

ASSESSMENT OF VARIABILITY IN M_3 GENERATION OF INDIAN MUSTARD (*Brassica juncea*) CZERN AND COSS

Anup Anasane¹, Beena Nair², A. P. Dhongade³ and D. Y. Upadhyay⁴

ABSTRACT

The present study was conducted with the objectives to estimate variances between family and within family, to estimate genetic parameters and to identify superior mutants for further utilization at experimental farm of Agricultural Botany Section, College of Agriculture Nagpur during *rabi* 2018 in M_3 generation. In *rabi* 2018, 90 mutants along with two checks (Bio 902 and Pusa bold) were evaluated in M_3 generation in two replications. Data were recorded on germination percentage, days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of siliqua plant⁻¹, seed yield plant⁻¹ and 1000 seed weight. The genetic parameter analysis revealed the importance of number of siliqua plant⁻¹ and seed yield plant⁻¹ for selection of better individual mutant from the progenies, based on genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance. Thus, 102 mutants were selected from Bio 902 variety treated with different doses of gamma rays and 38 mutants were selected from Pusa bold variety treated with different doses of gamma rays. All these mutants will be forwarded to M_4 generation in progeny rows for one or more generations so that homozygosity will be attained and the superior genotypes can be selected for forwarding to yield trials in further generation.

(Key words : *Brassica juncea*, mutation, genetic variability, gamma rays.)

INTRODUCTION

Availability of genetic variability is the prerequisite for any breeding programme. Besides conventional methods, induced mutation has been extensively used for developing new genetic variation in crop plants. Yield is one of the most important economic characters and is the product of multiplicative interaction of contributing characters. Hence, the important objective in mustard improvement is oriented to develop varieties which have high yielding potential. 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 a mutagenic agent, i.e. gamma rays.

MATERIALS AND METHODS

Dry healthy seeds of *Brassica juncea*, Pusa bold and Bio-902 treated with gamma rays of 900, 1000, 1100 Gy (Co^{60}) at BARC Trombay, Mumbai were used. The M_1 generation was raised during 2015-16 and individual plants in each treatment were harvested separately. The harvested seeds were used to raise M_2 generation. During *rabi* 2016-17 mutants were identified from Pusa bold and Bio-902 during

M_2 generation. In *rabi* 2017-18, on 12 Nov, all the harvested seeds from each (90) mutants of M_2 generation were sown to raise M_3 generation in replicated trial using Randomized Block Design. Data were recorded on germination percentage, days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of siliqua plant⁻¹, seed yield plant⁻¹ and 1000 seed weight. The data recorded during M_3 generation were subjected to the statistical analysis i.e. mean, range, genotypic variance, phenotypic variance, heritability (broad sense), genotypic coefficient of variation (%), phenotypic coefficient of variation (%), genetic advance (GA), standard error (SE) and co-efficient of variation (CV) (%).

RESULTS AND DISCUSSION

The observations were recorded on 90 mutants along with two checks for eight characters. 1000 seed weight were taken only for bold seeded mutants. Analysis of variance observed significance for between family and within family genetic variation. The results of this analysis were presented in table 1. The data on the analysis of variance resulted in highly significant mean square due to between family for all eight characters studied i.e. germination percentage, days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of siliqua plant⁻¹, seed yield plant⁻¹ and 1000 seed weight. This

1, 3 & 4. P.G. Students, Botany Section, College of Agriculture, Nagpur

2. Linseed Breeder, AICRP on Linseed, College of Agriculture, Nagpur

Table1. Analysis of variance for different characters in M₃ generation

Source of variation	df	Mean sum of square							
		Germination (%)	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches plant ⁻¹	Number of sliqua plant ⁻¹	Seed yield plant ⁻¹ (g)	1000 seed weight
Between families	92	192.67**	14.93**	71.31**	4294.40**	3.98**	18019.40**	86.36**	11.49**
Within families	2697	94.41	7.62	13.43	237.66	1.07	4860.74	22.52	2.99
Intra class correlation(t)		0.342	0.324	0.683	0.363	0.083	0.083	0.086	0.087

Table2. Genetic parameters estimates for different characters in M₃ generation

Parameters	Germination (%)	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches plant ⁻¹	Number of sliqua plant ⁻¹	Seed yield plant ⁻¹ (g)	1000 seed weight
CV (%)	7.85	3.81	5.38	7.30	8.22	15.79	20.4	10.56
SE	6.87	1.95	2.59	10.90	0.73	49.30	3.07	1.22
CD	19.29	5.48	7.28	30.22	2.03	136.69	8.50	3.39
Mean	89.34	50.13	100.02	159.39	3.78	132.63	7.06	5.04
Range	100 - 59.61	58.50-45.50	107 - 88	186.63-133.23	4.87 - 3.03	184.47 -88.90	12..19 -3.34	6.40-2.40
	(40.39)	(13)	(19)	(53.4)	(1.84)	(95.57)	(8.85)	(4)
Genotypic variance	49.13	3.66	28.94	135.22	0.10	438.62	2.00	0.28
Phenotypic variance	143.54	11.28	42.37	372.88	1.17	5299.37	20.81	3.27
GCV (%)	7.85	3.81	5.38	7.30	8.22	15.79	20.04	10.56
PCV (%)	13.41	6.70	6.51	12.12	28.59	54.89	64.62	35.89
Heritability(%)	34.23	32.41	68.30	36.26	8.26	8.28	9.62	8.66
G.A	7.22	1.92	7.83	12.33	0.16	10.61	0.77	0.28
G.A (as % of mean)	8.08	3.82	7.82	7.73	4.16	8	10.94	5.47

Table 3. Superior mutants selected for M₄ generation

Sr. No.	Doses of mutagen	Progeny selected	Character of progeny	Plant no. selected	Seed yield plant ¹ (g)	No. of siliqua plant ¹	No. of primary branches plant ¹	Plant weight (cm)	1000 seed weight (g)
1		M-1-14-2	More no. of siliqua	2	24.7	311	5	193	
2		M-1-11-16	High yield	16	55.2	560	6	172	
3		M-1-14-11	More no. of branches	11	26.9	423	10	192	
4		M-1-15-4	High yield	4	37.7	680	11	184	
5		M-1-4-13	High yield	13	25.2	315	5	184	
6		M-1-8-10	Bold and Tall	10	31.4	446	6	201	3.6
7		M-1-10-30	More no. of branches	30	29.9	222	9	195	
8		M-1-9-8	High yield	8	24.2	317	5	184	
9		M-1-13-24	More no. of siliqua	24	24.2	410	5	172	
10		M-1-9-11	More no. of siliqua	11	23.7	430	5	189	
11		M-1-2-16	Bold and More no. of siliqua	16	22.1	412	8	175	4.6
12		M-1-11-18	More no. of branches	18	21.4	221	9	210	
13	900 Gy	M-1-12-7	Bold	7	20.8	322	5	173	3.2
14		M-1-15-2	High yield	2	21.7	147	6	176	
15		M-1-15-27	High yield	27	20.7	210	6	162	
16		M-1-6-15	Tall	15	23	287	5	198	
17		M-1-1-3	Tall	3	22.5	273	5	198	
18		M-1-15-9	High yield	9	16.3	211	6	175	
19		M-1-11-29	High yield	29	16.4	245	4	179	
20		M-1-4-16	Bold	16	16.9	130	7	161	
21		M-1-2-28	More no. of branches	28	22.3	340	10	182	5.2
22		M-1-6-8	High yield	8	18.5	75	3	150	
23		M-1-15-19	Tall	19	18.4	263	4	210	
24		M-1-13-21	More no. of branches	21	18.3	270	10	189	
25		M-1-2-30	Bold	30	19.8	296	8	160	4.6
26		M-1-7-9	High yield	9	19.8	272	5	177	
27		M-1-15-15	Bold	15	19.6	213	4	191	5.2
28		M-1-4-11	High yield	11	16.8	157	5	179	
29		M-1-8-12	High yield	12	16.6	88	6	184	
30		M-1-13-13	High yield	13	16.5	122	5	130	
31		M-1-13-28	More no. of branches	28	16.2	366	8	187	
32		M-1-14-6	High yield	6	16.1	167	4	174	
33		M-1-8-11	Bold	11	15	168	7	168	3.6
34		M-1-15-3	Bold	3	15.3	296	5	171	5.2
35		M-1-9-10	High yield	10	16	245	6	174	
36		M-1-8-16	High yield	16	15.7	142	4	155	
37		M-1-10-15	Tall	15	15.7	172	5	188	
38		M-1-4-6	High yield	6	15.6	240	4	165	
39		M-1-9-2	High yield	2	15.2	270	5	167	
40		M-1-13-1	High yield	1	15.1	227	6	185	
41		M-2-20-14	High yield	14	23.7	277	4	167	
42		M-2-26-22	High yield	22	24.2	73	3	159	
43		M-2-19-13	High yield	13	23	185	6	152	
44		M-2-21-11	High yield	11	22.7	247	4	145	
45	1000 Gy	M-2-18-14	Tall	14	22.5	336	4	210	
46		M-2-16-3	High yield	3	21.5	330	4	181	
47		M-2-22-1	High yield	1	21.1	290	4	188	
48		M-2-17-11	Tall and More no. of siliqua	11	24.5	460	4	220	
49		M-2-22-3	High yield	3	43.2	825	6	166	
50		M-2-29-9	High yield	9	34	308	5	186	

51	M-2-19-7	More no. of branches	7	26.8	572	8	166	5.8
52	M-2-22-9	Bold and Tall	9	66.9	565	8	205	6.2
53	M-2-26-2	Bold	2	24.8	331	4	194	
54	M-2-24-3	Bold	3	27.2	413	5	172	
55	M-2-16-11	High yield	11	26.6	115	3	189	6
56	M-2-21-9	Bold	9	19.1	178	4	174	5.8
57	M-2-27-6	Bold and Tall	6	18.7	382	4	201	
58	M-2-21-5	Early	5	17.3	171	4	163	
59	M-2-20-13	More no. of siliqua	13	18.6	333	5	164	5.8
60	M-2-24-2	Bold	2	15.5	212	5	176	4.6
61	M-2-17-20	Bold	20	16	190	5	174	
62	M-2-28-15	More no. of siliqua	15	16	317	5	179	
63	M-2-29-6	Tall	6	16	247	5	192	
64	M-2-30-14	More no. of siliqua	14	15.8	313	4	162	
65	M-2-18-11	High yield	11	15.1	298	5	176	
66	M-2-23-17	High yield	17	15.1	121	6	162	
67	M-2-25-11	Bold	11	17.1	410	5	173	6.2
68	M-2-28-12	More no. of siliqua	12	16.8	347	5	189	
69	M-2-20-8	More no. of siliqua	8	16.5	545	4	169	
70	M-2-23-20	High yield	20	16.5	220	6	171	
71	M-2-23-3	Bold	3	16.4	292	5	167	5.2
72	M-2-28-5	High yield	5	16.4	302	4	173	
73	M-3-42-1	More no. of siliqua	1	23.8	489	5	185	4.4
74	M-3-42-13	Bold	13	21.7	436	7	166	
75	M-3-39-2	High yield	2	21	291	6	178	
76	M-3-31-2	More no. of branches	2	22.5	280	7	172	4.8
77	M-3-38-17	Bold	17	25.3	336	7	186	
78	M-3-39-5	High yield	5	24.4	334	5	177	6.4
79	M-3-34-2	Bold	2	17.3	148	3	193	
80	M-3-39-15	More no. of siliqua	15	17.6	389	5	168	5.2
81	M-3-36-21	Bold	21	22.8	412	4	186	5.8
82	M-3-38-3	Bold	3	27.4	352	5	189	
83	M-3-39-11	High yield	11	25.4	317	6	168	6.4
84	M-3-34-11	Bold	11	15.5	102	3	178	5
85	M-3-35-17	Bold	17	15.4	308	5	188	6.4
86	M-3-34-15	Bold	15	15.1	193	5	186	
87	M-3-36-7	High yield	7	15.1	63	2	155	
88	M-3-37-2	High yield	2	15.1	117	5	168	
89	M-3-37-27	High yield	27	15.1	278	5	140	4.8
90	M-3-45-28	More no. of branches	28	15.1	374	7	191	
91	M-3-31-15	More no. of branches	15	15	460	7	195	
92	M-3-41-13	Tall	13	16.7	97	5	183	
93	M-3-38-7	Bold & Appressed	7	16.8	161	4	180	
94	M-3-39-30	High yield	30	16.2	215	4	159	
95	M-3-44-6	Appressed	6	16.2	244	4	186	
96	M-3-37-8	High yield	8	16.1	212	4	180	
97	M-3-42-24	More no. of branches	24	16.1	257	7	166	
98	M-3-33-16	Appressed	16	18.2	150	5	171	
99	M-3-39-13	High yield	13	18.7	229	6	171	
100	M-3-36-25	High yield	25	19.1	268	6	175	
101	M-3-33-18	More no. of branches	18	19	385	7	178	
102	M-3-40-2	Bold	2	19.6	281	4	181	4.4

1100 Gy

Superior mutants selected from Pusa bold in M₃ generation

	Doses of mutagen	Progeny selected	Character of progeny	Plant no selected	Seed yield plant ⁻¹ (g)	No. of siliqua plant ⁻¹	No. of primary branches plant ⁻¹	Plant weight (cm)	1000 seed weight (g)
1	900Gy	M-1-51-10	Tall	10	16	146	5	187	
2		M-1-59-10	High yield	10	15.4	235	5	162	
3		M-1-57-8	Early	8	15.2	87	3	159	
4		M-1-55-15	Tall	15	15.3	195	5	191	
5		M-1-49-11	High yield	11	15.6	211	6	170	
6		M-1-57-4	More no. of siliqua	4	17.2	482	4	191	
7		M-1-54-15	High yield	15	16.3	144	5	159	
8		M-1-59-3	More no. of siliqua	3	20.8	544	4	167	
9		M-1-58-29	High yield	29	16.1	183	4	170	
10		M-1-59-4	Appressed	4	16.6	347	4	154	
11		M-1-59-15	High yield	15	16.6	210	4	184	
12		M-1-58-29	High yield	29	16.1	183	4	170	
13		M-1-48-15	High yield	15	18.8	245	4	172	
14	M-1-51-15	More no. of siliqua	15	22.1	401	6	172		
15	M-2-62-27	Bold	27	15.6	244	4	182	3	
16	M-2-75-29	More no. of siliqua	29	17.2	412	8	168		
17	M-2-61-24	High yield	24	15	217	2	172		
18	M-2-63-6	High yield	6	26.5	95	4	145		
19	M-2-71-22	More no. of branches	22	20.2	292	7	178		
20	M-2-71-2	Tall	2	18.8	302	5	190		
21	M-3-79-16	More no. of siliqua	16	21.5	512	8	140		
22	M-3-78-28	High yield	28	18	148	4	146		
23	M-3-76-26	Appressed	26	17.9	292	8	178		
24	M-3-78-7	Bold	7	17.9	238	6	198	5.4	
25	M-3-88-30	More no. of siliqua	30	17.7	310	5	171		
26	M-3-82-15	High yield	15	16.7	131	5	167		
27	M-3-77-5	High yield	5	15.8	203	6	155		
28	M-3-88-24	More no. of siliqua	24	15.8	310	6	185		
29	M-3-78-25	High yield	25	15.3	78	5	145		
30	M-3-45-28	More no. of branches	28	15.1	374	7	191		
31	M-3-87-4	High yield	4	16.1	210	4	172		
32	M-3-88-12	More no. of branches	12	24.7	273	6	184		
33	M-3-89-4	More no. of branches	4	23.3	390	7	167		
34	M-3-80-3	High yield	3	22	43	3	147		
35	M-3-76-20	More no. of branches	20	20.7	263	8	162	4.6	
36	M-3-81-10	Bold	10	16.6	245	7	157		
37	M-3-86-15	High yield	15	17.3	252	6	168		
38	M-3-77-2	High yield	2	19.9	55	4	170		
39	Bio 902	Checks	7.60	139.63	3.47	162			
40	Pusa bold		10.55	178	3.87	149.23			

indicated the presence of significant genetic variability between the families for all eight characters which allowed the estimation of genetic parameters. In accordance to this results significant variability between the families were also reported by Javed *et al.* (2000) in mustard.

Mean, range, genotypic variance, phenotypic variance, heritability (broad sense), genotypic coefficient of variation (%), phenotypic coefficient of variation (%), genetic advance (GA), standard error (SE) and co-efficient of variation (CV) (%) were calculated for eight characters in M_3 generation and are presented in table 2. Significant differences were observed between the progenies for all the eight characters studied. These results were line with that of Siddiqui *et al.* (2009) in rapeseed (*Brassica napus*), who also observed significant variation for all the characters studied. The phenotypic variance and phenotypic coefficient of variation was observed to be far higher than genotypic variance and genotypic coefficient of variation for all eight characters studied (Table 2). This indicated the higher influence of environment in the phenotypic expression of these characters. Similar results i.e. higher influence of environment were also reported by Bind *et al.* (2014) in mustard (*Brassica juncea*). Genotypic coefficient of variation exhibited in values from low to high category. Similarly phenotypic coefficient of variation was also observed to be low to high for different characters. In accordance to these results high genotypic coefficient of variation and phenotypic coefficient of variation for seed yield plant⁻¹ and number of siliqua were also reported by Akbar *et al.* (2003) in mustard (*Brassica juncea*). The heritability estimates provide in formation on transmission of traits from parents to offspring. Such estimate facilitates the evaluation of genetic and environmental effect aiding in selection. Estimation of heritability is often used to predict genetic advance under selection so that the plant breeder can anticipate improvement of different type and intensity of selection. The heritability and genetic advance estimated in material consisting 90 mutants along with two checks for eight characters are reported in table 2.

Genetic advance as a percentage of mean were moderate to low for all the characters under the present study. Similar to these results, moderate to low genetic advance as a percentage of mean was also reported by Kumar *et al.* (2012) in rapeseed (*Brassica napus*). When all the genetic parameters for eight characters were considered, it was found that seed yield plant⁻¹ exhibited high genotypic coefficient of variation, low heritability along with moderate genetic advance as a percentage of mean. Number of siliqua plant⁻¹ exhibited moderate genotypic coefficient of variation, low heritability with low genetic advance as a percentage of mean. Moderate heritability with low genetic advance was observed for plant height at maturity, germination % and days to 50% flowering. Number of primary branches plant⁻¹ and 1000 seed weight exhibited low heritability with low genetic advance whereas days to maturity exhibited

high heritability with low genetic advance. This indicated that seed yield plant⁻¹ exhibited low heritability with moderate genetic advance and were influenced by additive gene action in these traits in M_3 generation and helps as a criteria for selection.

One of the main objectives of this experiment was to identify superior mutants for forwarding to yield trial. Individual mutants were selected from M_2 generation on the basis of high seed yield plant⁻¹, number of siliqua plant⁻¹, earliness and boldness. The selected mutants from M_2 generation were raised in M_3 generation to test the performance and homozygosity. Selection of superior progenies on the basis of seed yield plant⁻¹ may not be effective and hence, plant breeder has to involve large number of component characters simultaneously in the selection programme. But handling of large number of component characters simultaneously becomes cumbersome and hence, selections of plants on the basis of seed yield plant⁻¹ and number of siliqua plant⁻¹ was considered. Superior plants from M_3 generation which were selected from different treatments on the basis of seed yield plant⁻¹, number of siliqua plant⁻¹, earliness, and bold seeded were presented in table 3. Thus, 102 mutants were selected from Bio 902 variety treated with different doses of gamma rays and 38 mutants were selected from Pusa bold variety treated with different doses of gamma rays.

All these 140 mutants which were selected from both Pusa bold and Bio 902 varieties were mainly on the basis of higher seed yield. A few of the mutants selected were also bold seeded. All these mutants will be forwarded to M_4 generation in progeny rows for one or more generations so that homozygosity will be attained and the superior genotypes can be selected for forwarding to yield trials in further generation.

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