

STUDIES ON GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND TRAIT ASSOCIATION IN INDIAN MUSTARD (*Brassica juncea*) CZERN AND COSS

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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 AICRP, College of Agriculture Nagpur during *rabi* 2018 in M_4 generation. In *rabi* 2017, 161 mutants were identified along with three checks in *rabi* 2018, these 161 mutants along with three checks (PM-21, Kranti and Shatabdi) were evaluated in M_4 generation in Randomized Block Design with two replications. Data were recorded on days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant⁻¹, number of siliqua plant⁻¹, length of siliqua (cm), number of seeds siliqua⁻¹, seed yield plant⁻¹(g) and 1000 seed weight (g). The genetic parameter analysis revealed the importance of number of siliqua plant⁻¹, 1000 seed weight 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, 93 mutants were selected from PM-21, variety treated with different doses of sodium azide ($T_1=0.03\%$ SA, $T_2=0.06\%$ SA and $T_3=0.09\%$ SA). All these mutants will be forwarded to M_5 generation in progeny rows for one or more generation 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, heritability, genetic variability, sodium azide)

INTRODUCTION

Agriculture sector plays a significant role in India's social security and overall economic welfare. Oilseed crops are the second most important determinant of agricultural economy, after cereals. Mustard is the second most important oilseed crop in India after groundnut. It accounts for nearly 20-22% of the total oilseeds produced in the country.

Indian mustard [*Brassica juncea* (L.) Czern & Coss] is an important oilseed crop, accounting more than 70% of the total area under rapeseed and mustard. 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. The breeding strategy to derive high yielding cultivar depends upon the nature and magnitude of variation for different yield components, the assessment of genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h_2) and genetic advance (GA%) is a pre-requisite for making effective selection. Hence, the important

objective in mustard improvement is oriented to develop varieties which have high yielding potential.

MATERIALS AND METHODS

PM 21 is a variety, which is low in erucic acid content and well adapted to Vidarbha region of Maharashtra. Dry, healthy and genetically pure seeds of *Brassica juncea* cv. Pusa mustard 21 were divided into 4 lots of 300 seeds each for giving the different doses sodium azide treatment, and one lot of 300 seeds among them was control. The three seed lots were treated with different doses of aqueous solution of sodium azide ($T_1=0.03\%$, $T_2=0.06\%$, $T_3=0.09\%$) for 18 hrs. After that, the seeds were washed with sterilized water and the treated seeds were sown after one hour along with control. 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, 71 mutants were identified from Pusa mustard 21 during M_2 generation. In *rabi* 2017-18, all the harvested seeds from individual (71) mutants of M_3 generation were sown to raise M_4 generation in

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Randomized Block Design with two replications. Data were recorded on days to 50% flowering, plant height, number of primary branches plant⁻¹, number of seeds siliqua⁻¹, number of siliqua plant⁻¹, seed yield plant⁻¹ and 1000 seed weight. The data recorded during M₄ generation were subjected to the statistical analysis i.e., mean, range, genotypic variance, phenotypic variance, heritability (broad sense) by Hanson *et al.* (1956), genotypic coefficient of variation (%) and phenotypic coefficient of variation (%) by Burton (1953), genetic advance (GA) by Robinson *et al.* (1949), standard error (SE) and co-efficient of variation (CV) (%).

RESULTS AND DISCUSSION

The observations were recorded on 161 mutants along with three checks for all characters. 1000 seed weight were taken only for bold seeded mutants. Analysis of variance observed significance for both, between family and within family genetic variation.

The results of this analysis are presented in table 1. The data on the analysis of variance resulted in highly significant mean squares due to between family for all nine characters studied i.e. days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of siliqua plant⁻¹, length of siliqua, number of seeds siliqua⁻¹, seed yield plant⁻¹ (g) and 1000 seed weight (g). This indicated the presence of significant genetic variability between the families for all nine characters which allowed the estimation of genetic parameters. In accordance to this results significant variability between the families were also reported by Pawar *et al.* (2018) in Indian mustard. They concluded that the analysis of variance recorded significant differences for all the characters under evaluation. Significant differences were observed between the progenies for all seven traits studied.

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 all characters in M₄ generation and are presented in table 2. Significant differences were observed between the progenies for all the traits studied. Significant differences were observed between the progenies for all the nine characters studied. The coefficient of variation (CV) ranged from 3.40% to 53.18% for various characters (Table 3). The low coefficient of variation (d" 20%) was observed for the characters days to maturity (3.40%), days to 50% flowering (5.51%), plant height (9.57%), no. of seed siliqua⁻¹ (11.57%), length of siliqua (12.70%) which showed the best genetic potential and its genetic influence. High coefficient of variation (> 20%) was observed for number of primary branches plant⁻¹ (27.46%), 1000 seed weight (34.65%), number of siliqua plant⁻¹ (39.17%) and seed yield⁻¹ (53.18%) which indicated more influence of environmental fluctuation. In accordance to these results there was a considerable increase in variance

for all the traits under study by Siddiqui *et al.* (2009) in rapeseed (*Brassica napus*). They concluded that the induced variation can be exploited in the evolution of new varieties of rapeseed with improved agronomic traits.

The phenotypic variance and phenotypic coefficient of variation was observed to be far higher than genotypic variance and genotypic coefficient of variation for all nine characters studied (Table 2). This indicated the higher influence of environment in the phenotypic expression of these characters. Similar results of higher influence of environment on days to flowering, days to maturity, plant height, number of primary branches plant⁻¹, number of siliqua plant⁻¹, seed yield plant⁻¹ were also reported by Bind *et al.* (2014) in Indian mustard.

Genotypic coefficient of variation exhibited in values from low, moderate and high. High genotypic coefficient of variation was observed for number of siliqua plant⁻¹ (32.79%) and seed yield plant⁻¹ (28.15%) and no one characters possessed moderate genotypic coefficient of variation and while length of siliqua (3.51), days to 50% flowering (4.05), days to maturity (5.38), number of primary branches plant⁻¹ (8.50%), seeds siliqua⁻¹ (8.99%), 1000 seed weight for bold seed (9.20), plant height (9.50%) exhibited low genotypic coefficient of variation.

Similarly phenotypic coefficient of variation was also observed to be low, moderate and high for different characters. High phenotypic coefficient of variation was observed for seed yield plant⁻¹ (60.14%), number of siliqua plant⁻¹ (51.08%), 1000 seed weight (35.85%), and number of primary branches plant⁻¹ (28.74%). Moderate phenotypic coefficient of variation for seeds siliqua⁻¹ (14.65%), plant height (13.49) and length of siliqua (13.18) and low phenotypic coefficient of variation for days to 50% flowering (7.63%) and days to maturity (6.37%). 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 summer mustard (*Brassica juncea* L.).

The heritability estimates provide information 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 161 mutants along with two checks for nine characters are reported in (table 3). Heritability per cent exhibited in values from low (0-30%), moderate (31-60%) and high (more than 61%) were categorized by Johnson *et al.* (1955). Heritability per cent ranged from 71.51% (days to maturity) to 6.59% (1000 seed weight for bold seeded mutant). High heritability was observed for days to maturity (71.51%), moderate heritability was observed for plant height (49.64%), number of siliqua plant⁻¹ (41.20 %), and seeds siliqua⁻¹ (37.64%) and low heritability was observed for days

Table 1. Analysis of variance for different characters in M₄ generation

Source	df	Mean sum of square									
		Days to 50% flowering	Days to maturity	Seeds siliqua ⁻¹	Plant height (cm)	Number of primary branches plant ⁻¹	Number of siliqua plant ⁻¹	Length of siliqua (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	
Between families	163	18.82**	70.03**	48.10**	8328.15**	9.25**	167354.98**	2.15**	203.32**	10.24**	
Within families	4756	10.55	11.63	2.52	272.40	0.96	5281.76	0.65	23.15	0.58	
Intra class correlation(t)		0.281	0.715	0.376	0.496	0.994	0.505	0.071	0.21	0.35	

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

Table 2. Genetic parameters estimates for different character in M₄ generation

Parameters	Days to 50% Flowering	Days to maturity	Days to maturity	Seeds siliqua ⁻¹	Plant height (cm)	Number of primary branches plant ⁻¹	Number of siliqua plant ⁻¹	Length of siliqua plant ⁻¹	Seed yield plant ⁻¹ (g)	1000 seed weight (g)
CV (%)	6.47	3.40	9.57	11.57	27.46	39.17	12.70	53.18	34.65	
SE(m) ±	2.30	2.41	11.67	1.12	0.73	54.11	0.57	3.48	1.23	
CD (5%)	6.41	6.73	32.35	3.11	2.03	150.00	1.58	9.64	3.40	
Mean	50.22	100.37	172.44	13.72	3.77	195.36	6.36	9.25	4.99	
Range	58.4-44 (14.5)	107-88 (19)	223.77-124.9 (98.87)	17.33-10.83 (6.5)	4.7-3.03 (1.67)	381.5-74.27 (307.23)	6.74-5.84 (0.9)	16.64-3.96 (12.68)	6.36- 3.24 (3.12)	
Genotypic variance	4.13	29.20	268.52	1.52	0.10	4102.32	0.05	6.78	0.21	
Phenotypic variance	14.68	40.83	540.93	4.04	1.18	9957.89	0.70	30.96	3.21	
GCV (%)	4.05	5.38	9.50	8.99	8.50	32.79	3.51	28.15	9.20	
PCV (%)	7.63	6.37	13.49	14.65	28.74	51.08	13.18	60.14	35.85	
Heritability (%)	28.14	71.51	49.64	37.64	8.75	41.20	7.10	21.92	6.59	
GA	1.90	8.04	20.32	1.33	0.17	72.35	0.10	2.15	0.21	
GA (as % of mean)	3.78	8.01	11.78	9.70	4.43	37.04	1.65	23.20	4.16	

Table 3. Superior mutants selected for M₅ generation

Sr. no.	Doses of Mutagen	Superior mutants selected in M ₂ generation									
		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 height (cm)	1000 seed weight (g)		
1	T ₂ =0.03% SA	NMM ₂ -1-1-2-9	Appressed Siliqua	9	18.9	211	5	193			
2		NMM ₂ -1-1-2-13	Appressed Siliqua	13	22.7	360	6	172			
3		NMM ₂ -1-1-2-15	Appressed Siliqua	15	26.7	423	5	192			
4		NMM ₂ -1-34-15-8	High Yield & Bold Seed	8	26.3	380	6	184	5.1		
5		NMM ₂ -2-4-1-12	High Yield & long siliqua	12	20.5	315	4	184			
6		NMM ₂ -2-4-4-2	High Yield & long siliqua	2	20.8	446	6	201			
7		NMM ₂ -2-4-9-1	High Yield & long siliqua	1	24.6	222	6	195			
8		NMM ₂ -2-4-9-2	High Yield & long siliqua	2	19.1	317	5	184			
9		NMM ₂ -2-4-14-9	High Yield & long siliqua	9	19.6	210	5	172			
10	T ₂ =0.06% SA	NMM ₂ -2-5-5-6	High Yield	6	39.3	430	5	189			
11		NMM ₂ -2-33-14-4	Early maturity & long siliqua	4	21.3	412	8	175			
12		NMM ₂ -2-33-14-12	Early maturity & long siliqua	12	33.7	221	9	210			
13		NMM ₂ -2-35-13-3	Appressed Siliqua	3	31.3	322	5	173			
14		NMM ₂ -2-37-12-1	Yellow seed & long siliqua	1	25.2	347	6	176			
15		NMM ₂ -2-37-12-2	Yellow seed & long siliqua	2	32.1	410	6	162			
16		NMM ₂ -2-37-12-3	Yellow seed & long siliqua	3	24.7	287	5	198			
17		NMM ₂ -2-37-12-10	Yellow seed & long siliqua	10	43.6	573	6	198			
18		NMM ₂ -2-35-4-10	Early maturity	10	36.8	211	6	175			
19		NMM ₂ -2-35-5-3	Early maturity	3	20.1	245	4	179			
20	T ₃ =0.09% SA	NMM ₂ -2-35-5-11	Early maturity	11	25.7	130	7	161			
21		NMM ₂ -2-39-12-13	Constructed	13	20.1	340	5	182			
22		NMM ₃ -3-5-8-3	Early maturity	3	26.3	375	4	150			
23		NMM ₃ -3-7-9-8	Early maturity	8	20.3	263	4	210			
24		NMM ₃ -3-7-8-13	Early maturity	13	21.6	270	4	189			
25		NMM ₃ -3-7-14-4	Early maturity	4	19.8	296	8	160			
26		NMM ₃ -3-9-3-3	Tall plant	3	19.8	272	5	177			
27		NMM ₃ -3-10-7-13	Bold seed	13	21.6	213	4	191	4.8		
28		NMM ₃ -3-11-3-3	Long siliqua	3	21.8	157	5	179			
29		NMM ₃ -3-11-3-5	Long siliqua	5	21.3	288	6	184			
30	T ₃ =0.09% SA	NMM ₃ -3-11-3-8	Long siliqua	8	24.7	322	5	130			
31		NMM ₃ -3-11-3-10	Long siliqua	10	24.1	366	8	187			
32		NMM ₃ -3-11-3-11	Long siliqua	11	20.3	267	4	174			
33		NMM ₃ -3-11-3-13	Long siliqua	13	19.6	168	7	168			
34		NMM ₃ -3-11-3-15	Long siliqua	15	20.4	296	5	171			
35		NMM ₃ -3-11-15-3	Long siliqua	3	23.7	245	6	174			
36		NMM ₃ -3-11-15-12	Long siliqua	12	20.9	242	4	155			
37		NMM ₃ -3-20-2-12	High yield	12	58.1	572	7	188			
38		NMM ₃ -3-20-2-14	High yield	14	24.3	240	4	165			
39		NMM ₃ -3-20-3-5	High yield	5	25.3	270	5	167			
40	NMM ₃ -3-20-4-2	High yield	2	32.7	227	6	185				

41	NMM ₃ -3-20-4-3	High yield	3	28.9	277	4	167	
42	NMM ₃ -3-20-5-3	High yield	3	20.8	273	3	159	
43	NMM ₃ -3-20-7-3	High yield	3	32.4	285	6	152	
44	NMM ₃ -3-20-15-2	High yield	2	19.3	247	4	145	
45	NMM ₃ -3-20-15-9	High yield	9	19.7	336	4	210	
46	NMM ₃ -3-21-1-7	High yield & Bold seed	7	21.4	330	4	181	4.8
47	NMM ₃ -3-21-10-7	High yield & Bold seed	7	18.8	290	4	188	4.1
48	NMM ₃ -3-21-10-14	High yield & Bold seed	14	20.4	460	4	220	4.4
49	NMM ₃ -3-21-11-14	High yield & Bold seed	14	21.3	325	6	166	4.3
50	NMM ₃ -3-22-4-1	Appressed siliqua	1	40.3	508	7	186	
51	NMM ₃ -3-22-4-3	Appressed siliqua	3	18.9	172	8	166	
52	NMM ₃ -3-22-4-10	Appressed siliqua	10	24.3	265	8	205	
53	NMM ₃ -3-22-4-15	Appressed siliqua	15	27.9	331	4	194	
54	NMM ₃ -3-23-2-5	Appressed & long siliqua	5	20.6	413	5	172	
55	NMM ₃ -3-23-2-11	Appressed & long siliqua	11	24.3	115	3	189	
56	NMM ₃ -3-23-4-5	Appressed & long siliqua	5	21.5	278	4	174	
57	NMM ₃ -3-25-3-1	Appressed & Bold seed	1	29.3	382	4	201	4.9
58	NMM ₃ -3-25-5-10	Appressed & Bold seed	10	21.3	171	4	163	4.6
59	NMM ₃ -3-25-6-11	Appressed & Bold seed	11	24.5	333	5	164	5.1
60	NMM ₃ -3-26-5-1	High yield	1	19.4	212	5	176	
61	NMM ₃ -3-26-7-3	High yield	3	31.3	290	5	174	
62	NMM ₃ -3-26-7-8	High yield	8	24.3	317	5	179	
63	NMM ₃ -3-26-7-10	High yield	10	21.9	247	5	192	
64	NMM ₃ -3-26-7-14	High yield	14	21.7	313	4	162	
65	NMM ₃ -3-26-7-15	High yield	15	21.2	298	5	176	
66	NMM ₃ -3-26-9-6	High yield	6	25.2	227	6	162	
67	NMM ₃ -3-26-9-9	High yield	9	24.1	310	5	173	
68	NMM ₃ -3-26-10-10	High yield	10	23.9	347	5	189	
69	NMM ₃ -3-26-10-14	High yield	14	19.7	245	4	169	
70	NMM ₃ -3-26-10-15	High yield	15	22.6	220	6	171	
71	NMM ₃ -3-34-14-6	Extra early maturity	6	19.1	292	5	167	
72	NMM ₃ -3-35-3-11	Dwarf plant & late maturity	11	26.1	302	4	173	
73	NMM ₃ -3-35-3-12	Dwarf plant & late maturity	12	19.8	389	5	185	
74	NMM ₃ -3-35-3-13	Dwarf plant & late maturity	13	23.9	336	7	166	
75	NMM ₃ -3-35-8-3	Dwarf plant & late maturity	3	19.8	291	6	178	
76	NMM ₃ -3-35-14-4	Dwarf plant & late maturity	4	19.2	280	7	172	
77	NMM ₃ -3-35-15-6	Dwarf plant & late maturity	6	28.1	336	7	186	
78	NMM ₃ -3-35-15-10	Dwarf plant & late maturity	10	24.6	334	5	177	

79	NMM ₃ -3-35-15-12	Dwarf plant & late maturity	12	23.4	248	3	193
80	NMM ₃ -3-37-14-4	Dwarf plant	4	26.6	389	5	168
81	NMM ₃ -3-37-14-5	Dwarf plant	5	27.4	412	4	186
82	NMM ₃ -3-37-14-12	Dwarf plant	12	20.1	352	5	189
83	NMM ₃ -3-37-14-15	Dwarf plant	15	22.3	317	6	168
84	NMM ₃ -3-38-15-4	Bold seed	4	21.9	288	3	178
85	NMM ₃ -3-38-15-12	Bold seed	12	34.3	308	5	188
86	NMM ₃ -3-39-13-9	High yield	9	21.4	193	5	186
87	NMM ₃ -3-40-8-3	Bold seed	3	24.4	263	2	155
88	NMM ₃ -3-41-4-8	Long siliqua & Bold seed	8	19.8	217	5	168
89	NMM ₃ -3-41-5-3	Long siliqua & Bold seed	3	20.6	278	5	140
90	NMM ₃ -3-41-5-5	Long siliqua & Bold seed	5	22.1	374	7	191
91	NMM ₃ -3-41-5-10	Long siliqua & Bold seed	10	20.3	460	7	195
92	NMM ₃ -3-42-4-5	Appressed & long siliqua	5	22.9	297	5	183
93	NMM ₃ -3-42-9-10	Appressed & long siliqua	10	33.6	461	6	180

to 50% flowering (28.14%), seed yield plant⁻¹ (21.92%), number of primary branches plant⁻¹ (8.75%), length of siliqua (7.10%) and 1000 seed weight (6.59%).

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 expressed as per cent exhibited in values from low (less than 10%), moderate (10-20%) and high (more than 20%) (Johnson *et al.*, 1955). Genetic advance as a percentage of mean were low, moderate and high for all the characters under the present study. High genetic advance as a percentage of mean was observed for number of siliqua plant⁻¹ (37.35%), seed yield plant⁻¹ (23.20%). Moderate genetic advance was observed for plant height (11.78%), and low genetic advance was seeds siliqua⁻¹ (9.70%), days to maturity (8.01%), number of primary branches plant⁻¹ (4.43%), 1000 seed weight (4.16%), days to 50% flowering (3.78%) and length of siliqua (1.65%). Similar to these results, high to low genetic advance as a percentage of mean was also reported by Kumar *et al.* (2012) in Indian mustard.

When all the genetic parameters for nine characters were considered, it was found that seed yield plant⁻¹ exhibited high genotypic coefficient of variation and phenotypic coefficient of variation, low heritability along with high genetic advance as percentage of mean. Number of siliqua plant⁻¹ exhibited high genotypic coefficient of variation and phenotypic coefficient of variation, moderate heritability with high genetic advance as a percentage of mean. High heritability and low genetic advance was observed for days to maturity. Moderate heritability and low genetic advance was observed for seeds siliqua⁻¹. Moderate heritability as well moderate genetic advance was observed for plant height at maturity. Number of primary branches plant⁻¹, days to 50% flowering, length of siliqua 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 there traits in M₄ generation and helps as a criteria for selection.

In M₅ generation 93 individual plants from progeny will be selected from 161 mutants of M₄ generation. These mutants will be further evaluated in M₅ generation and those found superior will be forwarded to yield trials.

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