.83	9.29	
T <sub>4</sub> MAL 13( 0.01M)	4-18	10.00	48.24	12.50	8.90	168-188	176.91	1.93	11.10	6.99	
T <sub>5</sub> MAL 13 (0.015M)	4–16	10.60	32.1	19.15	11.60	150-182	170.00	3.53	12.56	8.68	
T <sub>6</sub> MAL 13 (0.02M)	5–12	9.20	49.63	19.89	14.78	172-189	169.93	7.54	10.91	7.43	
T <sub>7</sub> MA 156 (Control)	2-10	5.79	22.32	23.49	10.71	183-197	189.00	3.2	7.15	4.52	
T <sub>8</sub> MAL 13(Control)	5–9	5.09	33.02	26.13	13.56	175–185	173.81	2.68	7.85	5.94	

variance are also reported by Upadhey et al.<sup>5</sup> in Soybean and Singh et al.<sup>6</sup> in urdbeans.

Higher and medium doses and/or conc. recorded maximum genotypic and phenotypic coefficient of variation in all the parameters. Coefficient of variation was maximum at higher doses of mutagen for plant height, number of primary branches, days to first flowering and number of pods per plant as this result is corroborate with

the findings of More et al.<sup>7</sup> in chickpea where as number of secondary branches, days to 50percent flowering, days to maturity, pod length, seeds per pod and yield per plant showed maximum coefficient of variation at lower doses of mutagen while it was highest for 100-seed weight at medium dose.

Highest genotypic and phenotypic coefficient of variation was recorded in both the genotype for number

Table 3. Range, Mean, coefficient of variation, PCV and GCV for Days to 50% flowering and days to maturity in  $M_2$  generation

	Days to 50 % flowering					Days to maturity					
Treatments	Range	Mean	C.V	PCV	GCV	Range	Mean	C.V	PCV	GCV	
T <sub>1</sub> MA 156 (0.01M)	186-206	190.26	6.83	8.00	3.90	<b>236</b> –245	240.47	7.34	5.12	3.19	
T <sub>2</sub> MA 156 (0.015M)	191-204	195.44	1.64	4.30	1.86	240-248	243.76	0.94	4.64	2.77	
T <sub>3</sub> MA 156 (0.02M)	189-209	194.69	2.74	9.91	4.75	241-251	244.77	1.07	5.52	4.09	
T <sub>4</sub> MAL 13( 0.01M)	175–197	184.60	3.18	7.71	4.59	235-243	239.48	1.09	5.56	3.99	
T <sub>5</sub> MAL 13 (0.015M)	170-193	182.58	2.29	6.20	4.16	236-243	241.00	1.68	7.58	5.11	
T <sub>6</sub> MAL 13 (0.02M)	178-191	193.58	1.62	6.49	4.35	239-245	241.29	1.54	5.11	3.62	
T <sub>7</sub> MA 156 (Control)	193-207	196.42	1.98	3.92	1.81	243-249	243.53	1.02	4.53	2.62	
T <sub>8</sub> MAL 13(Control)	179–191	182.59	1.56	5.24	3.30	237-245	240.75	0.98	5.54	3.69	

Table 4. Range, Mean, coefficient of variation, PCV and GCV for pod length and seeds per pod in M, generation

		Seeds per pod								
Treatments	Range	Mean	C.V	PCV	GCV	Range	Mean	CV	PCV	GCV
T <sub>1</sub> MA 156 (0.01M)	5.13-8.83	7.34	19.89	5.72	3.54	2.87-4.63	3.82	10.38	24.59	14.65
T <sub>2</sub> MA 156 (0.015M)	6.1-8.85	7.17	8.63	3.35	2.81	2.50-4.83	3.78	14.32	40.48	20.11
T <sub>3</sub> MA 156 (0.02M)	5.4-8.17	6.94	9.31	12.73	6.65	3.0-4.67	3.76	10.87	40.69	22.61
T <sub>4</sub> MAL 13( 0.01M)	4.52-6.33	5.61	7.16	4.63	2.85	2.83-4.27	3.74	16.50	32.89	18.18
T <sub>5</sub> MAL 13 (0.015M)	4.73-6.49	5.49	7.09	4.04	1.64	2.83-4.43	3.76	18.64	27.39	14.89
T <sub>6</sub> MAL 13 (0.02M)	4.72-6.55	5.51	6.03	5.26	2.90	3.32-4.17	3.72	14.56	35.48	20.16
T <sub>7</sub> MA 156 (Control)	5.02-7.45	6.23	8.15	3.05	1.93	2.46-4.69	3.56	9.86	27.25	21.35
T <sub>8</sub> MAL 13(Control)	4.73-8.73	5.05	6.25	4.16	2.57	2.67-4.67	3.74	10.23	32.09	27.01

Table 5. Range, Mean, coefficient of variation, PCV and GCV for number of pods/plant and 100-seed weight in  $\rm M_2$  generation

	Number of pods/plant					100-seed weight					
Treatments	Range	Mean	C.V	PCV	GCV	Range	Mean	C.V	PCV	GCV	
T <sub>1</sub> MA 156 (0.01M)	45-198	111.48	32.49	57.58	48.19	11.8- <b>18.65</b>	13.23	11.23	7.41	4.61	
T <sub>2</sub> MA 156 (0.015M)	59-205	126.41	29.03	49.45	36.57	12.20-18.60	15.02	11.021	8.19	3.73	
T <sub>3</sub> MA 156 (0.02M)	40-257	121.30	42.44	54.17	39.50	<b>9.16</b> –17.1	13.94	14.62	9.68	3.08	
T <sub>4</sub> MAL 13( 0.01M)	91-332	185.59	29.16	33.04	26.53	8.65-13.40	10.59	9.8	9.73	6.14	
T <sub>5</sub> MAL 13 (0.015M)	91-347	192.00	25.27	30.33	23.04	8.25-12.05	10.42	8.03	15.83	9.40	
T <sub>6</sub> MAL 13 (0.02M)	69-276	144.00	27.8	37.01	28.95	8.80-13.49	10.74	8.61	11.45	7.26	
T <sub>7</sub> MA 156 (Control)	45-185	106.71	17.63	54.85	39.56	10.02-16.23	12.86	9.65	6.77	2.64	
T <sub>8</sub> MAL 13(Control)	62-240	160.53	19.7	29.60	24.68	7.03-2.27	10.27	8.54	9.74	6.33	

**Table 6.** Range, Mean, coefficient of variation, PCV and GCV for yield/plant in M, generation

Treatments	Range	Mean	C.V	PCV	GCV
T <sub>1</sub> MA 156 (0.01M)	13.95-70.1	38.30	13.77	37.34	26.63
T <sub>2</sub> MA 156 (0.015M)	12.85-61.25	39.09	34.69	49.42	31.47
T <sub>3</sub> MA 156 (0.02M)	<b>05.6</b> –50.7	31.54	37.28	64.68	59.35
T <sub>4</sub> MAL 13( 0.01M)	19.85-74.5	41.67	26.97	55.96	24.31
T <sub>5</sub> MAL 13 (0.015M)	17.65- <b>87.4</b>	44.19	29.07	32.13	27.45
T <sub>6</sub> MAL 13 (0.02M)	18.30-62.87	38.11	27.11	50.91	34.77
T <sub>7</sub> MA 156 (Control)	11.65-49.62	24.61	12.39	54.86	50.10
T <sub>8</sub> MAL 13(Control)	10.20-57.30	30.23	25.06	45.65	37.15

of secondary branch, number of pods per plant and 100-seed weight while plant height, pod length and seeds per pod showed high genotypic and phenotypic coefficient of variation at lower dose of mutagen. The treatments showing maximum variation in quantitative characters may show stable gene mutations in subsequent generations and can be utilized in further breeding program. These results are also in confirmation for variability parameters as reported by Nandarajan et al.<sup>8</sup> in pigeon pea, Sinha and Bharati<sup>9</sup>, Charumati et al.<sup>10</sup>, Ramya et al.<sup>11</sup> in mungbean.

## 4. Conclusion

Mutation breeding is highly suitable among all the sources of genetic variability when natural variation does not provide the gene (s) for the desired traits. On the basis of the data presented in the Tables, results indicated wide range of genetic variations were predominant for most of the characters studied, mutagens have great scope in crop improvement.

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