

## EVALUATION OF INDUCED GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN INDIAN MUSTARD (*Brassica juncea* L.)

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### ABSTRACT

The present study was conducted with the objective to estimate between family and within family variances, to estimate genetic parameters and identify superior mutants for utilization. The experiment was conducted at farm of Agricultural Botany Section, College of Agriculture, Nagpur during *rabi* 2017 in  $M_3$  generation. 122 mutants along with four checks (Shatabdi, Kranti, Pusa bold and Bio 902) were evaluated in three replications. Data were recorded on germination percentage, days to flowering, days to maturity, plant height, number of primary branches plant<sup>-1</sup> number of siliqua plant<sup>-1</sup> and seed yield plant<sup>-1</sup>. Intra class correlation ( $t$ ) lead the conclusion that differences between individual within family is large and each family differentiated distinctly from the other one at lower level in  $M_3$  generation hence, equal weightage to  $\sigma^2_f$  and  $\sigma^2_w$  were suggested to be considered for selection in generation.  $M_3$  Genetic parameters estimated, revealed that number of siliqua plant<sup>-1</sup>, seed yield plant<sup>-1</sup> and early maturity where the characters influenced by additive gene action and selection would be effective in improving these traits.

(Key words: Genetic advance, genotypic coefficient of variability, heritability, phenotypic coefficient of variability and mustard)

### INTRODUCTION

Rapeseed (*Brassica napus* L.) is considered as one of the most important vegetable oil and protein meal crop worldwide. Its area under cultivation has substantiated during the last decade, and now a days it is the second largest contributor among the world supply of vegetable oils. In India, it is the second most important edible oilseed after groundnut sharing 27.8% in the India's oilseed economy. The share of oilseeds is 14.1% out of the total cropped area in India, rapeseed-mustard accounts for 3% of it. The important objective in mustard improvement is oriented to develop varieties which have high yielding potential (Labana and Banga, 1984). The other objectives are oriented to develop new varieties with wider adaptability, early maturity, disease resistance and high oil content along with high yield potential. To achieve this goal and to bring about desired improvement in mustard, technique of mutation breeding are exploited by plant breeders.

In  $M_3$  generation, homozygosity is not achieved. In order to find out extent of variability in  $M_3$  generation and to test whether homozygosity is attained or not, the present study was undertaken using the mutants selected in  $M_2$  generation of Pusa bold and BIO 902 variety of mustard with two mutagenic agent i.e. gamma rays alone and combination of gamma rays and EMS.

### MATERIALS AND METHODS

Dry healthy seeds of *Brassica juncea*, Pusa bold and BIO 902 treated with gamma rays and EMS. The gamma rays treatment of 900, 1000, 1100, 1200, 1300 Gy (<sup>60</sup>Co) was done at BARC, Trombay, Mumbai. Each of these treatments was treated with 0.5 per cent aqueous solution of EMS.

The harvested seed of  $M_1$  generation were used to raise  $M_2$  generation. During *rabi* 2015-16, 61 mutants were identified from Pusa bold and 61 mutants were identified from BIO 902 during  $M_2$  generation (Table 1). These identified mutants along with 4 checks (Pusa bold, BIO 902, Kranti and Shatabdi) were planted in Randomized Complete Block Design with three replications in *rabi* 2016-17. The details of treatment are presented in table 1.

The experiment was deliberately sown late in order to screen for powdery mildew infestation. All the cultural practices were followed to raise a good crop. No plant protection measures were adopted so that efficient screening of mutants for powdery mildew and aphid could be recorded. The sowing was undertaken on levelled piece of land at experiment farm of Agricultural Botany Section, College of Agriculture, Nagpur.

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Observations were recorded for estimation of coefficient of variation, standard error, critical difference, mean, range, Genotypic variance, Phenotypic variance, Genotypic and Phenotypic coefficient of variation (GCV and PCV) as per formula given by Burton (1953), Heritability percentage as per Hanson *et al.* (1956) and Genetic advance as per Robbinson *et al.* (1949).

## RESULTS AND DISCUSSION

Analysis of variance (Table 2) indicated the presence of significant genetic variability between the families for all seven characters which allowed the estimation of genetic parameters. In accordance to this results significant variability between the families were also reported by Cheema and Sadaquat (2005) and Javed *et al.* (2000) in mustard. They showed that the analysis of variance recorded significant difference for all the traits under evaluation. Significant differences were observed between the progenies for all the seven characters studied.

The lowest coefficient of variation ( $d'' 20$ ) was observed for the characters days to maturity (1.22%), days to first flower (4.74%) and for germination percentage (9.75%) which showed the best genetic potential and its genetic influence. The high coefficient of variation was observed for seed yield plant<sup>-1</sup> (25.42%), number of siliqua plant<sup>-1</sup> (21.58%), plant height (21.29%) and number of primary branches plant<sup>-1</sup> (21.26%) which indicates more influence of environmental fluctuation. These results were in line with that of Cheema and Sadaquat (2005) who also reported high coefficient of variability in primary branches, yield plant<sup>-1</sup> and number of siliqua plant<sup>-1</sup>.

The grand means (122 mutants along with six checks) for germination percentage was 86.25%, days to first flower 44.71 days, days for maturity 103.83 days, plant height 150.75 cm, number of primary branches plant<sup>-1</sup> 3.46, number of siliqua plant<sup>-1</sup> 118.26 and for seed yield plant<sup>-1</sup> 4.01 g (Table 3). Wide range of variation was exhibited for number of siliqua plant<sup>-1</sup> (215.27), germination percentage (76), plant height (57.85), seed yield plant<sup>-1</sup> (39.64), days to first flower (13.66), days to maturity (10.33) and number of primary branches plant<sup>-1</sup> (3.4), which indicated wild range of variation functioning for these characters. Seed yield plant<sup>-1</sup> (39.64 g), days to first flower (13.66), days to maturity (10.33) and number of primary branches plant<sup>-1</sup> (3.4) exhibited low range of variation. In accordance to these results wide range of variation for yield and yield component were also reported by Cheema and Sadaquat (2005).

The phenotypic variance and phenotypic coefficient of variation was observed to be far higher than genotypic variance and genotypic coefficient of variation for all seven characters studied (Table 3). This indicated the higher influence of environment in the phenotypic expression of these characters. Similar to this results higher influence of environment on germination percentage, days to flowering, days to maturity, plant height, number of

primary branches plant<sup>-1</sup>, number of siliqua plant<sup>-1</sup> and seed yield plant<sup>-1</sup> were also reported by Bind *et al.* (2014), all the characters showed positive correlation with seed yield plant<sup>-1</sup> both at phenotypic and genotypic levels except days to 50% flowering and days to maturity.

Genotypic coefficient of variation was found to range from low to high category. High genotypic coefficient of variation for seed yield plant<sup>-1</sup> (25.41%), number of siliqua plant<sup>-1</sup> (21.58%), plant height (21.28%) and number of primary branches plant<sup>-1</sup> (21.26%), and low genotypic coefficient of variation for days to maturity (1.22%), days to first flower (4.74%) and germination percentage (9.74%). Similarly phenotypic coefficient of variation was also observed to be low to high for different characters. High phenotypic coefficient of variation was observed for seed yield plant<sup>-1</sup> (72.37%), number of siliqua plant<sup>-1</sup> (43.99%), number of primary branches plant<sup>-1</sup> (37.09%) and plant height (24.70%). Moderate phenotypic coefficient of variation was observed for germination percentage (16.75%) and low phenotypic coefficient of variation of days to first flower (7.58%) and days to maturity (3.04%). In accordance to these results high genotypic coefficient of variation for seed yield plant<sup>-1</sup> (22.53) and number of siliqua plant<sup>-1</sup> (18.85) were also reported by Akbar *et al.* (2003).

The estimate of heritability and genetic advance estimated in material consisting 122 mutants along with four checks for seven characters are reported in table 3. Heritability per cent ranged from 74.23% (plant height) to 12.34% (seed yield plant<sup>-1</sup>). High heritability was exhibited by plant height (74.23%), moderate heritability was observed for days to first flower (39.11%) germination percentage (33.85%) and number of primary branches plant<sup>-1</sup> (32.85%) and low heritability was observed to be for number of siliqua plant<sup>-1</sup> (24.06%), days to maturity (16.17%) and seed yield plant<sup>-1</sup> (12.34%). The low estimate of heritability for above traits suggested the major role of environmental factor in the expression for these traits. In accordance to these result Ahmad *et al.* (2013) also reported major role of environmental factor in the expression of different traits in *Brassica* genotypes based on heritability.

Genetic advance as a percentage of mean were high for plant height (32.17%), number of primary branches plant<sup>-1</sup> (21.32%) and moderate for number of siliqua plant<sup>-1</sup> (18.59%), seed yield plant<sup>-1</sup> (15.25%) and germination percentage (10.01%) and low for days to first flower (5.19%) and days to maturity (0.85%). Similar to these results high genetic advance as a percentage of mean was also reported by Akbar *et al.* (2003). Heritability was observed to be maximum for number of siliqua plant<sup>-1</sup> and plant height (84%). Genetic advance as percent of mean was maximum for number of siliqua (35.66) followed by seed yield plant<sup>-1</sup> (33.53) and Ahmed *et al.* (2013) observed high 98.6% (heritability) and 42.54% (genetic advance) for seed yield in mustard.

**Table 1. Mutant selected in M<sub>2</sub> generation to raise M<sub>3</sub> generation**

<b>BIO 902</b>			
<b>Doses of mutagen</b>	<b>Sr. No.</b>	<b>Progeny Selected</b>	<b>Character of progeny</b>
900Gy	1.	M-1-1	Aphid Resistant and High yielding mutant.
	2.	M-1-2	High yielding mutant.
	3.	M-1-3	High yielding mutant.
	4.	M-1-101	Late mutant.
	5.	M-1-102	Tall mutant.
1000Gy	6.	M-2-4	Aphid Resistant mutant.
	7.	M-2-5	Aphid Resistant mutant.
	8.	M-2-6	Early mutant.
	9.	M-2-7	Dwarf and High yielding mutant.
	10.	M-2-8	Long and Bold siliqua mutant.
	11.	M-2-103	Orange color seed mutant
1100Gy	12.	M-3-9	Long siliqua and Aphid tolerance mutant
	13.	M-3-10	High yielding mutant
	14.	M-3-11	Powdery mildew resistant mutant
	15.	M-3-104	Aphid resistant mutant
	16.	M-3-105	Small seed mutant
1200Gy	17.	M-4-12	Early and Aphid resistant mutant
	18.	M-4-13	Early mutant
	19.	M-4-14	Early and appressed mutant
	20.	M-4-106	Tall mutant
	21.	M-5-15	Powdery mildew resistant mutant
1300Gy	22.	M-5-16	Aphid resistant mutant
	23.	M-5-17	Powdery mildew tolerant mutant
	24.	M-5-18	Aphid tolerant mutant
	25.	M-5-19	Aphid tolerant mutant
	26.	M-5-20	High yielding mutant
	27.	M-5-21	High yielding mutant
	28.	M-5-107	Extra late mutant
	29.	M-5-108	High yielding mutant
	30.	M-6-22	Aphid resistant mutant
	31.	M-6-23	High yielding and Aphid Resistant mutant
900Gy+EMS(0.5)	32.	M-6-24	High yielding mutant
	33.	M-6-25	High yielding mutant
	34.	M-6-26	High yielding mutant
	35.	M-6-109	Aphid resistant mutant
	36.	M-6-110	Powdery mildew tolerant mutant
	37.	M-7-27	High yielding mutant
1000Gy+EMS(0.5)	38.	M-7-28	Appressed mutant
	39.	M-7-29	Long siliqua mutant
	40.	M-7-30	Bold, late mutant
	41.	M-7-111	Small seed mutant
	42.	M-7-112	Powdery mildew tolerant mutant
1100Gy+EMS(0.5)	43.	M-8-31	Tall and bold mutant
	44.	M-8-32	Appressed mutant
	45.	M-8-33	Tall mutant
	46.	M-8-34	Appressed mutant
	47.	M-8-113	Late mutant
1200Gy+EMS(0.5)	48.	M-8-114	Aphid tolerant mutant
	49.	M-9-35	Bold, Aphid resistant mutant
	50.	M-9-36	High yielding mutant
	51.	M-9-37	Long siliqua mutant
	52.	M-9-38	Appressed mutant
	53.	M-9-39	Bold mutant
1300Gy+EMS(0.5)	54.	M-9-115	Appressed mutant
	55.	M-10-40	Dense siliqua mutant
	56.	M-10-41	Tall mutant
	57.	M-10-42	Appressed and long siliqua mutant
	58.	M-10-43	Tall mutant.
	59.	M-10-44	High yielding mutant
	60.	M-10-45	Appressed mutant
	61.	M-10-116	Dense siliqua mutant

**Pusa Bold**

<b>Doses of mutagen</b>	<b>Sr. No.</b>	<b>Progeny Selected</b>	<b>Character of progeny</b>
900Gy	1.	M-11-46	Bold and High yielding
	2.	M-11-47	Aphid resistant mutant
	3.	M-11-48	Early mutant
	4.	M-11-49	Early and more branched mutant
	5.	M-11-50	Early mutant
	6.	M-11-51	More branched mutant
	7.	M-11-117	Aphid tolerant mutant
1000Gy	8.	M-12-52	High yielding mutant
	9.	M-12-53	Early and more branches mutant
	10.	M-12-54	Aphid resistant mutant
	11.	M-12-55	Early mutant
	12.	M-12-56	High yielding mutant
	13.	M-13-57	Early and tall mutant
	14.	M-13-58	Short and High yielding mutant
1100Gy	15.	M-13-59	Bold seeded mutant
	16.	M-13-60	Long siliqua and more branches mutant
	17.	M-13-61	Aphid resistant and High yielding mutant
	18.	M-13-62	Dense siliqua mutant
	19.	M-13-118	Appressed mutant
1200Gy	20.	M-14-63	Powdery mildew tolerant mutant
	21.	M-14-64	High yielding mutant
	22.	M-14-65	Long siliqua mutant
	23.	M-14-119	Bold seeded mutant
	24.	M-15-66	Appressed mutant
1300Gy	25.	M-15-67	Appressed and early mutant
	26.	M-15-68	Early and High yielding mutant
	27.	M-15-69	Short siliqua mutant
900Gy+EMS(0.5)	28.	M-15-70	Appressed mutant
	29.	M-16-71	Appressed and High yielding mutant
	30.	M-16-72	Bold seed and dwarf mutant
	31.	M-16-73	Long siliqua mutant
	32.	M-16-74	Appressed and High yielding mutant
	33.	M-16-75	Appressed mutant
	34.	M-16-76	More branches mutant
	35.	M-16-77	Short siliqua mutant
	36.	M-16-120	Dense siliqua mutant
	37.	M-17-78	Bold mutant
1000Gy+EMS(0.5)	38.	M-17-79	High yielding mutant
	39.	M-17-80	High yielding mutant
	40.	M-17-81	More branched mutant
	41.	M-17-82	High yielding mutant
	42.	M-17-83	High yielding mutant
	43.	M-17-84	High yielding mutant
	44.	M-17-85	High yielding mutant
	45.	M-17-121	Dwarf mutant
1100Gy+EMS(0.5)	46.	M-18-86	Early and more branched mutant
	47.	M-18-87	Appressed and High yielding mutant
	48.	M-18-88	High yielding mutant
	49.	M-18-89	High yielding mutant
	50.	M-18-122	More branches and dwarf mutant
1200Gy+EMS(0.5)	51.	M-19-90	High yielding mutant
	52.	M-19-91	Small seed and late mutant
	53.	M-19-92	Yellow seeded mutant
	54.	M-19-93	More branches mutant
1300Gy+EMS(0.5)	55.	M-19-123	High yielding and small seeded mutant
	56.	M-19-124	Aphid resistant mutant
	57.	M-20-94	Late mutant
	58.	M-20-95	High yielding mutant
	59.	M-20-96	Long siliqua mutant
	60.	M-20-125	Yellow seeded and dwarf mutant
Control	61.	M-20-126	Bold seeded mutant
	62.	M-00-97	Shatabdi
	63.	M-00-98	Bio-902
	64.	M-00-99	Pusa Bold
	65.	M-00-100	Kranti

**Table 2. Analysis of variance for different character in M<sub>3</sub> generation**

Source of variation	df	Mean sum of square						
		Germination (%)	Days to first flower	Days to maturity	Plant height (cm)	Number of primary branches plant <sup>-1</sup>	Number of siliqua plant <sup>-1</sup>	Seed yield plant <sup>-1</sup> (g)
Between families	125	350.23*	20.49*	13.19*	55973.90*	30.46*	37244.95*	63.54*
Within families	6678	138.16	7.00	8.36	357.61	1.11	2056.22	7.39
Intra class correlation(t)		0.34	0.39	0.16	0.74	0.33	0.24	0.12

\*Significant at 5% level. \*\* Significant at 1% level

**Table 3. Genetic parameters estimates for different character in M<sub>3</sub> generation**

Parameters	Germination %	Days to first flower	Days to maturity	Plant height (cm)	Number of primary branches plant <sup>-1</sup>	Number of siliqua plant <sup>-1</sup>	Seed yield plant <sup>1</sup> (g)
CV (%)	9.75	4.74	1.22	21.29	21.26	21.58	25.42
S.E	4.85	1.22	0.73	18.53	0.43	14.73	0.59
C.D	13.45	3.39	2.03	51.35	1.18	40.84	1.63
Mean	86.25	44.71	103.83	150.75	3.46	118.26	4.01
Range	100-24 (76)	52-38.33 (13.66)	108.66-98.33 (10.33)	174.85-117 (57.85)	2.6-6 (3.4)	265.87-50.6 (215.27)	40.8-1.16 (39.64)
Genotypic variance	70.69	4.50	1.61	1029.9	0.54	651.64	1.04
Phenotypic variance	208.85	11.50	9.97	1387.5	1.65	2707.86	8.43
GCV (%)	9.74	4.74	1.22	21.28	21.26	21.58	25.41
PCV (%)	16.75	7.58	3.04	24.70	37.09	43.99	72.37
Heritability(%)	33.85	39.11	16.17	74.23	32.85	24.06	12.34
G.A	8.64	2.32	0.88	48.50	0.74	21.98	0.61
G.A(X of mean)	10.01	5.19	0.85	32.17	21.32	18.59	15.25

When all the genetic parameters for seven characters were considered, it was found that seed yield plant<sup>-1</sup>, exhibited high genotypic coefficient of variation, low heritability along with moderate genetic advance as a percentage of mean. Similarly, number of siliqua plant<sup>-1</sup> exhibited high genotypic coefficient of variation, low heritability with moderate genetic advance as a percentage of mean. Another character plant height also exhibited high heritability and high genetic advance as a percentage of mean, and moderate heritability were also observed for germination percentage, days to flower and number of primary branches plant<sup>-1</sup> and moderate genetic advance for germination percentage and low for other characters. This indicated that all these three characters i.e. seed yield plant<sup>-1</sup>, number of siliqua plant<sup>-1</sup> and plant height were influenced by additive gene action operating in the expression of these traits in M<sub>3</sub> generation and hence help as a criteria for making selection.

In M<sub>3</sub> generation 65 individual plants from 47 progeny were selected from 122 mutants of M<sub>2</sub> generation. Superior mutants from M<sub>3</sub> generation were selected on the basis of seed yield plant<sup>-1</sup>, number of siliqua plant<sup>-1</sup>, earliness, appressed and powdery mildew resistance. These mutants will be further evaluated in M<sub>4</sub> generation to test its homozygosity and if found stable can be evaluated in Preliminary yield trial.

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**Rec. on 28.05.2017 & Acc. on 09.06.2017**