



## Genetic Variability Analysis of M<sub>4</sub>-M<sub>5</sub> Mutants of Indian Mustard (*Brassica juncea* L.)

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### Abstract

Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is an important oilseed crop grown in India under diverse agro-ecological conditions in the temperate and subtropical regions during *Rabi* season. It fits well in the rainfed cropping system with low production cost and high potential to increase edible oil. Farmers in Assam grow rapeseed toria (*Brassica rapa*) due to its short duration but end up with low yield. Development of short-duration superior Indian mustard varieties is required to increase the average yield of rapeseed-mustard in Assam. Some Indian mustard genotypes were developed by induction of mutations at Assam Agricultural University, Jorhat. In the present study, 143 M<sub>4</sub> lines from the parent variety NRCHB-101 of Indian mustard developed through mutation breeding using gamma rays, were evaluated during *Rabi* 2020-21 followed by 116 M<sub>5</sub> selected lines during the *Rabi* 2021-22 to assess to genetic variability and interrelationships between yield component traits. Significant variation due to genotypes for the characters observed. Moderate genetic variation was observed for seed yield plant<sup>-1</sup>, number of primary and secondary branches plant<sup>-1</sup>. Moderate heritability coupled with high genetic advance was observed for number of siliquae in main shoot, number of primary branches, and number of secondary branches. The mutant lines JMM-NRCHB101-37, JMM-NRCHB101-57, JMM-NRCHB101-107 were found to be promising exhibiting superior performance for most of the yield attributing characters. The mutant line JMM-NRCHB101-86 and JMM-NRCHB101-95 also showed potentiality for early maturity with a high yield which could be exploited for the development of early maturing mustard varieties.

**Keywords:** *Brassica juncea*, Genetic advance, Genetic variability, Heritability, Mustard, Short duration

### Introduction

The oilseed brassica crops are commonly referred as rapeseed and mustard. After soya and palm oil, these crops are the third most important source of edible oil in the world. The word 'Rape' is derived from a Latin word meaning turnip and the word 'Mustard' from a Latin term *must/mustum* which means expressed juice of grapes and 'ardens' means hot and burning. Crop Brassicas are a group of six cultivated species, three diploids and three tetraploids,

five are rapeseed and mustard, and one is vegetable species. Among them, *Brassica rapa* L. (2n=20, AA) and *Brassica napus* L. (2n=38, AACC) are the rapeseed species; *Brassica nigra* Koch (2n=16, BB), *Brassica juncea* Czern & Coss. (2n=36, AABB) and *Brassica carinata* Braun (2n=34, BBCC) are the mustard species; and *Brassica oleracea* (2n=18, CC) is the vegetable species. *Brassica juncea*, *Brassica napus* and *Brassica rapa* are the major oilseed brassicas and each of them is polymorphic having oilseed, vegetable and fodder types. According to the Directorate of Rapeseed-Mustard

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Research (DRMR, 2020), rapeseed-mustard crops are grown over 6.23 million ha, producing 9.41 million tons in the country. In India, rapeseed-mustard yields about 1,511 kg ha<sup>-1</sup> against the world average yield of 1,980 kg ha<sup>-1</sup>. In Assam, these crops are cultivated over 2.80 lakh hectares yielding 1.67 lakh tonnes with average yield of 596 kg ha<sup>-1</sup>. Toria is the predominant brassica crop in Assam. Assam contributes 4.82% to the total acreage and 4.26% to the production of India (DRMR, 2020).

Indian mustard is the predominant brassica crop accounting for 75-80% of the acreage under oleiferous brassica as in 2018-19. In the important rapeseed-mustard growing states, Indian mustard is mainly cultivated. Yield potential of mustard is much higher than rapeseed (toria/ brown sarson/ yellow sarson) and it is one of the major reasons for high national average yield (1,511 kg ha<sup>-1</sup>) compared to low yield in Assam (596 kg ha<sup>-1</sup>). In Assam toria is mainly cultivated because of its adaptation to short crop duration (90 days) though there is yield penalty.

Rapeseed and mustard is a major crop in our country. Being a *Rabi* crop, it fits well in the rainfed cropping system. There is a high potential to increase the oil yield for the benefit of farmers. The production cost of rapeseed and mustard is also low. This crop is cultivated by both small and marginal farmers, and the cultivation also lies in the low resource and rainfed regions in the country. Therefore, improvement in the yield and quality characteristics of this crop will increase the income of small and marginal farmers. Mutation breeding is one of the plant breeding techniques to induce the desirable variability and develops high yielding varieties in shortest possible time (Jambhulkar and Shitre, 2009).

With the aim of developing short-duration high yielding Indian mustard varieties for Assam, mutations were induced in the variety NRCHB-101 by gamma irradiation (800, 1000 and 1200 Gy). Similar work was done by Julia et al. (2016) where higher mutagenic effectiveness has been reported at 1000 and 1200 Gy gamma ray treatment. NRCHB-101 is one of popular high yielding varieties of India developed by DRMR and released and notified in 2009. The variety was recommended for Assam in 2018. It gives seed yield of more than 1,100 kg ha<sup>-1</sup> with a crop duration of 108-115 days. Induced mutagenesis in this variety has resulted into the isolation of 217 number of putative mutants for various characters including yield and its components in M<sub>2</sub> generation. These mutants were advanced in M<sub>3</sub> generation and were analysed in M<sub>4</sub> and M<sub>5</sub> generations for assessment of genetic variation for seed yield and its component traits.

## Materials and Methods

Seeds of the variety NRCHB-101 were irradiated with 800 Gy, 1000 Gy and 1200 Gy during 2017-18 and sown in the field. Single plants were individually harvested. During 2018-19 M<sub>2</sub> generation was raised. As many as 331 M<sub>2</sub> plants were selected which showed early flowering and early maturing by more than 7 days and high yield of more than 20 g plant<sup>-1</sup>. In M<sub>3</sub> generation 29 selected putative mutants were grown, which were early in flowering and maturity by 8 to 12 days

compared to the parent, and 10 M<sub>3</sub> progenies with high yield of 40 g plant<sup>-1</sup> or more. M<sub>4</sub> and M<sub>5</sub> lines were derived from these selected M<sub>3</sub> progenies by isolating the variations.

The present study was conducted in two seasons, viz., *Rabi* 2020-21 and *Rabi* 2021-22. The experiment was carried out in the experimental farm of the Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat. The site is located at 26°44' N latitude and 94°10' E longitude having an elevation of 91 m above mean sea level. The genotypes were sown in a randomized block design having two replications. The lines were grown in 4 m single row plots with a spacing of 50 cm × 10 cm.

A total of 143 M<sub>4</sub> mutant lines were planted during *Rabi* 2020-21 followed by 115 M<sub>5</sub> selected lines during *Rabi* 2021-22 along with the parent.

Observations were recorded on five randomly sampled plants from each plot for plant height, main shoot length, number of siliqua in the main shoot, number of primary branches, number of secondary branches, and foot length. Similar characters were observed by Kumar et al. (2011) and Thakur et al. (2015) in their experiment on Indian mustard (*Brassica juncea* L.).

Analysis of variance was done using standard statistical procedures (Gomez and Gomez, 1984). Heritability (broad sense) was estimated according to Allard (1960). Genotypic and phenotypic coefficients of variation were estimated as per Burton and de Vane (1952). Genetic advance as% of mean was estimated according to Johnson et al. (1955).

## Results and Discussion

The analysis of variance for all the characters in both the seasons is shown in Table 1. The analysis revealed significant differences for all the characters indicating presence of variation among the genotypes.

*Estimates of Genetic Variability, Heritability and Genetic Advance (Table 2 and 3)*

The highest PCV and GCV were recorded for the characters number of primary branch, number of secondary branch and number of siliquae on main shoot indicating presence of ample variation among the genotypes. The genotypic coefficient of variation together with heritability estimates gives good indication of effectiveness of selection as suggested by Burton and de Vane (1952). High heritability coupled with genetic advance was observed for most of the characters indicating the presence of additive gene effects. Thus selection for these characters can serve as important criteria for further improvement of these lines in Indian mustard breeding programmes. Lyngdoh et al. (2017) observed high heritability with high genetic advance for the character plant height in their experiment on green mustard (*Brassica juncea*). Estimates of high heritability coupled with high genetic advance was observed by Tiwari et al. (2017) for number of primary branches, number of secondary branches, number of siliquae per plant and number of seeds per siliquae. Arifullah et al. (2013) observed both additive and dominance effects for the studied traits in Indian mustard.

Table 1: Analysis of variance for five plant characters during *Rabi* 2020-21 and *Rabi* 2021-22

Source	<i>Rabi</i> 2020-21						
	df	PH	MSL	SMS	PB	SB	FL
Replications	1	468.79	1479.28	16.61	0.57	0.91	13.03
Genotypes	141	1044.69**	1199.67**	144.23**	9.51**	33.39**	27.34**
Error	141	279.86	221.89	12.73	2.18	4.19	7.94
CV%		13.16	12.67	13.81	25.00	15.47	15.37

Table 1: Continue..

Source	<i>Rabi</i> 2021-22						
	df	PH	MSL	SMS	PB	SB	FL
Replications	1	1292.053	150.197	968.717	3.379	12.108	3.477
Genotypes	115	166.874**	308.176**	52.047**	4.221**	21.659**	11.293**
Error	115	34.405	162.505	27.095	1.875	9.369	6.224
CV%		4.18	19.28	14.21	23.43	23.65	13.57

Table 2: Genetic parameters for six yield component traits in  $M_4$  generation

Characters	Grand mean SEM±	Range		Coefficient of variance		Heritability $h^2$	Genetic Advance %
		Low	High	GCV	PCV		
1. Plant height (cm)	127.10 ± 9.66	87.67	171.00	12.56	18.19	47.67	17.87
2. Main Shoot length (cm)	117.58 ± 8.60	46.67	166.67	15.35	19.90	59.50	24.40
3. Number of siliqua in main shoot	25.83 ± 2.06	10.33	39.33	25.62	29.11	77.49	46.47
4. Number of primary branches	5.90 ± 0.85	2.33	13.00	26.50	36.43	52.92	39.71
5. Number of secondary branches	13.22 ± 1.18	2.67	22.00	23.60	28.22	69.93	40.65
6. Foot length (cm)	18.32 ± 1.63	10.67	24.33	13.88	20.71	44.90	19.15

Table 3: Genetic parameters for six yield component traits in  $M_5$  generation

Characters	Grand mean SEM±	Range		Coefficient of variance		Heritability $h^2$	Genetic Advance %
		Low	High	GCV	PCV		
1. Plant height (cm)	140.3 ± 4.15	110.7	159.1	5.80	7.15	65.81	9.69
2. Main Shoot length (cm)	66.1 ± 9.01	142.2	156.4	12.91	23.21	30.95	14.8
3. Number of siliqua in main shoot	36.6 ± 3.86	23.8	49.8	9.64	17.17	31.53	11.15
4. Number of primary branches	5.3 ± 0.97	3.0	10.5	18.53	29.87	38.48	23.68
5. Number of secondary branches	12.9 ± 2.16	4.0	21.5	19.15	30.43	39.61	24.83
6. Foot length (cm)	18.4 ± 1.76	13.0	23.5	8.66	16.10	28.94	9.6

*Mean Performance of the Genotypes*

The mean performance of all the traits under study has been observed during both the season (*Rabi* 2020-21 and *Rabi* 2021-22). During *Rabi* 2020-21 in the  $M_4$  generation, the genotype JMM-NRCHB101-120 and JMM-NRCHB101-65 exhibited maximum value for plant height while the genotype JMM-NRCHB101-87 revealed the least plant height. The genotype JMM-NRCHB101-120 revealed maximum main shoot length followed by JMM-NRCHB101-71, while the genotype JMM-NRCHB101-17 revealed the least main shoot length. The genotype JMM-NRCHB101-88 showed the maximum number of siliquae on main shoot followed

by JMM-NRCHB101-67. The highest value for number of primary branches was showed by the genotypes JMM-NRCHB101-128 and JMM-NRCHB101-129. The highest value for number of secondary branches was showed by the genotypes JMM-NRCHB101-56. The genotype JMM-NRCHB101-108 revealed the maximum foot length while the genotypes JMM-NRCHB101-15 showed the least foot length.

During *Rabi* 2021-22 in the  $M_5$  generation, the genotype JMM-NRCHB101-109 exhibited maximum value for plant height while the genotype JMM-NRCHB101-29 revealed the least plant height. The genotype JMM-NRCHB101-20 revealed maximum main shoot length while the genotype

JMM-NRCHB101-9 revealed the least main shoot length. The genotype JMM-NRCHB101-36 showed the maximum number of siliqua in main shoot. The highest value for number of primary branches was shown by the genotypes JMM-NRCHB101-4 while the highest value for number of secondary branches was shown by the genotype JMM-NRCHB101-105. The genotype JMM-NRCHB101-86 revealed the maximum foot length while the genotypes JMM-NRCHB101-9 showed the least foot length. The mutant lines showed better performance than the parent variety NRCHB-101 for all the characters in both the generations.

The present study revealed that the materials under this experiment contained significant variation for the important yield component traits which would help in designing a selection strategy. Therefore emphasis on these characters for selection will be advantageous for bringing improvement in Indian mustard genotypes.

### Conclusion

The present study was undertaken to estimate genetic variability of mutants in  $M_4$ - $M_5$  generation for six yield attributing characters. Additive gene effect for plant height was indicated high heritability coupled with high genetic advance. The mutant line JMM-NRCHB101-36 showed the highest number of siliquae main shoot<sup>1</sup>: whereas, JMM-NRCHB101-4 and JMM-NRCHB101-105 showed the highest number of primary and secondary branches. These characters could be exploited for the development of high yielding mustard varieties. The variability among the mutant lines can be used for selection of superior and short-duration genotypes for commercial cultivation for the farmers as well as for breeding new genotypes of Indian mustard.

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