EVALUATION OF SOME PROMISING M_6 MUTANT LINES OF INDIAN MUSTARD [*BRASSICA JUNCEA* (L) CZERN. & COSS.] CV. NRCHB-101 FOR SEED YIELD AND RELATED TRAITS

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By

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JORHAT – 785013 (ASSAM)

August 2023

Dedicated

to my

Beloved Parents

ASSAM AGRICULTURAL UNIVERSITY
FACULTY OF AGRICULTURE

CERTIFICATE – I

This is to certify that thesis titled **"Evaluation of Some Promising M_6 Mutant Lines of Indian Mustard [*Brassica juncea* (L) Czern. & Coss.] cv. NRCHB-101 for Seed Yield and Related Traits"** submitted to the Faculty of Agriculture, Assam Agricultural University, in partial fulfillment of the requirements for the degree of **Masters of Science (Agriculture)** in Plant Breeding & Genetics is a record of research work carried out by **Bhaskar Gogoi** under my personal supervision and guidance.

All kinds of help received by him have been duly acknowledged.

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Place: Jorhat

Date: August, 2023

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CERTIFICATE – II

This is to certify that the thesis titled **"Evaluation of Some Promising M_6 Mutant Lines of Indian Mustard [*Brassica juncea* (L) Czern. & Coss.] cv. NRCHB-101 for Seed Yield and Related Traits"** submitted by **Bhaskar Gogoi** bearing **Roll No. 2021-AMJ-152** to the Assam Agricultural University in partial fulfillment of the requirements for the degree of **Master of Science (Agriculture)** in the discipline of **Plant Breeding & Genetics** has been examined and approved by the Student's Advisory Committee after viva-voce.

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ABSTRACT

Rapeseed and mustard, two well-known oilseed brassica crops, are prominent source of edible oil worldwide. Indian mustard is the predominant oilseed brassica grown in India with high yield potential. In Assam, this crop is not yet popular mainly because of its longer duration compared to the predominant oilseed crop rapeseed toria. Therefore, an attempt had been made to develop early maturing mustard varieties by induced mutagenesis in a popular variety NRCHB–101. In this study, seventeen M_6 mutant lines and the parent variety were evaluated for mean performance, genetic variability and character interrelationships. Analysis of variance revealed highly significant genotypic variation for all the observed characters. High coefficients of genotypic and phenotypic variation were found for seed yield per plant and seed yield per hectare. High heritability and high genetic advance were found for seed yield per plant, yield per hectare, number of secondary branches per plant, plant height, foot length and 1000 seed weight, indicating that these characters were probably controlled largely by genes having additive gene action. Correlation analysis at genotypic level revealed that the characters plant height, number of secondary branches per plant and number of siliquae on main shoot had significant positive correlations with seed yield per plant. Path analysis showed positive direct effects of number of siliquae on main shoot, days to maturity, plant height, number of seeds per siliqua, days to 50% flowering and number of primary branches per plant on seed yield per plant. For these yield contributing traits heritability was high for days to 50% flowering, days to maturity and plant height and moderate for number of siliquae on main shoot and number of seeds per siliqua. Therefore, due attention should be given to these characters in selection for high seed yield. All the mutant lines matured in less than 105 days compared to 109 days of the parent variety. The mutant lines L-64, L-95, L-85, L-09, L-01 and L-107 were promising early maturing and high yielding genotypes, which could be exploited to develop desired varieties of Indian mustard.

LIST OF SYMBOLS AND ABBREVIATIONS

%	: Percent
/	: Per
@	: At the rate of
2n	: Diploid Chromosome number
ANOVA	: Analysis of variance
CD	: Critical difference
cm	: Centimeter
CV	: Coefficient of variation
df	: Degrees of freedom
DRMR	: Directorate of Rapeseed and Mustard Research
et al.	: et alia (and others)
Fig.	: Figure
g	: Gram
GA	: Genetic advance
GCV	: Genotypic coefficient of variation
h^2	: Heritability
ha	: Hectare
i.e.	: That is
PCV	: Phenotypic coefficient of variation
RBD	: Randomized block design
RF	: Rainfall
r_g	: Genotypic correlation coefficient
RH	: Relative humidity
r_p	: Phenotypic correlation coefficient
SE (m)	: Standard error of mean
t	: Tonne
USDA	: United States Department of Agriculture
σ^2_g	: Genotypic variance
σ^2_p	: Phenotypic variance

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Introduction…✍

CHAPTER I

INTRODUCTION

Rapeseed and mustard are two well-known oilseed crops, belonging to the genus Brassica. All oilseed brassicas yield edible oils of similar nutritional properties. In trade they are referred as rapeseed oil, which is the third most important source of edible oil in the world after palm oil and soybean oil. The term "rape" originates from the Latin word for turnip, while "mustard" is derived from the Latin words "must" and "ardens," meaning hot and scorching, respectively, which allude to the pungent nature of expressed mustard oil (Thomas et.al., 2012). The crop brassicas comprise of six cultivated species, three diploids and three tetraploids; five species are rapeseed and mustard and one is vegetable species. Among these, Indian rapeseed or rapeseed or turnip rape (*Brassica rapa* L., 2n=20, AA) and oilseed rape or Gobhi sarson (*Brassica napus* L., 2n=38, AACC) are rapeseed species. Black mustard (*Brassica nigra* Koch, 2n=16, BB), Indian mustard or brown mustard or Rai [*Brassica juncea* (L) Czern & Coss., 2n=36, AABB] and Ethiopian mustard or Karan rai (*Brassica carinata* Braun, 2n=34, BBCC) are mustard species. *Brassica oleracea* (2n=18, CC) is vegetable brassica (Prakesh, *et al*., 2009). *Brassica juncea*, *Brassica napus* and *Brassica rapa* are economically important major oilseed brassicas. These species exhibit high polymorphism and each of them has oilseed, vegetable and fodder variants.

In India, rapeseed-mustard crops cover more than 8.6 million hectares, producing approximately 11.963 million tonnes. The average production of rapeseed-mustard in India is 1511 kg/ha, whereas the global average yield stands at 1980 kg/ha (USDA, 2022). In the state of Assam, these crops are cultivated on 2.88 lakh hectares, resulting in a production of 1.86 lakh tonnes (DRMR, 2022). Indian mustard accounted for 75 to 80 percent of the rapeseed-mustard area planted in the country during the 2018-19, making it the most significant oilseed brassica cultivated in India. However, in Assam the main brassica crop is toria (*B. rapa*). The seed yield potential of rapeseed varieties such as toria, brown sarson, and yellow sarson is considerably lower compared to mustard. This disparity in yield potential plays a crucial role in the variation between the high national average production (1511 kg/ha) and the relatively low yield observed in Assam (596 kg/ha). Due to its short growth cycle of approximately 90 days, toria is primarily and popularly cultivated in Assam, despite its lower yield.

To increase the cultivation of Indian mustard in Assam, it is essential to develop varieties with a shorter lifespan. One effective method for creating desirable genotypes is mutation breeding. Jambhulkar and Shitre (2009) in India and Malek *et al.* (2011) in Bangladesh reported the successful generation of beneficial mutants of Indian mustard through gamma irradiation.

In order to cater to the needs of Assam, a popular high yielding variety, NRCHB-101 (developed by DRMR, Bharatpur and released in 2009) was subjected to gamma irradiation (800 Gy, 1000 Gy and 1200 Gy) during 2017 to create short-duration, high-yielding types of Indian mustard. NRCHB-101 was recommended for cultivation in Assam in 2018 and it exhibits seed yield of over 1100 kg per hectare with maturity duration of 108-115 days. A number of mutant lines were developed and the selected lines were carried forward to M_5 generation in 2021-22 (Bora, 2022). The present study is focused on assessment of genetic variation for agro-morphological characters in selected M_6 lines during 2022-23. The specific objectives of the study are:

i. To evaluate the mean performance of genotypes in terms of agro-phenological traits;

ii. To assess genetic variation among the genotypes; and

iii. To analyze genotypic correlations and causal relationships among different traits.

Review of Literature…✍

CHAPTER II

REVIEW OF LITERATURE

Genetic variation is a crucial factor in conducting successful breeding programs. Having information about the diversity of genotypes is essential for identifying and selecting desired individuals with unique traits. Previous studies on oilseed brassicas have demonstrated the existence of genetic variation within the species.

2.1 Genetic variation

Bora (2022) conducted a study on morphological and molecular characterization of M_5 mutant lines of Indian mustard cultivar NRCHB-101. She evaluated 115 M_5 lines along with the parent during *Rabi* 2021-22 to assess to genetic variability and mean performance for yield and duration related traits. She reported significant variation for all the traits. High GCV was observed for stem thickness, siliqua density, oil yield per hectare and seed yield per hectare. High heritability was observed for days to maturity, stem thickness, seed yield per hectare, oil yield per hectare, seed oil content, thousand seed weight and plant height. Genetic advance was high for seed yield per plant, number of secondary branches, number of primary branches and thousand seed weight. As many as 57 lines, including the high yielding lines, were of significantly shorter duration (99-105 days) compared to the parent (110.5 days).

Devi (2021) conducted a study on evaluation of some mutant and non-mutant lines of Indian mustard for seed yield and related traits. In this study 29 genotypes comprising of 21 M_{4-5} mutant lines, 5 newly developed F_{6-7} lines and three varieties were evaluated during *Rabi* 2019-20 and 2020-21 to assess genetic variability and interrelationships between yield component traits. The pooled analysis of variance revealed significant variation due to genotypes, environment and genotype x environment interaction for most of the characters observed. High heritability coupled with high genetic advance was observed for number of secondary branches per plant. The mutant lines JMM-TM2-15, JMM-TM2-28 and recombinant line JM13-4 showed potentiality for early maturity with high yield.

According to Saroj *et al.* (2021) examined 289 accessions of mustard collected from four different continents for yield and associated characteristics. They found considerable genetic variation and heritability for days to flowering, plant height, seed size, and seed output per plant. They identified some potentially good genotypes.

Chakraborty *et al.* (2021) revealed that there was genetic variation among 33 genotypes of Indian mustard collected from various agro-climatic regions of India. They reported high GCV and PCV for number of primary branches per plant, the number of secondary branches/plant, the number of siliquae and the seed yield per plot.

Pradhan *et al.* (2021) conducted a study on 24 different genotypes of Indian mustard to examine the seed yield and traits associated with yield. They found that plant height, number of primary branches per plant, number of secondary branches per plant, 1000-seed weight, and seed production per plant exhibited high level of genotypic and phenotypic variation. Most of these traits showed significant correlations with one another.

Patel *et al.* (2021) found considerable variation in 45 genotypes for all 18 parameters linked to seed yield and quality. Significant phenotypic and genotypic diversity was found for number of branches per plant, seed output per plant, myristic, palmitic, and stearic acid. High heritability estimates were recorded for Myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid and glucosinolates, number of branches per plant, siliquae per plant, seeds per siliqua, siliqua length, 1000-seed weight, and seed yield per plant.

Prajapati *et al.* (2020) found notable genetic variation in 161 M_4 mutant lines and three check varieties of Indian mustard for all the traits examined. They observed significant amount of genetic and phenotypic variation for seed yield per plant and number of siliquae per plant. They concluded that the number of siliquae per plant, 1000-seed weight and seed yield per plant were important traits for effective selection.

Kumar *et al.* (2018) assessed genetic parameters in 26 genotypes of Indian mustard. The study showed that the number of secondary branches, harvest index, biological yield, seed yield per plant, and number of primary branches had high genotypic (GCV) and phenotypic coefficient of variation (PCV). Most of the traits exhibited high heritability, except for harvest index and seeds per siliqua. The study also revealed a high genetic advance for all the traits, except for days to first flower, which suggests that selection based on these traits would be effective.

Gadi *et al.* (2020) examined thirty-six germplasms of Indian mustard and analyzed the variation in ten quantitative traits. They found that there was a highly significant genotypic variation for all the traits, except for the harvest index.

Singh *et al.* (2019) conducted a study on ten genotypes of Indian mustard, evaluating various parameters of genetic variability. Based on their findings, they selected the best performing lines from the studied genotypes.

Srivastava *et al.* (2019) evaluated thirty-eight genotypes of Indian mustard, including the Giriraj check variety, focusing on seed yield and other traits associated with yield. The study found that traits such as days to 50% flowering, biological yield, and seed yield per hectare exhibited high heritability and genetic advance.

Aktar *et al.* (2019) conducted a study on Brassica genotypes to investigate genetic parameters and diversity in relation to yield and yield-contributing traits. The findings indicated high heritability ranging from 61.54% to 98.64% across the traits studied. Additionally, the study revealed high genetic advance (greater than 60%) and genetic advance as a percentage of mean. Among all the genotypes evaluated, BD-7114 was identified as the top-performing genotype considering all the traits analyzed.

Jat *et al.* (2019) conducted an assessment of genetic diversity in twenty genotypes of Indian mustard by examining thirteen different characteristics. The findings demonstrated that there was significant variation among the genotypes across all traits studied. The researchers also observed high levels of heritability and genetic advance for key traits such as seed yield per plant, number of siliquae per plant, days to 50% flowering, and siliqua length.

Maurya *et al.* (2018) conducted a study on fifty accessions of Indian mustard germplasm to assess the genetic variability, heritability, and genetic advance of different quantitative traits. They observed significant variations among all the traits studied. The researchers found that the genotypes showed moderate to high levels of PCV and GCV.

Julia *et al.* (2018) conducted a study at Central Agricultural University in Imphal, India, to assess the effectiveness and efficiency of gamma rays on Indian mustard. Three genotypes of Indian mustard were selected for the study, and it was found that the LD50 values ranged from 1000 Gy (resulting in pollen sterility) to 1200 Gy of gamma rays. The researchers observed that the treatment with 1000 Gy of gamma rays demonstrated high efficiency and effectiveness. Additionally, the highest lethality was observed at 800 Gy. The study also revealed that the mutagenic efficiency, in terms of both injury and sterility, was highest at the 1000 Gy gamma ray treatment.

Devi (2018) conducted a study to evaluate twelve Indian mustard germplasm lines for thirteen different quantitative traits. The results showed significant variation for all the traits studied. The traits with high estimates of PCV, GCV, heritability and genetic advance were biological yield per plant, number of seeds per siliqua, siliquae on main raceme and grain yield per plant.

Raliya *et al.* (2018) conducted a study on a set of crosses of Indian mustard, focusing on genetic variability and character association related to seed yield per hectare, 1000-seed weight, siliqua length, plant height, and number of primary branches. The study identified that the cross NRCHB 101 x NPJ 112 exhibited the highest seed yield of 3293.01 kg/ha, followed by RH 406 x F1 with 3077.37 kg/ha and NPJ 112 x RRN 727 with 2975.31 kg/ha, while the mean seed yield across all crosses was 2090.25 kg/ha. The oil content of the seeds ranged from 38.6 to 42.33 percent, with an average oil content of 41.13 percent.

Sapkal *et al.* (2018) studied the genetic variability in 88 biparental progenies of Indian mustard, comparing them to six check varieties. The results showed significant differences among the traits, except for days to maturity. The study also estimated genetic parameters, which indicated that seed yield per plant and siliquae per plant were influenced by additive gene effects. Based on these findings, the researchers concluded that selection would be an effective approach for improving these traits.

Chandra *et al.* (2018) conducted a study on Indian mustard to assess the variability and heritability of branching behavior in rainfed conditions. They examined fifty genotypes and categorized them into 9 groups based on their branching behavior and grain yield. The research revealed significant variation in basal and non-basal branching patterns. Traits such as the number of siliquae per plant, plant height, height of the first primary branch, height of the first siliqua, and harvest index exhibited high heritability and genetic advance, indicating the influence of additive gene action. The authors recommended selecting for these traits as an effective breeding strategy. They also identified specific plant characteristics that were important for Indian mustard in rainfed conditions, including lower positioned primary basal branches with at least two secondary branches, lower height of the first siliqua, superior root volume, reduced non-basal branching, higher number of siliquae, medium-tall plant stature, high harvest index, and efficient dry matter utilization.

Saleem *et al.* (2017) carried out a multivariate analysis experiment on 107 accessions, which included one check cultivar of Indian mustard. The study focused on both qualitative and quantitative traits. Significant variation was observed in traits such as pod shattering, plant height, main raceme length, and days to 100% flowering. Out of the 20 principal components analyzed, seven components had eigenvalues of ≥1.0, accounting for approximately 73.92% of the total variation observed among the 107 accessions.

Lyngdoh *et al.* (2017) conducted a study on mustard genotypes, focusing on genetic variability, character association, and path coefficient analysis. They evaluated seven different genotypes of green mustard to assess the genetic variability and the degree and direction of association between yield and its component characters. The genotype 204/MGVAR-4 displayed the highest yield per plant, followed by the genotype MGVAR-1.

Priyamedha *et al.* (2017) conducted a study on ten genotypes of Indian mustard. They found significant variations among the genotypes for all the studied characteristics. The findings indicated that traits such as plant height, seed yield, and siliqua length exhibited high heritability and genetic advance, suggesting the influence of additive genetic factors in these traits.

Helal *et al.* (2016) evaluated a collection of rapeseed and mustard lines with the objective of developing a short duration variety suitable for rice fallow land. They assessed eight different varieties and four promising lines of rapeseed-mustard. The results revealed significant positive correlations for multiple traits. They identified four genotypes, namely Improved Tori, BARI Sarisha-8, BARI Sarisha-14, and BARI Sarisha-15, as suitable varieties for cultivation.

Uzair *et al.* (2016) examined ten genotypes of Indian mustard to assess genetic variability, heritability, and genetic advance for several traits including plant height, number of primary branches, days to 50% flowering, days to 70% maturity, seeds per siliqua, siliqua length, 1000-seed weight, and seed yield. The results indicated significant variability across all the traits studied. Notably, seed yield, siliqua length, and plant height exhibited both high heritability and high genetic advance, implying that these traits are strongly influenced by genetic factors and can be improved through selective breeding.

Yadav *et al.* (2015) studied on the determination of the LD50 (lethal dose 50) of ethyl methane sulfonate (EMS) for inducing mutations in two varieties of Indian mustard (RH-749 and NRCHB-101) and one wild relative, Sinapis alba. The study identified that EMS doses of 0.42%, 0.73%, and 0.3% were found to be optimal for both Indian mustard and Sinapis alba.

Merah (2015) conducted a study on the genetic variability of glucosinolates in *Brassica juncea* seed and their relationship with agronomical traits among the genotypes used for condiment purposes. The study included 190 genotypes from various origins and was carried out in Dijon, France. The research focused on parameters such as oil content, total glucosinates, sinigrin, and gluconapin levels in the seeds. Additionally, characteristics such as flowering and maturation durations were observed. The results revealed that the average value of total glucosinolates exceeded 103 μmolg^{-1}, while the sinigrin content ranged from 0 to more than 134 μmolg^{-1}.

Iqbal *et al.* (2014) conducted a study on genetic diversity analysis of different germplasms of Indian mustard to identify short-duration genotypes for cultivation. They identified BARI Sarisha-15, BINA Sarisha-4, and BARI Sarisha-14 as suitable genotypes for cultivation. However, genotypes such as BARI Sarisha-8, Tori-7, and NAP-0763 were found to be more susceptible to environmental fluctuations.

Shekhawat *et al.* (2014) observed significant variability among sixty genotypes of Indian mustard for thirteen different traits. Notably, traits such as the number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, number of siliquae per plant, and seed yield per plant exhibited high estimates of genetic coefficient of variation. Additionally, these traits also displayed high heritability along with high genetic advance. These findings suggest that phenotypic selection based on the number of secondary branches per plant, number of siliquae per plant, and seed yield per plant could be an effective approach for improving yield in Indian mustard.

Ali *et al.* (2013) examined thirty-five advanced M_5 mutant lines along with a check variety of winter rapeseed (*Brassica napus*). They found significant differences were observed among the advance mutant lines for various traits, including oil content, glucosinolates, protein content, linolenic acid, oleic acid, and erucic acid. Erucic acid and glucosinolates exhibited high genetic variability but low heritability and genetic advance.

Malek *et al.* (2011) reported mutagenesis on the well-adapted and popular mustard variety BARIsarisha-11 using gamma irradiation. The research revealed that two mutants, MM-10-04 and MM-08-04, selected from 700 Gy irradiation, displayed higher seed yield compared to BARIsarisha-11. These mutants also demonstrated tolerance to Alternaria blight disease and aphid infestation. Consequently, these two mutants were registered as Binasarisha-7 and Binasarisha-8 in 2011, and recommended for commercial cultivation.

Jambhulkar and Shitre (2009) studied mutation induction, evaluation and utilization for the development of high-yielding varieties in Indian mustard and sunflower at BARC, Trombay, India. A wide spectrum of mutations was revealed for seed coat colour, chlorophyll, plant height, maturity, flower morphology, seed weight and oil content. Two high yielding varieties of Indian mustard viz., TM1 and TM50 were developed and exploited in hybridization to develop bold, yellow seeded and high yielding genotypes. Mutants for drought tolerance were isolated besides zero erucic and zero glucosinates genotypes.

Javed *et al.* (2000) studied thirteen gamma-irradiated mutants of Indian mustard along with the parent variety and observed significant variability among the entries for all the traits. The mutants had shorter plant height but produced higher grain yield than their parent variety indicating a significant improvement in the genetic constitution as a result of gamma irradiation.

Velasco *et al.* (1997) evaluated the effects of ethyl methane sulphonate (EMS) on seeds of Ethiopian mustard (*Brassica carinata* A. Braun) line C-101. The mutant N2-6230 showed very low oleic acid content (4.7%) and high erucic acid (40-49.3%). After selection for high erucic acid content in M_3 and M_4 generation, the mutation was fixed in M_5 generation and the line was declared to be the first high erucic line in *Brassica* species through mutation breeding.

2.2 Character interrelationships

Devi (2021) conducted a study on evaluation of 29 genotypes comprising of 21 M_{4-5} mutant lines, 5 F_{6-7} recombinant lines and three varieties of Indian mustard for seed yield and related traits. Seed yield per plant was positively correlated with number of siliquae on main shoot and negatively correlated with days to 50% flowering at genotypic level. Path analysis based on genotypic correlations showed positive direct effects on seed yield per plant of number of siliquae on main shoot, number of primary and secondary branches per plant.

Chakraborty *et al.* (2021) revealed that there was genetic variation among 33 genotypes of Indian mustard from various agro-climatic regions of India. There was strong positive correlation of seed yield with plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, and 1000 seeds weight.

Lakra *et al.* (2020) examined the genetic diversity and phenotypic associations in 30 genotypes of Indian mustard. They reported that seed yield per plot was positively correlated with number of plants per plot, number of siliquae per plant, siliqua length and number of seeds per siliqua.

Srivastava *et al.* (2019) evaluated thirty-eight genotypes of Indian mustard, including a check variety, Giriraj, focusing on seed yield and other traits associated with yield. Positive genotypic correlations were observed between seed yield and other traits, including plant height, number of secondary branches, siliquae per plant, siliqua length, seed yield per plot, seed yield per plant, and biological yield per plant.

Materials and Methods…✍

CHAPTER III

MATERIALS AND METHODS

3.1 Location and Period of the Experiment

The experiment was conducted in the experimental area of the Department of Plant Breeding & Genetics, Assam Agricultural University, Jorhat, during the Rabi season of 2022-23. The specific location of the site is situated at 26°44' N latitude and 94°10' E longitude, with an elevation of 91 meters above mean sea level (source: www.aau.ac.in).

3.2 Experimental Materials

A total of 17 selected M_6 mutant lines developed through gamma irradiation from Indian mustard cultivar NRCHB-101 along with the parent variety were grown during 2022-23. The details of the experimental materials are presented in Table 3.1.

3.3 Design of Experiment and Layout

Experimental design: Randomized block design (RBD) with three replications.

Plot size: 4 m x 1.2 m (four rows, 4 m long).

Spacing: row to row 30 cm, plant-to-plant 10 cm (plant to plant spacing within row was adjusted to approximately 10 cm by thinning operations at seedling stage).

Date of sowing: 17^{th}November 2022.

The recommended package of practices was followed to raise and manage the crop.

3.4 Crop Management

3.4.1 Field preparation and fertilizer application

The experimental field underwent a thorough process of pulverization, planking, and levelling to achieve a fine tilth, ensuring optimal soil conditions. Meticulous efforts were made to remove weeds, stones, and stubbles etc. from the field.

Manures and fertilizers application:

Well-decomposed cow dung manure was applied @ 2 tonnes per hectare as basal. Fertilizers were applied @ 60:40:40 kg/ha $N:P_2O_5:K_2O$ in the form of Urea, Single Super Phosphate and Muriate of Potash, respectively. Half of N fertilizer and the whole of P_2O_5 and K_2O fertilizers were applied as basal. The remaining half of nitrogen fertilizer was top-dressed at the time of flowering. In addition to these, Borax was applied as basal @ 10 kg/ha. In addition to these, two foliar sprays consisting of a 1% urea solution and micronutrient Tracel were applied during flowering to pod filling stage.

Table 3.1 Genotypes used in the study

S. No.	Line No.	Designation of line	Gamma dose used in the origin	Source of seeds
1	L-1	JMM-NRCHB101-1	From 800 Gy	Department of Plant Breeding & Genetics, AAU, Jorhat
2	L-4	JMM-NRCHB101-4	From 800 Gy	
3	L-6	JMM-NRCHB101-6	From 800 Gy	
4	L-8	JMM-NRCHB101-8	From 800 Gy	
5	L-9	JMM-NRCHB101-9	From 800 Gy	
6	L-10	JMM-NRCHB101-10	From 800 Gy	
7	L-17	JMM-NRCHB101-17	From 800 Gy	
8	L-23	JMM-NRCHB101-23	From 800 Gy	
9	L-26	JMM-NRCHB101-26	From 800 Gy	
10	L-29	JMM-NRCHB101-29	From 800 Gy	
11	L-64	JMM-NRCHB101-64	From 1000 Gy	
12	L-86	JMM-NRCHB101-86	From 1000 Gy	
13	L-89	JMM-NRCHB101-89	From 1000 Gy	
14	L-94	JMM-NRCHB101-94	From 1000 Gy	
15	L-95	JMM-NRCHB101-95	From 1000 Gy	
16	L-107	JMM-NRCHB101-107	From 1200 Gy	
17	L-111	JMM-NRCHB101-111	From 1200 Gy	
18	Parent	NRCHB-101		

3.4.2 Irrigation

To fulfil the water requirements of the plants, irrigation was done manually four times at pre-sowing, active vegetative stage, flowering stage and pod filling stage.

3.4.3 Intercultural Operations

To maintain an appropriate plant population, thinning, weeding and earthing operations were carried out manually as per needs. These activities were conducted twice during the vegetative growth period, around 15-20 days after sowing.

3.4.4 Plant Protection

At the stage of pod development, Imidachlorpid @ 1.5 ml/L of water was sprayed twice to keep the plants free from aphids. No other serious pests and diseases were observed in the field.

3.4.5 Recording of Observations

For data collection, five competitive plants were randomly sampled from the middle rows of each plot. Seventeen different quantitative characters were observed on these sampled plants. The observations on days to 50% flowering and days to maturity were recorded on plot basis. The plot mean data were computed and were used for statistical analysis.

3.5 Data recorded on whole plot basis

3.5.1 Days to 50% flowering (DFF)

The number of days from the date of sowing to the date when about 50 percent of plants in a plot opened first flower was counted and recorded as days to 50% flowering.

3.5.2 Days to maturity (DM)

The number of days from the date of sowing to the date when about 75 percent of the plants in each plot attained physiological maturity, indicated by the turning of pods to a yellow and golden brown colour, was counted and recorded as days to maturity.

3.6 Data recorded on individual sampled plants (5 plants per plot)

3.6.1 Plant height (PH)

The height of each sampled plant was measured in centimetres by a metre scale from the ground level to the tip of the highest inflorescence at maturation stage.

3.6.2 Number of primary branches per plant (NPB)

Number of primary branches was counted on each sampled plant after finishing of flowering and recorded.

3.6.3 Number of secondary branches per plant (NSB)

The number of secondary branches on all the primary branches of a plant was counted and recorded while observing the number of primary branches.

3.6.4 Foot length (FL)

The foot length from each sampled plant was measured in centimetre from the ground level to the point at which the first branch was borne.

3.4.5 Main shoot length (MSL)

The length of the main shoot (inflorescence or raceme) of each sampled plant was measured in centimeter from the base to the tip of the main inflorescence using a metre scale at the crop maturation stage.

3.6.6 Number of siliquae on the main shoot (SMS)

The number of siliquae in the main shoot of each sampled plant was counted while measuring the main shoot length.

3.6.7 Siliqua density on main shoot

Siliqua density was derived as number of siliquae per centimetre of the main shoot.

3.6.8 Number of seeds per siliqua (SPS)

From the middle portion of the main shoot in each sampled plant, five siliquae were collected at maturation stage. The number of seeds per siliqua was counted and the average per siliqua was recorded.

3.6.9 Number of siliquae on the terminal 15 cm of main shoot (STS)

The number of siliquae on the terminal 15 cm of the main shoot of the sampled plants was counted at the time of maturity and recorded.

3.7 Characters observed after harvesting:

3.7.1 Maximum root length (MRL)

The roots of the sampled plants were carefully dug out after harvest of the plants. Adhering soils were removed and the maximum root length of each sampled plant was measured in centimeter from the main stem to the tip of the longest root.

3.7.2 Thousand seed weight (TSW)

After harvest, threshing, cleaning and drying 1000 seeds were counted from seeds of the sampled plants and weighed in an electronic balance (Afcoset, model ER-200A) in grams (g).

3.7.3 Seed oil content (OC)

After harvesting, threshing, cleaning and drying the oil content of the seeds in percentage from each plot was determined by using the FOSS InfatecTM 1241 Grain Analyzer.

3.7.4 Seed yield per plant (SYPP)

The total seeds from the 5 sampled plants per plot were cleaned and dried and weighed in an electronic balance (Afcoset, model ER-200A) and recorded in grams (g), and divided by 5 to express as seed yield per plant.

3.7.5 Seed yield per hectare (SYPH)

Seed yield per plot including the seeds of the sampled plants was recorded in gram after threshing, cleaning and drying. Then it was converted to seed yield per hectare in Kg/ha.

3.8 Qualitative character

3.8.1 Seed colour

Seeds obtained from each plot were observed for the colour of the seed coats.

3.9 STATISTICAL ANALYSIS

3.9.1 Analysis of variance

The plot mean values of each quantitative trait were obtained and systematically tabulated. Plot mean values were then subjected to analysis of variance by following the standard statistical procedure (Gomez and Gomez, 1984).

Structure of ANOVA:

Source of variance	Degree of freedom	Mean square	F ratio	Expected mean square
Replications	r-1	M_r	Mr/Me	-
Genotypes	g-1	M_g	Mg/Me	$\sigma^2_e + r\sigma^2_g$
Error	(r-1)(g-1)	M_e		σ^2_e
Total	rg-1	-		-

Where, r=no. of replications

g= no. of genotypes

σ^2_e= error or environmental variance

σ^2_g= genotypic variance

F-test was applied to test the significance of differences in replications and genotypic variance against error variance at 5% and 1% levels of significance.

Critical difference (CD) was calculated to test the difference between two genotype means as follows:

CD = SEd x t at error d.f. at 0.05 and 0.01 level of significance.

SEd is the standard error of difference of two genotypic means to be tested.

$$\text{SEd} = SQRT\left(\frac{2Me}{r}\right)$$

3.9.2 Coefficient of variation (CV)

The ratio of the standard deviation of error variance (error mean square) to the grand mean was obtained and expressed as percentage.

3.9.3 Estimation of genetic parameters

The genetic parameters were estimated for each character from the analysis of variance. Genotypic variance (σ^2g) and phenotypic variance (σ^2p) were computed following Burton and Devane (1953). The expected genetic advance was calculated for each character following Allard (1960) which was then expressed as percent of grand mean.

3.9.4 Genotypic variance (σ_g^2) is the variance due to the genotypes present in the population. This was computed from analysis of variance as suggested by Burton and Devane (1953).

$$\sigma^2_g = (Mg - Me)/r$$

3.9.5 Phenotypic variance (σ_P^2) was calculated by following formula:

$$\sigma^2_p = \sigma_g^2 + \sigma^2_e$$

3.9.6 Standard error of mean SE(m) was calculated by following formula:

$$SE(m) = SQRT\left(\frac{EMS}{r}\right)$$

3.9.7 Phenotypic coefficient of variation (PCV) for each character was calculated in percentage as:

$$PCV\ (\%) = SQRT(\sigma^2_p)/(\bar{X}) \times 100$$

3.9.8 Genotypic coefficient of variation (GCV) for each character was calculated in percentage as:

$$GCV\ (\%) = SQRT(\sigma_g^2)/\ (\bar{X}) \times 100$$

Where, $\bar{X}$ is the grand mean

3.9.9 Heritability in broad sense (h^2_{bs}) in percentage

$$h^2_{bs} = (\sigma^2_g)/\sigma^2_p \times 100$$

3.9.10 Expected genetic advance (GA) for each character was calculated by using the formula given by Johanson, Robinson and Comstock (1955) as follows:

$$GA = k.\ \sigma_p.h^2$$

Where,

k = 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h^2_{bs} = Heritability (broad sense) in fraction

Genetic advance as percent of population mean = GA/($\bar{X}$) x 100

For estimation of the genetic parameters Singh and Chaudhary (1979) was consulted.

All computations and statistical analysis were worked out using Microsoft Office Excel 2007.

3.10 CORRELATION AND PATH ANALYSIS

Genotypic correlation coefficient between two characters, say X and Y, was computed with the help of formula given by Al-Jibouri *et al.* (1958). The genotypic and phenotypic correlation coefficients between two characters, say X and Y, were obtained from the analysis of variance X and Y and the analysis of covariance between X and Y following the procedure given in Singh and Chaudhary (1979) and Dabholkar (1999).

3.10.1 Genotypic correlation coefficient, $r_{g(xy)}$

$$\mathbf{r}_{\mathbf{g(xy)}} = \frac{\sigma gxy}{\sqrt{\sigma 2gx} \times \sqrt{\sigma 2gy}}$$

Where, $r_{g(xy)}$ = Genotypic correlation coefficient between x and y.

σ^2_{gx} = Genotypic variance of x

σ^2_{gy} = Genotypic variance of y

σ_{gxy} = Genotypic covariance between x and y and it is given by

$$\sigma_{gxy} = \frac{MSPg - MSPe}{r}$$

Where, MSP_g = Genotypic mean sum of product

MSP_e = Error mean sum of product

r = Number of replications

3.10.2 Phenotypic correlation coefficient (rpxy)

$$r_{p(xy)} = \frac{\sigma pxy}{\sqrt{\sigma 2px \times \sigma 2py}}$$

Where, $r_{p(xy)}$ = Phenotypic correlation coefficient between x and y.

σ^2_{px} and σ^2_{py} = Phenotypic variances of x and y, respectively

σ_{pxy} = Phenotypic covariance between x and y and is given by

$\sigma_{pxy} = \sigma_{gxy} + \sigma_{exy}$

The significance of the correlation coefficient was tested by comparing the observed value of correlation coefficient with the table value at 5% and 1% probability level at (g-2) degree of freedom, where 'g' is the number of genotypes.

3.10.3 Path coefficient analysis

Path coefficient is a simple standardized partial regression coefficient. Path coefficient analysis was given by Wright (1921). It is a method to measure the direct and indirect effects of independent variables on the dependent variable. It allows the separation of correlation coefficients into components of direct and indirect effects. Path coefficient analysis was carried out by the method given by Dewey and Lu (1959) by taking seed yield per plant as the dependent variable. Genotypic correlation coefficients were used for this analysis.

In path coefficient analysis, the correlation coefficient of any character with seed yield per plant was split into direct and indirect effects as follows:

$r_{iy}= r_{1i}P_1+r_{2i}P_2+r_{3i}P_3+............+r_{ni}P_n+.........r_{ii}P_1$

Where,

r_{iy} = Correlation of the character on seed yield per plant

$r_{1i}P_1$ =Indirect effect of ith character on seed yield per plant through first character

r_{ni} = Correlation between nth and ith characters

n = Number of independent variables (yield attributing characters)

P_i = Direct effect of the ith character on seed yield per plant

The direct effect of component characters on seed yield per plant was obtained by solving the following equations in matrix form:

$[r_{ry}] = [P_{1y}] [r_{ij}]$

Therefore, $[P_i] = [r_{ij}]^{-1}[r_{iy}]$

Where,

$[P_i]$ = Matrix of direct effects (path coefficients)

$[r_{iy}]$ = Matrix of correlation coefficients between component traits and seed yield per plant

$[r_{il}]$ = Matrix of correlation coefficients between all component characters

The residual effect in path analysis measures the influence of other possible independent factors on the dependent variable but not included in the study. Direct effects and correlation coefficients are used to estimate the residual effect as follows:

Residual effect = Pr = $(1-P_i r_{iy})^{1/2}$

Where, P_i and r_{iy} are as given above.

Statistical analysis and computations of the data were carried out using Microsoft Office Excel 2007. The correlation and path analysis coefficients were computed using O. P. Sheoran, Hisar. Statistical Package for Agricultural Scientists (OPSTAT), CCS HAU.

Experimental Findings…✍

CHAPTER IV

EXPERIMENTAL FINDINGS

The study was carried out during Rabi 2022–23 to evaluate mean performance of 18 genotypes of Indian mustard including 17 M_6 mutant lines and the parent genotype NRCHB–101, to assess genetic variability for 16 quantitative characters and to analyze correlations and path coefficients between characters. The results of the investigation are described in this chapter.

4.1 Analysis of variance

The analysis of variance of the plot mean values was done for each character, and is presented in Tables 4.1.1 and 4.1.2. The analysis revealed highly significant variation among the genotypes for all the characters studied. Variation among the M_6 lines was also significant for all the characters. Thus, the mutant lines could provide a basis for selection of desired types of Indian mustard. The difference between mean of mutant lines and the parent was significant for days to maturity, number of primary branches per plant, number of secondary branches per plant, main shoot length, number of siliquae on main shoot, number of siliquae on terminal shoot, foot length and 1000 seed weight. These showed that on the average the mutant lines were diverse from the parent for these characters.

4.2 Mean Performance of M_6 Lines

The mean performances of the genotypes for the 16 quantitative traits are presented in Tables 4.3 and 4.4.

4.3 Days to 50% flowering

Days to 50% flowering ranged from 41 to 45 days with a mean value of 43.5 days (Table 4.3). It was observed that the mutant line L-04 (41 days) exhibited the least number of days to 50% flowering followed by L-23 (41.7 days) and L-17 (42 days). These three lines were statistically at par. The line L-95 took the longest time for flowering (45 days). The mean of the mutant lines was 43.51 days. In comparison to that, the parent variety NRCHB-101 took 43.7 days to 50% flowering and the difference was non-significant.

Table 4.1 ANOVA (mean squares) for for growth related yield parameters in M_6 lines of Indian mustard

Source	df	DFF (days)	DM (days)	PH (cm)	NPB (no.)	NSB (No.)	MSL (cm)	FL (cm)	MRL (cm)
Replications	2	5.13**	12.17**	16.05	0.07	1.19	13.79	77.69	1.31
Genotypes	17	3.62**	13.50**	949.51**	0.42**	6.00**	123.27**	110.55**	3.64**
M_6 lines	16	3.84**	5.96**	1005.17**	0.34**	5.68**	125.23**	91.76**	3.85**
M_6 lines vs Parent	1	0.07	134.21**	58.94	1.61**	11.16**	91.99**	411.21**	0.19
Error	34	0.35	1.28	58.88	0.07	0.38	7.22	11.16	0.61
CV%	5.54	1.35	1.11	5.54	6.81	7.87	4.03	9.20	4.78

*Significant at P=0.05 and ** Significant at P=0.01

DFF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, MSL= Main shoot length, FL= Foot length, MRL= Maximum root length

Table 4.2 ANOVA (mean squares) for seed yield and related yield attributes in M_6 lines of Indian mustard

Source	df	NSMS (No.)	SD (No./cm)	STS (No.)	SPS (No.)	TSW (g)	OC (%)	SYPP (g)	SYPH (Kg/ha)
Replications	2	12.32	0.0008	0.54	0.95	1.13	0.73	0.29	2717.28
Genotypes	17	24.50**	0.0039**	6.02**	1.75**	0.69**	3.84**	8.75**	31821.46**
M_6 lines	16	24.19**	0.0042**	4.17*	1.30**	0.71**	3.83**	9.17**	33723.34**
M_6 lines vs Parent	1	29.51*	0.0002	35.61**	8.89**	0.35**	4.00	1.89	1391.47
Error	34	5.54	0.0012	2.14	0.43	0.04	1.21	0.46	2481.73
CV%	5.54	7.18	6.94	14.45	5.47	5.20	3.19	15.37	10.64

*Significant at P=0.05 and ** Significant at P=0.01

NSMS= Number of siliquae on main shoot, SD= Siliqua density, STS= Number of siliquae on terminal 15 cm shoot, SPS= Number of seeds per siliqua, TSW=Thousand seed weight, OC= Seed oil content, SYPP= Seed yield per plant, SYPH= Seed yield per hectare

Table 4.3 Mean performance of the M_6 mutant lines of Indian mustard for growth related yield parameters

Genotype	DFF (days)	DM (days)	PH (cm)	NPB (No.)	NSB (No.)	FL (cm)	MRL (cm)	MSL (cm)
L-01	44.00	101.67	145.40	4.33	9.33	39.93	17.40	73.33
L-04	41.00	101.33	117.47	3.60	8.20	34.33	17.00	63.00
L-06	43.67	103.67	126.93	4.07	9.73	31.27	17.07	63.53
L-08	43.67	102.33	125.80	3.73	6.73	34.80	18.00	70.27
L-09	44.67	101.33	147.33	4.13	8.47	35.27	13.80	72.87
L-10	44.00	102.67	122.07	3.53	6.67	40.33	17.67	54.80
L-17	42.00	102.67	138.00	4.07	8.73	39.67	16.67	70.93
L-23	41.67	100.00	131.13	3.60	6.80	31.33	15.73	65.67
L-26	44.33	100.67	123.27	4.27	8.33	31.67	16.53	59.80
L-29	43.33	104.67	142.00	4.00	7.47	44.13	16.67	63.67
L-64	44.00	103.67	145.33	3.67	8.87	24.27	15.60	59.80
L-86	42.67	100.00	147.13	3.40	6.67	36.07	15.67	68.27
L-89	44.33	100.33	125.40	3.47	5.33	37.47	14.40	67.27
L-94	44.33	102.67	110.40	3.87	6.07	32.20	16.73	59.20
L-95	45.00	101.33	158.47	3.60	7.73	45.93	16.53	74.73
L-107	42.67	100.00	183.33	4.47	9.47	38.13	14.93	76.73
L-111	44.33	101.33	159.47	4.27	10.00	28.73	16.27	74.53
M_6 Mean	43.51	101.78	138.17	3.89	7.92	35.62	16.27	66.96
Parent	43.67	108.67	142.73	3.13	5.93	47.67	16.53	61.27
Mean	43.52	102.17	138.43	3.84	7.81	36.29	16.29	66.65
SE(m)	0.34	0.65	4.43	0.15	0.35	1.93	0.45	1.55
CD5%	0.69	1.33	9.05	0.31	0.71	3.94	0.92	3.17
CD1%	0.94	1.79	12.18	0.41	0.96	5.31	1.24	4.26

DFF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, FL= Foot length, MRL= Maximum root length, MSL= Main shoot length

4.4 Days to maturity

The range for days to maturity was from 100 (L-26, L-94, L-107) to 108.7 (parent variety) days. The mean maturity duration was 102.2 days and the mean of the mutant lines was 101.8 days. As the mutant lines were selected for early maturity in previous generations, therefore, all the mutant lines matured in less than 105 days compared to the parent variety NRCHB-101, which was the latest in maturity (108.7 days). The difference between the parent and the mutant lines (101.78 days) was highly significant. All the mutant lines were early in maturity, 6.88 days earlier on the average. The genotypes L-86 (100.3 days) and L-29 (100.7 days), L-04 (101.3 days), L-09 (101.3 days), L-95 (101.3), L-111 (101.3) and L-01 (101.7 days) also exhibited early maturity and all of them were statistically at par. Therefore, from these it was evident that the mutant lines were significantly early in maturity.

4.5 Plant height (cm)

Plant height ranged from 110.4 cm (L-94) to 183.33 cm (L-107) with mean value of 138.43 cm. The mean of the mutant lines was 138.17 cm while the parent variety NRCHB-101 was 142.73 cm tall. The difference was non-significant. Plant height has positive effect on seed yield in mustard, but extremely tall genotypes suffer from lodging. Therefore, medium tall genotypes in the height category of 130-150 cm could be ideal for early maturing varieties. L-107 was the only genotype which was significantly taller than all others. L-111 (159.5 cm), L-95 (158.47 cm), L-09 (147.3 cm) and L-86 (147.1 cm) were at par. The ideal height category also included L-01, L-64, L-29, L-17, L-23 and the parent NRCHB-101 having plant height 131.1 cm to 145.4 cm.

4.6 Number of primary branches per plant

The mutant line L-107 produced the highest number of primary branches per plant (4.47) and parent variety produced the least number (3.13). The mean value for this character was 3.84 while the mean of the mutant lines was 3.89. There was highly significant difference between the mutant lines and the parent; the mutants produced 0.75 more primary branches on the average than the parent. The genotypes L-01 (4.33), L-26 (4.27), L-111 (4.27), L-09 (4.13), L-06 (4.07) and L-17 (4.07) also developed higher number of primary branches per plant, and all of them were at par.

4.7 Number of secondary branches per plant

Number of secondary branches per plant ranged from 5.33 (L-89) to 10.00 (L-111). The mean value for this character was 7.81 and the mean of the mutant lines was 7.92 against the parent value of 5.93 secondary branches per plant. There was highly significant difference between the mutants and the parent. The mutants produced on the average 1.98 more secondary branches than the parent. The genotypes L-06 (9.73), L-107 (9.47) and L-01 (9.33) also developed high number of secondary branches per plant. They were at par for this character.

4.8 Foot length (cm)

Foot length ranged from 24.27 cm (L-64) to 47.67 cm (parent). The mean foot length was 36.29 cm and the mean of the mutants was 35.62 cm. There was highly significant difference between mutants and the parent. The mutants were 12.05 cm shorter than the parent. Short foot length is a desirable trait and it was selected in the previous generations in the present materials, though variation existed. The genotype L-111 (28.73 cm) was at par with the shortest genotype L-64. L-06, L-26 and L-29 were other genotypes that exhibited short foot length and they were at par statistically.

4.9 Maximum root length (cm)

The maximum root length varied from 13.80 cm in L-09 to 18 cm in L-08 with a mean value 16.29 cm (Table 4.3). The parent mean was 16.53 cm and the mean of the mutants was 16.27 cm. The difference between the mutants and the parent was not significant. Other mutant genotypes having long roots were L-10, L-01, L-06, and L-04, all of them being statistically at par along with the longest genotype L-08.

4.10 Main shoot length (cm)

The main shoot length ranged from 54.80 cm (L-10) to 76.73 cm (L-107) with a mean value 66.65 cm (Table 4.3). The parent mean was 61.27 cm and the mean of the mutants was 66.96 cm, and the difference (5.70 cm) was highly significant. Other mutant genotypes having long main shoots were L-95, L-111, L-01 and L-09, all of them being statistically at par with the longest genotype L-107.

4.11 Number of siliquae on main shoot

Number of siliquae on main shoot varied from 26.27 (L-10) to 37.20 (L-08) with a mean value of 32.78 siliquae while the parent mean was 29.73 (Table 4.4). The difference between the mutants and the parent (3.23) was significant. Higher number of siliquae is desirable trait. Other than L-08 the genotypes having high number of siliquae were L-111, L-64, L-95, L-89, L-01, L-107, L-09 and L-17, which were statistically at par with L-08.

4.12 Siliqua density (No./cm)

Siliqua density on main shoot ranged from 0.44/cm for the genotype L-107 to 0.60/cm for genotype L-64 (Table 4.4). There was no difference between the mutant lines and the parent, both the values were 0.49/cm. Siliqua density is an important yield attribute. L-64 exhibited the highest siliqua density, significantly higher than the others. Other genotypes showing high siliqua density following L-64 were L-29, L-08, L-86, L-04, L-26, L-111, parent NRCHB-101, L-10, L-17 and L-95; all of them were statistically at par for siliqua density.

4.13 Number of siliquae on the terminal 15 cm main shoot

The number of siliquae on the terminal 15 cm main shoot (siliquae on terminal shoot) ranged from 7.67 (genotype L-107) to 13.47 (parent variety) with a mean value 10.12 siliquae. The mean of the mutants was 9.92. The difference between the mutants and the parent was highly significant. The parent variety showed the highest number of siliquae on the terminal shoot. Some other genotypes, which were statistically at par with the parent, were L-64 (12), L-26 (11.73) and L-29 (11.07).

4.14 Siliqua density (No./cm) on terminal shoot

The genotypic variation for siliqua density on the terminal shoot was highly significant. Also, there was highly significant difference (0.24/cm) between the mutant lines (0.66/cm) and the parent (0.90/cm). Siliqua density on the terminal shoot ranged from 0.51/cm in L-107 to 0.90/cm in the parent variety. Three other genotypes, viz. L-64 (0.80/cm), L-23 (0.78) and L-26 (0.74/cm) were with high siliqua density on the terminal shoot and they were statistically at par with the parent.

4.15 Number of seeds per siliqua

The number of seeds per siliqua ranged from 10.33 (parent variety) to 13.38 (L-08 and L-64) with a mean value of 12.01 seeds per siliqua (Table 4.4). The mean of the mutants was 12.10 and the difference (1.77 seeds/ siliqua) between the mutants and the parent (10.33) was highly significant. The number of seeds per siliqua is an important yield component trait, and higher number is desirable. Following L-08 and L-64 other mutant lines having high number of seeds per siliqua were L-94 (12.65 seeds/ siliqua), L-95 (12.60) and L-86 (12.41), all of them being statistically at par with L-08 and L-64.

4.16 Thousand seed weight (g)

Thousand seed weight ranged from 3.050 g (genotype L-107) to 4.693 g (L-06) with a mean of 3.893 g against the parent value of 3.560 g (Table 4.4). There was highly significant difference between the mutants and the parent. The mutants had on the average 0.353 g more weight/1000 than the parent. Seed weight is one of the components of seed yield. Therefore higher values are desirable. In addition to the highest genotype L-06, the other genotypes having high seed weight were L-10 (4.557 g) and L-26 (4.373 g) and L-95 (4.363 g), and all of them were statistically at par with L-06.

4.17 Seed oil content (%)

Seed oil content ranged from 32.6 percent (L-111) to 36.64 percent (L-08). The mean oil content was 34.49 percent while that of the parent variety was 33.37 percent (Table 4.4), the difference being statistically non-significant. High oil content is a desirable trait in an oilseed crop. In addition to L-08, some other genotypes viz., L-26 (35.74%), L-01 (35.57%), L-94 (35.52%), L-17 (35.49%) and L-89 (35.39%) were having high oil content and all of them including L-08 were statistically at par for this trait.

4.18 Seed yield per plant (g/plant)

Seed yield per plant ranged from 2.05 g (L-10) to 8.95 g (L-64) with mean of 4.44 g against 3.67 g per plant yield of the parent variety NRCHB-101 (Table 4.4). The average difference between the mutants and the parent was non-significant. L-64 produced significantly higher yield per plant than the others. Other high yielding genotypes on per plant basis following L-64 were L-111, L-01, L-107, L-06, L-09 and L-08, and all of them were statistically at par.

4.19 Seed yield per ha (Kg/ha)

Seed yield per hectare ranged from 469.79 Kg (L-10) to 881.60 Kg/ha (L-64) (Table 4.4). The mean yield was 676.49 Kg/ha, and the mean of the mutants was 677.72 Kg/ha against the yield of the parent variety 655.56 Kg/ha. L-64 was the highest yielding genotype, giving significantly higher seed yield than all others. Following L-64 some other high yielding genotypes were L-95 (796.18 Kg/ha), L-86 (779.51 Kg/ha), L-09 (762.85 Kg/ha), L-01 (745.49 (Kg/ha) and L-107 (740.97 Kg/ha), which yielded significantly better than the parent, and all of them were statistically at par.

4.20 Seed coat colour

The seed coat colour of all the mutant lines was brown or dark brown, except the line L-23 that exhibited light yellow seed coat colour although there was some mix type of seed coat colour (i.e., light yellow and brown.

Table 4.4 Mean values of the M_6 mutant lines of Indian mustard for seed yield and related yield attributes

Genotype	NSMS (No.)	SD (No./cm)	STS (No.)	SPS (No.)	TSW (g)	OC (%)	SYPP (g)	SYPH (Kg)
L-01	34.13	0.47	9.00	11.31	3.353	35.57	5.80	745.49
L-04	32.53	0.51	10.13	12.21	3.553	34.80	3.05	568.40
L-06	29.80	0.47	10.13	11.13	4.693	34.18	5.53	734.03
L-08	37.20	0.53	9.67	13.38	3.217	36.65	5.30	718.75
L-09	33.80	0.46	10.00	12.26	3.767	33.41	5.43	762.85
L-10	26.27	0.48	10.33	11.44	4.557	34.68	2.05	469.79
L-17	33.73	0.47	8.33	12.09	3.887	35.49	3.25	625.00
L-23	32.60	0.50	11.73	11.71	4.150	33.25	3.32	663.54
L-26	31.87	0.53	11.07	11.29	4.373	35.74	2.15	565.28
L-29	31.47	0.49	10.87	12.13	3.590	34.49	4.45	612.50
L-64	36.00	0.60	12.00	13.38	3.443	33.82	8.95	881.60
L-86	31.53	0.46	9.40	12.41	4.073	34.80	3.30	779.51
L-89	34.53	0.52	10.73	12.00	3.940	35.39	3.88	661.46
L-94	28.93	0.49	9.53	12.65	4.323	35.52	3.03	547.22
L-95	35.53	0.47	8.33	12.60	4.363	34.40	4.85	796.18
L-107	33.93	0.44	7.67	12.11	3.050	32.71	5.68	740.97
L-111	36.47	0.49	9.73	11.67	4.183	32.61	6.17	648.61
M_6 Mean	32.96	0.49	9.92	12.10	3.913	34.56	4.48	677.72
Parent	29.73	0.48	13.47	10.33	3.560	33.37	3.67	655.56
Mean	32.78	0.49	10.12	12.01	3.893	34.49	4.44	676.49
SE(m)	1.36	0.02	0.84	0.38	0.117	0.64	0.39	28.76
CD5%	2.78	0.04	1.72	0.78	0.338	1.31	0.80	58.73
CD1%	3.74	0.06	2.31	1.05	0.455	1.76	1.07	79.09

NSMS= Number of siliquae on main shoot, STS= Number of siliqua on terminal 15 cm shoot, SD= Siliqua density, SPS= Number of seeds per siliqua, TSW= Thousand seed weight, OC= Seed oil content, SYPP= Seed yield per plant, SYPH= Seed yield per hectare.

4.20 Study of genetic variability parameters

The genotypic coefficient of variation, phenotypic coefficient of variation, broad-sense heritability and expected genetic advance as a percentage of mean were estimated from the analysis of variance in order to draw inference about the extent of genetic variation and the degree of genetic determination. The genetic variability parameters including the range of values are given in Table 4.5. Good ranges of mean values were observed for all the traits.

High genotypic coefficient of variation (GCV >20%) was observed for yield per plant (37.44%), seed yield per ha (21.12%); medium GCV (10-20%) was observed for number of secondary branches (17.53%), foot length (15.86%), plant height (12.45%), 1000 seed weight (11.93%) and number of siliquae on terminal shoot (11.24%). For the other characters GCV was low GCV (<10%).

High estimates of phenotypic coefficient of variation (PCV) was observed for yield per plant (40.47%) and seed yield per ha (23.65%). Medium PCV was observed for number of secondary branches (19.21%), foot length (18.33%), number of siliquae on terminal shoot (18.30%), plant height (13.62%), number of primary branches (13.44%), 1000 seed weight (13.01%), number of siliquae on main shoot (10.50%) and main shoot length (10.16%). For the other characters low PCV (<10%) was recorded.

High heritability (broad sense) was recorded for seed yield per plant (85.58%), main shoot length (84.28%), 1000 seed weight (84.02%), plant height (83.44%), number of secondary branches (83.24%), seed yield per ha (79.76%), days to maturity (76.02%), days to 50% flowering (75.94%) and foot length (74.80%). Moderate heritability (40-70%) was observed for the characters maximum root length (62.53%), number of siliquae on main shoot (53.27%), number of seeds per siliqua (50.52%), siliqua density (43.89%) and oil content (41.90%), while the heritability value was low (<40%) for the other characters.

Estimate of genetic advance as percent of mean was high (>20%) for yield per plant (71.35%), seed yield per ha (38.86%), number of secondary branches per plant (32.95%), foot length (28.26%), plant height (23.42%) and 1000 seed weight (22.52%). Medium genetic advance (10-20%) was found for maximum root length, main shoot length, number of siliquae on terminal shoot and number of siliquae on main shoot. On the other hand genetic advance was low (<10%) for the rest of the characters.

From the above it was seen that high estimates of GCV, high heritability and high genetic advance were observed for yield per plant and seed yield per ha. High genetic advance and high heritability were observed for seed yield per plant, seed yield per ha and number of secondary branches per plant. These characters were presumably controlled by additive genes and simple selection for these traits was likely to be effective. Plant height, 1000 seed weight, main shoot length, days to maturity, days to 50% flowering and foot length exhibited high heritability with medium or low genetic advance. These characters were presumably preponderantly influenced by non-additive gene action.

Table 4.5 Estimates of genetic parameters for yield and yield attributes in Indian mustard

Character	Range	GCV %	PCV %	h^2(bs) %	Genetic advance%
Days to 50% flowering	41.00-45.00	2.40	2.75	75.95	4.31
Days to maturity	100.00-108.67	1.98	2.27	76.02	3.55
Plant height (cm)	110.40-183.33	12.45	13.63	83.45	23.42
No. of primary branches/ plant	3.13-4.47	7.09	13.45	27.76	7.69
No. of secondary branches/plant	5.33-10.00	17.53	19.22	83.25	32.96
Main shoot length (cm)	54.80-76.73	9.33	10.17	84.28	17.65
No. of siliquae on main shoot	26.27-37.20	7.67	10.51	53.28	11.53
Siliqa density (No./cm)	0.44-0.60	6.14	9.27	43.90	8.38
Siliquae on terminal 15 cm shoot	7.67-13.47	11.24	18.31	37.71	14.22
Terminal siliqa density (No./cm)	0.51-0.90	11.24	18.31	37.71	14.22
No. of seeds per siliqua	10.33-13.38	5.52	7.77	50.53	8.09
Foot length (cm)	24.27-47.67	15.86	18.34	74.81	28.26
Maximum root length (cm)	13.80-18.00	6.17	7.80	62.53	10.05
1000 Seed weight (g)	3.05-4.69	11.93	13.01	84.02	22.52
Oil content (%)	32.61-36.65	2.71	4.19	41.90	3.62
Seed yield per plant (g)	2.05-8.95	37.44	40.47	85.59	71.36
Seed yield per hectare (Kg)	469.79-881.60	21.12	23.65	79.76	38.86

4.21 Character association studies

4.21.1 Genotypic correlation

The correlation coefficients between different traits at genotypic and phenotypic levels are presented in Table 4.6

From the analysis of the correlation coefficients at genotypic level it was found that seed yield per plant had significant positive correlation with plant height, number of secondary branches and number of siliquae on main shoot.

Days to maturity showed strong positive correlation with number of siliquae on terminal shoot, but negative correlation with number of primary branches per plant and main shoot length. Days to 50% flowering did not show significant correlation with any of the characters including seed yield per plant.

Plant height exhibited significant positive correlation with seed yield per plant, number of secondary branches, main shoot length and number of siliquae on main shoot; and negative correlation with oil content. Number of primary branches per plant was observed to be positively correlated with number of secondary branches per plant and main shoot length. Both number of primary branches per plant and number of secondary branches per plant exhibited negative genotypic correlation with number of siliquae on terminal shoot.

There was strong positive correlation between main shoot length and number of siliquae on main shoot. However, main shoot length showed negative correlation with siliqua density, number of siliquae on terminal shoot and days to maturity. Number of siliquae on main shoot was positively correlated with plant height, main shoot length and number of seeds per siliqua, and negatively correlated with number of siliquae on terminal shoot and 1000 seed weight. Siliqua density was positively correlated with number of siliquae on terminal shoot and number of seeds per siliqua, whereas it was negatively correlated with main shoot length and foot length.

Number of siliquae on terminal shoot was correlated with a number of characters. It was positively correlated siliqua density and days to maturity. On the other hand it was negatively correlated with number of primary branches per plant, number of secondary branches per plant, main shoot length, number of siliquae on main shoot and number of seeds per siliqua.

Number of seeds per siliqua exhibited positive genotypic correlation with number of siliquae on main shoot and siliqua density but negative correlation with number of siliquae on terminal shoot. Foot length showed only one significant correlation that was negative correlation with siliqua density. Maximum root length also exhibited only one significant correlation, i.e. positive correlation with oil content. Similarly, thousand seed weight showed only one significant correlation, i.e. a negative correlation with number of siliquae on main shoot. Seed oil content was positively correlated with maximum root length and negatively correlated with plant height.

4.21.2 Phenotypic correlation

At phenotypic level seed yield per plant showed significant positive correlation with plant height, number of secondary branches and number of siliquae on main shoot.

Plant height exhibited strong positive correlation with main shoot length and negative correlation with oil content. Number of primary branches per plant was positively correlated with secondary branches per plant. Main shoot length was positively correlated with plant height and number of siliquae on main shoot but negatively correlated with number of siliquae on terminal shoot. Number of siliquae on main shoot was positively correlated with siliqua density apart from seed yield per plant as mentioned earlier. Siliqua density was positively correlated with number of siliquae on terminal shoot. Oil content was negatively correlated with plant height.

Table 4.6 Genotypic correlation (above diagonal) and phenotypic correlation (below diagonal) between different characters in M_6

	PH	NPB	NSB	MSL	SMS	SD	STS	SPS	FL	MRL	TSW	OC	DM	DF	SYPP
PH	1	0.457	0.507*	0.736**	0.542*	-0.393	-0.435	0.065	0.219	-0.457	-0.426	-0.772**	-0.144	0.102	0.560*
NPB	0.265	1	0.875**	0.597**	0.420	-0.383	-0.842**	-0.120	-0.356	0.077	-0.179	-0.073	-0.564*	0.230	0.375
NSB	0.437	0.622**	1	0.446	0.389	-0.142	-0.509*	-0.062	-0.375	0.037	-0.108	-0.409	-0.199	-0.044	0.567*
MSL	0.680**	0.326	0.376	1	0.821**	-0.498*	-0.780**	0.214	0.184	-0.365	-0.377	-0.240	-0.462*	0.031	0.408
SMS	0.327	0.128	0.277	0.550*	1	0.132	-0.577*	0.597**	-0.252	-0.331	-0.572*	0.125	-0.366	0.099	0.691**
SD	-0.333	-0.164	-0.097	-0.419	0.488*	1	0.567*	0.488*	-0.630**	0.110	-0.178	0.453	0.184	0.133	0.328
STS	-0.292	-0.333	-0.273	-0.527*	0.019	0.499*	1	-0.535*	-0.190	-0.090	0.019	-0.198	0.797**	0.054	-0.079
SPS	-0.028	0.045	-0.042	0.121	0.436	0.376	-0.155	1	-0.352	-0.137	-0.361	0.427	-0.399	0.074	0.432
FL	0.189	-0.178	-0.281	0.116	-0.221	-0.422	-0.015	-0.331	1	0.184	-0.164	0.098	0.383	0.024	-0.370
MRL	-0.329	-0.166	-0.013	-0.245	-0.157	0.037	0.011	-0.083	0.111	1	0.154	0.609**	0.433	-0.125	-0.223
TSW	-0.348	-0.074	-0.086	-0.342	-0.384	-0.089	0.078	-0.201	-0.095	0.099	1	0.048	-0.146	0.264	-0.464
OC	-0.477*	-0.091	-0.273	-0.197	-0.164	0.058	-0.150	0.110	0.064	0.377	0.009	1	-0.040	0.058	-0.391
DM	-0.078	-0.137	-0.105	-0.353	-0.301	0.071	0.323	-0.250	0.343	0.205	-0.049	-0.122	1	0.146	0.091
DF	0.054	0.025	-0.023	0.016	0.065	0.060	0.010	-0.065	0.087	-0.053	0.273	0.069	0.117	1	0.309
SYPP	0.468*	0.217	0.489*	0.337	0.554*	0.311	0.003	0.313	-0.323	-0.221	-0.379	-0.322	0.090	0.227	1

***** Significant at P=0.05; ** Significant at P=0.01

4.22 Path coefficient analysis

The path coefficient analysis aids in the deciphering of a cause and effect relationship between seed yield and its direct and indirect component traits. It was done to separate the direct and indirect effects on seed yield per plant on the basis of genotypic correlation coefficients and given in Table 4.7.

It was observed that number of siliquae on main shoot showed the maximum positive direct effect (1.035) on seed yield per plant and this character was also positively correlated with seed yield per plant. Similarly, plant height showed high direct positive effect and positive correlation with seed yield per plant. Therefore, number of siliquae on main shoot and plant height had true positive relationship with seed yield.

Days to maturity showed high direct effect on seed yield but its correlation was not significant because its indirect effects via other yield attributes, mainly number of siliquae on main shoot and foot length. Number of seeds per siliqua also showed positive direct effect on seed yield per plant but its correlation with yield though positive but fell short of statistical significance. Similar is the case with days to 50% flowering and number of primary branches per plant. These two characters also showed positive direct effects but correlation with yield, though positive, fell short of statistical significance.

The character main shoot length had high negative direct effect on seed yield per plant but non-significant positive correlation with seed yield per plant**.** There were considerable positive indirect effects of main shoot length via number of siliquae on main shoot, siliqua density and plant height. Siliqua density showed high negative direct effect on yield though its correlation with yield was non-significant positive because of its positive indirect effects via other characters, mainly foot length and main shoot length.

Foot length exhibited high negative direct effect on yield and non-significant negative correlation with yield. A few other characters showing low negative direct effects were number of secondary branches per plant, number of siliquae on terminal shoot, maximum root length and 1000 seed weight. Out of these characters, number of secondary branches per plant was positively correlated with yield. It was because it's positive indirect effects via number of siliquae on main shoot, foot length and plant height.

The residual effect in path analysis was 0.047, which indicated that component traits accounted for 95 percent of variation in seed yield per plant.

Table 4.7 Direct and indirect effects of yield attributes on seed yield per plant on the basis of genotypic correlations

	PH	NPB	NSB	MSL	SMS	SD	STS	SPS	FL	MRL	TSW	OC	DM	DF	r (SYP)
PH	**0.608**	0.052	-0.051	-0.727	0.561	0.358	0.048	0.023	-0.192	0.036	0.024	-0.066	-0.127	0.014	0.560*
NPB	0.278	**0.114**	-0.105	-0.591	0.435	0.349	0.093	-0.041	0.312	-0.006	0.010	-0.006	-0.498	0.032	0.375
NSB	0.308	0.119	**-0.100**	-0.441	0.403	0.129	0.056	-0.021	0.328	-0.003	0.006	-0.035	-0.176	-0.006	0.567*
MSL	0.447	0.068	-0.045	**-0.989**	0.849	0.453	0.086	0.074	-0.161	0.029	0.021	-0.021	-0.408	0.004	0.408
SMS	0.330	0.048	-0.039	-0.811	**1.035**	-0.120	0.064	0.206	0.220	0.026	0.032	0.011	-0.323	0.014	0.691**
SD	-0.239	-0.044	0.014	0.492	0.137	**-0.910**	-0.063	0.168	0.552	-0.009	0.010	0.039	0.162	0.018	0.328
STS	-0.264	-0.096	0.051	0.771	-0.597	-0.516	**-0.111**	-0.184	0.166	0.007	-0.001	-0.017	0.703	0.007	-0.079
SPS	0.040	-0.014	0.006	-0.211	0.618	-0.444	0.059	**0.344**	0.308	0.011	0.020	0.037	-0.352	0.010	0.432
FL	0.133	-0.041	0.038	-0.182	-0.260	0.573	0.021	-0.121	**-0.876**	-0.015	0.009	0.008	0.337	0.003	-0.370
MRL	-0.278	0.009	-0.004	0.361	-0.343	-0.100	0.010	-0.047	-0.161	**-0.079**	-0.009	0.052	0.382	-0.017	-0.223
TSW	-0.259	-0.020	0.011	0.373	-0.592	0.162	-0.002	-0.124	0.143	-0.012	**-0.056**	0.004	-0.128	0.036	-0.464
OC	-0.470	-0.008	0.041	0.237	0.130	-0.412	0.022	0.147	-0.086	-0.048	-0.003	**0.086**	-0.035	0.008	-0.391
DM	-0.087	-0.064	0.020	0.457	-0.379	-0.167	-0.088	-0.137	-0.335	-0.034	0.008	-0.003	**0.882**	0.020	0.091
DF	0.062	0.026	0.004	-0.030	0.102	-0.121	-0.006	0.025	-0.021	0.010	-0.015	0.005	0.129	**0.138**	0.309

Residual=0.047

Bold faced diagonal values are direct effects.

Discussion…✍

CHAPTER V

DISCUSSION

Oilseed brassicas, commonly known as rapeseed-mustard, hold a prominent position in the edible oil industry. They are winter loving crops and typically grown during the Rabi season. They are the third most important source of edible oils in the world after palm oil and soybean oil. They are the most popular cooking oil in India and ranks second to soybean among the oilseeds grown in the country. Among the oilseed brassicas, Indian mustard stands out the most important oilseed brassica crop in India and it occupies 75-80 percent areas under rapeseed-mustard (DRMR, 2022).

Breeding programs have led to continuous genetic enhancement in mustard, resulting in varieties with nutritionally superior edible oil and meal, which also serve as a valuable protein-rich livestock feed. As per the USDA Report (2022), the global cultivation area for rapeseed-mustard spans 37.72 million hectares, yielding a production of 73.88 million metric tons resulting in average yield of 1959 Kg/ha. However, India's oilseeds production is insufficient to meet the domestic demand and therefore, India relies heavily on imported edible oils spending substantial foreign exchange. Consequently, there is a pressing need to augment edible oil production to cater to the demands of ever-growing population.

Rapeseed toria (*Brassica rapa*) is the predominant oilseed crop in Assam. The farmers prefer to cultivate toria due to its short duration even though it yields lower than Indian mustard. Toria plants have shallow roots, hollow stems, and exhibit low biological yield, and mature within 85-90 days (Barua, 1992). In contrast, Indian mustard has superior seed yield potential but requires a longer duration than toria. Consequently, there is a focus on developing short-duration Indian mustard varieties. Mustard varieties take about 110 days or more, characterized by thick and solid stems and deep roots (DA&FW document). Therefore, for enhancing the productivity of rapeseed-mustard in Assam, it is necessary to develop short-duration high yielding Indian mustard varieties. Such improvement in yield, duration, quality, and resistance to biotic and abiotic stresses would augment the income of small and marginal farmers. Mutation breeding has emerged as an effective plant breeding method for development of high-yielding and early maturing varieties (Jambhulkar and Shitre, 2009; Venugopalan and Suprasanna, 2022).

To meet the demand for suitable short-duration, high-yielding Indian mustard varieties for Assam, gamma irradiation was employed to induce mutations in a popular high-yielding variety, NRCHB-101. The mutant lines were selectively advanced to M_5-M_6 generations. In the present investigation, 17 M_6 mutant lines along with the parent variety were evaluated for mean performance of the lines, genetic variability among the genotypes for yield, duration and associated traits and to study character interrelationships. The experiment was conducted during Rabi season of 2022-23.

5.1 Mean performances of the M_6 lines

The mean performances of the genotypes were evaluated for 16 quantitative characters. The analysis of variance revealed significant genotypic variation with wide ranges of mean values. The mutant genotypes exhibited desirable yield attributing traits. Notably, certain M_6 mutant lines showed promise compared to the parent variety for all traits, as was seen in Tables 4.4 and 4.5. The best 5 lines for each character are listed here in Table 5.1. These lines can be carried forward for further improvement.

For Assam, the most desirable mustard varieties would be medium-tall, approximately 130-150 cm height, with a short duration of 100-105 days and high seed and oil yield. It is note-worthy that all the mutant lines were early maturing; they matured in less than 105 days, compared to the parent variety (108.7 days). Genotypes L-23, L-26, L-86, L-89, and L-107 were the earliest in maturity (100 days). Table 5.2 presents the early-maturing lines (100-105 days) that displayed high seed yield per hectare, significantly superior to the parent variety. Notably, some lines demonstrated combination of short duration and high seed yield.

The M_6 genotype L-64 showed the highest seed yield of 881.6 Kg/ha and oil content of 33.82% with a maturity duration of 103.6 days. This was followed by L-95 (796.2 Kg/ha, 34.40% oil), L-86 (779.5 Kg/ha, 34.4%), L-09 (762.9 Kg/ha, 33.41%), L-01 (745.5 Kg/ha, 35.57%) and L-107 (741 Kg/ha, 32.71%), and all of them maturing within 102 days. All of them were statistically at par for seed yield per ha, but all of them yielded significantly higher than the parent genotype (655.56 Kg/ha, 108.7 days duration, 33.4% oil). Other short-duration, high-yielding lines are listed in Table 5.2. These lines were in the tall or medium-tall categories. The highest oil content was observed in genotype L-08 (36.65%), followed by L-26 (35.74%), L-01 (35.57%), L-94 (35.52%), L-17 (35.49%), and L-89 (35.39%).

Table 5.1: Best five lines for seed yield and related characters

Character	**Best 5 lines**	**Range of values**
Days to 50% flowering - early	L-04, L-23, L-17, L-86, L-107	41-43 days
Days to maturity - early	L-23, L-86, L-107, L-89, L-26	100-101 days
Plant height (cm) - ideal	L-111, L-95, L-09, L-86, L-01, L-64	159.5-145.3 cm
No. of primary branches per plant	L - 107, L-01, L-111, L-26, L-09	4.5-4.1
No. of secondary branches per plant	L- 111, L-06, L-107, L-01, L-64	10-8.9
Foot length (cm) - Low	L- 64, L-111, L-06, L-23, L-26	24.3-31.7 cm
Maximum root length (cm)	L- 08, L-10, L-01, L-06, L-04	18-17 cm
Main shoot length (cm)	L-107, L-95, L-111, L-01, L-09	76.7-72.9 cm
No. of siliquae on main shoot	L- 08, L-111, L-64, L-95, L-89	37.2-34.5
Siliqua density (No./cm)	L- 04, L-08, L-10, L-23, L-26	0.60-0.51
No. of siliquae on terminal shoot	NRCHB-101, L-64, L-23, L-26. L-29	13.5-10.9
Number of seeds per siliqua	L-64, L-08, L-94, L-95, L-86	13.4-12.4
Thousand seed weight (g)	L- 06, L-10, L-26, L-95, L-94	4.68-4.32 g
Seed oil content (%)	L-08, L-26, L-01, L-94, L-17	36.7-35.5%
Seed yield per plant (g)	L- 64, L-111, L-01, L-107, L-06	8.95-5.53 g/plant
Seed yield per hectare (Kg)	L- 64, L-95, L-86, L-09, L-01	882-745 kg/ha

Table 5.2 Characteristics of the high yielding M_6 genotypes of Indian mustard

Genotype	SYPH (Kg/ha)	DM (Days)	PH (cm)	NPB (No.)	NSB (No.)	FL (cm)	MSL (cm)	NSMS (No.)	SD (No./cm)	STS (No.)	TSW (g)	OC (%)
L-64	881.6	103.7	145.3	3.7	8.9	24.3	59.8	36.0	0.60	12.0	3.44	33.8
L-95	796.2	101.3	158.5	3.6	7.7	45.9	74.7	35.5	0.48	8.3	4.36	34.4
L-86	779.5	100.0	147.1	3.4	6.7	36.1	68.3	31.5	0.46	9.4	4.07	34.8
L-09	762.8	101.3	147.3	4.1	8.5	35.3	72.9	33.8	0.46	10.0	3.77	33.4
L-01	745.5	101.7	145.4	4.3	9.3	39.9	73.3	34.1	0.47	9.0	3.35	35.6
L-107	741.0	100.0	183.3	4.5	9.5	38.1	76.7	33.9	0.44	7.7	3.05	32.7
L-06	734.0	103.7	126.9	4.1	9.7	31.3	63.5	29.8	0.47	10.1	4.69	34.2
L-08	718.8	102.3	125.8	3.7	6.7	34.8	70.3	37.2	0.53	9.7	3.22	36.6

SYPH: Seed yield per ha, DM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NSB: Number of secondary branches per plant, FL: Foot length, MSL: Main shoot length, NSMS: Number of siliquae on main shoot, SD: Siliqua density, STS: Number of siliquae on terminal shoot, TSW: 1000 seed weight, OC: Seed oil content

5.2 Assessment of genetic variation

Genetic variability within a population is essential for the success of a crop improvement program. Remarkable variation was observed among the genotypes for duration and yield-related characters. This suggested that induced genetic variation existed among the genotypes. These findings were similar to the research conducted by Raliya *et al.* (2018), where they also reported significant differences among genotypes for various traits in Indian mustard. Similarly, Meena *et al.* (2017) reported a substantial amount of genetic variability across 39 genotypes of Indian mustard for 12 quantitative characters.

Existence of genetic variability is crucial for successful selection in a breeding programmes. Genotypic and phenotypic coefficients of variation (GCV and PCV) are good measures to assess the extent of genetic variation. Burton and Devane (1953) suggested that comparing genotypic and phenotypic coefficients of variation was the most effective method for evaluating genetic variability for different traits. Knowledge of genetic parameters is indispensable for any practical breeding program (Raliya *et al.*, 2019). In the present study, seed yield per plant and seed yield per hectare exhibited high estimates of GCV and PCV, high heritability and high genetic advance. Similarly, number of secondary branches per plant, plant height and 1000 seed weight showed combination of high genetic advance and high heritability with moderate GCV. These characteristics were likely to be preponderantly influenced by additive genes (Panse, 1957), and thereby implying that simple selection for these traits would be effective. Singh *et al.* (2019) reported similar findings regarding high GCV and PCV for seed yield per plant, number of primary branches per plant, number of secondary branches per plant and 1000-seed weight. Yadava *et al.* (2011) and Chakraborty *et al.* (2021) also observed high GCV and PCV for these traits.

In addition to the traits mentioned earlier, high heritability was also observed for main shoot length, days to maturity and days to 50% flowering. Estimate of heritable variation becomes more meaningful when heritability is assessed in conjunction with genetic advance, as highlighted by Kumar *et al.* (2018). However, genetic advance was low for these characters. Probably non-additive gene action was involved for governing these characters. High heritability and high genetic advance were reported by Kumar and Misra (2007). Yadava *et al.* (2011) reported similar findings of high heritability combined with high genetic advance for thousand seed weight and other related traits in a population of 30 released varieties of Indian mustard.

5.3 Character Inter-relationships

5.3.1 Correlation studies

For enhancing complex quantitative traits like seed yield for which direct selection may not be effective, plant breeders need knowledge about the interrelationships of yield attributes (Nandi *et al.*, 2021). In addition to obtaining information on the nature and magnitude of variation, it is also important to understand the relationships between seed yield and related characters, as well as their cause and effect relationships in order to identify the characters for defining an ideal plant type and for increasing the efficiency of direct and indirect selection (Kumari and Kumari, 2018).

Genotypic correlation is generally caused by linkage or pleiotropic effects of genes and selection effects, which can act independently or together (Falconer, 1989). The genetic improvement can be enhanced only if the pleiotropy or linkage involves two desirable traits (Singh and Narayanan, 2017). From the correlation studies, it was revealed that plant height, number of secondary branches, number of siliquae on main shoot were positively correlation with yield per plant at genotypic level. A strong positive correlation was observed between number of primary branches and number of secondary branches, and between main shoot length and number of siliquae on main shoot. A similar association of plant height with number of primary branches, number of secondary branches, main shoot length and number of siliquae on main shoot was observed by Kumar *et al.* (2018) and Swetha *et al.* (2019). A negative correlation was observed between foot length and seed yield per plant, which was desirable. Devi (2018) and Nandi *et al.* (2021) reported a similar association of foot length with seed yield per plant.

5.3.2 Path analysis

The theory of path analysis was given by Wright (1921) and Dewey and Lu (1959) illustrated the method of path coefficient analysis for plant breeding application, which has since been widely employed to assess the direct and indirect effects of contributing traits on yield. By combining correlation coefficients with path coefficients, researchers gain better insight about character interrelationship, enabling them to effectively design a crop improvement programme. This integrated methodology has proven invaluable in advancing agricultural science and facilitated targeted enhancement in crop productivity and quality**.**

If the association between yield and a yield character is due to a character's direct effect, it indicates the true relationship between them, and direct selection for this character will improve yield. However, if the correlation is primarily due to the character's indirect effect *via* other component traits, indirect selection through that character would be less successful for enhancing yield (Kumar *et al*., 2018). In the present study, number of siliquae on main shoot exhibited the maximum direct effect on seed yield per plant as well as a high positive correlation with the latter. Plant height also showed similar relationship with yield per plant. Number of primary branches, number of seeds per siliqua, and days to 50% flowering showed positive direct effects on seed yield per plant and to some extent positive correlations with yield. Days to maturity exhibited high positive direct effect on yield without any correlation. In such situation, indirect effects of days to maturity via characters like main shoot length were important. Similar findings were also reported by Gupta *et al.* (2018).

The character main shoot length had the highest negative direct effect on seed yield per plant but depicted a non-significant positive correlation with seed yield per plant**.** Similarly, the character foot length had high negative direct effect with non-significant negative correlation with seed yield per plant. Therefore, it could be presumed that foot length expressed a true relationship with seed yield per plant. From the breeder's point of view it was a desirable relationship; because breeders want to develop varieties with high yield and short foot length. Moreover, number of secondary branches and siliqua density showed negative direct effects with positive correlations with seed yield per plant.

A character with wide genetic variability, high heritability, high genetic advance, the high positive correlation and high direct effect on seed yield would be an ideal situation for the breeder for effective selection for enhancing seed yield potential (Bhaduriya and Kumar, 2021). The characters plant height, siliquae on main shoot and foot length were identified to be such yield attributing variables in the present investigation. Heritability for plant height and foot length was high and moderate for siliquae on main shoot.

5.4 Implications of the results and future prospects

The present investigation provided information regarding, mean performance, genetic variability and their interrelationship between yield per plant and yield attributing characters in a mutant population of Indian mustard variety NRCHB-101. Some of the important implications of the findings are given below.

a) Induced mutagenesis through gamma irradiation was effective means of creating genetic variation for agronomically desirable traits including seed yield in Indian mustard.

b) Short duration high yielding genotypes of mustard with low feet are requirement for cultivation in Assam. Few such genotypes were identified in M_6 generation. These genotypes need to be carried forward for multi-location and on-farm testing and then released as varieties. For comparison a toria check variety could be included in future trials.

c) There was genetic variation in the mutant population for seed yield and related traits, which could be exploited for crop improvement to increase oilseed production

d) Resistance to biotic factors such as alternaria blight and mustard aphids, and abiotic stresses such as high temperature, moisture stress and late sowing need to be evaluated and incorporated in the potential varieties.

e) Oil and meal quality attributes are important aspects in rapeseed-mustard. Thees traits need to be enhanced by making appropriate breeding techniques including mutation breeding.

f) Molecular markers are important tools of modern plant breeding. Suitable molecular markers need to be identified and applied in breeding programme to make the breeding process more efficient.

Summary and Conclusion… ✍

CHAPTER VI

SUMMARY AND CONCLUSION

6.1 Summary

The family Brassicaceae comprises plants of significant economic importance, as nearly every part of these plants finds utility in human or animal use. Among them, Indian mustard stands out as the predominant brassica crop, accounting for approximately 75-80 percent of the oleiferous brassica acreage in India during the 2018-19 period. On the other hand, in Assam, toria is the primary brassica crop cultivated, covering about 80-90 percent of the total area. This preference for toria is mainly due to its adaptability to a short crop duration of around 90 days, even though its seed yield is lower compared to mustard. To encourage the expansion of mustard cultivation in Assam, it becomes crucial to develop varieties with reasonably short crop durations.

In the present investigation, an experiment was conducted with 17 M6 mutant lines of Indian mustard along with the parent variety NRCHB-101 to evaluate mean performance, genetic variability and character interrelationships among the genotypes. The genotypes were grown in the experimental area of the Department of Plant Breeding & Genetics, Assam Agricultural University, Jorhat during *Rabi* 2022-23. The mutant lines were derived from mutagenesis by gamma irradiation @ 800, 1000 and 1200 Gy.

Significant variation was observed among the mutant lines for all the characters. Mutant lines vs. parent difference was significant for days to maturity, number of primary branches, number of secondary branches, main shoot length, number of siliqua on main shoot, number of siliqua on terminal 15 cm shoot, number of seeds per siliqua, foot length and thousand seed weight. Compared to the parent variety, the mutants were earlier in maturity by 6.9 days, shorter plants by 15.51 cm, main shoots shorter by 2.88 cm, siliquae longer by 0.70 cm, seed yield per plant lesser by 0.8 g per plant and seed yield per hectare is more by 14.9 kg/ha.

More than 10 lines were isolated from the M_6 mutants which were superior to the parent by 82.8 per cent for seed yield per ha with maturity duration of 100-103 days. These lines could be exploited for development of early maturing mustard varieties by further evaluation. The genotype L-64 was the highest performing line for seed yield and oil yield per hectare with maturity duration 103 days.

High genotypic coefficient of variation (GCV) was observed for yield per plant (37.44%), yield per hectare (21.12%); medium GCV (10-20%) was observed for number of secondary branches (17.53%), foot length (15.86%), 1000 seed weight (11.92%) and number of siliquae on terminal shoot (11.24%). For the other characters GCV was low GCV (<10%). High phenotypic coefficient of variation (PCV) was observed for the yield per plant (40.47%) and yield per ha (23.65%). Medium PCV was observed for main shoot length (10.16%), number of siliquae on main shoot (10.50%), 1000 seed weight (13.01%), number of primary branches (13.44%), plant height (13.62%), number of siliquae on terminal shoot (18.30%), foot length (18.33%) and number of secondary branches (19.21%). For the other characters low PCV (<10%) was recorded.

High heritability (broad sense) was recorded for yield per plant (85.58%), main shoot length (84.28%), 1000 seed weight (84.02%), plant height (83.44%), number of secondary branches (83.25%), yield per ha (79.76%), days to maturity (76.02%), days to 50% flowering (75.94%) and foot length (74.80%). Moderate heritability (40-70%) was observed for the characters oil content (41.90%), siliqua density (43.89%), number of seeds per siliqua (50.52%), number of siliquae on main shoot (53.27%) and maximum root length (62.53%). On the other hand, low heritability (<40%) was recorded for number of primary branches (27.75%) and number of siliquae on terminal shoot (37.7%).

Genetic advance as percent of mean was high (>20%) for yield per plant (71.35%), yield per ha (38.86%), number of secondary branches per plant (32.95%), foot length (28.26%), plant height (23.42%) and 1000 seed weight (22.52%). Medium genetic advance (10-20%) was obtained for root length, number of siliquae on main shoot, number of siliquae on terminal shoot and main shoot length. On the other hand, genetic advance was low (<10%) for days to maturity, days to 50% flowering, seed oil content, number of primary branches, siliqua density and number of seeds per siliqua.

From the correlation analysis of *Rabi* 2022-23, it was observed that plant height, number of secondary branches, number of siliquae on MS exhibited positive correlation with seed yield per plant. Plant height showed strong positive correlation with number of secondary branches, main shoot length and number of siliqua on main shoot. Number of primary branches per plant exhibited significant positive correlation with number of secondary branches per plant and main shoot length. A significant positive correlation was also observed between the traits number of siliqua on main shoot and number of seeds per siliqua. Main shoot length exhibited significant positive correlation with number of siliqua. The character siliqua density exhibited significant positive correlation with number of siliqua on terminal 15 cm of main shoot and number of seeds per siliqua. Number of siliqua on terminal 15 cm of main shoot exhibited significant positive correlation with days to maturity .The character maximum root length exhibited significant positive correlation with oil content. A positive correlation indicates that an increase in one character would lead to a simultaneous increase in the correlated character, while in the case of negative correlation it is just the opposite. It was also observed that seed yield per plant exhibited negative correlation with thousand seed weight. The character plant height exhibited significant negative correlation with oil content. Number of secondary branches per plant was also negatively correlated with number of siliqua on terminal 15 cm of main shoot.Number of primary branches per plant exhibited significant negative correlation with number of seeds on terminal 15 cm of main shoot. The character number of siliqua on main shoot was also negatively correlated with number of siliqua on terminal 15 cm of main shoot and thousand seed weight. The character siliqua density exhibited significant negative correlation with foot length. Number of siliqua on terminal 15 cm of main shoot exhibited significant negative correlation with number of seeds per siliqua.

From the path analysis it was observed that number of siliqua on main shoot showed the maximum positive direct effect towards seed yield per plant while the character main shoot length showed a high negative direct effect on seed yield per plant and exhibited significant positive correlation with seed yield per plant. The character number of plant height, number of primary branches per plant, number of seeds per siliqua, days to maturity and days to fifty per cent flowering showed positive direct effect towards seed yield per plant and all of these characters exhibited significant positive correlation with seed yield per plant. Although the character oil content showed positive direct effect on seed yield per plant, it has a negative correlation with seed yield per plant. The characters main shoot length, number of secondary branches per plant, siliqua density, per siliqua number of siliqua on terminal 15 cm of main shoot, foot length maximum root length and thousand seed weight showed negative direct effect on seed yield per plant.

6.2 Conclusion

Significant variation was present among the 17 M6 mutant lines along with the parent variety NRCHB-101 for seed yield and its attributing traits. The mean of the mutants was significantly different from the parent line for several yield attributes. Therefore, mutagenesis was effective and it offered scope for selection to bring about for the genetic improvement of the crop.

High genotypic coefficient of variation (GCV) and (PCV) was observed for yield per plant and yield per hectare. High heritability was observed for yield per plant, yield per ha, 1000 seed weight, foot length, main shoot length, number of secondary branches, plant height, days to maturity and days to 50% flowering. High estimates of genetic advance were observed for number of secondary branches, seed yield per plant and seed yield per ha.

Based on short duration (100-105 days) all of the 17 M_6 mutant lines performed better than the parent. The mutant lines L-64, L-95, L-86, L-9, L-1 and L-107 were promising with significantly superior seed yield per hectare with maturity duration less than 105 days compared to the parent variety. The genotype L-64 exhibited the highest seed yield (881.6 Kg/ha) and oil content (33.82%) with maturity duration of 103 days. L-23, L-86, L-107 and L-89 (100 days) were the earliest maturing and high yielding line. Medium tall (around 120-140 cm) genotypes with short duration (100-105 days) and high seed and oil yield would be the most desirable mustard varieties for Assam.

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Photo Gallery…✍

PHOTO GALLERY

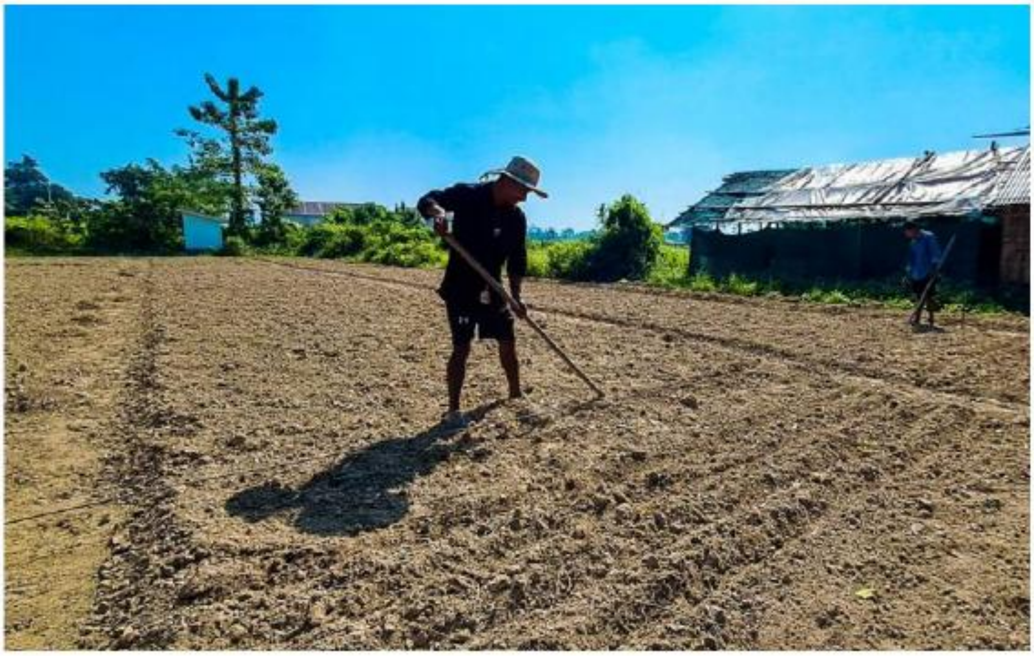

Plate 1: Land Preparation

Plate 2: Fertilizer and Fym Application

Plate 3: Flowering Stage

Plate 4: Field View

Plate 5 (a): Genotypes used in the study

Plate 5 (b): Genotypes used in the study

Plate 6: Harvested lots

Plate 7: Threshing

Plate 8: Winnowing

Appendix…✍

APPPENDIX – I

Meteorological data during the period of experimentation

SMW	Weekly Met. Data	Temp. (ºC)		RH %		Total RF (mm)	Rainy days	Total BSSH (hrs.)
		Max.	Min.	Morn.	Even.			
2022								
46	12 Nov - 18 Nov	28.3	14.4	99	57	0	0	7.9
47	19 Nov - 25 Nov	28.2	12.3	97	51	0	0	9
48	26 Nov - 2 Dec	28.4	11.6	99	53	0	0	9
49	3 Dec - 9 Dec	27.7	11.3	100	53	0	0	8.3
50	10 Dec -16 Dec	26.7	11.5	99	58	0	0	7.5
51	17 Dec - 23 Dec	26.2	11.8	99	57	0	0	7.1
52	24 Dec- 31 Dec	22.1	10.9	100	69	0	0	2.7
2023								
1	1 Jan - 7 Jan	23.7	7.9	99	52	0	0	6.6
2	8 Jan - 14 Jan	25.2	8.8	98	54	0	0	7.4
3	15 Jan -21 Jan	21.4	8.5	99	62	0	0	3.3
4	22 Jan - 28 Jan	24.9	8.8	98	53	0	0	6.6
5	29 Jan - 4 Feb	27.2	11.5	99	53	0	0	9.7
6	5 Feb - 11 Feb	23.3	12.9	99	67	8.5	1	0.1
7	12Feb - 18 Feb	25.1	11.9	98	49	0.2	0	5.7
8	19Feb - 25 Feb	25	15.2	97	70	31.8	3	1.8
9	26 Feb - 4 Mar	27.9	13.2	95	44	0	0	7.4
10	5 Mar - 11 Mar	29.3	14.8	94	49	0	0	5.9
11	12 Mar - 18 Mar	28.8	15.7	95	55	7.0	1	3.7
12	19 Mar - 25 Mar	22.8	15.6	99	86	73.0	5	0.8
13	26 Mar - 1 Apr	26.8	16.8	96	67	6.0	1	3.8

Source: Department of Agro-Meteorology, AAU, Jorhat