

**“Genetic studies on yield and its related attributes
in Indian mustard [*Brassica juncea* (L.) Czern. &
Coss.]”**



THESIS
SUBMITTED IN
PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR THE DEGREE
OF
MASTER OF SCIENCE
IN
AGRICULTURE IN GENETICS AND PLANT BREEDING
2024

**Submitted by:
guidance of**

Suraj Dwivedi

Id. No. CA-12478/2022
botanist

Under the

Dr. Mahak Singh

Professor /economic
(oil seed)

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
**CHANDRA SHEKHAR AZAD UNIVERSITY OF AGRICULTURE &
TECHNOLOGY, KANPUR- 208002 (U.P.) INDIA**



**DEDICATED TO GOD &
MY BELOVED PARENTS**

SURAJ DWIVEDI...

MAHAK SINGH
Professor /economic botanist
(oil seed)
Department of Genetics and Plant
Breeding

Department of Genetics and Plant
Breeding
C. S. Azad University of Agriculture and
Technology, Kanpur-208 002



CERTIFICATE

This is to certify that thesis entitled “**Genetic studies on yield and its related attributes in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]**” submitted in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture** with major in **Genetics and Plant Breeding** from College of Agriculture, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, (U.P.) is a record of bonafide research work carried out by **Mr Suraj Dwivedi, Id. No. CA-10478/22**, under my guidance and supervision. The thesis embodies the work of candidate herself.

Place: Kanpur

(Mahak Singh)

Dated: / / 2024

Chairman
Advisory Committee

DEPARTMENT OF GENETICS AND PLANT BREEDING
CHANDRA SHEKHAR AZAD UNIVERSITY OF AGRICULTURE
AND TECHNOLOGY, KANPUR-208 002 (INDIA)



ADVISORY COMMITTEE CERTIFICATE

We, the undersigned members of the advisory committee of **Suraj Dwivedi**, Id. No. CA-12478/22, a candidate for the degree of **Master of Science in Agriculture** with major **Genetics and Plant Breeding**, agree that the thesis entitled, "**Genetic studies on yield and its related attributes in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]**" is submitted by him in partial fulfillment of the requirements for the degree.

(Mahak Singh)

(Chairman)

Professor/economic botanist (oil seed)
Department of Genetics & Plant
Breeding

(R.K. Yadav)

(Member) Professor & Head
Department of Genetics & Plant
Breeding

(C. L. Maurya)

(Member) Dean & Professor
Department of Seed Science
& Technology

(Vijay Kumar Yadav)

(Member) Professor
Department of Genetics & Plant
Breeding
Breeding

(Shweta)

(Member) Assistant Professor
Department of Genetics & Plant

ACKNOWLEDGEMENT

I dedicate my unfeigned thanks to “GOD” who invigorated me with the fortitude and capability to aptly complete my research work.

I feel privileged to express my sincere gratitude toward my respected guide and chairman of my advisory committee, [Dr. mahak singh](#) (professor/ economic botanist (oil seed) Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.) for always being there for me and guiding me throughout. I am grateful for her excellent and praise worthy guidance, keen interest, patience, encouragement and parental affection during whole of my degree. This journey would not have been possible without her effort.

I am also very thankful to the members of my advisory committee, [Dr. R.K. Yadav](#) (Head, Department of Genetics and Plant Breeding), [Dr. C.L. Maurya](#) (Dean & Professor, Department of Seed Science and Technology), [Dr. Sweta](#) (Assistant Professor) Department of Genetics and Plant Breeding, [Dr. Vijay kumar Yadav](#) (professor) Department of Genetics and Plant Breeding. for their technical guidance, keen interest, sympathetic attitude & help at different stages of the investigation. I am also thankful to [Md. Zaheer](#) and [Mr. Manish Gupta](#) and all the members of Department of Genetics and Plant Breeding who timely helped me for successfully finishing my research work.

I am overwhelmed with rejoice to evince my profound sense of veneration towards my Grandfather [Dr. P.N. Dwivedi](#), grand mother late. [smt. kewalpati devi](#). my mother [Mrs. Kanchan](#), my father [Mr. Krishan Kumar Dwivedi](#) who have always been my role models, for providing me with their constant immense affection, blessings, moral support, enthusiasm and their untiring efforts as a source of inspiration and encouragement to strive harder in life. I want to express my heartfull gratitude to all my family members, [Mr. Ram Sewak Dwivedi](#), [Mr. Vijay Dwivedi](#) [Mr. sanjay kumar Dwivedi](#), [Mr. Arun Kumar Dwivedi](#). thanks for all that you do, your support means the world to me .also for believing in me and empowering me to be and do my best.

I pay obeisance to my sister [Alpana Dwivedi](#), and brother [Mr. Atul kumar Dwivedi](#), for the encouragement they brought out in my life and whose support silently worked in bringing me near to my long-cherished aspiration.

Friends are like rare, priceless pearls from the depths and I truly have some of gems in my life. My best friend [Nilesh Dwivedi](#), [Ashutosh Pandey](#) deserves a particular mention since he constantly stood by me in all good and bad times and inspires me to accomplish my goals.

The limited world of words hampers me to express the feeling of my indebtedness towards my friend Mohit Shukla ,Prabhujeet, Jay, Kshitij, Shivam, Devendra, Ashish Singh, Sandeep Nirdesh, Ratish whose love, frolic and affection always made me feel at home here in the leather city of India. My batchmates Abhishek dimri, Ayush mishra, Ramjeewan. Manish sankhalyan, Saloni singh, for providing the friendly amiable environment to me during my thesis work.

I gratefully express my deep sense gratitude to my respected seniors kirti singh

My cordial thanks to Dr.Bhanupratap (Associatet professor, fruit science at Acharya Narendra Deva University of Agriculture & Technology, Ayodhya) for his extremely support, encouragement and best help for completing this manuscript. His constant guidance went a long way in successful completion of this herculean task.

Lastly the co-operation provided by the entire staff of Department of Genetics and Plant Breeding and all the respondents of the study area who help me directly or indirectly are greatly acknowledged.

Date:

Place: KANPUR

(SURAJ DWIVEDI)

INDEX

CHAPTERS	PARTICULARS	PAGE NO.
I	INTRODUCTION	1-5
II	REVIEW OF LITERATURE	6-32
III	MATERIALS AND METHODS	33-51
IV	EXPERIMENTAL FINDINGS	52-115
V	DISCUSSION	116-126
VI	SUMMARY AND CONCLUSION	127-130
*	BIBLIOGRAPHY	i-xv
**	APPENDIX	1-3

List of Tables

S. No.	Title	Page No.
1	Details of genotypes used as parents in the experiment	34
2	Twenty-one F ₁ s obtained from 7x7 diallel crosses of Indian mustard	35
3	Analysis of variance (ANOVA)	38
4	ANOVA for Combining ability	43
5	Scale for Genetic advance in percent of mean	46
6	Scale for Path Coefficient	51
7	Analysis of variance of parents and F ₁ s for twelve traits in Indian mustard	53
8	Mean performance and range of variability of 7 parents and F ₁ for 12 characters in Indian mustard	56
9	Maximum and minimum mean values of parents and crosses for 12 traits in Indian mustard	57-58
10	Uniformity test for W _r -V _r using regression coefficient and 't ² ' for 12 characters in Indian mustard	63
11	Estimates of variance components analysis and related parameters for 12 traits in Indian mustard	65-66
12	Analysis of variance of combining ability and their ratios for 12 traits in Indian mustard	70
13	Estimates of gca effects of parents for 12 traits in Indian mustard	73
14	Ranking top three desirable parents based on per se performance and GCA effects for 12 attributes in Indian mustard	74-75
15	Estimates of SCA effects of 21 F ₁ s for 12 characters in Indian mustard	80-81
16	Ranking top three desirable parents based on per se performance and SCA effects for 12 attributes in Indian mustard	82-83
17	Estimates of heterosis for hybrids for 12 characters in Indian mustard	88-92

18	Genetic variability, heritability, genetic advance and genetic advancement in percent over mean for 12 characters in Indian mustard	96
19(a)	Genotypic correlation coefficient among the seed yield and it's contributing characters for 12 characters in Indian mustard	98
19(b)	Phenotypic correlation coefficient among the seed yield and it's contributing characters for 12 characters in Indian mustard	104
20(a)	Direct & indirect effect of 12 characters on seed yield of Indian mustard as independent variable at genotypic level	108
20(b)	Direct & indirect effect of 12 characters on seed yield of Indian mustard as independent variable at phenotypic level	112

LIST OF SYMBOLS AND ABBREVIATIONS

SYMBOLS	ABBREVIATION
/	Per
%	Percentage
°C	Degree celsius
&	And
ANOVA	Analysis of Variance
σ	Standard deviation
CD	Critical Difference
CV	Coefficient of variation
SC	Standard Check
BP	Better Parent
EP	Economic Parent
Cov.	Covariance
Inter.	International
d.f.	Degrees of freedom
<i>et al.,</i>	et-alai (and others)
F ₁	First filial generation
g	Gram
cm.	Centimeter
<i>i.e.</i>	That is
GCA	General combining ability
SCA	Specific combining ability
<i>Per se</i>	Actual
R	Replication
T	Treatment
P	Parent
No.	Number of
MT	Million Tonne
v/s	Versus
SEm	Standard error of mean
X	General mean
Min.	Minimum
<i>Viz.,</i>	Videlict (Namely)
*	Significant at 5%
**	Significant at 1%

Genetic and combining ability analysis of seed yield and its contributing traits in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]

Name of the student : Suraj Dwivedi
I.D. Number : CA-12478/2022
Advisor : Dr. Mahak Singh
Year : 2022-2024
Degree : Master of Science in Agriculture
Department : Genetics and plant breeding

**Chandra Shekhar Azad University of Agriculture & Technology, Kanpur-208002 (U.P.),
India.**

ABSTRACT

The present investigation, "**Genetic studies on yield and its attributing traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]**" was carried out at Oilseed Research Farm, Kalyanpur of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.), India during *rabi* 2023-24 with 28 treatments [7 parents and their 21 crosses] following diallel cross analysis excluding reciprocals in 3 replications laid out in randomized block design. Observations were made on 12 quantitative characters namely days to 50% flowering, days to maturity, length of main raceme (cm), plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae on main raceme, number of siliquae per plant, average seeds per siliquae, 1000-seed weight (g), oil content (%) and seed yield per plant (g) during the course of investigation.

The genetic component of variance showed significant values for both additive \hat{D} & the dominance \hat{H}_1 \hat{H}_2 components for almost all the characters. The degree of dominance showed over-dominance for the characters such as Days to 50% flowering, days to maturity, length of main raceme, plant height, number of primary branches, number of secondary branches, number of siliquae on main raceme, number of siliquae per plant, average seeds per siliquae, and seed yield per plant.

Analysis of Variance for combining ability revealed the significant values for both *gca* & *sca* various for most of the characters. The estimated values of variance due to specific combining

ability (σ^2_{gca}) were higher than the variance of general combining ability (σ^2_{sca}) for all the characters except oil content (%). It indicated these characters are under the control of non-additive gene action. Hybrids NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8 and NDR8501 x AZAD MAHAK showed high heterosis over both better and economic parent (Azad Mahak) for seed yield per plant. NARENDRA AGETI RAI-8 x AZAD MAHAK showed high heterosis for oil content.

The parents AZAD MAHAK, NDR8501 were good general combiners for a number of traits especially for oil content (%) and seed yield per plant (g). NARENDRA AGETI RAI-4 X AZAD MAHAK showed high sca effect for oil content (%) whereas NDR8501 X AZAD MAHAK showed high sca effect for seed yield per plant (g).

Genotypic correlation coefficient was higher in magnitude than their corresponding phenotypic correlation coefficient for all the characters. Significant positive correlations were found in seed yield per plant with all the characters except Days to maturity.

Phenotypic path analysis values revealed that positive and indirect effects were exerted on seed yield per plant by all the traits except Days to maturity. Thus, the selection pressure on these traits may lead to overall increase in the yield. To harvest maximum yield potential, a certain degree of heterozygosity should be maintained in a population.

Chapter 1

INTRODUCTION

[*Brassica juncea* (L.) Czern & Coss.] commonly known as Indian mustard, is a major oil seed crop that has been grown in India for centuries and is both versatile and economically significant. Among the first crops to be domesticated was this one as well. The Latin word "mustum," which meaning "condiment," is where the term "mustard" originated. The ecotypes of Brassica that are primarily grown in India include *Brassica juncea*, also known as Indian mustard, *Brassica nigra*, also known as black mustard, and *Brassica campestris*, also known as yellow sarson, brown sarson, and toria. Within the Brassica family of oil seed crops, Indian mustard (*Brassica juncea*(L.) Czern.and Coss.), sometimes referred to as rai, raya, or laha, makes up a sizable component.

Mustard's origins are unknown and diverse. Vavilov (1949) identified the principal centre of origin of mustard as Afghanistan and its neighbouring regions, with subsidiary centres of origin consisting of central and western China, Eastern India, and minor Asia, including Iran. Given that wild variations of Brassica rapa and Brassica nigra exist in this area, the Middle East has been suggested as the most likely origin of *Brassica juncea* (Olsson, 1960a,b); Mizushima et al., 1967 and Prakash et al., 1980). The hypothesis that the regions of northwestern Himalayas and southwestern China may represent two secondary centres of origin where there is significant variation in *Brassica juncea* forms is supported by biochemical research (Vaughan et al., 1963). It was brought from China to India. The prime mustard growing countries world are India, China, Canada, Pakistan, Poland, Bangladesh and Sweden.

Indian mustard is an amphidiploid ($2n=36$), according to U 1935. It was produced via interspecific crossing of *Brassica campestris* ($2n=20$) with *Brassica nigra* ($2n=16$), followed by spontaneous chromosomal doubling. Along with other closely related cultivated Brassica species, such as Black mustard (*B. nigra* (L.) Koch $2n$ (BB) = 16), Yellow mustard (*B. campestris* syn. *Brassica rapa* (L.) var. Yellow sarson, $2n$ (AA) = 20), Brown mustard (*B. campestris* syn. *Brassica*

rapa (L.) var. Brown sarson, 2n (AA) = 20), Taramira [*Eruca sativa*. Mill. 2n (EE) = 22], Ethiopian mustard or Karan rai (*B. carinata* A. Braun, 2n (BBCC) = 34], and Gobhi sarson (*B. Napus sp.oleifera* DC var. *annua* (L.), 2n (AACC) = 38). Indian mustard accounts for more than 80% of the total acreage used for rapeseed and mustard cultivation.

Mustard plants are erect, multibranched, and tall (90–200 cm). The leaves are pinnate, broad, and stalked. The erect, 2–6.5 cm long fruits with short, and robust beaks. The thick seed coat has a brown or dark brown colour. The inflorescence of Indian mustard (*Brassica juncea*) like a corymbose raceme. Uncertain flowering could last for two to three weeks. The stigma becomes receptive even two or three days before the flower opens, facilitating bud pollination selfing easier. *Brassica juncea* is self-compatible despite being an amphidiploid. It is an autogamous species by nature, with 5–30% of offspring resulting from environmental factors and random fluctuations in pollinating insects (Kumar et al., 2013).

The mustard seed has 2.56 g of protein, 1.41 g of sugar, 2 g of fibre, 0.47 g of fat, and 4.51 g of filled with nutrients carbs per 100 g. About 36–38% protein, 14–16% carbohydrate, 10–15% fibre, 6–8% moisture, 4–6% ash, 3–4% minerals, 0.7–0.9% vitamins, 2–3% glucosinolate, 3–6% phytic acid, 1–1.5 percent sinapine, and 1.6–3.1 percent tannin are present in the brassica seed oil cake (Agnihotri et al., 2004). A total of 10.70% of saturated fatty acids, such as arachidic acid (6.9%), stearic acid (0.9%), and palmitic acid (2.9%), are present in *Brassica juncea*. Of these, 56% are monosaturated fatty acids, such as erucic acid (46.5%), oleic acid (8.9%), and palmitoleic acid (0.6%). The remaining 32.6% are polyunsaturated fatty acids, such as linoleic acid (18.1%) and linolenic acid (14.5%) (Gopalan et al., 2007).

Erucic acid, a fatty acid that makes up 40–50% of Indian mustard, and sulfur-rich glucosinolates (100–280 μ moles/g of defatted seed meal) are the two main antinutritional components of the plant. A high concentration of erucic acid causes heart problems and an unpleasant frying smell. Yet, the utilisation of seed meal cake as animal feed for monogastric animals is hampered by high quantities of glycosinolates. Varieties with reduced erucic acid and glucosinolate content have recently been created. The globally approved specifications are Canola grade odd rapeseed cultivars, sometimes referred to as double low or double zero '00', with 2%

erucic acid and 30 μ moles/g glucosinolates. Triple zero (000) types are those that have low concentrations of erucic acid, glucosinolate, and crude fibre.

According to Bhowmik et al. (2014), Indian mustard seeds contain between 37 and 49% oil, which has a strong aroma and is regarded as the healthiest and most nutritious cooking medium. Oil and seeds are used as condiments when making pickles. Because mustard oil contains antibacterial and anti-inflammatory qualities, it is utilised in the tanning industry, soap manufacturing, and medical fields. Since the young plant's leaves provide enough minerals and sulphur for the diet, they can be consumed as a green vegetable.

Cattle can find plenty of green food in the green leaves and stem.

In India's major crop-growing regions, it is grown during the Rabi season. In India in 20121–22 it had 8.06 million ha area, a production of 11.75 million tonnes (*E&S Division, DA&FW 2023*)

The seven Indian states of Gujarat, Assam, West Bengal, Rajasthan, Madhya Pradesh, and Uttar Pradesh are among those where it is grown nationwide. These states account for more than 90% of its production and more than 80% of its land (*E&S Division, DA&FW 2023*). More over half of India's land is in the state of Rajasthan. Indian mustard has significantly increased in size in the past; nevertheless, because the majority of the cultivated area is rainfed, resources are scarce, and there are biotic and abiotic obstacles, present output levels are still modest. This crop is currently facing extra challenges from limited genotypic potential, price instability, and climate change. In both traditional and non-traditional locations of India, this crop has enormous potential to increase output with technological breakthroughs, sufficient inputs, and a suitable legislative framework.

In india rajathan is the leading producer of rape seed and mustard accounts 5.48 million tonnes and its area is 3.37 million ha. Uttarpradesh rank fourth in terms of area and production ,area of up is 0.76 million and production 1.03 million tonnes (*E&S Division, DA&FW 2023*). Per capita availability of edible oil in india is 19.7 kg (PIB.Goi.in 2023)

In order to meet the anticipated demand for oil, this crop's productivity potential must be drastically expanded. The development of hybrids with high seed yield and oil content is essential to bridging the gap between oil output and human population. Gaining an understanding of heterosis is crucial for understanding the breeding techniques that will be applied to improve crops

through hybridization. Heterosis studies also help select only the crosses with the highest yield potential by eliminating many from the F1 generation itself. Heterosis breeding is one of the most feasible ways to get over the yield barrier (Allard, 1960). Because very effective cytoplasmic genetic male sterility and fertility restoration systems such as *mori*, *ogura*, and 126-1 are available, brassica heterosis may be exploited inexpensively. Cytoplasmic male sterility, or CMS, is a useful tool in this species for taking advantage of heterosis and making useful hybrid seeds.

In both tropical and sub-tropical regions, mustard is grown since it is a cold-loving crop. It is grown from the north-eastern/northwestern hill to the south under a range of agro-climatic circumstances, such as irrigated/rainfed, timely/late planted, saline, and mixed cropping. Mostly temperate regions are preferred to cultivate mustard.

It is a Rabi crop, which requires dry conditions during the harvesting season, moderate soil moisture during the growth season, and fairly cool temperatures. Light loam, which can be found in soil types ranging from clay loam to sandy loam, is the best soil for growing mustard. Mustard crops require a pH range of 6.0 to 7.5 to grow in heavy soils during water logging scenarios (Madhusoodanan 2016) et al., Two essential and challenging elements in the effectiveness of a breeding endeavour are the quantity of genetic variety that is available and the ability of the parents to undergo hybridization. The conventional method of choosing parents based on their personal achievement does not guarantee success (Allard,1960)

The best breeding strategy for maximising genetic potentiality and breaking through in crop productivity relies on an extensive understanding of the genetic system underlying character inheritance, as well as knowledge of the type and degree of gene action, correlations between different characters, heritability, and genetic advancement.

In plant breeding, combining ability has been widely utilised to determine how effectively parental lines function in hybrid combinations. In 1942, Sprague and Tatum invented it. In order to identify the best performing lines for commercial release and lines that may be used as parents in future heterosis breeding, the majority of crop breeding programmes prioritise the use of combining ability (Oakey et al., 2006). Parental lines can be selected using certain mating designs, such as North Carolina designs I, II, and III, diallel, and line x tester. With the help of such mating designs, the genetic effects of a line can be divided into two categories: additive (fixable) and non-additive (non-fixable) (Oakey et al.,2006;Topal, 2004)

.. Only when the gene frequencies of the parental cultivars used to produce F1 differ may heterosis occur. Selecting parents for a hybrid development plan based on ability analyses combined with diversity estimates may prove beneficial. Using phenotypic features, a number of studies have already evaluated genetic diversity (Gupta et al., 1991; Vaishnava et al., 2006; Alie et al., 2009; Yadava et al., 2012a; Singh et al., 1966). Analysing the combining potential of two parental lines is one of the best ways to tell if they will produce better offspring. Combining ability analysis is essential to finding desirable parents and crosses.

In both self-pollinated and cross-pollinated species, the design of diallel mating has been extensively utilised to study the type of gene activity responsible for the expression of quantitative traits. It offers reliable information on variance components, the effects of GCA and SCA variances, and their composition. Consequently, it facilitates the choice of appropriate parents for hybridization as well as the optimal breeding practises (Hayman, 1954; Griffing, 1956). When applicable, parallel techniques (Griffing, 1956) have been widely used in a number of species to provide information on GCA x ENV, SCA x ENV, maternal x ENV, and non-maternal x ENV interactions. It considerably boosts researchers' efficiency while studying and interpreting dial-cross data.

Therefore, keeping in view the above background, the present investigation entitled **“Genetic studies on yield and its related attributes in Indian mustard (*Brassica juncea* L. Czern & Coss)”** was undertaken with the following objectives:

- ◆ to estimate the extent of variability among parents and their F1s progenies,
- ◆ to study the genetic components based on analytical approaches,
- ◆ to estimate general and specific combining ability variances and effects,
- ◆ to estimate the heterosis for the characters studied,
- ◆ to estimate heritability and genetic advance for different traits,
- ◆ to estimate the genotypic and phenotypic correlation coefficients, and
- ◆ to determine the direct and indirect effect of different characters on seed yield.

♦ Chapter 2

REVIEW OF LITERATURE

Indian mustard [*Brassica juncea* (L.) Czern & Coss.; $2n = 36$] is a naturally amphidiploid plant. Combining ability analysis is one of the powerful techniques available for the development of high yielding crop plant varieties. It provides estimates of combining ability effects and aids in selecting only desirable parents for various breeding programmes and further exploitation. Several researchers calculated heterosis, specialised combining ability, and general combining ability for several attributes in different crop species using the Diallel mating design. The current evaluation attempted to compile the existing knowledge on heterosis and combining ability analyses for several features in Indian mustard.

The following is a brief review of literature studies on genetic variability, diallel crossanalyses, combining ability and gene action, heterosis, heritability, genetic advance, correlation and path coefficients of different quantitative characteristics of mustard relevant to the objectives of the current study:

1. Genetic variability, heritability and genetic advance
2. Combining ability and gene action
3. Nature and magnitude of heterosis for yield and its components
4. Correlation and path coefficients

1. Genetic variances, heritability and genetic advance:

Genetic variability is the fundamental component of a crop improvement project. To produce a crop to the appropriate degree of development and for selection to be effective, it is necessary to evaluate genetic variability for yield and its constituents. In other words, selection and to a large part the breeding approach itself depend on genetic diversity. Any selection plan must take into account genetic variation since it is heritable.

Sohan and Nutan (2010) investigated the genetic variability of 36 genotypes for eight quantitative traits in Indian mustard, and they found substantial genetic variations across genotypes (parent vs. crosses) for all the variables except for number of seeds/siliqua. For quantitative features, the phenotypic coefficient of variance (PCV) value was greater than the genotypic coefficient of variance (GCV), indicating the importance of environmental variance. Both the test weight and the quantity of siliquae/plant showed high heritability.

Mishra *et al.* (2010) discovered that secondary branches per plant (CV 47.3%) had the most variability, followed by siliqua beak length (CV 43.6%), while oil content (CV 4.3%) had the lowest variability, followed by protein content (CV 6%).

Lohia *et al.* (2013) reported that analysis of variance obtained a substantial difference between genotypes for all variables, showing the presence of a broad spectrum of genetic variability. High heritability estimates suggested that these features were influenced primarily by additive genetic variation and had only a little involvement in their inheritance.

Meena *et al.* (2014) conducted an inquiry to evaluate heritability, genetic advancement, and inter-se relationship in varied accession of the Indian mustard and discovered that the harvest index had significant heritability and genetic advancement.

Abkari and Niranjan (2015) investigated the relationship between a high coefficient of variation and a genotypic coefficient of variation for the number of secondary branches, number of siliquae per plant, number of seeds per siliqua, and yield per plant, as well as the presence of a higher magnitude of variability among the test genotypes, for vital selection in relation to the aforementioned characters.

Iqbal *et al.* (2015) analysed 49 genotypes of Indian mustard and found that for the studied morphological features, phenotypic coefficient of variance (PCV) was larger than genotypic coefficient of variation (GCV). High GCV was detected for seed output per plant, whereas moderate GCV was discovered for the quantity of primary and secondary branches per plant.

Chawla *et al.* (2016) conducted an experiment on four different genotypes of Indian mustard in order to calculate the coefficient of variation owing to genotype and phenotype with heritability and genetic advancement. They demonstrated the highest genotypic coefficient of variation for the number of siliqua on the main raceme followed by seed yield per plant and the highest phenotypic coefficient of variation for variables like number of siliqua on the major raceme followed by oil content. Test weight, pod length, oil content, and

number of siliqua on the main raceme all showed high heritabilities. Additionally, they discovered a substantial genetic progress for the quantity of siliqua on the major raceme and seed output per plant.

Raliya et al. (2018) discovered that the mean sum of squares owing to genotypes (treatments) were significant for all characteristics studied. For all the qualities studied, the phenotypic coefficient of variance was greater than the genotypic coefficient of variation. Most of the characteristics, including yield/ha, had significant GCV, PCV, and narrow sense heritability. The genetic progress expressed as a percentage of the mean was similarly greater for 1000-seed weight, siliqua length, plant height, and number of major branches.

Devi (2018) discovered that GCV and PCV coefficients of variation were high for the following traits: biological yield per plant, grain yield per plant, and siliquae on main raceme. Biological yield per plant, siliquae on main raceme, grain yield per plant, and seed quantity per siliquae all showed better heritability and genetic progress.

Kumari and Kumari (2018) used morphological features to explore the genetic diversity pattern in thirty-one *Brassica juncea* L. genotypes. The collective analysis of variance revealed highly significant genotypic variances for days to flowering, days to 50% flowering, days to 75% maturity, plant height, siliqua length, 1000- seed weight, and harvest index, confirming the possibility of improving these traits through selection.

Tiwari et al. (2019) conducted an experiment to investigate the morphological features of Indian mustard. He discovered that the number of secondary branches per plant had a large genotypic coefficient of variation, followed by the number of siliqua per plant, test weight, and seed output per plant. The number of siliqua per plant showed significant genetic progress. He also noticed a high heritability associated with a strong genetic progress and deduced the significance of additive gene action in determining siliqua length, seed yield per plant, test weight, number of secondary branches per plant, and siliqua number per plant.

Yadav and Yadav (2020) reported that the number of secondary branches per plant had the highest phenotypic coefficient of variation (PCV), followed by seed yield per plant, 1000-seed weight, length of main raceme, number of primary branches per plant, and number of seeds per siliqua.

Tripathi et al. (2020) discovered that an analysis of variance revealed significant differences between treatments for all characteristics under normal and saline/alkaline conditions. In both conditions, the genotypic correlation coefficients between most of the traits were greater

than the phenotypic correlation coefficients, indicating a strong association between the various characters studied and that the genotypic expression of the association was relatively less influenced by the environmental aberration.

Gadi et al. (2020) examined thirty-six different genotypes of Indian mustard (*Brassica juncea* L. Czern and Coss.) for 10 quantitative traits. According to the variability, the genotypic coefficient of variation (GCV) was moderate for 50% blooming, days to maturity, total number of siliqua per plant, biological weight, test weight, and seed yield; and low for plant height, number of siliqua on main branch, number of seed per siliqua, and harvest index. The phenotypic coefficient of variation (PCV) assessment was high for biological weight and moderate for all other features except the number of seeds per siliqua, which had a low PCV. Character days to maturity (94.1%) had the highest heritability, followed by 50% flowering (92.4%) and Test weight (92.0%). The parameters total number of siliqua per plant (48.7%), plant height (43.8%), number of seed per siliqua (39.8%), number of siliqua on main shoot (22.3%), biological weight (17.9%), and harvest index (7.1%) had poor heritability. The biggest genetic gain as a percentage of mean was seen in days to 50% blooming (20.995%), days to maturity (21.320%), total number of siliqua per plant (20.066%), and test weight (35.936%). Genetic progress has a low value for plant height, number of siliqua on main stem, number of seeds per siliqua, biological weight, harvest index, and seed yield.

Singh et al. (2021) discovered that analysis of variance indicated significant differences between treatments for all variables except siliqua length, days to 50% blooming, and days to 80% maturity. For all the traits, phenotypic coefficients of variability (PCV) were greater than genotypic coefficients of variability (GCV). For total number of siliquae per plant, plant height, and seed yield/plant, high heritability was associated with strong genetic progress.

Chaturvedi et al. (2021) discovered that genotypes QM 16-2, QM 16-3, QM 16-4, NDRE 7 and NDRS 2008 had high GCV and PCV for all characteristics, and that these five lines represented a significant group for increased seed output per plant. The genotypes indicated above also demonstrated high to extremely high mean performance for various additional yield components.

Prasad et al. (2021) found moderate GCV and moderate PCV (10-20%) estimations for number of secondary branches per plant, number of siliqua per plant, seed index, harvest index, and erucic acid in both generations. Heritability estimations ranged from 4.8% (number of seed

per siliqua) to 31% (days to maturity) in F1 generation to 1.8% (oil content) to 41.0% (leaf area index) in F2 generation. In the F1 generation, the estimated genetic progress over the mean of the character ranged from 4.03% (days to 50% flowering) to 52.39% (total glucosinolate) and 3.65% (days to maturity) to 48.87% (total glucosinolate).

Nishad et al. (2022) conducted research to determine genetic diversity for 20 distinct genotypes of Indian mustard. The analysis of variance reveals that there is a lot of variation among the genotypes investigated. GCV and PCV estimations range from high to moderate for the parameters number of siliqua per plant, harvest index (%), seed yield per plant, and number of secondary branches per plant. For characteristics such as number of siliqua per plant, harvest index (%), seed yield per plant (g), and number of secondary branches per plant, strong heritability along with high genetic advanced as a percentage of mean were observed.

2. Combining ability and gene action:

Combining ability has been frequently used in plant breeding to identify the performance of parental lines in hybrid combinations. It was invented in **1942** by **Sprague** and **Tatum**. Most crop breeding projects prioritise the use of combining ability in the identification of the best performing lines for commercial release and lines that may be utilised as parents in future heterosis breeding (**Oakey et al., 2006**). Specific mating designs, such as line x tester, diallel, and North Carolina designs I, II,

and III can be used to choose parental lines. The genetic impacts of a line may be partitioned into two genetic components using such mating designs: additive (fixable) and non-additive (non-fixable) (**Oakey et al., 2006, Topal**).

Combining ability is an evaluation of the worth of genotypes based on their progeny performance in a certain mating design (**Allard, 1960**). Crossing a line with numerous others yields the average performance of the line in all its cross combinations. General combining ability and specific combining ability, two ideas of combining ability, have had a significant impact on inbred line appraisal and population formation in crop breeding (**Sprague** and **Tatum, 1942**). General combining ability was described by **Sprague** and **Tatum** as the average performance of a line in

a series of cross combinations. They defined special combining ability as the capacity of certain cross combinations to perform better or worse than would be predicted based on the average performance of the parental lines. Parents with a high average combining ability in crosses are called good general combiners, but parents with the potential to combine well with a specific cross are termed good specific combiners. According to statistics, the general combining ability is the major effect, whereas the specific combining ability is an interaction effect (**Kulembeka et al., 2012**).

Griffing (1956a) proposed a model to demonstrate that GCA variation was mostly caused by additive genetic influences, whereas SCA was caused by dominance and epistatic components of genetic variance. In the absence of epistasis, **Hayman** claimed that general combining ability consists of additive and dominant components, whereas specific combining ability comprises over-dominance.

Griffing (1956b) developed two models, each with four approaches, for estimating general and specific combining abilities in a collection of diallel crossings. Combining ability analysis is a strong method for identifying excellent and bad combiners and selecting appropriate parental material in breeding efforts. The relative size of different components of variation influences the selection of an effective breeding approach for quantitative character enhancement.

Sarkar and Singh (2001) assessed the combining ability and reciprocal cross effects of 10 *Brassica juncea* (L.) cultivars for thirteen characteristics. GCA and SCA variances for seed yield, days to 50% flowering, days to maturity, number of primary and secondary branches, early vigour, plant height, length of siliqua, number of siliquae on main shoot, seeds per siliqua, oil content, and 1000-seed weight were significant in reciprocal crosses. They proposed three parental lines, Zem-1, Zem-2, and EC-322092, as well as crosses combining either two high GCA parents or one high GCA parent, to get improved outcomes for seed yield and associated yield contributing qualities.

Ghosh et al. (2002) performed a $L \times T$ study on eleven quantitative variables in *Brassica juncea* (L.) utilising 29 female and 7 male parents. SKM 93-28, VSL-5, YSRL-10, STRAIN-26, AD-2041, DBS-10, and KBJ-3 were shown to be considerably superior general combiners for seed yield and yield components among the parents.

Singh and Sachan (2003) used 8×8 diallel analysis to analyse *Brassica juncea* (L.) parents and F1s omitting reciprocals. Estimates of combining ability for different yield attributes and oil contents revealed significant general and specific combining ability mean 10 squares for

all characters, indicating that both additive and non-additive gene effects were important in the inheritance of studied traits. Except for the quantity of siliquae on the main shoot, they defined the relevance of GCA and SCA interactions with the surroundings for all the characters.

Kumar and Rathore (2004) used an 8×8 diallel analysis to estimate combining ability in two distinct soil environmental conditions, normal and saline. Significant GCA and SCA variation was detected on normal soil for days to 50% blooming, days to maturity, number of siliquae per plant, 1000-seed weight, and seed production per plant. In saline soil, however, GCA variance for days to 50% blooming and SCA variance for the quantity of siliqua per plant were shown to be significant.

Singh et al. (2005) tried crosses with the parents 'Seeta', 'BR 40', 'Pusa Barani', 'Pusa Bold', 'CM 3', 'Varuna', 'Narendra Rai', and 'RCC 4' utilising a half diallel mating design. The F1 findings revealed that the parents, 'CM 3', 'Pusa Barani', 'Pusa Bold', and 'BR 40' were good general combiners for seed yield per plant, number of seeds per siliqua, oil content, and number of primary branches per plant.

Dhaliwal et al. (2006) performed line \times tester study on a set of 44 F1's involving four CMS lines and eleven inbred lines to evaluate combining ability impacts and its environmental interaction for fatty acids in seed oil. The experimental design's analysis of variance revealed that parents and hybrids differed substantially. Significant parents versus hybrids \times environment interaction revealed that heterotic and combining ability impacts vary with environment. The combining ability study revealed that non-additive gene effects dominated oleic acid and linoleic acid inheritance.

Noshin et al. (2007) conducted a 6×6 diallel experiment with *Brassica juncea*(L.) to estimate seed yield and component attributes for combining ability. The effects of SCA on seed production were determined to be statistically insignificant. Other yield contributing variables have quite substantial GCA and SCA variations evaluated. GCA mean squares were greater than SCA mean squares, demonstrating the importance of additive effects.

Mahak et al. (2008) demonstrated highly significant GCA and SCA variances were observed for days to 50% flowering, plant height, number of primary branches, number of siliquae per plant, 1000-seed weight, and oil content; however, the extent of GCA variance was greater than SCA variance for most of the characters. The GCA impact estimates revealed that the parents, Varuna, Urvashi, and Maya, were good general combiners for seed yield per plant. For seed output per plant, cross combinations Varuna \times Urvashi, Varuna \times Maya, Maya \times Urvashi,

and Maya × Kantishown substantial and desired SCA effects.

Aher et al. (2009b) tried crosses with 10 lines and four testers using the line x tester mating strategy. The ratio of variance estimates due to general combining ability and specific combining ability was less than unity, indicating that non-additive gene action was involved in the expression of days to 50% flowering, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, 1000- seed weight, oil content, and seed yield per plant. The additive kind of gene action was predominately engaged in the expression of plant height, main shoot length, and primary branch number per plant. SCA never mentioned the participation of parents with a strong GCA impact. Crosses with strong SCA effects did not necessarily involve parents with high GCA effects. SKM-95-85 × GM-2, RSK-87 × Varuna, and RSK-87 × GM-2 were the top three hybrids in terms of per se performance, with positive significant SCA effects in desired impacts for seed yield per plant.

Gupta et al. (2010) performed half diallel analysis in *Brassica juncea* (L.) to uncover general combining capacity, particular combining ability, and high heterotic hybrids. GCA and SCA variations were found to be significant for all characteristics.

The GCA variation was shown to be greater for days to 50% blooming, days to maturity, plant height, and 1000-seed weight, whereas the SCA variance was greater for seed yield and all remaining parameters.

Dey et al. (2011) performed line × tester analysis in snowball cauliflower using three CMS lines as female parents and nine different lines of snowball cauliflower as testers. The parent Ogu2A had the most GCA effect for curd yield (4.51) and harvest index (1.97) whereas Ogu1A had the greatest GCA effect for earliness (-2.73). The GCA for curd length (0.39) was important in Ogu2A (parent).

Lal et al. (2011) tested a set of 8 × 8 diallel crosses in Indian mustard with their parents in a randomised block design with three replications in two settings. Estimates of GCA effects based on pooled analysis revealed that variety RH 8812 had the greatest potential as a good general combiner for all six characters, while BIO 902 and RH 9304 also had favourable GCA effects for yield/plant, days to 50% flowering, primary branches per plant, and number of siliquae/plants. SCA study found that the ten crossings had positive and substantial SCA for seed yield. Two of these crosses, RH 8812 × PUSA JAI KISAN and PUSA JAI KISAN × RH 819, were shown to be the best cross combinations for early blooming and oil content. The GCA/SCA ratio suggested

that additive gene effects were more important for plant height, days to 50% blooming, and primary branches per plant; however, additive and non-additive gene effects were equally important for number of siliquae/plants, seeds yield/plant, and oil content.

Yadava et al. (2012) analysed 19 parents (14 lines and 5 testers) for both additive and non-additive gene activities involved in influencing yield and its contributing attributes. The best general combiner among the parents was found as Pusa Mustard-25. Significant and positive SCA effects were observed for seed yield in 17 crosses, number of primary branches in six crosses, number of secondary branches in four crosses, point to the first siliqua in six crosses, number of siliquae on the main shoot in nine crosses, main shoot length in five crosses, and 1000-seed weight in nine crosses, whereas significant negative SCA effects were observed for plant height in two crosses and point to the first siliqua in nine crosses.

Arifullah et al. (2012) showed considerable general combining ability for most of the parameters except plant height and siliqua length in an 8 x 8 diallel cross of eight promising genotypes in Indian mustard. Parents UCD-8/4, KJ-119, and BRS-2 were effective general combiners for yield-related characteristics. A hybrid between BRS-2 and UCD-8/4 produced the highest desired SCA for the number of main branches and siliquae per plant. S-9 Canola Raya for siliqua length, Canola Raya UCD-8/4 for number of seeds per siliqua, KJ-119 BRS-2, BARD-1 NIFA Raya for 1000-seed weight, and cross BRS-2 UCD-8/4 for seed yield all exhibited strong positive SCA, with at least one of the potential general combiner parents involved.

Singh et al. (2013) investigated the impacts of combining ability and discovered that the genotypes RH-9617, RH-9806, and RH-9615 were good general combiners for earliness, siliqua length, 1000-seed weight, number of seeds per siliqua, primary branches per plant, and oil 12 content. As a result, these parents might be utilised in crossover schemes to achieve even greater success.

Gami and Chauhan (2013) studied the combining ability, gene action, and heterosis in *Brassica juncea* (L.) by crossing six parental lines and four testers in a line × tester mating method. Parents Pusa Bold and Bio-902 had strong and beneficial GCA impacts on seed output per plant, but parent PCR-7 was discovered to be an excellent general combiner for 1000-seed weight. SCA effects were greatest in hybrids SKM- 9820 × GM-2 and PCR-7 × Varuna.

Kumar *et al.* (2013) used a diallel analysis of seven parents, omitting reciprocal crosses, to discover high heterotic crossings and their association in terms of GCA and SCA. Except for secondary branches per plant, the analysis of variance research of GCA and SCA variances revealed that most of the features were significant. RK03-2 and Varuna were determined to be suitable parents for practically all features because to their high GCA and per se performance. Varuna \times RK03-1 and Varuna \times RK03-4 demonstrated both high per se performance and SCA effects. The best parent and best crosses mentioned above can be employed for further development via hybridization and heterosis breeding, respectively.

Chaurasia and Ram Bhajan (2014) discovered that three parents, SKM-401, PRQ-2005, PWR-9541, and CS-609-B-10, had large GCA impacts on seed output per plant. For oil content, high GCA effects were reported in four parents: RGN-142, PRB-2006-12, Vardan, and PRQ-2005. PRQ-2005 had high GCA impacts on seven characteristics, including seed output per plant and oil content. Similarly, the strains

PWR-9541, SKM-401, and CS-609-B-10 demonstrated favourable GCA effects for six, seven, and five traits, including seed yield, respectively. PRQ-2005 \times PAB-9534, PRQ-2006-12 \times Kanti, CS-609-B-10 \times SKM401, CS-609-B-10 \times Kanti, PRB-2006-12 \times NDRE-4, and four additional crosses were discovered to have acceptable SCA effects for seed production per plant. Similarly, the crosses PRQ-2005 \times NDRE-4, NDRE-4 \times PWR-9541, PRB-2006-12 \times NDRE-4, and CS-609-B10 \times Kanti for blooming earliness were promising, as did SKM-401 \times PAB-9534, PRQ-2005 \times CS-609-B-10, NDRE-4 \times Kanti, and Kanti \times Vardan for maturity earliness.

Prajapati *et al.* (2014) discovered that in all crosses, both additive and non-additive gene activities were engaged in seed yield per plant. The degree of non-additive gene action for character inheritance was larger in the crosses GM 1 \times Vardan and IC 491446 \times GM 2. All three types of digenic interactions between linked pairs of genes, additive additive, additive dominance, and dominance dominance, contributed considerably to the inheritance of the number of seeds per siliquae. Main branch length in cross IC-491446 \times GM 2; test weight in cross IC-491446 \times GM 2 and PM 67 \times Varuna with increased magnitude of dominance interaction. The degree of the additive interaction was larger in the cross IC-491446 \times GM 2. Most yield and attribute traits showed duplicate epistasis in distinct crosses of the Indian mustard.

Dholu *et al.* (2014) investigated the ability of Indian mustard to combine in an 8×8 diallel. Except for days to 50% flowering, plant height, siliquae length, seeds per siliquae, and 1000 seed weight, the GCA and SCA ratios indicated that non-additive gene action was dominant in the

inheritance of all traits. The parents GM-2 and IC- 560696 were excellent general combiners for seed yield per plant and related traits. For aphid resistance, the gca and sca mean squares were significant. According to the estimates of general combining ability, parents GM-1 and GM-3 were good general combiners for aphid resistance. Specific combining ability estimates revealed that the cross combinations IC-491446 × GM-2, IC-560696 × Vardan, IC-491446 × GM-1, Laxmi × Vardan, and Laxmi × IC-560696 were the most promising for aphid resistance.

Meena et al. (2015) used line x tester analysis with nine lines and four testers to assess GCA and SCA impacts of parental lines and improved parent heterosis of 36 crosses of Indian mustard. Some crosses showed significant SCA effects for seed production, 1000-seed weight, oil content, and other contributing factors in the desired direction. NRCHB 101, the best general combiner, had significantly substantial positive GCA impacts for seed yield and yield contributing characteristics. Some high yielding crossings were also discovered, which might be used to create better 13 genotypes, and the parents involved could be transformed to well-adapted cytoplasmic male sterile or restorer lines.

Patel et al. (2016) investigated heterosis in 40 *Brassica juncea* (L.) F1s by integrating ability and genetic variance components for different quantitative and qualitative features. The parents SKM 0518, SKM 0907, and SKM 0445 were found to be good general combiners for seed yield per plant, and SKM 0518 was found to be a good general combiner for days to flowering, days to maturity, number of siliques per plant, oleic acid, erucic acid, and glucosinolate content. These findings imply that breeding strategies such as biparental mating followed by recurrent selection, diallel and line x tester mating design, and so on, might be used to discover attractive transgressive segregants for further enhancement of these characteristics.

Vineet et al. (2016) used seven genotypes crossed in a diallel fashion to investigate combining ability and heterosis for seed yield and its component traits in Indian mustard. GCA variance was significant for all characters, whereas SCA variance was significant for all traits except days to flowering. For seed yield and its components, Kranti was found to be the best general combiner among the parents, followed by Varuna and EC 399301.

Meena et al. (2017) calculated combining ability and heterosis for 18 hybrids created by crossing 9 lines with 2 *Brassica juncea* (L.) testers. Both additive and non-additive gene actions were identified in influencing seed yield and its attributing attributes, with non-additive gene action predominating. RH 0749, RH 0406, Rohini, NRCHB 101, and NPJ 112 were good general combiners among the parents. Significant SCA effects for seed output, 1000-seed weight, number

of seeds per siliqua, and other favourable attributing qualities were seen in a series of hybrids. Three crosses, NRCHB 101 × NPJ 112, RH-749 × NPJ 112, and RH-406 × RRN-727, out of 18 crosses, exhibited high magnitude over better parent, standard parent, and mid-parent heterosis with highly significant SCA effects, as well as higher per se performance for seed yield and its component traits.

Shrimali et al. (2017) A diallel analysis excluding reciprocals was performed on ten parents and their hybrids to identify high heterotic crosses and their relationship in terms of GCA and SCA. GCA and SCA analysis of variance reveal differences in all traits. The ratio of GCA and SCA variances was less than one for all characters except days to flowering, plant height, and harvest index. SKM851 × RGN-303 (30.26%), GDM 4 × RH-055 (27.72%), GDM 4 × RGN-282 (25.06%), and GDM 4 × SKM 518 (18.63%) out of 45 crosses. The parent GM 3, GDM 4, RH-0555, and RSK-29 were effective combiners for seed yield and component characteristics. RGN-303 and RSK-29 were good general combiners for oil content.

Kumar et al. (2018) began combining ability analysis on a $L \times T$ of F_1 and F_2 generations in *Brassica juncea* (L.), which demonstrated that the parents' general combining ability impacts had a positive correlation with their per se performance. The parents EC401574, Pusa Bold, and Rajendra Sufalam were good general combiners for seed yield and number of siliquae on the main raceme, RAURD 153, RAURD 34, and RAURD 32 for days to flowering and main shoot length, and EC 399788 for number of siliquae per plant and number of secondary branches per plant. Based on improved parent heterosis and specific combining ability, EC 401574 × Rajendra Sufalam for the number of siliquae per plant, seed yield per plant, and number of secondary branches per plant were selected as possible cross combinations.

Thanmichon et al. (2018) developed 21 crosses from seven lines and three testers to determine the combining ability impacts in *Brassica juncea* (L.). Combining ability impacts indicated that of the 14 parents, DRMR-150-35, RH-932, and TM-2 were strong general combiners, while DRMR 150-35 × Pusa Bold, GM-3 × SEJ-2, RH932 × TM-2, and MCP 802 × SEJ-2 were the best particular combiners.

Chaurasiya et al. (2018) used a set of seven parental crosses in half diallel fashion to estimate heterosis and combining ability effects, as well as variances, in Indian mustard. They discovered that the genotypes Urvashi and Pusa Bold were the best parents for almost all studied traits, as their GCA and per se performance were the highest, while the crosses Maya NRCDR-2,

Maya Urvashi, Maya Pusa Bold, NRCHB-101 Pusa M-21, and Urvashi Pusa Bold showed high per se performance as well as SCA effects.

Sahib *et al.* (2019) found the best parents and hybrids for yield attributes based on GCA, SCA, and high heterotic performance, using crosses of five mustard lines and three testers in a line \times tester configuration. For GCA effects, parent IC-317528 was deemed the best general combiner for the greatest number of characteristics, whereas for SCA effects, cross IC-589669 IC-571683 was deemed the best general combiner for most traits. Based on mean performance and heterosis calculations, the cross IC-589669 IC-571655 was deemed to be the most promising for seed yield per plant.

Kaur *et al.* (2019) in a set of 55 diallel crosses, studied combining ability for yield and its attributes in Indian mustard and found significant differences for both general combining ability (GCA) and specific combining ability (SCA) for all traits studied. The presence of both additive and non-additive gene interactions for the inheritance of various studied traits was indicated by the high magnitude of GCA and SCA effects. The crosses IC-589681 IC-571649, IC-589680 IC-589681 had a high potential for seed yield and its component traits based on SCA effects.

Yadav *et al.* (2020) estimated combining ability for seed yield and its component traits under late sown conditions using seven parents crossing in half diallel fashion. The combining ability analysis of variance revealed highly significant differences for both GCA and SCA for all characters except harvest index for GCA and days to maturity and harvest index for SCA effect. Kranti, RLM-198, RGN-291, and Vardan were excellent general combiners for most of the characters. Kranti NRCHB-101, Kranti Ashirwad, NRCHB101 RLM-198, NRCHB-101 RGN-291, RLM-198 Ashirwad, RGN-291 Ashirwad, RH-30 Ashirwad, and Vardan Ashirwad were the best specific combiners for seed yield per plant based on per se performance and desirable significant SCA effects for seed yield per plant and associated 12 characters.

Kapadia *et al.* (2021) proposed that the best general combiners for seed yield and a few other traits were GDM-4 in females and IC-399819 and EC-766060 in males based on estimates of general combining ability effects. The SCA estimates revealed that the hybrids GM-2 \times EC-766437, GM-2 \times RH-406, and GDM-4 \times EC-766378 had positive SCA effects in the desired direction for seed yield per plant. The hybrids GDM-4 \times EC-766043, GDM-4 \times RH-749, and GDM-4 \times EC-766495 had significant negative SCA effects for days to 50% flowering, while GM-3 \times EC-766437 had

significant negative SCA effects for days to maturity. While the GDM-4 × EC-766043 hybrid demonstrated significant SCA effects in the desired direction for oil and protein content.

Singh et al. (2022) studied ten parents and found that only one parent, EC 511664, had significantly positive GCA for relative water content, chlorophyll content, membrane stability index, and excised leaf water loss. For 1000 seed weight, parent DRMR 1165-40 showed significantly positive GCA effects. As a result, these are excellent general combiners of these traits.

3. Nature and magnitude of heterosis for yield and its components:

Shull (1914) coined the term heterosis, which he defined as "hybrid vigour." Heterozygosity is defined as increased vigour, fertility, and so on in a cross between two genetically different lines when compared to growth in either of the parental lines. The identification of hybrids that are more productive than the best parents/cultivars is a critical factor in heterosis breeding. Male sterility and fertility restoration systems, as well as self-incompatibility mechanisms, have made the use of heterosis relatively simple in some species. Heterozygosity (**East, 1936**), the accumulation of favourable dominant genes from each parent in heterozygotes, and non-allelic interaction or epistasis (**Castle, 1946** and **Jinks, 1955**) have all been linked to the phenomenon of heterosis. (**Fonesca and Patterson 1968**) defined heterobeltiosis as an increase or decrease in the mean value of an F1 hybrid over the better parent. To be commercially viable, the hybrid must outperform the most widely used commercial variety. Standard heterosis or economic heterosis refers to the superiority of hybrid over the standard check or the best variety.

It is critical to study the magnitude of heterosis to exploit it. The magnitude of genetic differences between the parents involved in the crosses has a significant impact on the heterosis experiment. Maximum heterosis will be observed in parents with optimal to intermediate genetic diversity (**Moll and Stuber, 1974**). The following paragraphs provide a brief overview of heterosis reports in oilseed:

Verma et al. (2000) evaluated heterosis for five traits in 21 F₁s derived from seven genotypes of *Brassica juncea* (L.). RK-8902 × DLM-2, PR-8903 × RK-8902, and RSK-28 × DLM-2 hybrids displayed advantageous heterosis for seedling vigour, seed yield, and days to 50% Flowering, oil content, and 1000-seed weight are all elements to consider.

Ghosh *et al.* (2002) reported that two crosses, YSRL-10 × Pusa Bold and DB5-10 × Pusa Bold, demonstrated robust heterosis for seed yield and several of the yield contributing traits. For most of the main traits, including seed yield, both additive and non-additive gene action was critical.

Sharma and Sharma (2003) revealed that under adverse environmental conditions, the spectrum of heterosis was larger for both seed and oil yield. For seed and oil yields, the crosses RC-781 × RH-781 and PHR-1 × RH-781 revealed significantly superior parent heterosis in both environmental circumstances. Under moisture stress, none of the crosses displayed appreciable economic heterosis in seed and oil output. Under irrigated conditions, four crosses demonstrated substantial economic heterosis: T59 × PHR-1, Pusa Bold × PHR-1, Pusa Bold × RH-781, and PHR-1 × RH-781 for seed production and oil output per plant.

Goswami *et al.* (2004) reported 30 crosses of Indian mustard and discovered that cross RH-9404 × RH-30 exhibited the highest heterosis for seed output per plant in E1 and E2, respectively. This hybrid also showed significant heterosis for 1000 seed weight. Because of the high heterosis for all the characteristics examined, the crosses RH-9617 × RWH-1 and RH-9621 × RWH-1 were chosen.

Beena *et al.* (2005) reported that the cross Bio-902 × Rohini was the finest of all the crosses investigated. It exhibited the largest mean and economic heterosis for seed yield per plant, number of siliquae per plant, number of branches per plant, and days to maturity, as well as a substantial negative heterosis. Although heterosis was discovered at a greater level in preponderance of the seed yield hybrids.

Dixit *et al.* (2005) reported that cross RLM-198A × YRT-3 (104.40%) followed by PCMS-106A × Jatai ral (98.12%), RLM-198A × Jatai ral (81.13%), Pusa Bold A siifolia' × JMM-1628 (73.28%) and PCMS-106A × RK-8401 (63.19%) showed heterobeltiosis for seed yield with significant and favourable SCA impacts. For oil content, three crosses showed desired heterobeltiosis (6.91%), followed by Pusa Bold A siifolia' × JMM-1628 (4.49%) and RLM-198A × BIOYSR (3.21%), while two crosses showed considerable and positive standard heterosis (3.76%) and Pusa Bold Asiifolia' × Local mustard (3.66%).

Mahto *et al.* (2006) detected heterotic crossovers in Indian mustard using 45 genotypes (nine progenitors and their diallel, eliminating reciprocals). For the preponderance of yield contributing characteristics, the crosses RH-843 × RH-851 and PR 18 × BR 40 revealed a bigger

magnitude of relative heterosis and heterobeltiosis, respectively. In terms of heterotic effects, three combinations stood out: PR-18 × BR-40, PR-830 × RH-851, and RH-843 × RH-851.

Nair et al. (2007) studied fifteen elite genotypes of *Brassica juncea* (L.) were crossed with two testers in a L × T pattern, and F₁s, along with parents, were evaluated to assess heterosis magnitude for yield and yield contributing characteristics. The highest degree of heterosis for seed yield per plant was reported in three crosses: Vardhan × TM-17, Vardhan × Laxmi, and Vardhan × RL-1359.

Singh (2007) revealed that fourteen crosses, namely Laxmi × BR-40 (90.48%), Laxmi × Pusa Bold (71.43%), Pusa Bold × CM-3 (54.76%), Pusa Bold × Varuna (54.76%), BIO-902 × CM-3 (54.76%), RH-30 × BIO-902 (54.76%), BR40 × CM-3 (38.9%), Pusa Bold × BR-40 Seed yield heterosis ranged from 35.71% (BIO-902 × SEJ-2) to 90.48% (Laxmi × BR-40). In general, crosses with substantial heterobeltiosis also exhibited large standard heterosis and per se seed yield performances. The results demonstrated that the increase in seed yield was mostly attributed to the increased number of siliquae.

Nasrin et al. (2008) reported that the cross 3-8 × 3-I I demonstrated desirable heterosis for primary branches, secondary branches, and seed yield per plant: J-7 × J-9 for primary branches, seed yield per plant, and thousand seed weight: J-7 × i-II for days to maturity; i-LU × 3-I I for 50% flowering and maturity.

Aher et al. (2009b) investigated the amount of heterosis in Indian mustard by crossing 10 lines and 4 testers. The results demonstrated a substantial degree of heterosis for seed yield per plant, number of siliquae per plant, and number of secondary branches per plant, but a low quantity of heterosis for the remaining parameters. The cross RSK-87 × GM-2 exhibited the highest economic heterosis for seed yield (42.95%), followed by SKM-95-85 × GM-2 (40.11%), and RSK-87 × Varuna (36.77%).

Sabhagnia et al. (2010) observed the significant positive heterotic effects including mid-parent and high parent heterosis were observed for all the traits studied but for different number of crosses.

Gupta et al. (2010) revealed that relative heterosis and heterobeltiosis were highest for seed yield per 100 siliquae and days to 50% blossoming. The crosses IC-199715 × IC-199714 and EC-289602 × Prakash displayed the greatest relative heterosis and heterobeltiosis in terms of the number of primary branches per plant and harvest index. Agra Local × Pusa Bahar was a promising cross for the length of the main axis; Poorbi Jaya × Agra Local for the number of

siliquae on the main axis; and EC-289602 × Pusa Bahar for biological yield per plant and seed yield per plant.

Dey *et al.* (2011) reported that heterosis for curd yield was highest in the hybrid Ogu2A Kt-22 (63.5%), followed by Ogu1A WF (36.9%). The finest hybrid for earliness was Ogu1A Kt-15, followed by Ogu3A Kt-22, with heterosis of 14.4% and 11.7%, respectively.

Yadava *et al.* (2012b) studied 10 hybrids and demonstrated >15% heterobeltiosis, highly significant SCA effects, and greater per se performance. The progenitors utilised to develop these hybrids were determined to be suitable for conversion to cytoplasmic male sterile and restorer lines for commercial heterosis exploitation.

Kumar *et al.* (2013) attempted crossings in a diallel fashion while deleting the reciprocals of seven parents to uncover high heterotic crossovers and their linkages in terms of GCA and SCA. Five crosses out of twenty-one displayed substantial economic heterosis for seed yield. The cross with the highest standard heterosis was RK03-3 × RK03-4 (43.90%), followed by RK03-2 × RK03-4 (34.55%), Varuna × RK03-4 (31.75%), RH-819 × RH9801 (25.00%), and RH-819 × RK02-4 (24.22%).

Singh *et al.* (2013) observed that the cross combinations RH-9710 × RH9806 and RH-9707 × RH9806 should be utilised via heterosis breeding or employed in recombination breeding to enhance seed yield. SKM-9820 × GM-2 and PCR-7 × Varuna (T-59) crosses produced the strongest heterosis and SCA effects over superior parent and standard checks.

Gami and Chauhan (2013) taking into account heterosis, mean performance, and combining ability effects, the parents Pusa Bold, GM-2, SKM-9820, and SKM-9033, as well as hybrids PCR-7 × Varuna, SKM-9033 × Varuna, and SKM-9820 × Varuna, were found to be promising for exploitation of heterosis and undertaking crossing programmes to obtain desirable recombinants.

Chaurasia and Ram Bhajan (2014) reported that six crosses demonstrated strong heterobeltiosis: CS-609-B-10 × NDRE-4 (170.50%), PRQ-2005 × NDRE-4 (152.84%), RGN-142 × PRB-2006-12 (126.88%), CS-609-B-1 × Kanti (118.53%), PRB-2006-12 × Kanti (117.16%), and PAB9534 × Kanti (104). These crosses also revealed considerable relative and economic heterosis when compared to the mid parent and standard types, respectively. For oil content, three crosses, SKM-401 × Vardan, PRB-2006-12 × Vardan, and NDRE-4 × PWR-9541, revealed considerable relative heterosis (3.5%), heterobeltiosis (3.3%), and standard heterosis (5.24%), respectively.

Meena et al. (2015) employed line- \times -tester analysis with nine lines and four testers to execute an experiment containing 36 crossings of *Brassica juncea* (L.). Hybrids DRMR-2269 \times NRCHB-101, DRMR-2243 \times NRCHB-101, DRMR-2613 \times NRCDR-2, DRMR-2341 \times NRCDR-2, DRMR-2398 \times NRCHB-101, DRMR-2326 \times NRCHB-101, and DRMR-2486 \times Ashirwad demonstrated the highest proportion of heterobeltiosis with higher per se performance and highly significant SCA impacts for seed yield.

Patel et al. (2016) revealed that the cross combinations SKM-0820 \times GDM-4(15.5), SKM-0715 \times SKM-0445 (13.5), and SKM-0907 \times SKM-0445 (12.5) were significant for seed yield per plant. For seed yield per plant, the cross combinations SKM-0820 \times GDM-4 exhibited strong per se performance, standard heterosis, and SCA effects.

Barupal et al. (2017) made crosses GM-3 \times RGN-145, RGN-48 \times Kranti, and GM-3 \times Kranti took fewer days to flower since they possessed the highest negative and significant heterosis and heterobeltiosis. Five hybrids displayed negative and severe heterosis and heterobeltiosis, with RGN-48 \times RGN-145 and RGN-48 \times Geeta maturing first. RGN-48 \times Kranti was the most heterotic cross in terms of days to 50% flowering, days to maturity, plant height, number of primary branches per plant, and biological yield per plant.

Kumar et al. (2017) computed heterotic crossings using sixty crosses (two lines plus thirty testers). CMS Mori \times NPJ-135 (13.17%) and CMSNDRE-4 \times PRE2007-06 (12.83%) hybrids revealed a large SCA effect and heterosis over the conventional varieties Kranti and Maya, respectively.

Adhikari et al. (2017) revealed that all the factors, save plant height and glucosinolate concentration, exhibited very high heterosis in the desired direction. RRN778 \times Maya and RB-57 \times Maya for early maturity; Maya \times RMM-09-4; RB-57 \times PM-25; and PRL-2012-13 \times DRMR-675-39 for seed yield; PRL-2012-13 \times RRN-778; and DRMR-675-39 \times Maya for oil content were the most promising heterotic crosses for relative heterosis, heterobeltiosis, and standard heterosis, respectively.

Thanmichon et al. (2018) employed seven lines and three testers to construct 21 crosses to estimate heterosis over superior parent in *Brassica juncea* (L.). In DRMR-15 \times SEJ-2, DRMR 150-35 \times Pusa Bold, RH-932 \times TM-2, and GM-3 \times SEJ-2, heterobeltiosis (over superior parent) was high. Based on mean performance and GCA impacts, the most promising progenitors were DRMR 150-35, TM-2, and RH-932, whereas the most

promising crosses were DRMR 150-35 × Pusa Bold, MCP 802 × SEJ-2, RH 932 × TM-2, and GM-3 × SEJ-2.

Kumar *et al.* (2018) revealed that hybrid RAURD 153 × Pusa Bold for number of primary branches per plant, EC 399788 × Pusa Bold for secondary branches per plant, EC 401574 × Rajendra Sufalam for seed yield per plant, number of siliques per plant and siliqua on main raceme, RAURD 214 × Rajendra Sufalam for silique length and RAURD 32 × Vardan for seeds per silique manifested high SCA as well as heterotic effects.

Wolko *et al.* (2019) reported that for the first category, we include plant height, silique length, and the quantity of seeds per silique—a high percentage of hybrids showed significant positive heterosis for these parameters, regardless of year of observation or hybrid type. For the second group, we can include the number of branches and siliques per plant as well as the thousand seed weight. Hybrids revealed both positive and negative significant heterosis for these features, with no apparent trend for the years and types of hybrids.

Malviya *et al.* (2019) calculated heterosis for seed yield, component characteristics, and oil content in Indian mustard under late and timely seeded circumstances using 15 lines and 4 testers in a line tester mating system. Based on this study, they identified several genotypes as superior donor for seed yield viz., TERIWBJ-32-1, RK-08-1, PARASMANI-2-10, SKM-0301, Maya, RGN228 and RRN-631 among the lines and Kranti and NDYR-8 among testers in timely sown condition whereas, TERIWBJ-32-1, JMM-08-1, TERIHOJ-48, Sahib-36 and LET-14-1 among the lines and 24 Basanti among testers under late sown condition. The superior and high yielding crosses were Pusa Karishma NDRE-4, RK-08-1 NDRE-4, PARASMANI-2-10 NDRE-4 under timely sown condition and the crosses viz., RRN-631 Basanti, TERIWBJ-32-1 Basanti, Sahib-36 Basanti, Pusa Karishma NDRE-4 under late sown condition.

Srivastava *et al.* (2020) studied the amount of relative, heterobeltiosis, and standard heterosis for seed yield and its components in nine Indian mustard genotypes, including the standard check, RB-50, and their hybrids, under timely seeded irrigated conditions. For most of the variables under consideration, the analysis of variance revealed significant genetic diversity among the parents and hybrids. For 1000 seed weight, RB-50 Kranti exhibited a favourable and significant value for all three types of heterosis. Rh-1 Standard heterosis was observed for seed yield per plant as well as the number of primary and secondary branches in 19 Giriraj, RGN-298RH-749, RGN-298 Giriraj, Vardan RH-749, and Vardan Giriraj. Based on standard heterosis

and perse performance for seed yield per plant, the cross combinations Vardan Giriraj, RGN-298RH-749, Vardan RH-749, and Vardan RGN-73 were identified.

Kumar *et al.* (2021) estimated heterosis in Indian mustard (*Brassica juncea* L.) using 77 half diallel mating designs and their parents, and data were collected for eleven quantitative characters cross combination RAURD 14-18 RAURD-214 was identified as the best heterotic cross for all three types of heterosis, estimated over bestcheck NRCHB101. As a consequence of re-examining the CMS influence on the identified performance, the female parent of the best heterotic cross combination may be changed into CMS line and male as restorer line for commercial exploitation.

Patel *et al.* (2021) evaluated 35 hybrids, five CMS lines, seven testers, and the standard check GDM 4 for ten different traits and discovered that three hybrids, Kranti \times Mori 'R' 1-18, SKM 9928 \times Pusa Agrani, and SKM 9928 \times Mori 'R' 1-18, were found promising for seed yield over the standard check GDM 4. In terms of heterosis, one of the hybrids Kranti \times Mori 'R' 1-18 (17.85%) plants demonstrated considerable and positive standard heterosis for seed yield.

Kumawat *et al.* (2022) tested ten parents in three different contexts using a randomised complete block design with three replications. Data on quantitative characters were collected, and heterosis and heterobeltiosis were determined, revealing a suitable degree of heterosis and heterobeltiosis for all attributes. The RGN-13 \times RH-406 cross was identified for days to 50% flowering, days to maturity, number of secondary branches per plant, number of siliquae per plant, 1000-seed weight, oil content, leaf area index, and harvest index, while the RGN-303 \times RGN-229 cross was identified for days to 50% flowering, days to maturity, number of secondary branches, number of seed per siliqua, and 1000-seed weight. RGN-13 and RH-406 were revealed as good heterotic and heterobeltiotic crosses for seed yield and other contributing characteristics among the 45 crosses.

4. Correlation and path coefficient:

Correlation coefficients analysis enables to identify the type and degree of association between any two quantifiable qualities. **Galton (1908)** first proposed the idea of correlation, which was further developed by **Fisher (1918)** and **Wright (1921)**, and which states that correlations between botanical markers and breeding quality are to be taken into account as trustworthy guides

in the process of association. It converts complex relationships between the occurrences into a straightforward form of association. However, the correlation coefficient does not reflect an intentional reliance of one variable on another.

Path coefficient analysis was first developed by **Write (1921)**, but **Dewey & Lu (1959)** used the method to select plants. Path coefficient analysis provides efficient ways to determine the direct and indirect causes of associations, enabling a given correlation to gauge the relative weight of each causal factor. Here, an overview of the literature on path coefficient analysis is presented.

Gangapur *et al.* (2009) investigated 46 germplasms of Indian mustard for seed production and contributing characteristics (11 attributes) in both protected (against pests and diseases) and unprotected conditions. Path coefficient analysis of 11 yield contributing characters clearly demonstrated that the number of siliquae per plant had the greatest positive direct effect on seed yield in both protected and unprotected environments, despite the fact that the number of primary and secondary branches per plant, biological yield per plant, harvest index, and other traits had positive direct effects in decreasing order and contributed indirectly to seed yield.

Nagendra Maurya *et al.* (2013) discovered that days to 50% blooming (0.404) had the greatest direct influence, followed by plant height (0.226) and number of seeds per silique (0.114). The length of the silique (-0.198) and 1000 seed weight (-0.139) had significant unfavourable direct impacts. Whereas the essential yield contributing variables under observation were plant height, followed by the number of siliquae on the main axis via days to 50% blooming, the indirect largest positive consequence was applied by plant height.

Maurya *et al.* (2013) reported that genotypic path analysis revealed that days to 50% blooming (0.404) generated the most direct impression, followed by plant height (0.226) and number of seeds per silique (0.114). The length of the silique (-0.198) and weight of 1000 seeds (-0.139) were the most unfavourable direct impacts. Whereas the important yield contributing factors under observation were plant height, number of siliquae on main raceme, and days to 50% blooming, the unanticipated highest favourable impression was exerted by plant height.

Lodhi *et al.* (2014) observed that seed yield per plant was found to be negatively correlated with oil content and positively correlated with the number of primary branches per plant, secondary branches per plant, angle of the primary branch, main shoot length, silique length, and number of seeds / siliquae.

Kumar and Pandey (2014) reported that at both the genotypic and phenotypic levels, seed yield per plant was positively and highly substantially connected with secondary branches per

plant, siliqua length, 1000 seed weight, biological yield per plant, and harvesting index. Only at the phenotypic level do days to maturity show a significant link with siliqua / plant and days to 50% blooming; beak length and primary branch per plant exhibited a negative correlation with days to maturity.

Bind *et al.* (2014) reported that all characteristics except for days to 50% blooming and days to maturity showed positive connection with seed yield per plant at both phenotypic and genotypic phases. The path coefficient analysis at the genotypic level showed that biological yield per plant, followed by harvest index, 1000 seed weight, number of seeds per siliqua, and number of primary branches per plant, had the biggest direct positive influence on seed production per plant. Plant height at the phenotypic level had the most direct negative impact on seed output per plant.

Sirohi *et al.* (2015) observed a notable and favourable correlation between seed production and biological yield, harvest index, and number of siliquae per plant. According to a path coefficient study, biological yield and harvest index had more favourable and immediate effects on seed yield. The biggest indirect factor affecting seed yield was harvest index.

Devi (2017) reported that grain yield per plant was shown to be negatively connected with secondary branches per plant and biological yield per plant, whereas siliquae on the main raceme employed strong positive significant genotypic association with grain production per plant. The biggest positive indirect influence of this feature was shown by days to 50% blooming, according to path analysis, whereas the highest direct effect was demonstrated by biological yield per plant.

Roy *et al.* (2018) studied diverse genotypes of Indian mustard genotypes for seed yield and its components and evaluated correlation of the entire traits with seed yield. They observed that seed yield per plant was positively and significantly associated with oil content, number of siliqua per plant, siliqua length, number of seeds per siliqua while days to flowering and biological yield showed negative correlation with seed yield. They also analysed the path coefficient analysis and observed that seed yield per plant had positive and direct influence on oil content, number of siliqua per plant, siliqua length, number of seeds per siliqua, days to first flowering, biological yield and harvest index.

Devi (2018) stated that path analysis revealed that days to 50% blooming had the greatest positive direct influence, but biological yield per plant had the greatest indirect effect.

Rout *et al.* (2018) reported that path coefficient analysis revealed a high positive and

direct influence of harvest index, biological yield, and number of siliquae per plant on seed yield at the genotypic level, and a high positive and direct influence of harvest index and biological yield per plant on seed yield at the phenotypic level in Indian mustard.

Pandey (2018) reported that path coefficient analysis of 17 yield contributing characters clearly indicated that the number of primary branches as well as biological yield per plant had the highest positive direct effect on seed yield, followed by harvest index, test weight, length of siliqua, silique on main axis, which had positive direct effects in descending order, and other characters contributed indirectly to seed yield in Indian mustard.

Awasthi et al. (2020) revealed that path co-efficient analysis found a low residual impact (0.00482, 0.00304, and 0.00167) during Rabi 2016-17 and 2017-18, indicating that most of the important yield components were included in the research. The harvest index % had the most direct beneficial influence on seed yield per plant, siliquae per plant, seeds per siliqua, secondary branches per plant, and days to maturity. Based on the findings, it was determined that two parameters, seed yield per plant and harvest index, which showed a strong positive association as well as a direct influence on seed yield, might be well-considered for selection and advancement of mustard germplasm seed yield.

Singh (2020) discovered that at both genotypic and phenotypic levels, days to 50% blooming had the most beneficial direct influence, followed by oil content, days to maturity, and test weight.

Singh et al. (2021) used a randomised block design with two replications to assess fourteen quantitative features in 50 Indian mustard (*Brassica juncea* L.) germplasm lines. Plant height, secondary branch, main shoot length, siliqua on main shoot, and maturity all had a strong positive significant genotypic association with seed output per plant, according to correlation research. Main shoot length, siliqua on main shoot, and maturity were shown to have a highly significant and positive link with seed yield per plant in phenotypic correlation.

Lavanya et al. (2022) studied the correlation and path coefficient analysis of twelve yield contributing features in fifty mustard genotypes. Correlation study found that at the genotypic level, seed yield per plant is positively and strongly connected with harvest index, followed by the number of secondary branches per plant and the number of siliquae per plant. Days to maturity, number of secondary branches per plant, number of siliquae per plant, siliqua length, 1000 seed weight, harvest index, and oil content all had a

direct positive influence on seed production per plant, according to path coefficient analysis. Days to 50% blooming, plant height, number of major branches per plant, and number of seeds per siliqua, on the other hand, had a direct negative influence on seed output per plant at both the genotypic and phenotypic levels. According to the findings, harvest index, number of secondary branches per plant, and number of siliquae per plant all had a significant association and a direct impact on seed output per plant.

Chapter-3

MATERIALS AND METHODS

3.1. Experimental site:

The present investigation entitled “Genetic studies on yield and its related attributes in Indian mustard (*Brassica juncea* L. Czern & Coss)” was carried out to elicit the information on magnitude of heterosis, correlation, path analysis, general and specific combining ability effects of parents and their hybrids for seed yield and its component traits. The field experiment was conducted at Oilseed Research Farm, Chandra Shekhar Azad University of Agriculture and Technology, situated at Kalyanpur, Kanpur, 208024 (U.P.) during, Rabi 2022-23 & 2023-24.

3.2. Experimental material and method:

Production of F₀ seeds:

Seven diverse parents were sown in five rows each during Rabi 2022-23 at Oilseed Research Farm, Kalyanpur, Kanpur for crossing programme. All possible cross combination excluding reciprocals were attempted in diallel fashion to produce F₀ seeds.

Testing of Parents and their 21 crosses:

The final experiment was conducted at Oilseed Research Farm, Kalyanpur, Kanpur during Rabi 2023-24. Each Parent and F₁s were evaluated in a Randomized Compact Block design with three replication. Each genotype was sown in single row of 5.0m long spaced at 45cm. The plant to plant distance was maintained at 20cm by thinning at 15 DAS. All the recommended package of practices were adopted to raise good crop.

Table 3.1: Details of genotype used as parents in the experiment:

S. S.N.	G genotypes	Pe pedigree	Ch characters
1.	L LAHAR	Fa farmer's variety	Days to maturity: 120-125 days, Oi oil content: 41-42%
2.	NRCDR-2	IC ICAR-DRMR	Days to maturity: 133-135 days, Oi oil content: 38-40%
3.	N NARENDRA AGETI RAI-4	N NDU&T AYODHYA	Days to maturity: 130-133 days, Oi oil content: 38-39%
4.	N NARENDRA AGETI RAI-8	N NDU&T AYODHYA	Days to maturity: 131-133 days, Oi oil content: 39.2-40.6%
5.	N NDR8501	Se selection from Atwa local(Fatehpur)	Days to maturity: 132-133 days, Oi oil content: 38.4-39.6%
6.	JA JAGRATI	Se selection from local	Days to maturity: 134-135days, Oi oil content: 39.8-40 %
7.	A AZAD MAHAK	M mathura Rai × JD- 6	Days to maturity: 120-125 days, Oi oil content: 41-42%

Table 3.2: Twenty one F₁s obtained from 7x7 diallel crosses of Indian mustard

S S.N.	C CROSSES	S.N.	Cr CROSSES
		11.	N NRCDR-2 x AZAD MAHAAK
1.	L LAHAR X NRCDR-2	12.	NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8
2.	L LAHAR x NARENDRA AGETI RAI-4	13.	N NARENDRA AGETI RAI-4 x NDR8501
3.	L LAHAR x NARENDRA AGETI RAI-8	14.	N NARENDRA AGETI RAI-4 x JAGRATI
4.	L LAHAR X NDR8501	15.	N NARENDRA AGETI RAI-4 x AZAD MAHAK
5.	L LAHAR x JAGRATI	16.	N NARENDRA AGETI RAI-8 x NDR8501
6.	L LAHAR x AZAD MAHAK	17.	N NARENDRA AGETI RAI-8 x JAGRATI
7.	N NRCDR-2 x NARENDRA AGETI RAI-4	18.	N NARENDRA AGETI RAI-8 x AZAD MAHAK
8.	N NRCDR-2 x NARENDRA AGETI RAI-8	19.	N NDR8501 x JAGRATI
9.	N NRCDR-2 x NDR8501	20.	N NDR8501 x AZAD MAHAK
10.	N NRCDR-2 x JAGRATI	21.	JA JAGRATI x AZAD MAHAK

3.4. Observations recorded:

The observations were recorded by five randomly selected plant for:

(i) Days to 50% flowering: The number of days were counted from the date of sowing to flowering of fifty per cent plants in a plot.

(ii) Days to maturity: The number of days were counted from the date of sowing to yellowing of seventy five per cent of siliquae in a plot was considered as maturity period.

(iii) Plant height (cm): Height of a plant was measured from base of the plant to tip of main shoot of individual plant at the time of harvest and the mean values for a plot were recorded.

(iv) Length of main raceme (cm): Length of main raceme from point of its emergence to tip was measured in cm.

(v) Number of primary branches: Number of branches arising from the main shoot was counted from the same tagged plants used for plant height at the time of harvest and mean values were obtained.

(vi) Number of secondary branches: The number of secondary branches arising from the main primary branches bearing siliquae were counted at the time of harvest from five randomly selected plants per plot and mean values over five plants were recorded.

(vii) Number of siliquae per plant: The number of siliquae bearing seeds per plant were recorded by counting total number of siliquae on five randomly selected plants in each plot and then values were averaged.

(viii) Seed yield per plant (g): All the five tagged plants were harvested and threshed as well as cleaned. The seeds so obtained were weighed in gram and averaged.

(ix) 1000-seed weight (g): Exact one thousand seeds were counted from bulk of seeds with the help of electronic balance and weighed in gram upto two decimal points.

(x) Oil content (%): Oil content was estimated in percentage by using Petroleum Ether method in Biochemistry Laboratory of Agriculture Biochemistry Department of CSAUAT, Kanpur.

(xi) Protein content (%): Protein content in percentage was estimated using NIRS (Near Infrared Spectrometer) in Directorate of Research Laboratory CSAUAT, Kanpur.

(xii) Methionine content (%): Methionine content in percentage was estimated using NIRS (Near Infrared Spectrometer) in Directorate of Research Laboratory CSAUAT, Kanpur.

(xiii) Tryptophan content (%): Tryptophan content was estimated in percentage using NIRS (Near Infrared Spectrometer) in Directorate of Research Laboratory CSAUAT, Kanpur.

(xiv) 3.5. Statistical Analyses:

The experimental data was compiled by taking the mean over selected plants of each treatment in each replication. The mean data was subjected for the following statistical analyses:

1. Analysis of variance
2. Diallel crosses analysis
3. Combining ability variances and their effects
4. Estimation of heterosis over economic parents.
5. Selection parameters

3.5.1. ANALYSIS OF VARIANCE

The analysis of variance for the design of experiment was carried out according to the procedure outlined by **Panse and Sukhatme (1967)**. The significance of difference among treatment means was tested by 'F' test. To test the hypothesis $H_0 : t_1 = t_2 = \dots = t_v$, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = Mean Performance of the i th genotype in j th replication

μ = General mean

g_i = Effect of i th genotype

r_j = Effect of j th replication

e_{ij} = Random experimental error associated with i th genotype and j th replication.

The usual form of analysis of variance is given in Table 3.5.1 to provide comparison; genotypic sum of square were partitioned in to parents, hybrids and parents vs. hybrids.

Table 3.3: Analysis of variance (ANOVA)

Source of variation	Degrees of freedom	Mean Sum of Squares	Expected MS	Cal. F
Replications	(r-1)	M_r	$\sigma^2_e + g \sigma^2_r$	
Genotypes	(g-1)	M_g	$\sigma^2_e + r \sigma^2_g$	
Parents	(p-1)	M_p	$\sigma^2_e + r \sigma^2_p$	
F ₁ 's Hybrids	(h-1)	M_h	$\sigma^2_e + r \sigma^2_h$	
Parents vs. Hybrids	1	M_{ph}	$\sigma^2_e + r \sigma^2_{ph}$	
Error	(g-1)(r-1)	M_e	σ^2_e	
Total	(rg-1)	-	-	

Where,

r=Number of replications

g=Number of genotypes (Parents +Hybrids)

p=Number of parent

h=Number of F₁'s hybrids

$\sigma^2 r$ = Variance due to replications

$\sigma^2 g$ = Variance due to genotypes

$\sigma^2 p$ = Variance due to parents

$\sigma^2 h$ = Variance due to hybrids

$\sigma^2 ph$ = Variance due to parents vs. hybrids

$\sigma^2 g$ = Variance due to genotypes

$\sigma^2 e$ = Error variance

Standard error of difference: Standard error of difference between two treatment means was formulated by using the given equation:

$$S. Ed \pm = \sqrt{\frac{2EMS}{r}}$$

Where, EMS = Error mean sum of square

r = number of replications in the experiment

Critical difference (CD): Critical difference was estimated by the formula:

$$CD = S. Ed \pm \times t$$

Where, t-value = table value of error difference at 5 per cent or 1 per cent level of significance.

Coefficient of variation (CV): CV is the ratio of standard deviation to the arithmetic mean. It is expressed as percentage.

$$CV\% = \frac{\sigma}{\bar{X}} \times 100$$

Where,

σ = standard deviation

\bar{X} = mean

3.5.2. DIALLEL ANALYSIS:

A set of crosses produced by involving 'n' lines in all possible combinations is designated as diallel cross and the analysis of such crosses is known as diallel analysis.

Such an analysis provides information on (1) the nature and amount of genetic parameters and (2) general and specific combining ability of parents and their crosses, respectively. The following two approaches were followed for diallel analysis:

1. Hayman's approach
2. Griffing's approach

The graphical analysis and components of genetic variance was done according to **Hayman (1954 a, b)**. The diallel analysis technique developed by **Hayman (1954a, b)** and **Jinks (1956)** and applied by **Aksel and Johnson (1963)** was used to understand the inheritance mechanism of different plant characters to ascertain the genetic basis of variation of various characters. This technique provided information regarding gene action governing different traits, proportion of positive and negative genes, distribution of genes among the parents, maternal and reciprocal effects, ratio of dominant and recessive genes, presence or absence of gene interactions and degree of dominance.

\hat{D} = Component of variation due to additive effects of genes

\hat{H}_1 = Component of variation due to dominance effects of gene

$\hat{H}_2 = H_1 [1-(u-v)^2]$

u = Proportion of positive genes in parents

v = Proportion of negative genes in parents

\hat{F} = The mean of F_r over arrays, where F_r is the covariance of additive and dominance gene effects in a single array.

\hat{E} = The expected environmental component of variation

Estimation of components of variation:

The estimates of these components of genetic variation were determined using following formulae as suggested by Hayman (1954a)

$$\hat{D} = V_0L_0 - \hat{E}$$

$$\hat{F} = 2 V_0L_0 - 4W_0L_{01} - \frac{2(n-2)}{n} \hat{E}$$

$$\hat{H}_1 = V_0L_0 + 4V_0L_1 - \frac{(3n-2)}{n} \hat{E}$$

$$\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\hat{E}$$

$$h^2 = 4(ML_1 - ML_0)^2 - 4 \frac{(n-1)}{n^2} \hat{E}$$

The statistics in the above formula may be explained as here as:

V_0L_0 = Variance of parents

V_r = Variance of r^{th} array

V_1L = Mean variance of the array

W_r = The covariance between the parents and their offspring in the r^{th} array.

W_0L_1 = Mean of covariance between the parents and their arrays

V_0L_1 = the variance of the means of arrays.

Testing of hypothesis: Uniformity of $(W_r - V_r)$ would indicate the validity of the hypothesis as postulated by Hayman (1954a) with ungrouped randomization, this may be tested by using the formula mentioned below:

$$t^2 = \frac{n-2}{4} \times \frac{(\text{Var.}V_r - \text{Var.}W_r)^2}{(\text{Var.}V_r \times \text{Var.}W_r) \text{Cov}^2(V_r, W_r)}$$

This is tested against the table value of F with 4 and $(n-2)$ degree of freedom where n is number of parents. Significant value indicates failure of the 56ty`hypothesis. Another way of testing the hypothesis is through the regression coefficient.

These values are tested against table value of 't' for $n-2$ degree of freedom.

Standard error of estimates

In order to estimate the accuracy of the above components of variance, the terms of main diagonal of the matrix given by **Hayman (1954a)** with common multipliers S^2 was used, where:

$$S^2 = (1/2) [\text{Var} (W_r - V_r)]$$

The formula being:

$$\text{S.E. } (\hat{D}) = \pm [S^2 (n^5 + n^4)/n^5]^{0.5}$$

$$\text{S.E. } (\hat{H}_1) = \pm [S^2 (n^5 + 41 n^4 - 12 n^3 + 4n^2)/n^5]^{0.5}$$

$$\text{S.E. } (\hat{H}_2) = \pm [S^2 (36 n^4/n^5)]^{0.5}$$

$$\text{S.E. } (\hat{F}) = \pm [S^2 (4n^5 + 20n^4 - 16 n^3 + 16 n^2) /n^5]^{0.5}$$

$$\text{S.E. } (\hat{h}^2) = \pm [S^2 (16n^4 + 16n^2 - 32 n + 16)/n^5]^{0.5}$$

$$\text{S.E. } (\hat{E}) = \pm [S^2 (n^4/n^5)]^{0.5}$$

After testing the significance of the components of variation for, \hat{D} , \hat{H}_1 , \hat{H}_2 , \hat{F} , and \hat{E} . The mean degree of dominance was calculated as $[(\hat{H}_1 / \hat{D})]^{0.5}$,

the proportion of genes with positive and negative effects as $(\hat{H}_2/4\hat{H}_1)$,

the proportion of dominant and recessive genes in the parents as $(4 \hat{D} \hat{H}_1)^{0.5} + \hat{F} / (4\hat{D} \hat{H}_1)^{0.5} - \hat{F}$ or KD / KR and the number of groups of genes, which control the character that exhibit dominance as (\hat{h}^2 / \hat{H}_2) .

3.5.3. COMBINING ABILITY ANALYSIS

The combining ability analysis was carried out by the procedure suggested by **Griffing's (1956 b) Method 2, Model 1**. The mathematical model for the combining ability analysis is assumed to be:

$$X_{ijkl} = \mu + g_i + g_j + S_{ij} + 1/bc \sum_k \sum_l e_{ijkl}$$

$$ij = 1,2,3, \dots, n;$$

$$k =$$

$$1,2,3, \dots, b;$$

1,2,3,.....c)

where,

μ = the population mean

g_i = the general combining ability (gca) effect of i^{th} parent

g_j = the gca effect of j^{th} parent

S_{ij} = the specific combining ability (gca) effect for the cross between i^{th} and j^{th} parents such that $S_{ij} = S_{ji}$

b = number of replication

c = number of plant per replication.

e_{ijkl} = the environmental effect associated with the $ijkl^{th}$ individual observation on i^{th} individual in the k^{th} block with i^{th} as female parent and j^{th} as male parent.

The usual restrictions, such as [$g_i = 0$ and $S_{ij} = S_{ii} = 0$ for each i] are imposed.

Table 3.4: ANOVA for combining ability:

Source of variation	Degree of freedom	Sum of square	Mean	Expected MS	F-test

GCA	(n- 1)	Sg	Mg	$\sigma^2e + \sigma^2s + (n + 2)\sigma^2g$	Mg/Me
SCA	$\frac{n(n - 1)}{2}$	Ss	Ms	$\sigma^2e + \sigma^2s$	Ms/Me
Error	(r-1)(t-1)	Se	Me	σ^2e	

Where,

$$S_g = \frac{1}{n+2} [\sum_i (X_i + X_{ii})^2 - 4/n \sum_i X_i^2 \dots \dots \dots]$$

$$= \frac{1}{n+2} \sum_i (X_i + X_{ii})^2 + 2/(n+1) (n+2) X^2 \dots$$

Where,

r = number of replications

Me = the error MS obtained from main ANOVA

Sg = the sum of squares (SS) due to gca

Ss = sum of squares due to sca

n = number of parents

Xi = total of the array involving Ith as a female

the i^{th} parents of the array

X_{ii} = the value of

total

$X_{..}$ = the grand

cross, with i^{th} as a female parent and j^{th} as a male parent

X_{ij} = value of the

C. Estimates of components of variances were obtained as under:

Component due to gca: $\hat{\sigma}_g^2 = \frac{Mg - Me}{n-2}$

Component due to sca: $\hat{\sigma}_s^2 = Ms - Me$

Estimates of various effects: The general and specific combining ability effects were estimated as follows:

$$\hat{g}_i = 1/n+2 [(X_i + X_{ii}) - 2/n X_{....}]$$

$$\hat{s}_{jib} = X_{ij} - 1/n+2 (X_i + X_{ii} + X_j + X_{jj}) + 2/(n+1) (n+2) X_{..}$$

where,

$$\hat{g}_i =$$

estimates of gca effects for the parent

estimates of gca

\hat{s}_{ij} = estimates of sca effects for ij^{th} cross

$X_{..}$ = and X_{ij} are the same as explained earlier

X_{ij} = total of the arrays involving j^{th} parent as a male

j^{th} parent of the array

X_{jj} = the value of the

Estimation of standard errors:

$$\begin{aligned} \widehat{\sigma}_e^2 / n(n+2)]^{0.5} & \text{SE}(\widehat{g}_i) = [(n-1) \\ \widehat{\sigma}_e^2 / (n+2)]^{0.5} & \text{SE}(\widehat{g}_i - \widehat{g}_j) = [2 \\ [(n(n-1) \widehat{\sigma}_e^2 / (n+2)]^{0.5} & \text{SE}(\widehat{s}_{ij}) = \\ (n+1) \widehat{\sigma}_e^2 / (n+2)]^{0.5} & \text{SE}(\widehat{s}_{ij} - \widehat{s}_{ik}) = [2 \\ (n+1) \widehat{\sigma}_e^2 / (n+2)]^{0.5} & \text{SE}(\widehat{s}_{ij} - \widehat{s}_{kl}) = [2n \\ \widehat{\sigma}_e^2 / (n+2)]^{0.5} & \end{aligned}$$

where, $\widehat{\sigma}_e^2 = M_{e/r}$ taken as error MS from the combining ability analysis

Estimates of degree of dominance:

The average degree

of dominance in the ratio of σ^2_s / σ^2_g was calculated using following formula:

$$D.D. = (\widehat{\sigma}_s^2 / \widehat{\sigma}_g^2)^{0.5}$$

where,

$\widehat{\sigma}_s^2$ = estimate of variance component due to specific combining ability

$\widehat{\sigma}_g^2$ = estimate of variance component due to general combining ability

Where,

$$M_{ssgca} - M_{sserror} / N + 2 \text{ as per Griffing method 2 model I}$$

$$\widehat{\sigma}_{sca}^2 = M_{ssca} - M_{sserror}$$

Testing the significance of *gca* and *sca* effects. Each *gca* and *sca* effects were subjected to ‘t’ test for testing of the significance.

The value of calculated ‘t’ is regarded as significant if it exceeds 1.96 and 2.58 at 5 per cent and 1 per cent levels of significance, respectively.

Alternatively *gca* and *sca* effects were compared with critical difference calculated by following formula:

$$C. D._{(gi)} = S.E._{(gi)} \times \text{table } t_{0.05} \text{ and } t_{0.01}$$

$$C. D._{(sij)} = S.E._{(sig)} \times \text{table } t_{0.05} \text{ and } t_{0.01}$$

3.5.4. Estimation of Economic Heterosis

The economic heterosis was estimated by formulae:

$$\text{Heterosis EP} = [F1 - EP/EP] / EP \times 100$$

Where, EP is the mean value over replication of economic parent.

3.5.5. ESTIMATION OF SELECTION PARAMETERS

Direct Selection

Parameters:

(a) Genetic

advance: The genetic advance was calculated as per the formula given by **Robinson *et al.* (1949)**.

$$\text{Genetic Advance} = (\sigma_{ph}) \times (K) \times (h^2)$$

Genetic advance in percent of mean of the character

$$G.A. (\%) = \frac{GA}{\bar{X}} \times 100$$

Where,

G. A. = Estimate of genetic advance

K = Selection differential at 5% selection intensity (K = 2.06)

h^2 = Heritability coefficient in narrow sense.

σ_{ph} = Phenotypic standard deviation.

\bar{X} = Mean value of the character concerned

Table 3.5: Scale for Genetic advance in percent of mean, classified by

(Johnson et al., 1955)

S. No.	Values of Genetic Advance (per cent)	Scale
1.	Less than 10	Low
2.	10 to 20	Medium
3.	Above 20	High

(c) **Heritability (in narrow sense)** in F_1 generation was calculated by the formula suggested by **Crumpacker and Allard (1962)**, which is as follows:

$$\hat{h}^2 = \frac{(1/4) \hat{D}}{[(1/4) \hat{D} + (1/4) \hat{H}_1 - (1/4) \hat{F} + \hat{E}]}$$

where,

\hat{h}^2 = estimate of heritability coefficient and \hat{D} , \hat{H}_1 , \hat{F} and \hat{E} are the same as explained earlier.

Heritability (in per cent) = heritability coefficient (\hat{h}^2) x 100

Searle (1965) suggested the scales of narrow sense heritability:

Below 40 =Low

41-50 =Medium

Above 50 =High

Indirect Selection Parameters:

Correlations Coefficient Analysis:

The form of analysis taken up for obtaining co-variance components among different pairs of observations was the same as that for analysis of variance except that sum of squares were replaced by sum of products and mean squares were replaced by mean

products. The phenotypic and genotypic correlation coefficients for all the characters under present investigation were calculated as per the method advocated by **Singh and Chaudhary (1985) and Al-Jibouri *et al.* (1958)**.

Genotypic covariance (Cov_{gxgy})

$$Cov_{gxgy} = \frac{MSPg - MSPe}{r}$$

Where,

Cov_{gxgy} : Genotypic co-variance between x^{th} and y^{th} character,

MSPg : Mean sum of products due to genotypes between two variable i and j,

MSPe : Mean sum of products due to error between variable i and j

r: number of replication.

Phenotypic covariance (Cov_{pxpy}):

$$Cov_{pxpy} = Cov_{gxgy} + Cov_{exey}$$

Where, Cov_{exey} and Cov_{pxpy} are environmental covariance and phenotypic co-variance between x^{th} and y^{th} character respectively.

The estimates of co-variance and variance were utilized for computation of genotypic and phenotypic correlation coefficients.

Genotypic correlation coefficient (r_{gxgy}):

It was reckoned by formulae as presented under:

$$r_{gxgy} = Cov_{gxgy} / \sqrt{(\sigma^2_{gx} \times \sigma^2_{gy})}$$

Where,

r_{gxgy} Cov_{gxgy} σ^2_{gx} σ^2_{gy} are Genotypic correlation coefficient between x^{th} and y^{th} character, Genotypic co-variance between x^{th} and y^{th} character, and Genotypic variance for x^{th} and y^{th} character, respectively.

Phenotypic correlation coefficient ($r_{p_{ij}}$):

It was computed with the help of formulae given below:

$$r_{p_{xy}} = \text{Cov}_{p_{xy}} / \sqrt{(\sigma^2_{px} \times \sigma^2_{py})}$$

where, $r_{p_{xy}}$, $\text{Cov}_{p_{xy}}$ and σ^2_{px} , σ^2_{py} are phenotypic correlation coefficient between x^{th} and y^{th} character, phenotypic co-variance between x^{th} and y^{th} character and phenotypic variance for x^{th} and y^{th} character, respectively.

Test of significance: The 't' values were approximated to test the significance of the correlation coefficients with (n-2) degrees of freedom by utilizing the formula advocated by **Panse and Sukhatme (1985)**, as :

$$t = \frac{r}{\sqrt{(1-r^2)}} \times \sqrt{(n-2)} ; \text{taking degree of freedom as } (n-2)$$

Where,

't' : Calculated value of 't'

r : Correlated coefficient between two variables and n: total number of observations.

Path Coefficient Analysis:

Wright (1921) suggested the procedure for path coefficient analysis and further elaborated by Dewey and Lu (1959) for plant breeding. It was carried out on the basis of genotypic correlation ($r_{g_{ij}}$). In order to devise path analysis three steps were followed calculation of direct effect, indirect effect and residual effect.

Direct effects: To estimate direct effect of various characters, simultaneous equations are solved from the path matrix.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \dots + r_{1(12)}P_{12y}$$

Similarly for all the 13 characters, simultaneous equations are solved to obtain direct effects.

Where, $r_{1Y}, r_{2Y}, r_{3Y}, \dots, r_{13Y}$ are the genotypic correlations of days to maturity, days to 50% flowering, plant height (cm), length of main raceme (cm), number of primary branches, number of secondary branches, number of siliquae per plant, 1000 seed weight (g), oil content (%), protein content (%), methionine content, tryptophan content (%) respectively towards seed yield per plant.

$P_{1Y}, P_{2Y}, P_{3Y}, \dots, P_{13Y}$ are the direct effects of days to maturity, days to 50% flowering, plant height (cm), length of main raceme (cm), number of primary branches, number of secondary branches, number of siliquae per plant, 1000 seed weight

(g), oil content (%), and protein content (%), methionine content, tryptophan content (%) respectively towards seed yield per plant.

Indirect effects: It is effect of an independent character on dependent character via other independent characters. It is estimated by putting correlation coefficient values and those of direct effect values in equation forms as depicted below.

Indirect effect of X_1 via

$$X_2 = r_{12} \cdot P_{2y}$$

$$X_3 = r_{13} \cdot P_{3y}$$

$$X_{12} = r_{1(12)} \cdot P_{12y}$$

Where X_1, X_2, X_{12}

are the independent variables.

Similarly indirect effects were computed by using above mentioned formula.

Residual effects: The residual effects are those variations which occurred due to other possible independent variables and which cannot be explained under the present investigation. It is evaluated by deducting the value of coefficient of determination from unity. Here residual effect was estimated by using the values of direct effects and correlation coefficients,

$$R = 1 - \sqrt{(\sum_{i=1}^c (P_{iy} \cdot r_{iy}))}$$

Where, R = Residual effect.

P_{iy} = Direct effect of i^{th} independent character.

R^2 is the coefficient of determination and is the amount of variation in yield and that can be accounted for the yield component trait. Path-coefficient at phenotypic level was calculated using phenotypic correlation coefficient.

Table 3.6: Scales for Path Coefficient (Lenka and Mishra, 1973)

S. No.	Values of direct and indirect effects	Scale
1.	0.00 to 0.09	Negligible
2.	0.10 to 0.19	Low
3.	0.20 to 0.29	Moderate
4.	0.30 to 0.99	High
5.	More than 1.00	Very high

Chapter 4

EXPERIMENTAL FINDINGS

The findings of the present investigation entitled, “**Genetic studies on yield and its related attributes in Indian in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]**” to collect the information in genetic architecture of seedyield and its attributes based on seven parents diallel cross excluding reciprocals. The traits viz. days to 50% flowering, days to maturity, length of main raceme

(cm), plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae on main raceme, number of siliquae per plant, average seeds per siliquae, 1000-seed weight (g), oil content (%) and seed yield per plant (g) are considered as contributing characters are described under the following heads:

1. Analysis of variance
2. Diallel cross analysis : Genetic components of variance analysis
3. Combining ability analyses
4. Extent of heterosis in F₁ generation
5. Selection parameters
 - a. Genetic advance
 - b. Heritability
 - c. Correlation coefficient
 - d. Path coefficient

1. Analysis of variance:

The variance analysis of data based on the mean values of all 12 characters independently of the mean sum of squares (M.S.S) is presented in **Table 7**. It demonstrated highly significant variations in treatment for most of the traits under study, indicating a large range of variance in parents and F₁s that provides enough opportunity for parent selection.

Table 1. Mean performance and range of variability of 7 parents and F1 for 12 characters in Indian mustard

Sourced of variation	df	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yeild per plant (g)
REP	2	1.08	2.68	1.61	0.71	0.57	0.96	1.69	13.09	0.37	0.02	0.05	0.34
Treat.	27	20.01**	58.21**	112.63**	273.56**	8.30**	5.09**	199.90**	2815.31**	3.80**	0.65**	2.66**	5.21**
PAR	6	36.49**	89.65**	150.76**	118.30**	4.97**	2.03**	191.05**	3317.83**	2.65**	0.88**	2.19**	5.99**
F1	20	12.45**	39.29**	67.52**	188.27**	6.49**	4.12**	146.63**	1975.63**	3.25**	0.42**	2.51**	3.97**
PVF1	1	72.32**	248.00**	786.10**	2911.37*	64.57**	42.68**	1318.39*	16590.17*	21.65**	3.88**	8.50**	25.46*
EROR	54	1.34	4.41	1.92	2.19	0.49	0.66	1.36	10.22	0.47	0.02	0.09	0.15

***, ** significant at 5% and 1% level, respectively**

Mean and Range :

Days to 50% flowering:

For each character, the mean and range of parents and their F₁s were determined, and the results are shown in **Table 8** & maximum and minimum mean values of parents and crosses are shown in **Table 9**.

Based on the population mean (63.62 days), three of the seven parents, JAGRATI, NARENDRA AGETI RAI MAHAK, and LAHAR were discovered to be early flowering. Other parents were late flowering. The days to 50% flowering lies between 56.67 days to 68 days.

Among the crosses, days to 50% flowering varied from 58.33 to 65.33 days, with a mean of 61.68 days. Among the 21 crossings investigated, NARENDRA AGETI RAI×JAGRATI, NDR8501×JAGRATI, JAGRATI×AZAD MAHAK exhibited early flowering, while the others were late in 50% Flowering.

Days to maturity:

Three of the seven parents, AZAD MAHAK, LAHAR NDR8501 were assessed to be early maturing based on the population mean (131.48days). Other parents were late to mature. The days to maturity range from 119.33 to 135.33 days.

Days to maturity varied from 120.33 to 132.33 days for crosses, with a mean of 127.51 days. Among the 21 crossings tested, five combinations, namely NARENDRA AGETI RAI-4×NARENDRA AGETI RAI-8, NARENDRA AGETI RAI-8×JAGRATI, NARENDRA AGETI RAI-8×AZAD MAHAK exhibited early maturity, while the others were late in maturity.

Length of main raceme (cm):

Out of seven parents three namely, LAHAR, AZAD MAHAK and NRCDR-2, were found to have long length of main raceme based on population mean (75.56 cm). The length of main raceme lies between 66.47 cm to 80.07 cm.

Among crosses length of main raceme ranged between 72.87 cm to 89.40cm with mean 82.62 cm. Among 21 crosses evaluated 5 best combinations namely, NARENDRA AGETI RAI-4×AZAD MAHAK, LAHAR×AZAD MAHAK, NRCDR-2×AZAD MAHAK, LAHAR×NRCDR-2, NDR8501×AZAD MAHAK

Plant height (cm):

Out of seven parents three namely JAGRATI, NARENDRA AGETI RAI-8, NDR8501, were found short height based on population mean(180.22cm). The plant height lies between 168.40 cm to 188.40 cm.

Among crosses plant height ranged between 180.53 cm to 203.27 cm with mean 193.82 cm. Among 21 crosses evaluated 5 combinations namely, NARENDRA AGETI RAI×JAGRATI, NDR8501 × JAGRATI, NARENDRA AGETI RAI-4 × JAGRATI, NRCDR-2× JAGRATI, LAHAR×JAGRATI showed short height, while remaining were found long in length.

Number of primary branches per plant:

Out of seven parents two namely, AZAD MAHAK, NDR8501, were found to have more number of primary branches based on population mean (9.09). Then number of primary branches lies between (8.13 to11.80)

Among crosses number of primary branches ranged between (8.93 to 13.33) with mean 8.93 Among 21 crosses evaluated 10. best 5 combinations namely, NDR8501× AZAD MAHAK, NARENDRA AGETI RAI-8× AZAD MAHAK, JAGRATI × AZAD MAHAK, NARENDRA AGETI RAI-4× AZAD MAHAK, NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8 combiners have number of primary branches above mean.

Table 8: Mean performance and range of variability of 7 parents and F₁ for 12 characters in Indian mustard

Traits	Mean		Range			
			Parent		F ₁ s	
	Parent	F ₁ s	Minimum	Maximum	Minimum	Maximum
Days to 50% flowering	63.62	61.48	56.67	68.00	58.33	65.33
Days to maturity	131.48	127.51	119.33	135.33	120.33	132.33
Length of main raceme (cm)	75.56	82.62	66.47	85.27	72.87	89.40
Plant height (cm)	180.22	193.83	168.40	188.40	180.53	203.27
Number of primary branches	9.09	11.11	8.13	11.80	8.93	13.33
Number of secondary branches	17.73	19.38	16.40	18.73	17.53	21.97
Number of siliquae on main raceme	64.45	73.60	54.13	77.40	61.40	88.53
Number of siliquae/plant	443.11	475.57	409.67	491.33	422.40	510.40
Average seeds per siliquae	13.49	14.66	12.53	15.40	13.07	16.30
533	4.28	4.77	3.55	4.94	3.53	5.33
Oil Content (%)	40.10	40.84	38.56	41.40	339.15	42.36
Seed yield per plant (g)	18.00	19.28	15.87	19.43	16.60	20.80

Table 9: Maximum and minimum mean values of parents and crosses for 12 traits in Indian mustard

Source	Days to 50% flowering				Days to maturity				Length of main raceme (cm)			
	Minimum		Maximum		Minimum		Maximum		Minimum		Maximum	
	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross
Parents	56.67	Jagrati	68.00	Narendra Ageti Rai	119.33	Azad Mahak	135.33	Nrcdr-2	66.477	Narendra Ageti Rai	85.27	Azad Mahak
F_{1s}	58.53	Jagrati×Azad Mahak	65.33	Nrcdr-2×Narendra Ageti Rai-4	120.33	Narendra Ageti Rai-4×Narendra Ageti Rai-8	132.33	Lahar×Ndr8501	72.87	Narendra Ageti Rai-4×Jagrati	89.40	Narendra Ageti Rai-4×Azad Mahak

Source	Plant height (cm)				Number of primary branches				Number of secondary branches			
	Minimum		Maximum		Minimum		Maximum		Minimum		Maximum	
	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross
Parents	168.40	Jagrati	188.40.	Azad Mahak	8.13	Jagrati	11.80	Azad Mahak	16.40	Jagrati	18.73	Azad Mahak
F_{1s}	180.53	Ndr8501×Jagrati	203.27	Narendra Ageti Rai-4×Azad Mahak	8.93	Nrcdr-2×Jagrati	13.33	Narendra Ageti Rai-4×Azad Mahak	17.53	Lahar×Jagrati	21.97	Narendra Ageti Rai-4×Azad Mahak

Source	Number of siliquae on main raceme				Number of siliquae/ plant				Average seeds per siliquae			
	Minimum		Maximum		Minimum		Maximum		Minimum		Maximum	
	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross
Parents	54.13	Narendra Ageti Rai-4	77.40	Azad Mahak	409.67	Lahar	491.33	Azad Mahak	12.53	Lahar	15.40	Azad Mahak
F₁s	61.40	Lahar× Narendra Ageti Rai-4	88.53	Narendra Ageti Rai-4× Azad Mahak	422.40	Lahar× Narendra Ageti Rai-4	510.40	Nrcdr-2× Azad Mahak	13.07	Nrcdr-2× Narendra Ageti Rai-4	16.30	Narendra Ageti Rai-4× Azad Mahak

Source	1000 grain weight (g)				Oil content (%)				Seed yield per plant (g)			
	Minimum		Maximum		Minimum		Maximum		Minimum		Maximum	
	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross	Value	Cross
Parents	3.55	Lahar	4.94	Azad Mahak	38.56	Narendra Ageti Rai-4	41.40	Azad Mahak	15.87	Jagrati	19.43	Ndr8501
F₁s	3.53	Lahar× Narendra Ageti Rai-4	5.33	Narendra Ageti Rai-4× Azad Mahak	39.15	Narendr a Ageti Rai-4× Narendra	42.36	Narendra Ageti Rai-8× Azad Mahak	16.60	Narendra Ageti Rai-4× Jagrati	20.80	Narendra Ageti Rai-4× Narendra Ageti Rai-

						a Ageti Rai-8						8
--	--	--	--	--	--	------------------	--	--	--	--	--	---

Number of secondary branches per plant:

Out of seven parents five parents had more number of secondary branches per plant as compared to the population mean (17.73) namely, AZAD MAHAK, NDR8501, NARENDRA AGETI RAI-4, NARENDRA AGETI RAI-8, NRCDR-2. The number of secondary branches lies between 16.40 to 18.73.

Among crosses number of secondary branches ranged between 17.53 to 21.97 with mean 19.38. Among 21 crosses evaluated 10 combiners have number of secondary branches above mean. Best 5 combinations namely, NARENDRA AGETI RAI-4 × AZAD MAHAK, NARENDRA AGETI RAI-4 × NDR8501, NARENDRA AGETI RAI-4 × NARENDRA AGETI RAI-8, NRCDR-2 × AZAD MAHAK, NDR-8501 AZAD MAHAK have number of secondary branches above mean.

Number of siliquae on main raceme:

Out of seven parents three namely, AZAD MAHAK, NDR8501, NRCDR-2 and were found to have more number of siliquae on main raceme based on population mean (64.45). The number of siliquae on main raceme lies between (54.13 to 77.40)

Among crosses number of siliquae on main raceme ranged between 61.40 to 88.53 with mean 73.60. Among 21 crosses evaluated 5 best combinations namely, NARENDRA AGETI RAI-4 × AZAD MAHAK, NRCDR-2 × AZAD MAHAK, JAGRATI × AZAD MAHAK, NDR8501 × AZAD MAHAK, NRCDR-2 × NDR8501.

Number of siliquae per plant:

Out of seven parents two parents had more number of siliquae per plant as compared to the population mean (443.11) namely, AZAD MAHAK, NRCDR-2. The number of siliquae lies between 409.67 to 491.33

Among crosses number of siliquae per plant ranged between 422.40 to 510.40 with mean 475.57. Among 21 crosses evaluated 11 combiners have number of siliquae per plant above mean. Best 5 combinations namely, JAGRATI × AZAD MAHAK, NARENDRA AGETI RAI-8 × AZAD MAHAK, NRCDR-2 × AZAD MAHAK, NRCDR-2 × NDR8501, LAHAR × NRCDR-2 have number of siliquae per plant above mean.

Average seeds per siliquae:

Out of seven parents three parents had more average seeds per siliquae as compared to the

population mean (13.49) namely, AZAD MAHAK, JAGRATI, NDR8501. The value of average seeds per siliquae lies between 12.53 to 15.40.

Among crosses value of average seeds per siliquae ranged between 13.07 to 16.30 with mean 14.66. Among 21 crosses evaluated 9 combiners have value of average seeds per siliquae above mean. Best 5 combinations namely, NARENDRA AGETI RAI-4×AZAD MAHAK, LAHAR×AZAD MAHAK, JAGRATI×AZAD MAHAK, NDR8501×AZAD MAHAK, NARENDRA AGETI RAI-4×NDR8501 have value of average seeds per siliquae above mean.

1000-seed weight (g):

Out of seven parents four parents had more 1000-seed weight as compared to the population mean (4.28) namely, AZAD MAHAK, NDR8501, NARENDRA AGETI RAI-8, NRCDR-2 and. The value of 1000-seed weight lies between 3.55 to 4.94.

Among crosses value of 1000-seed weight ranged between 3.53 to 5.33 with mean 4.77. Among 21 crosses evaluated 13 combiners have value of 1000 seed weight (g) above mean. Best 5 combinations namely, JAGRATI×AZAD MAHAK, NARENDRA AGETI RAI-8×AZAD MAHAK, NARENDRA AGETI RAI-4×AZAD MAHAK, AGETI RAI-4×NDR8501, NRCDR-2×AZAD MAHAK have value of 1000-seed weight above mean.

Oil content (%):

Out of seven parents four parents had more oil content % as compared to the population mean (40.10%) namely, LAHAR, NRCDR-2, AZAD MAHAK, NDR8501. The value of oil content lies between 38.56% to 41.40%.

Among crosses value of oil content % ranged between 39.15% to 42.36% with mean 40.84%. Among 21 crosses evaluated 9 combiners have value of oil content above mean. Best 5 combinations namely, LAHAR×AZAD MAHAK, NRCDR-2×AZAD MAHAK, NARENDRA AGETI RAI-8×AZAD MAHAK, LAHAR×NARENDRA AGETI RAI-8, NARENDRA AGETI RAI-4×AZAD MAHAK have value of oil content above mean.

Seed yield per plant (g):

The seed yield per plant (g) amongst parents varied from 15.87(jagrati) to 19.48(Azad

Mahak) with a mean value of 18.00g. one parents had lesser seed yield per plant than the rest four two as compared to the mean.

Amongst F₁s, it ranged from 16.60 g (NARENDRAAGETI RAI-4×JAGRATI) to 20.80 g (NARENDRA AGETI RAI-4×NARENDRA AGETI RAI-8) with a mean values of 19.28g. eleven crosses had lesser seed yield per plant than the rest ten as compared to the mean.

2. Diallel Cross analyses:

Genetic component of variance analysis:

The regression “b”, its standard error “sb”, regression deviation from zero (b-0), unity(1-b) and t² value for all the 12 traits are depicted in **Table 10**. The regression coefficient for all 12 traits is described as below:

Days to 50% flowering:

In F₁ generation, non-significant regression coefficient deviation was observed positive and non-significant for zero and positive non-significant for unity and t² value.

Days to maturity:

In F₁ generation, non-significant regression coefficient deviation was observed for zero, unity and t² value was also found non-significant.

Length of main raceme (cm):

In F₁ generation, positive non-significant regression coefficient deviation was observed for zero while unity and t² value were found positive non-significant.

Plant height (cm):

In F₁ generation, positive non-significant regression coefficient deviation was observed for zero while unity and t² value were found positive non-significant.

Number of siliquae on main raceme:

In F₁ generation, positive non-significant regression coefficient deviation was observed for

zero while unity and t^2 value were found positive non-significant.

Number of siliquae per plant:

In F_1 generation, positive non-significant regression coefficient deviation was observed for zero and unity while and t^2 value was found positive non-significant.

In F_1 generation, positive non-significant regression coefficient deviation was observed for zero and unity while and t^2 value was found positive non-significant.

1000-seed weight (g):

Average seed per siliqua

In F_1 generation, positive non-significant regression coefficient deviation was observed for zero and unity while t^2 value was found positive significant.

Oil content (%):

In F_1 generation, positive non-significant regression coefficient deviation was observed for zero and unity while and t^2 value was found positive non-significant.

Seed yield per plant (g):

F_1 generation, positive non-significant regression coefficient deviation was observed for zero and unity while and t^2 value was found positive non-significant.

Table No 10: Uniformity test for Wr-Vr using regression coefficient and 't²' for 12 characters in Indian mustard

S.No.	Chracters	b	Se±b	T test		
				IFB=0	IF B=1	T ²
1	Days to 50% flowering	0.507	0.486	1.044	1.015	0.202
2	Days to maturity	0.331	0.329	1.005	2.032	0.279
3	Length of main raceme (cm)	0.720	0.165	4.349	1.695	1.089
4	Plant height (cm)	0.209	0.225	0.930	3.515*	2.442
5	Number of primary branches	0.448	0.143	3.134	3.856*	5.929**
6	Number of secondary branches	0.079	0.173	0.456	5.311**	5.913**
7	No of siliquae on main raceme	0.685	0.197	3.479	1.601	0.733
8	Number of siliquae / plant	0.969	0.043	22.565	0.713	0.353
9	Average seeds per siliquae	0.843	0.136	6.221	1.154	0.526
10	1000 grain weight (g)	0.770	0.095	8.142	2.431	3.668*
11	Oil content (%)	0.754	0.122	6.201	2.020	2.153
12	Seed yeild per plant (g)	0.796	0.101	7.901	2.030	2.468

* Significant at 5% level; ** Significant at 1% level

SE \pm b = Standard error

(b-0) = regression deviation from zero (1-b) = regression deviation from unity

Genetic component analysis and related statistics

The estimate of all the component of variation is presented in **Table 11** and following results were observed:

The Additive Component (\hat{D}): The estimates of additive component (\hat{D}) was highly significant for majority of all of the traits.

The Dominant Component (\hat{H}_1 and \hat{H}_2): The estimated dominance component (\hat{H}_1) and (\hat{H}_2) was highly significant for all characters. The estimated values of $1H^{\wedge}$ were higher than that of the estimates of $2H^{\wedge}$ for all the characters.

The Components (\hat{h}^2): The estimates of \hat{h}^2 were positive and highly significant for all the characters.

The environmental Component (\hat{E}): The estimate values of \hat{E} component were positive and non-significant for all the characters indicating negligible role of environment for expression of characters.

Components	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yield per plant (g)
D	11.72*	28.44*	49.62**	38.72**	1.49*	0.45	63.22**	1102.58**	0.728**	0.287**	0.699**	1.945**
	1.07	6.87	7.55	14.87	0.49	0.36	13.06	33.81	0.111	0.047	0.098	0.193
F	4.83	46.75*	11.12	-35.03	-0.24	-0.96	-12.81	189.04**	0.961**	0.143	-0.600**	0.001
	2.56	16.49	18.12	35.67	1.18	0.88	31.34	81.10	0.267	0.113	0.235	0.464
H1	8.93**	75.25*	61.85**	199.16*	7.40*	3.38**	101.98*	1134.94**	1.491**	0.493**	1.053**	2.911**
	2.57	16.54	18.19	35.80	1.18	0.88	31.45	81.39	0.268	0.113	0.236	0.465
H2	7.39**	41.62*	59.36**	180.46*	7.15*	2.99**	86.78**	1119.24**	1.345**	0.446**	0.867**	2.739**
	2.26	14.58	16.02	31.54	1.04	0.77	27.71	71.72	0.236	0.100	0.208	0.410
h2	13.28*	45.57*	146.37*	542.91*	11.97**	7.85**	245.77*	3093.92**	3.964**	0.721**	1.571**	4.725**
	1.52	9.79	10.76	21.19	0.70	0.52	18.61	48.17	0.158	0.067	0.140	0.275
E	0.44	1.45	0.63	0.71	0.16	0.22	0.46	3.42	0.156	0.006	0.030	0.052
	0.38	2.43	2.67	5.26	0.17	0.13	4.62	11.95	0.039	0.017	0.035	0.068
sqrt(h1/d)	0.87	1.63	1.12	2.27	2.23	2.73	1.27	1.01	1.43	1.31	1.23	1.22
H2/4h1	0.21	0.14	0.24	0.23	0.24	0.22	0.21	0.25	0.23	0.23	0.21	0.24
((4DH1)^.5+F)/((4DH1)^.5-F)	1.62	3.04	1.22	0.67	0.93	0.44	0.85	0.84	0.37	1.47	0.48	1.00
h^2/H2	1.80	1.09	2.47	3.01	1.67	2.62	2.83	2.76	2.95	1.62	1.81	1.72

h²	64.76	39.24	56.98	50.22	33.61	48.05	67.31	69.77	65.08	44.86	75.02	58.95
r	-0.166	-0.561	-0.968	-0.348	-0.867	-0.222	-0.779	-0.944	-0.916	-0.919	-0.621	-0.892

Table 11: Estimates of variance components analysis and related parameters for 12 traits in Indian mustard

Proportion of Genetic Components:

The estimates of mean degree of dominance $(\hat{H}_1/\hat{D})^{1/2}$ more than unity for most of the characters except for days to flowering (0.87).

The proportion of genes with positive and negative effects $(\hat{H}_2/4\hat{H}_1)$ were near or equal to theoretical value (0.25) for no of siliqua per plant (0.25) and Length of main raceme (0.24) Number of primary branches(0.24) Seed yeild per plant (g) (0.24) while a few characters have values lesser than the theoretical value (0.25) such as days to 50% flowering, days to maturity, plant height , Number of secondary branches, Average seeds per siliquae, 1000 grain weight (g), Oil content (%),

The proportion of dominant and recessive genes $[(4\hat{D}^{\wedge} \hat{H}^{\wedge}_1)^{1/2} + F^{\wedge} / (4\hat{D}^{\wedge} \hat{H}^{\wedge}_1)^{1/2} - F^{\wedge}]$ were less than unity for all the characters except days to 50% flowering (1.62), main days to maturity

(3.05) Length of main raceme (cm(1.22)and 1000grain weight (1.47).

The ratio \hat{h}^2 / \hat{H}_2 depicted the number of group of genes which control the character and exhibit dominance. Days to 50% flowering (1.80), days to maturity (1.09), length of main raceme (2.47), plant height (3.01), number of primary branches(1.67), number of secondary branches (2.62), number of siliquae on main raceme (2.83), number of siliquae per plant (2.76), average seeds per siliquae (2.95), and seedyield per plant (1.62) showed its value more than unity while remaining other characters had its value less than unity such as average seeds per siliquae (1.81), 1000grain weight (1.72). Indicating that these characters are under control of at least one gene group more than one gene group was responsible for the expression of the traits.

Table 12: Analysis of variance of combining ability and their ratios for 12 traits in Indian mustard

Source of variation		Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae /plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yield per plant (g)
Gca	6	20.33**	28.99**	96.02**	174.44**	4.23**	3.39**	185.68*	2835.19**	3.633**	0.464*	2.892*	4.643**
sca	21	2.77**	16.67**	20.83**	67.41**	2.35**	1.21**	32.62**	396.43*	0.590**	0.147*	0.314*	0.907**
Error	54	0.45	1.47	0.64	0.73	0.16	0.22	0.46	3.36	0.158	0.006	0.031	0.049
□□g		2.21	3.06	10.60	19.30	0.45	0.35	20.58	314.65	0.386	0.051	0.318	0.510
□□s		2.32	15.20	20.20	66.68	2.19	0.99	32.16	393.08	0.433	0.141	0.283	0.858
□□g/□□□s		0.95	0.20	0.52	0.29	0.21	0.35	0.64	0.80	0.89	0.36	1.13	0.60

□□s/□□□g) ^0.5		1.02	2.23	1.38	1.86	2.20	1.68	1.25	1.12	1.06	1.66	0.94	1.30
-------------------	--	------	------	------	------	------	------	------	------	------	------	------	------

*, ** significant at 5% and 1% level, respectively

2. Combining ability analyses:

Analysis of variance for combining ability:

The analysis of variance for combining ability is depicted in **Table 12**. The general combining ability and specific combining ability were significant for most of the characters. The estimated variance of general combining ability (σ^2_{gca}) was lower than variance of specific combining ability (σ^2_{sca}) for all the characters except Oil content (%).

General combining ability (GCA) effect:

The estimated values of general combining ability effects of 7 parents for all the 12 characters are presented in **Table 13** and **14** ranking top three desirable parents on the basis of per se performance and gca effect character wise result are described as follows:

Days to 50% flowering:

The minimum value of gca effect for days to 50% flowering was revealed by parent LAHAR (-0.01) and maximum for NARENDRA AGETI RAI-4 (2.51)

Significant negative gca effects were observed from the parents NDR850 (-0.43) and NARENDRA AGETI RAI-8 (-0.53) JAGRATI (2.57). The positive and significant value of gca effect for days to 50% flowering was observed in NDR8501, NARENDRA AGETI RAI-4.

Days to maturity:

The gca effect for days to maturity trait varied from -0.48(LAHAR) to 2.70 (NRCDR-2). The significant negative gca effect for days to maturity was shown by NARENDRA AETI RAI-4(-1.30), NARENDRA AETI RAI-8(-1.26),JAGRATI(-0.48), AZAD MAHAK(-2.22) The positive and significant value of gca effect for days to maturity was observed in NDR8501(0.89), NRCDR-2(2.70) LAHAR(1.67). Negative and non-significant gca effects were observed from the parent LAHAR(-0.48).

Length of main raceme (cm):

The gca effect for length of main raceme (cm) varied from -3.96 (NARENDRA AETI RAI-4) to 4.99 (Azad Mahak). Positive and significant gca effects were observed in AZAD MAHAK (4.99), NRCDR-2(3.92). Negative and significant effect were revealed in NDR 8501 (-1.17), NARENDRA AETI RAI-8 (-2.08) and JAGRATI.

Plant height (cm):

The gca effect for plant height (cm) varied from -9.22 (JAGRATI) to 4.22(AZAD MAHAK). Significant negative gca effect were shown by parents NDR8501(-1.59) and JAGRATI (-9.22). Significant positive gca effect were shown by AZAD MAHAK (4.99),NARENDRA AGETI RAI-8(0.93), NARENDRA AGETI RAI-4 (1.84) and NRCDR-2(2.19)LAHAR(1.78).

Number of primary branches per plant:

Genotypes were revealed positive and significant for gca effect for number of primary branches per plant in parents AZAD MAHAK (1.39). Negative gca effects were observed in JAGRATI (-0.59), NRCDR-2 (-0.54), LAHAR (-0.39).The gca effects varied from -0.59 (JAGRATI) to 1.39 (AZAD MAHAK).

Table 12: Analysis of variance of combining ability and their ratios for 12 traits in Indian mustard

Source of variation		Days to flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliqua on main raceme	Number of siliquae /plant	Average seeds per siliqua	1000 grain weight (g)	Oil content (%)	Seed yield per plant (g)
Gca	6	20.33**	28.99**	96.02**	174.44*	4.23**	3.39**	185.68**	2835.19**	3.633*	0.464*	2.892*	4.643**
sca	21	2.77**	16.67**	20.83**	67.41**	2.35**	1.21**	32.62*	396.43*	0.590*	0.147*	0.314*	0.907**
Error	54	0.45	1.47	0.64	0.73	0.16	0.22	0.46	3.36	0.158	0.006	0.031	0.049
σ^2_g		2.21	3.06	10.60	19.30	0.45	0.35	20.58	314.65	0.386	0.051	0.318	0.510
σ^2_s		2.32	15.20	20.20	66.68	2.19	0.99	32.16	393.08	0.433	0.141	0.283	0.858
$\sigma^2_{g/s}$		0.95	0.20	0.52	0.29	0.21	0.35	0.64	0.80	0.89	0.36	1.13	0.60

□□s/□□□g) ^0.5		1.02	2.23	1.38	1.86	2.20	1.68	1.25	1.12	1.06	1.66	0.94	1.30
-------------------	--	------	------	------	------	------	------	------	------	------	------	------	------

*, ** significant at 5% and 1% level, respectively

3. Combining ability analyses:

Analysis of variance for combining ability:

The analysis of variance for combining ability is depicted in **Table 12**. The general combining ability and specific combining ability were significant for most of the characters. The estimated variance of general combining ability (σ^2_{gca}) was lower than variance of specific combining ability (σ^2_{sca}) for all the characters except Oil content (%).

General combining ability (GCA) effect:

The estimated values of general combining ability effects of 7 parents for all the 12 characters are presented in **Table 13** and **14** ranking top three desirable parents on the basis of per se performance and gca effect character wise result are described as follows:

Days to 50% flowering:

The minimum value of gca effect for days to 50% flowering was revealed by parent LAHAR (-0.01) and maximum for NARENDRA AGETI RAI-4 (2.51)

Significant negative gca effects were observed from the parents NDR850 (-0.43) and NARENDRA AGETI RAI-8 (-0.53) JAGRATI (2.57). The positive and significant value of gca effect for days to 50% flowering was observed in NDR8501, NARENDRA AGETI RAI-4.

Days to maturity:

The gca effect for days to maturity trait varied from -0.48(LAHAR) to 2.70 (NRCDR-2). The significant negative gca effect for days to maturity was shown by NARENDRA AETI RAI-4(-1.30), NARENDRA AETI RAI-8(-1.26), JAGRATI(-0.48), AZAD MAHAK(-2.22) The positive and significant value of gca effect for days to maturity was observed in NDR8501(0.89), NRCDR-2(2.70) LAHAR(1.67). Negative and non-significant gca effects were observed from the parent LAHAR(-

0.48).

Length of main raceme (cm):

The gca effect for length of main raceme (cm) varied from -3.96 (NARENDRA AETI RAI-4) to 4.99 (Azad Mahak). Positive and significant gca effects were observed in AZAD MAHAK (4.99), NRCDR-2(3.92). Negative and significant effect were revealed in NDR 8501 (-1.17), NARENDRA AETI RAI-8 (-2.08) and JAGRATI.

Table 13: Estimates of gca effects of parents for 12 traits in Indian mustard

Var	Parent/Hybrids	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yield per plant (g)
1	LAHAR	-0.01	1.67 **	0.30	1.78 **	-0.39 **	-0.71 **	-4.82 **	-18.89 **	-0.68 **	-0.38 **	0.18 **	-0.66 **
2	NRCDR-2	0.40	2.70 **	3.92 **	2.19 **	-0.54 **	0.10	3.44 **	25.15 **	-0.49 **	0.20 **	-0.05	0.06
3	NARENDRA AGETI RAI-4	2.51 **	-1.30 **	-3.23 **	1.84 **	0.12	0.69 **	-2.83 **	-14.88 **	0.14	-0.15 **	-0.92 **	0.11
4	NRENDRA AGETI RAI-8	-0.53 *	-1.26 **	-2.08 **	0.93 **	-0.19	-0.13	-2.58 **	-9.13 **	-0.38 **	-0.01	0.08	0.08
5	NDR8501	0.43 *	0.89 *	-1.17 **	-1.59 **	0.20	0.06	0.77 **	-1.29 *	0.09	0.04	0.04	0.60 **
6	JAGRATI	-2.57 **	-0.48	-2.73 **	-9.22 **	-0.59 **	-0.79 **	-2.25 **	-4.86 **	0.08	-0.01	-0.30 **	-1.16 **
7	AZAD MAHAK	-0.23	-2.22 **	4.99 **	4.07 **	1.39 **	0.78 **	8.27 **	23.89 **	1.24 **	0.31 **	0.98 **	0.97 **
	gca(j)	0.206	0.374	0.247	0.264	0.125	0.145	0.208	0.566	0.123	0.024	0.054	0.069

	se gi-gj	0.315	0.571	0.377	0.403	0.190	0.221	0.318	0.864	0.187	0.037	0.083	0.105
--	-----------------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

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

Table 14. Ranking of top three desirable parents based on per se performance and GCA effects for 12 attributes in Indian mustard

Sl. No	Characters	Good parents based on per se mean performance	Good general combiners based on gca effect	Best common parents based per se performance and gca effects
1	Days to 50% flowering	JAGRATI	NARENDRA AGETI RAI -8	JAGRATI
		NARENDRA AGETI RAI -8	JAGRATI	NARENDRA AGETI RAI -8
			LAHAR	
2	Days to maturity	AZAD MAHAK	NARENDRA AGETI RAI -4	
			NARENDRA AGETI RAI -8	
			JAGRATI	
3	Plant height(cm)	JAAGRATI	NDR8501	JAAGRATI
		NDR8501	JAGRATI	NDR8501
		NARENDRA AGETI RAI-4		
4	No..of primary branches per plant	AZAD MAHAK	AZAD MAHAK	AZAD MAHAK
		NRCDR-2	NDR8501	
		LAHAR		
5	No. of secondary branches per plant	AZAD MAHAK	AZAD MAHAK	AZAD MAHAK
		NDR8501	NARENDRA AGETI RAI-4	
6		AZAD MAHAK	AZAD MAHAK	NRCDR-2

7	No. of siliquae per main raceme Length of main raceme	AZAD MAHAK	AZAD MAHAK	AZAD MAHAK
		NDR8501 NARENDRA AGETI RAI-	NDR8501	NDR8501
		NRCDR-2	NRCDR-2	AZAD MAHAK NRCDR-2
8	No. of siliquae per plant	AZAD MAHAK NRCDR-2	AZAD MAHAK LAHAK	AZAD MAHAK
		NRCDR-2	NRCDR-2	NRCDR-2
9	AVERAGE of seeds per siliqua	AZAD MAHAK	AZAD MAHAK	AZAD MAHAK

AVERAGE of seeds per siliqua	AZAD MAHAK	AZAD MAHAK	AZAD MAHAK
	NDR8501	NDR8501	NDR8501
	JAGRATI	JAGRATI	JAGRATI
1000 seed weight (g)	AZAD MAHAK	AZAD MAHAK	AZAD MAHAK
	NDR8501	NRCDR-2	NDR8501
	NRCDR-2	NDR8501	
Oil content	AZAD MAHAK	AZAD MAHAK	AZAD MAHAK
	NDR8501	NDR8501	NDR8501
	LAHAR		
Seed yield per plant	NDR8501	AZAD MAHAK	NDR8501
	AZAD MAHAK	NDR8501	AZAD MAHAK
	NARENDRA AGETI RAI - 4	NRCDR-2	

Plant height (cm):

The gca effect for plant height (cm) varied from -9.22 (JAGRATI) to 4.22(AZAD MAHAK). Significant negative gca effect were shown by parents NDR8501(-1.59) and JAGRATI (-9.22). Significant positive gca effect were shown by AZAD MAHAK (4.99),NARENDRA AGETI RAI-8(0.93), NARENDRA AGETI RAI-4 (1.84) and NRCDR-2(2.19)LAHAR(1.78).

Number of primary branches per plant:

Genotypes were revealed positive and significant for gca effect for number of primary branches per plant in parents AZAD MAHAK (1.39). Negative gca effects were observed in JAGRATI (-0.59), NRCDR-2 (-0.54), LAHAR (-0.39).The gca effects varied from -0.59 (JAGRATI) to 1.39 (AZAD MAHAK).

Number of secondary branches per plant:

Minimum value of the gca effect for number of secondary branches per plant was observed in JAGRATI (-0.79) and maximum in AZAD MAHAK (0.78). All genotypes were found significant for this characters except NRCDR-2(0.10), NARENDRA AGETI RAI-8 (-0.13), NDR8501(0.06). AZAD MAHAK and NARENDRA AGETI RAI-4 have good per se performance for this trait.

Number of siliquae on main raceme:

Genotypes were revealed positive and significant for gca effect for number of on main raceme in parents AZAD MAHAK (8.27) and NDR8501 (0.77) NRCDR-2(3.44). Positive gca effect were found good general combiners. Negative gca effects were observed in JAGRATI (-2.25), NARENDRA AGETI RAI-8(-2.58) NARENDRA AGETI RAI-4 (-2.83) LAHAR (-4.82) The gca effects variedfrom --2.25 (JAGRATI) to 8.27(AZAD MAHAK).

Number of siliquae per plant:

The minimum value for gca effect for number of siliquae per plant was found inLAHAR (-18.89) while maximum in NRCDR-2 (25.15). The genotypes AZAD MAHAK (23.89), NRCDR-2(25.15) showed positive and significant gca effects while all negative and significant effects were

found.

Average seeds per siliquae:

Minimum gca effect for average seeds per siliquae was observed in LAHAR (- 0.68) and maximum in AZAD MAHAK(1.24). Positive significant effects were revealed in AZAD MAHAK. Genotypes namely NRCDR-2 (-0.49) NARENDRA AGETI RAI-8(-0.38) LAHAR(0.68) showed negative significant effects while positive non-significant in NARENDRA AGETI RAI-8 NDR8501, JAGRATI

1000-Seed weight (g):

The gca effect for 1000-seed weight (g) varied from -0.01 NARENDRA AGETI RAI-8 to 0.31 (AZAD MAHAK). Genotypes exhibited positive and significant gca effects for 1000-seed weight (g) AZAD MAHAK (0.31), NRCDR-2 (0.37) and with negative significant gca effects parents namely; NRENDRA AGETI RAI-4 (-0.15) LAHAR (-0.38).

Oil content (%):

The gca effect for oil content (%) varied from -0.92 (NRENDRA AGETI RAI-4) to (0.98) AZAD MAHAK. The parents namely:, LAHAR (0.18) and AZAD MAHAK (0.98) showed positive significant gca effect and they were superior with per se performance for this trait. Negative significant gca effect were showed in NRENDRA AGETI RAI-4 (-0.92), JAGRATI (-0.30) and negative non-significant for NRCDR-2 (-0.05) while positive non-significant for NRENDRA AGETI RAI-4(0.08) NDR8501(0.04).

Seed yield per plant (g):

The gca effect for seed yield per plant (g) varied from -1.16 (JAGRATI) to 0.97 (AZAD MAHAK). Genotypes exhibited positive and significant gca effect for seed yield per plant AZAD MAHAK (0.97), NDR8501 (0.60). The parents namely: JAGRATI(-1.16), LAHAR (-0.66) showed negative and significant gca effects.

Specific combining ability (SCA) Effect:

The specific combining ability effect of all the 21 hybrids for 12 characters were estimated and depicted in **Table 15** and **16** (Ranking top three desirable cross combinations on the basis of per se performance and sca effect). The character wise results are described below:

Days to 50 % flowering:

The estimates of sca effect for days to 50% flowering varied from -3.95 (NARENDRA AGETI RAI-4×AZAD MAHAK) to 1.71(NARENDRA AGETI RAI-4×JAGRATI). For days to 50 % flowering, early flowering plants with negative sca effects are preferred. The crosses namely, LAHAR × NRCDR-2 (-1.40), LAHAR× NARENDRA AGETI RAI-8 (-1.14), LAHAR × AZAD MAHAK (-1.10) and NRCDR-2× NARENDRA AGETI RAI-8 (-0.88) , NRCDR-2× NDR8501(-1.18), NARENDRA AGETI RAI-8 × NARENDRA AGETI RAI-4(0.66), NARENDRA AGETI RAI-4× AZAD MAHAK(-3.95) NARENDRA AGETI RAI-8×NDR8501(1.58) were found negatively significant and hence are desirable on the basis of sca effects and these crosses were superior in per se performance for early flowering.

Days to maturity:

The negative and significant sca effect for days to maturity is considered desirable. The minimum sca effect for this character was observed in NARENDRA AGETI RAI-8 ×JAGRATI (-6.09), and maximum in NDR85013×AZAD MAHAK. (3.17) For days to 50 % flowering, early flowering plants with negative sca effects are preferred. The best cross combination namely, NARENDRA AGETI RAI-8 ×JAGRATI (-6.09), NARENDRA AGETI RAI-8×JAGRATI (5.39) NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8 (-5.61) showed significant and negative sca effect followed by NARENDRA AGETI RAI-4× NDR8501 (-2.43)were superior in per se performance for early maturity.

Length of main raceme (cm):

The sca effect for length of main raceme (cm) varied from -2.89 (NDR8501× JAGRATI)to 9.68 (NARENDRA AGETI RAI-4×). The positive and significant sca effect for main raceme length is considered desirable. The positive and significant sca effect were found maximum in 9.68 (NARENDRA AGETI RAI-4) followed by NARENDRA AGETI RAI-4×AZAD MAHAK(6.79) NRCDR-2× JAGRATI(4.39), NARENDRA AGETI RAI-8×JAGRATI (3.22) These crosses have high per se performance for these trait.

Plant height (cm):

The range of sca effect for plant height (cm) varied from (-4.27) LAHAR × NDR8501 to (8.35) LAHAR× NRCDR. The negative and significant sca effect for plant height is considered desirable. The cross combinations NDR8501 ×JAGRAATI (0.92) showed significant and least positive sca effect and was found superior in performance for dwarf plant height.

Number of primary branches per plant:

The estimate of sca effects for number of primary branches per plant varied from(-1.01) LAHAR× NARENDRA AGETI RAI-4 to (3.00) LAHAR× NRCDR-2. The positive and significant sca effect for number of primary branches per plant is considered desirable. Positive and significant sca effect were found in cross combinations namely, LAHAR× NRCDR-2 ,LAHAR×NDR 8501, NRCDR-2× NARENDRA AGETI RAI-8, NRCDR-2 × AZAD MAHAK, NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8, NARENDRA AGETI RAI-4× NDR8501, NARENDRA AGETI RAI-4× JAGRATI, JAGRATI×AZAD MAHAK.these crosses were found superior in performance for producing more number of primary branches per plant.

Table 15: Estimates of SCA effects of 21 F1s for 12 characters in Indian mustard

V a r	Hybrids	Days to 50% flower ing	Days to maturi ty	Len ^t h of main racem e (cm)	Plant height (cm)	Numb er of prima ry branc hes	Number of seconda ry branche s	Numbe r of siliqua e on main raceme	Numbe r of siliqua e/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yeild per plant (g)
8	LAHAR X NRCDR-2	-1.40 **	-2.20 **	1.32 **	8.35 **	3.00 **	1.01 **	5.74 **	21.35 **	0.34 *	0.46 **	0.03	0.65 **
9	LAHAR x NARENDRA AGETI RAI-4	0.16	-0.20	0.48	6.49 **	-1.01 **	-0.32	-2.26 **	-11.29 **	-0.62 **	-0.58 **	-0.25 **	0.65 **
10	LAHAR x NARENDRA AGETI RAI-8	-1.14 **	-0.91	2.46 **	2.34 **	0.18	0.38 *	1.56 **	-10.17 **	0.03	0.03	0.83 **	0.55 **
11	LAHAR X NDR8501	-0.44	1.28 *	0.28	-4.27 **	1.51 **	-0.40 *	1.31 **	18.18 **	0.35 *	0.05	-0.10	0.10
12	LAHAR x JAGRATI	0.56 *	-0.69	2.98 **	3.09 **	-0.62 **	0.07	1.06 **	-1.11	-0.29	0.34 **	0.06	-0.44 **

1	LAHAR	x	-1.10	3.06	1.26	4.28	-1.00		23.07		0.37	0.29	1.17	
3	AZAD MAHAK		**	**	**	**	**	0.60 **	-0.22	**	1.14 **	**	**	
1	NRCDR-2	x			0.92	-4.02	-0.98		19.94		0.16			
4	NARENDRA				**	**	**	-0.16	0.51	**	0.18	**	-0.08	0.10
4	AGETI RAI-4		0.42	-0.91										
1	NRCDR-2	x												
5	NARENDRA													
5	AGETI RAI-8		-0.88 **	1.06 *	2.70 **	5.96 **	1.00 **	-0.40 *	2.16 **	7.19 **	-0.43 **	0.10 **	-0.01	-0.70 **
16	NRCDR-2	x	-1.18 **	-2.09 **	1.72 **	7.45 **	-0.60 **		2.08 **	11.68 **			0.41 **	-0.08
	NDR8501							0.33			0.03	-0.06		
17	NRCDR-2	x			4.39 **	1.01 **	-0.54 **		-0.74 **	4.79 **				0.81 **
	JAGRATI		0.16	-0.72				0.19			0.31	-0.04	-0.13	
18	NRCDR-2	x			2.02 **	-2.64 **	3.65 **	0.35 *	5.31 **	-6.10 **		-0.16 **	0.60 **	0.55 **
	AZAD MAHAHA		-0.18					0.72 **			0.61 **			
19	NARENDRA		-0.66 *	-5.61 **		8.34 **	2.13 **		4.60 **	2.99 **		0.35 **	-0.66 **	1.65 **
	AGETI RAI-4				-0.01			2.11 **			0.61 **			

	x NARENDRA AGETI RAI-8												
20	NARENDRA AGETI RAI-4 x NDR8501	0.38	-2.43 **	9.68 **	10.72 **	1.00 **	0.81 **	5.02 **	4.51 **	1.17 **	0.66 **	0.34 **	0.53 **
21	NARENDRA AGETI RAI-4 x JAGRATI	1.71 **	-5.39 **	-2.02 **	-0.45 **	2.42 **	0.49 *	3.40 **	2.92 **	0.85 **	0.38 **	0.31 **	-1.31 **
22	NARENDRA AGETI RAI-4 x AZAD MAHAK	-3.95 **	-0.98 *	6.79 **	6.93 **	1.22 **	1.52 **	11.78 **	22.17 **	0.55 **	0.52 **	0.87 **	-0.44 **
23	NARENDRA AGETI RAI-8 x NDR8501	-1.58 **	-3.13 **	0.72 *	6.71 **	-0.22 **	-0.26	0.94 **	16.96 **	0.15	0.05	0.62 **	-0.44 **
24	NARENDRA AGETI RAI-8 x JAGRATI	-0.25	-6.09 **	3.22 **	-1.59 **	-0.19 **	-0.14	0.95 **	17.73 **	0.64 **	-0.06	0.20 **	0.52 **

Table 16: Ranking top three desirable parents based on per se performance and SCA effects for 12 attributes in Indianmustard

Traits	Good specific combiners based on per se performance	Superior specific combiners based on SCA effects	Common specific combiners based on SCA & per se performance
Days To 50% Flowering	NARENDRA AGETI RAI-8 X JAGRATI, NDR8501 X JAGRATI, NARENDRA AGETI RAI-4 X AZAD MAHAK	NARENDRA AGETI RAI-4 X AZAD MAHAK NARENDRA AGETI RAI-8 X NDR8501 LAHAR X NRCDR-2	NARENDRA AGETI RAI-4 X JAGRATI
Days To Maturity	NARENDRA AGETI RAI-8 X JAGRATI, NARENDRA AGETI RAI-4 X NARENDRA AGETI RAI-8, NARENDRA AGETI RAI-4 X JAGRATI	NARENDRA AGETI RAI-8 X NDR8501, NARENDRA AGETI RAI-8 X NDR8501, NARENDRA AGETI RAI-8 X JAGRATI	NARENDRA AGETI RAI-8 X JAGRATI
Length of Main Raceme (cm)	JAGRATI X AZAD MAHAK, NDR8501 X AZAD MAHAK, NARENDRA AGETI RAI-4 X AZAD MAHAK	NARENDRA AGETI RAI-8X JAGRATI, LAHAR X NARENDRA AGETI RAI-4, NRCDR-2 XJAGRATI	
Plant Height (cm)	NDR8501 X JAGRATI, NARENDRA AGETI RAI-4 X JAGRATI	NRCDR-2 X NARENDRA AGETI RAI-4, NARENDRA AGETI RAI-8 X JAGRATI, LAHAR X NDR8501	NARENDRA AGETI RAI-8 X JAGRATI

Number of Primary Branches	NDR8501X AZAD MAHAK, NARENDRA AGETI RAI-8X AZAD MAHAK, LAHAR X NRCDR-2,	NARENDRA AGETI RAI- 4 X JAGRATI, LAHAR X NRCDR-2, NARENDRA AGETI RAI-4NARENDRA AGETI RAI-8	LAHAR X NRCDR-2
Number of Secondary Branches	NDR8501 X AZAD MAHAK, JAGRATI X AZAD MAHAK JAGRATI X AZAD MAHAK	NARENDRA AGETI RAI-4 X NARENDRA AGETI RAI-8 NARENDRA AGETI RAI-4 X	NARENDRA AGETI RAI-4 X AZAD MAHAK

Number of Siliquae/Plant	NARENDRA AGETI RAI-8 X AZAD MAHAK, NRCDR-2 X AZAD MAHAK, NARENDRA AGETI RAI-4 X AZAD MAHAK	NARENDRA AGETI RAI-8 X JAGRATTI, NARENDRA AGETI RAI-4 X AZAD MAHAK, NRCDR-2 X NARENDRA AGETI RAI-4	NARENDRA AGETI RAI-4 X AZAD MAHAK
Average Seeds Per Siliquae	NDR8501 X AZAD MAHAK, NARENDRA AGETI RAI-4 X AZAD MAHAK, NRCDR-2 X AZAD MAHAK	NARENDRA AGETI RAI-8 X JAGRATI, LAHAR X AZAD MAHAK, NARENDRA AGETI RAI-4 X JAGRATTI	
1000 Grain Weight (G)	NARENDRA AGETI RAI-4 X AZAD MAHAK, JAGRATI X AZAD MAHAK, NARENDRA AGETI RAI-8 X AZAD MAHAK	NARENDRA AGETI RAI-8 X JAGRATI, NARENDRA AGETI RAI-4 X AZAD MAHAK, LAHAR X NRCDR-2	NARENDRA AGETI RAI-4 X AZAD MAHAK
Oil Content (%)	NARENDRA AGETI RAI-8 X AZAD MAHAK, NRCDR-2 X AZAD MAHAK, LAHAR X AZAD MAHAK	NARENDRA AGETI RAI-4 X AZAD MAHAK, NARENDRA AGETI RAI-8 X NDR8501 NARENDRA AGETI RAI-8X AZAD MAHAK	
Seed Yield Per Plant	NDR8501 X AZAD MAHAK, NARENDRA AGETI RAI-4 X NARENDRA AGETI RAI-8	NDR8501 X AZAD MAHAK, NARENDRA AGETI RAI-4 X NARENDRA AGETI RAI-8	NDR8501 X AZAD MAHAK
Number of Siliquae on Main Raceme	NRCDR-2 X AZAD MAHAK, NARENDRA AGETI RAI-4 X AZAD MAHAK	NARENDRA AGETI RAI-4 X NDR8501, NRCDR-2 X AZAD MAHAK	NARENDRA AGETI RAI-4 X AZAD MAHAK

Number of primary branches per plant:

The estimate of sca effects for number of primary branches per plant varied from (-1.01) LAHAR× NARENDRA AGETI RAI-4 to (3.00) LAHAR× NRCDR-2. The positive and significant sca effect for number of primary branches per plant is considered desirable. Positive and significant sca effect were found in cross combinations namely, LAHAR× NRCDR-2 ,LAHAR×NDR 8501, NRCDR-2× NARENDRA AGETI RAI-8, NRCDR-2 × AZAD MAHAK, NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8, NARENDRA AGETI RAI-4× NDR8501, NARENDRA AGETI RAI-4× JAGRATI, JAGRATI×AZAD MAHAK.these crosses were found superior in per se performance for producing more number of primary branches per plant.

Number of secondary branches per plant:

The sca effects for number of secondary branches per plant ranged from (-0.40)LAHAR × NDR8501 to (2.11) NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8. The positive and significant sca effectfor number of secondary branches per plant is considered desirable. The best cross combinations which showed positive and significant effect were NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8 (2.11) NARENDRA AGETI RAI-4×AZAD MAHAK, NDR8501×JAGRATI (1.36), NDR8501× AZAD MAHAK.

Number of siliquae on main raceme:

The sca effect for number of siliquae on main raceme varied from -2.26 (LAHAR× NARENDRA AGETI RAI-4) to (NARENDRA AGETI RAI-4× AZAD MAHAK) (11.78). The positive and significant sca effect for number of siliquae per plant is considered desirable. Significant and positivesca effect were found in cross combination namely, NARENDRA AGETI RAI-4× AZAD MAHAK (11.78), LAHAR× NRCDR-2 (5.74) which was found most superior in per se performance.

Number of siliquae per plant:

The sca effect for number of siliquae per plant varied from -14..75 (NDR 8501 ×AZAD MAHAK) to 23.07 (LAHAR× AZAD MAHAK). The positive and significant

sca effect for number of siliquae per plant is considered desirable. Significant and positive sca effectwere found in cross combinations namely, LAHAR× AZAD MAHAK (23.07),LAHAR

× NRCDR-2(21.75) , NARENDRA AGETI RAI-4× AZAD MAHAK(22.17), NRCDR-2× NARENDRA AGETI RAI-4 (19.94), LAHAR ×NDR8501 (18.18) which were found superior in per se performance.

Average seeds per siliquae:

The sca effect for average seeds per siliquae ranged from -0.62 (LAHAR× NARENDRA AGETI RAI-4) to 1.17 (NARENDRA AGETI RAI-4× NDR8501). The positive and significant sca effect for protein content is considered desirable. The cross namely, NARENDRA AGETI RAI-4× NDR8501 (1.17) was found significant and desirable on the basis of sca effects and this crosses was superior in per se performance for average seeds per siliquae.

1000-seed weight (g):

The estimate of sca effects 1000-seed weight (g) varied from -0.58 (LAHAR× NARENDRA AGETI RAI-4) to 0.66 (NARENDRA AGETI RAI-4× NDR8501). The positive and significant sca effect for 1000 seed weight is considered desirable. The best cross combination which showed significant positive sca effect were NARENDRA AGETI RAI-4× NDR8501(0.66) NARENDRA AGETI RAI-4× AZAD MAHAK (0.52), LAHAR× NRCDR-2 (0.46) These crosses were found superior in per se performance for test weight.

Oil content (%):

The estimate of sca effect for oil content (%) ranged from -0.66 (NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8) to 0.87 (NARENDRA AGETI RAI-4× AZAD MAHAK). The positive and significant sca effect for oil content is considered desirable. The best cross combinations having positive significant sca effect were found in crosses namely, NARENDRA AGETI RAI-4× AZAD MAHAK (0.87), LAHAR×NARENDRA AGETI RAI-4(0.83).

Seed yield per plant (g):

The minimum value of seed yield per plant (g) for sca effect was found in lahar × jagrati (-0.44) and maximum in NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8 (1.65). The positive and significant sca effect for number of seed yield per plant is considered desirable. Positive and significant effect were observed in NARENDRA

AGETI RAI-4 × NARENDRA AGETI RAI-8 (1.65), LAHAR × AZAD MAHAK (1.17) these crosses showed higher per se performance for seed yield per plant

4. Estimation of heterosis in F₁ generation

- Hybrids NARENDRA AGETI RAI-4 × NARENDRA AGETI RAI-8 and NDR8501 × AZAD MAHAK showed high heterosis over both better and economic parent (azad mahak) for seed yield per plant NARENDRA AGETI RAI-8 × AZAD MAHAK showed high heterosis for oil content.

The estimates of heterosis over better and economic parent for 12 traits were estimated and depicted in **Table 17**. The character wise description is given below:

Days to 50% flowering:

All 21 crosses showed negative significant heterosis over better parent in desirable direction. Heterosis over better parent for days to 50% flowering ranged from -9.79 (JAGRATI × AZAD MAHAK) to -1.55 (NARENDRA AGETI RAI-4 × JAGRATI).

The cross combination namely: JAGRATI × AZAD MAHAK (-9.79), NDR8501 × JAGRATI(8.64), NARENDRA AGETI RAI-4 × AZAD MAHAK(6.70), NARENDRA AGETI RAI-8 × NDR8501(6.70), LAHAR × NARENDRA AGETI RAI-8(6.70), LAHAR × JAGRATI(7.22). 18 out of 21 crosses showed negative significant heterosis over better parent. Heterosis over economic parent ranged from (-9.79) JAGRATI × AZAD MAHAK to (-1.55) (NARENDRA AGETI RAI-4 × JAGRATI).

Days to maturity:

Out of 21 crosses only 18 crosses showed negative and significant heterosis and 3 showed negative non-significant heterosis over economic parent in desirable direction. Heterosis over economic parent ranged from (-9.98) NARENDRA AGETI RAI-4 × NARENDRA AGETI RAI-8 (-0.50) LAHAR × NDR8501. For heterosis over economic parent all crosses showed negative significant heterosis in desirable direction except LAHAR × AZAD MAHAK (-0.50), LAHAR × AZAD MAHAK(-0.51), NDR8501 × AZAD MAHAK (-201) which were found non-

significant.

Length of main raceme (cm):

Out of 21 crosses 8 crosses were positive significant heterosis over economic parent in desirable direction and varied from 18.21 (NARENDRA AGETI RAI-4 x NDR8501) to 0.30 (JAGRATI x AZAD MAHAK). The cross combinations (NARENDRA AGETI RAI-4 x NDR8501) exhibited maximum heterosis over economic parent (18.21), followed by NARENDRA AGETI RAI-8 x JAGRATI (11.21).

Plant height (cm):

Three crosses out of 21 crosses showed negative significant heterosis over economic parent in desirable direction, heterosis over economic parent ranged between -4.28 (NARENDRA AGETI RAI-8 x NDR8501) to 7.89 (NARENDRA AGETI RAI-4 x AZAD MAHA). The cross combination exhibited maximum heterosis over economic parent (-4.28) NARENDRA AGETI RAI-8 x NDR8501, followed by -4.18 (NARENDRA AGETI RAI-8 x JAGRATI). 2 crosses out of 21 crosses showed negative non-significant heterosis over economic parent, 12 crosses out of 21 crosses showed positive significant heterosis over economic parent while the rest of the crosses showed positive non-significant heterosis over economic parent.

Va r	Hybrids	Days to 50% flowering			Days to maturity			Length of main raceme (cm)			Plant height (cm)		
		BP	MP	Azad	BP	MP	Azad	BP	MP	Azad	BP	MP	Azad
8	LAHAR X NRCDR-2	-5.18 **	-4.69 **	-5.67 **	-3.45 **	-2.12	9.50 **	2.25	6.95 **	1.33	10.28 **	10.35 **	7.61 **
9	LAHAR x NARENDRA AGETI RAI-4	-4.90 **	-1.77	0.00	-3.74 **	-3.02 **	7.82 **	1.73	9.24 **	-8.05 **	9.08 **	10.20 **	6.44 **
10	LAHAR x NARENDRA AGETI RAI-8	-5.24 **	-4.49 **	-6.70 **	-4.00 **	-3.40 **	7.26 **	5.80 **	9.83 **	-4.38 **	6.33 **	7.73 **	3.75 **
11	LAHAR X NDR8501	-5.10 **	-3.88 **	-4.12 **	-0.50	0.00	10.89 **	4.15 **	7.07 **	-5.86 **	1.36 *	2.94 **	-1.10
12	LAHAR x JAGRATI	-5.76 **	-0.28	-7.22 **	-3.73 **	-2.89 *	8.10 **	5.62 **	9.70 **	-4.53 **	1.21	5.65 **	-1.24
13	LAHAR x AZAD MAHAK	-6.19 **	-5.45 **	-6.19 **	-0.51	4.38 **	9.78 **	2.50	7.68 **	2.50	6.45 **	7.76 **	6.45 **
14	NRCDR-2 x NARENDRA AGETI RAI-4	-3.92 **	-1.26	1.03	-4.68 **	-4.09 **	8.10 **	-2.41	9.25 **	-3.28 *	3.72 **	4.72 **	1.08
15	NRCDR-2 x NARENDRA AGETI RAI-8	-5.18 **	-3.94 **	-5.67 **	-3.20 *	-2.48 *	9.78 **	1.07	9.56 **	0.16	8.66 **	10.03 **	5.89 **
16	NRCDR-2 x NDR8501	-5.61 **	-4.88 **	-4.64 **	-3.94 **	-3.11 **	8.94 **	0.99	8.45 **	0.08	8.10 **	9.71 **	5.34 **
17	NRCDR-2 x JAGRATI	-6.74 **	-0.83	-7.22 **	-3.94 **	-3.47 **	8.94 **	2.29	10.93 **	1.37	0.44	4.77 **	-2.12 **
18	NRCDR-2 x AZAD MAAHAAK	-4.12 **	-3.88 **	-4.12 **	-3.20 *	2.88 *	9.78 **	2.19	2.65 *	2.19	6.33 **	7.71 **	6.33 **
19	NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8	-6.86 **	-3.06 *	-2.06	-9.98 **	-9.86 **	0.84	5.79 **	9.57 **	-11.42 **	11.90 **	12.23 **	6.97 **
20	NARENDRA AGETI RAI-4 x NDR8501	-3.92 **	-2.00	1.03	-5.99 **	-5.75 **	5.31 **	18.21 **	23.64 **	1.02	11.83 **	12.42 **	6.90 **
21	NARENDRA AGETI RAI-4 x JAGRATI	-6.37 **	2.14	-1.55	-9.45 **	-9.34 **	1.68	2.15	5.76 **	-14.54 **	1.39 *	4.79 **	-3.08 **
22	NARENDRA AGETI RAI-4 x AZAD MAHAK	-11.27 **	-9.05 **	-6.70 **	-7.23 **	-1.98	3.91 **	4.85 **	17.84 **	4.85 **	7.89 **	10.32 **	7.89 **

23	NARENDRA AGETI RAI-8 x NDR8501	-7.65 **	-5.73 **	-6.70 **	-6.25 **	-6.13 **	4.75 **	7.50 **	8.60 **	-8.13 **	9.74 **	9.99 **	4.28 **
24	NARENDRA AGETI RAI-8 x JAGRATI	-6.38 **	-1.68	-9.28 **	-9.95 **	-9.73 **	1.12	11.02 **	11.07 **	-7.04 **	0.84	3.92 **	-4.18 **
25	NARENDRA AGETI RAI-8 x AZAD MAHAK	-3.61 *	-2.09	-3.61 *	-6.25 **	-1.06	4.75 **	0.00	8.85 **	0.00	6.23 **	8.94 **	6.23 **
26	NDR8501 x JAGRATI	-9.69 **	-3.28 *	-8.76 **	-5.47 **	-5.12 **	6.15 **	1.65	2.73 *	-13.14 **	1.31	4.17 **	-4.18 **

Table 17: Estimates of heterosis for hybrids for 12 characters in Indian mustard

27	NDR8501 x AZAD MAHAK	-6.63 **	-6.15 **	-5.67 **	-2.01	3.30 **	9.22 **	1.44	9.39 **	1.44	0.57	3.36 **	0.57
28	JAGRATI x AZAD MAHAK	-9.79 **	-3.85 **	-9.79 **	-4.48 **	1.05	7.26 **	0.31	9.24 **	0.31	0.57	6.20 **	0.57
	sca(ii)	0.95	0.82		1.71	1.48		1.13	0.98		1.21	1.05	
	sca(ij)	1.92	1.66		3.47	3.01		2.29	1.98		2.45	2.12	
	se(sij-ik)	2.52	2.19		4.57	3.96		3.01	2.61		3.22	2.79	

V ar	Hybrids	Number of primary branches			Number of secondary branches			No of siliquae on main raceme			Number of siliquae/plant		
		BP	MP	Azad	BP	MP	Azad	BP	MP	Azad	BP	MP	Azad
8	LAHAR X NRCDR-2	43.94 **	47.29 **	7.34	5.64	10.03 **	3.38	7.08 **	17.56 **	-2.24	1.38 *	10.26 **	0.76

9	LAHAR x NARENDRA AGETI RAI-4	6.06	8.11	-20.90 **	2.76	6.47	-0.53	5.74 **	9.45 **	-20.67 **	1.28 *	2.19 **	-14.03 **
10	LAHAR x NARENDRA AGETI RAI-8	15.91 *	18.60 **	-13.56 **	3.54	6.52	-1.25	7.09 **	9.84 **	-15.42 **	0.97	2.84 **	-12.63 **
11	LAHAR X NDR8501	24.31 **	29.71 **	1.13	0.67	3.37	-4.34	1.13	8.95 **	-11.41 **	6.24 **	9.81 **	-5.26 **
12	LAHAR x JAGRATI	2.27	6.30	-23.73 **	3.93	5.40	-6.41	5.44 **	8.83 **	-15.63 **	2.42 **	5.16 **	-9.92 **
13	LAHAR x AZAD MAHAK	-10.17 *	2.91	-10.17 *	4.80	10.29 **	4.80	-3.70 **	10.04 **	-3.70 **	0.85	10.00 **	0.85
14	NRCDR-2 x NARENDRA AGETI RAI-4	8.66	9.09	-22.03 **	6.91	7.50 *	4.63	2.50	16.08 **	-6.42 **	1.91 **	9.93 **	1.29 *
15	NRCDR-2 x NARENDRA AGETI RAI-8	29.37 **	29.37 **	-7.91	1.09	2.39	-1.07	5.19 **	12.80 **	-3.96 **	0.48	7.43 **	-0.14
16	NRCDR-2 x NDR8501	0.69	7.41	-18.08 **	6.18	7.75 *	3.91	9.81 **	12.08 **	0.26	3.00 **	8.58 **	2.37 **
17	NRCDR-2 x JAGRATI	6.35	8.06	-24.29 **	0.73	6.33	-1.42	1.56	8.25 **	-7.28 **	0.86	7.02 **	0.24
18	NRCDR-2 x AZAD MAAHAAK	0.00	16.83 **	0.00	9.79 **	10.97 **	9.79 **	14.13 **	19.32 **	14.13 **	3.88 **	4.20 **	3.88 **
19	NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8	49.61 **	50.20 **	7.34	19.30 **	20.19 **	15.48 **	15.32 **	22.33 **	-8.91 **	5.01 **	6.02 **	-9.14 **
20	NARENDRA AGETI RAI-4 x NDR8501	24.31 **	32.10 **	1.13	13.24 **	14.29 **	9.61 **	9.54 **	21.82 **	-4.05 **	4.03 **	6.59 **	-7.23 **
21	NARENDRA AGETI RAI-4 x JAGRATI	48.27 **	51.24 **	6.38	6.76	12.12 **	3.35	12.43 **	19.99 **	-10.03 **	4.28 **	6.13 **	-8.28 **
22	NARENDRA AGETI RAI-4 x AZAD MAHAK	12.99 **	31.58 **	12.99 **	17.26 **	19.17 **	17.26 **	14.38 **	34.62 **	14.38 **	1.49 **	9.78 **	1.49 **

23	NARENDRA AGETI RAI-8 x NDR8501	8.33	15.56 **	-11.86 *	4.29	4.49	-0.53	3.88 **	9.26 **	-9.00 **	8.19 **	9.82 **	-3.53 **
24	NARENDRA AGETI RAI-8 x JAGRATI	14.68 *	16.53 **	-18.36 **	0.19	4.47	-4.45	8.88 **	9.59 **	-12.88 **	9.04 **	9.93 **	-4.10 **

25	NARENDRA AGETI RAI-8 x AZAD MAHAK	6.21	24.09 **	6.21	4.63	7.10 *	4.63	-0.78	10.88 **	-0.78	0.88	8.17 **	0.88
26	NDR8501 x JAGRATI	10.42	19.55 **	-10.17 *	10.11 **	14.62 **	4.63	4.18 **	8.89 **	-8.74 **	9.14 **	9.90 **	-2.67 **
27	NDR8501 x AZAD MAHAK	9.60 *	20.87 **	9.60 *	9.79 **	12.59 **	9.79 **	3.70 **	10.56 **	3.70 **	-3.26 **	2.28 **	-3.26 **
28	JAGRATI x AZAD MAHAK	6.21	25.75 **	6.21	1.25	7.97 *	1.25	5.47 **	17.18 **	5.47 **	1.04 *	7.52 **	1.04 *
	sca(ii)	0.57	0.49		0.66	0.58		0.95	0.83		2.59	2.24	
	sca(ij)	1.16	1.00		1.35	1.16		1.93	1.67		5.25	4.54	
	se(sij-ik)	1.52	1.32		1.77	1.53		2.55	2.20		6.91	5.99	

Var	Hybrids	Average seeds per siliquae			1000 grain weight (g)			Oil content (%)			Seed yeild per plant (g)		
		BP	MP	Azad	BP	MP	Azad	BP	MP	Azad	BP	MP	Azad
8	LAHAR X NRCDR-2	5.18	6.56	-12.12 **	2.28	17.80 **	-0.20	0.58	1.12 *	-1.45 *	3.26	9.51 **	-2.06
9	LAHAR x NARENDRA AGETI RAI-4	-0.53	2.31	-14.29 **	-2.12	-1.30	-28.48 **	-2.22 **	0.27	-4.19 **	2.51	9.26 **	-1.72
10	LAHAR x NARENDRA AGETI RAI-8	2.56	4.44	-13.42 **	-2.36	7.94 **	-13.29 **	2.89 **	3.62 **	0.82	4.99 **	10.29 **	-2.41
11	LAHAR X NDR8501	3.41	7.89 *	-8.23 *	-1.80	9.21 **	-11.61 **	0.49	0.95	-1.53 *	-2.23	6.34 **	-2.06
12	LAHAR x JAGRATI	-1.46	2.80	-12.55 **	9.79 **	18.86 **	-6.88 **	0.05	0.94	-1.96 **	2.45	3.83 *	-13.92 **
13	LAHAR x AZAD MAHAK	4.33	15.04 **	4.33	0.13	16.53 **	0.13	1.69 **	2.72 **	1.69 **	5.33 **	14.47 **	5.33 **
14	NRCDR-2 x NARENDRA AGETI RAI-4	7.01	8.66 *	-7.79 *	0.90	15.38 **	-1.55	-1.33 *	0.65	-4.35 **	3.41 *	3.96 **	-0.86
15	NRCDR-2 x NARENDRA AGETI RAI-8	0.51	1.03	-15.15 **	2.35	7.17 **	-0.13	1.33 *	1.50 **	-1.77 **	0.00	1.01	-5.15 **
16	NRCDR-2 x NDR8501	2.44	5.53	-9.09 *	0.28	4.32 *	-2.16	2.11 **	2.19 **	-0.85	0.51	3.26 *	0.69
17	NRCDR-2 x JAGRATI	4.39	7.54 *	-7.36 *	-0.41	6.55 **	-2.83	0.08	0.44	-2.98 **	1.45	8.95 **	-3.78 *

18	NRCDR-2 x AZAD MAHAHA	2.16	11.32 **	2.16	1.35	2.60	1.35	1.88 **	3.46 **	1.88 **	5.84 **	8.64 **	5.84 **
19	NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8	11.03 *	12.17 **	-4.33	10.18 **	20.88 **	-2.16	-2.12 **	-0.32	-5.43 **	11.83 **	13.56 **	7.22 **
20	NARENDRA AGETI RAI-4 x NDR8501	15.37 **	17.06 **	2.38	16.94 **	29.09 **	5.26 *	-0.21	1.87 **	-3.10 **	3.95 *	6.22 **	4.12 *
21	NARENDRA AGETI RAI-4 x JAGRATI	12.93 **	14.59 **	0.22	16.15 **	24.79 **	-1.48	-0.27	1.38 *	-4.00 **	-10.75 **	-3.68 *	-14.43 **
22	NARENDRA AGETI RAI-4 x AZAD MAHAK	5.84	13.71 **	5.84	7.96 **	24.76 **	7.96 **	0.45	4.02 **	0.45	1.03	3.16 *	1.03
23	NARENDRA AGETI RAI-8 x NDR8501	4.15	6.75	-7.58 *	6.45 *	7.17 **	-4.18	2.96 **	3.22 **	-0.02	-1.20	2.49	-1.03
24	NARENDRA AGETI RAI-8 x JAGRATI	7.56	10.25 **	-4.55	4.10	6.49 **	-7.56 **	1.58 *	1.77 **	-1.85 **	2.03	8.55 **	-5.15 **
25	NARENDRA AGETI RAI-8 x AZAD MAHAK	0.22	8.69 *	0.22	0.13	6.08 **	0.13	2.31 **	4.07 **	2.31 **	6.19 **	10.06 **	6.19 **
26	NDR8501 x JAGRATI	5.85	5.85	-6.06	7.20 **	10.38 **	-3.51	0.09	0.53	-2.81 **	0.34	10.48 **	0.52
27	NDR8501 x AZAD MAHAK	2.81	8.94 **	2.81	-2.83	2.27	-2.83	0.43	1.91 **	0.43	6.86 **	6.95 **	7.04 **
28	JAGRATI x AZAD MAHAK	3.46	9.63 **	3.46	3.37	11.87 **	3.37	0.08	1.99 **	0.08	1.20	11.34 **	1.20

Length of main raceme (cm):

Out of 21 crosses 8 crosses were positive significant heterosis over economic parent in desirable direction and varied from 18.21 (NARENDRA AGETI RAI-4 x NDR8501) to 0.30 (JAGRATI x AZAD MAHAK). The cross combinations (NARENDRA AGETI RAI-4 x NDR8501) exhibited maximum heterosis over economic parent (18.21), followed by NARENDRA AGETI RAI-8 x JAGRATI (11.21).

Plant height (cm):

Three crosses out of 21 crosses showed negative significant heterosis over economic parent in desirable direction, heterosis over economic parent ranged between -4.28 (NARENDRA AGETI RAI-8 x NDR8501) to 7.89 (NARENDRA AGETI RAI-4 x AZAD MAHA). The cross combination exhibited maximum heterosis over economic parent (-4.28) NARENDRA AGETI RAI-8 x NDR8501, followed by -4.18 (NARENDRA AGETI RAI-8 x JAGRATI). 2 crosses out of 21 crosses showed negative non-significant heterosis over economic parent, 12 crosses out of 21 crosses showed positive significant heterosis over economic parent while the rest of the crosses showed positive non-significant heterosis over economic parent.

Number of primary branches per plant:

Out of 21 crosses only two cross showed positive significant heterosis over economic parent in desirable direction. Heterosis over economic parent for this trait varied from -24.99 (NRC DR-2 x JAGRATI) to 12.99 (NARENDRA AGETI RAI-4 x AZAD MAHAK). The cross combination NARENDRA AGETI RAI-4 x AZAD MAHAK exhibited maximum heterosis 12.99 over economic parent and showed positive significant heterosis over economic parent. The rest of the crosses showed negative heterosis over economic parent out of which 8 were negative and significant.

Number of secondary branches per plant:

Out of 21 crosses 5 crosses showed positive significant heterosis over economic parent in desirable direction and ranged between -6.41 LAHAR x JAGRATI to 17.26 (NARENDRA AGETI RAI-4 x AZAD MAHAK)

Number of siliquae on main raceme:

Out of 21 crosses showed positive significant heterosis over economic parent in desirable

direction. Heterosis over economic parent varied from -14.38 (NARENDRA AGETI RAI-4 x AZAD MAHAK) to 3.70 (NDR8501 x AZAD MAHAK).

Number of siliquae per plant:

Out of 21 crosses 15 crosses showed positive significant heterosis over better parent in desirable direction. Heterosis over better parent varied from -3.26 (ANDR8501 x AZAD MAHAK) to 9.14(NDR8501 x JAGRATI). The cross combination () exhibited maximum (NDR8501 x JAGRATI) heterosis over better parent (9.14), followed by(9.04) NARENDRA AGETI RAI-8 X JAGRATI,

Average seeds per siliquae:

Only one cross out of 21 crosses show positive significant heterosis over economic parents in desirable direction over better parents ranging from -1.46 (LAHAR x JAGRATI) to 15.37 (NARENDRA AGETI RAI-4 x NDR8501). The cross combination (NARENDRA AGETI RAI-4 x NDR8501) exhibited maximum heterosis over better parent (15.37). 16 out of 21 crosses showed positive non-significant heterosis over better parent while the rest showed negative non-significant heterosis over economic parent.

1000-seed weight (g):

Seven crosses out of 21 crosses show positive significant heterosis over better parents in desirable direction over better parent ranging from -2.83 (NDR8501 x AZAD MAHAK) to 16.94 (NARENDRA AGETI RAI-4 x NDR8501). The cross 16.94 (NARENDRA AGETI RAI-4 x NDR8501), 16.15 (NARENDRA AGETI RAI-4 x JAGRATI), (10.18) NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8. were best cross combination for heterosis over better parent.

Oil content (%):

Nine crosses of total 21 crosses were found to have positive and significant heterosis over better parent in desirable direction and varied from -2.22 (LAHAR x NARENDRA AGETI RAI-4) to 2.96

(NARENDRA AGETI RAI-8 x NDR8501) 2.89 (NARENDRA AGETI RAI-8 x NDR8501). The cross combination NARENDRA AGETI RAI-8 x NDR8501 exhibited maximum heterosis over better parent followed by 2.89 (NARENDRA AGETI RAI-8 x NDR8501).

7 crosses of total 21 crosses were found to have positive and non-significant heterosis over better parent, 3 crosses out of total 21 crosses were found to have negative and significant heterosis over better parent and the rest exhibited negative and non-significant heterosis over better parent.

Seed yield per plant (g):

Six crosses out of 21 crosses showed positive significant heterosis over economic parent in desirable direction. Heterosis over economic parent varied from - 14.43 (NARENDRA AGETI RAI-4 x JAGRATI) to 7.22 (NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8). The cross combination NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8 exhibited maximum heterosis over economic parent (7.22), followed by NDR8501 x AZAD MAHAK (7.04) and NARENDRA AGETI RAI-8 x AZAD MAHAK (6.19). 4 crosses of total 21 crosses were found to have positive and non-significant heterosis over economic parent, 5 crosses out of total 21 crosses were found to have negative and non-significant.

5 Selection parameters

Selection parameters are classified as direct and indirect and described as follows:

Direct selection parameters

Heritability and genetic advance are the most important direct selection parameters. The amount of genetic variability present in parents was transmitted from parent to progenies. These both parameters in % for 21 crosses are depicted in **Table 18**.

Table 18: Genetic variability, heritability, genetic advance and genetic advancement in percent over mean for 12 characters in Indian mustard

Genotypes	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to 50% flowering	62.01	56.67	68.00	6.22	7.57	82.25	4.66	7.52	4.02	4.44
Days to maturity	128.50	119.33	135.33	17.93	22.34	80.27	7.82	6.08	3.30	3.68
Length of main raceme (cm)	80.86	66.47	89.40	36.90	38.82	95.06	12.20	15.09	7.51	7.71
Plant height (cm)	190.42	168.40	203.27	90.45	92.66	97.62	19.36	10.17	4.99	5.06
Number of primary branches	10.60	8.13	13.33	2.60	3.09	84.19	3.05	28.77	15.22	16.59
Number of secondary branches	18.97	16.40	21.97	1.47	2.14	69.03	2.08	10.96	6.40	7.71
No of siliquae on main raceme	71.31	54.13	88.53	66.18	67.54	97.98	16.59	23.26	11.41	11.52
Number of siliquae/plant	467.46	409.67	510.40	935.07	945.18	98.93	62.65	13.40	6.54	6.58
Average seeds per siliquae	14.37	12.53	16.30	1.11	1.58	70.11	1.82	12.64	7.33	8.75
1000 grain weight (g)	4.65	3.53	5.33	0.21	0.23	92.16	0.91	19.54	9.88	10.29
Oil content (%)	40.65	38.56	42.36	0.86	0.95	90.18	1.81	4.45	2.28	2.40

Seed yeild per plant (g)	18.96	15.87	20.80	1.69	1.84	91.93	2.57	13.54	6.85	7.15
---------------------------------	--------------	--------------	--------------	-------------	-------------	--------------	-------------	--------------	-------------	-------------

GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation

a. Heritability:

The estimate of (bs) heritability varied from 69.03% (Number of secondary branches) to 98.93% (Number of siliquae/plant). Low estimate of (bs) heritability was found in Number of secondary branches (69%), whereas medium estimate of (bs) heritability was found in Number of primary branches (84.19%), Days to 50% flowering (82.25%), Days to maturity (80.27%).

Number of siliquae on main raceme (97.98%), number of siliquae per plant (98.13%), length of main raceme (95.06%), plant height (97.62%), oil content (90.18%) and 1000 grain weight (92.16%) exhibited high estimates of heritability.

b. Genetic advance in percent over mean

Genetic advance in percent over mean varied from 0.91% for 1000 grain weight (g) to 62.25% for Number of siliquae /plant

Low estimates of GAM was exhibited by 1000 grain weight (0.91%), number of primary branches (3.05%), average seeds per siliquae (1.82%), number of secondary branches (2.08%), seed yield per plant (2.57%), oil content (1.81 %), days to 50% flowering (4.66%), days to maturity (7.82%), length of main raceme (12.20%) and number of siliquae on main raceme (16.59%). Plant height (19.36%) showed moderate GAM while number of siliquae per plant (62.25%) exhibited high genetic advance mean.

Indirect selection parameters

Selection parameter in indirect selection is classified into two types via correlation coefficient analysis and Path coefficient analysis.

c. Correlation coefficient analysis

Genotypic and phenotypic correlation coefficients for 12 characters in all possible combinations were computed and the results are presented in **Table-19(a)** for genotypic correlation & **19(b)** for phenotypic correlation and described as follows:

Table 19(a): Genotypic correlation coefficient among the seed yield and it's contributing characters for 12 characters in Indian mustard

Parent/Hybrids	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yeild per plant (g)
Days to 50% flowering	1.000	0.068	-0.238*	0.080	-0.115	0.117	-0.265*	-0.289**	-0.223*	-0.288**	-0.462**	0.155
Days to maturity			-0.137	-0.303**	-0.576**	-0.491**	-0.303**	-0.186	-0.625**	-0.407**	-0.136	-0.254*
Length of main raceme (cm)				0.673**	0.487**	0.522**	0.802**	0.773**	0.514**	0.675**	0.709**	0.485**
Plant height (cm)					0.601**	0.749**	0.572**	0.446**	0.386**	0.432**	0.457**	0.651**
Number of primary branches						0.813**	0.742**	0.470**	0.797**	0.645**	0.480**	0.586**
Number of secondary branches							0.779**	0.543**	0.826**	0.700**	0.267*	0.826**
Noof siliquae on main raceme								0.860**	0.791**	0.866**	0.669**	0.625**
Number of siliquae/plant									0.587**	0.822**	0.566**	0.530**
Average seeds per siliquae										0.742**	0.535**	0.630**
1000 grain weight (g)											0.463**	0.504**

Oil content (%)												0.409**
Seed yeild per plant (g)												1.000

***Significant at 5% level; **Significant at 1% level**

Genotypic correlation coefficient:

Days to 50% flowering:

Days to 50% flowering showed positive correlation with days to maturity (0.068), plant height (0.080), number of secondary branches (0.117), seed yield per plant (0.155). Negative and significant correlation with length of main raceme (-0.238), number of siliquae on main raceme (-0.265), number of siliquae per plant (-0.289), average seeds per siliquae (-0.223), 1000 grain weight (-0.288), oil content (-0.462).

Days to maturity:

Days to maturity showed significant and negative correlation with length of main raceme (-0.137) plant height (-0.303), number of primary branches (-0.576), Number of secondary branches, (-0.491), number of siliquae on main raceme (-0.303), number of siliquae per plant (-0.186), average seeds per siliquae (-0.625), 1000 grain weight (-0.407), oil content (-0.136), seed yield per plant (-0.254). Days to maturity showed positive correlation with days to 50% flowering (0.068).

Length of main raceme (cm):

Length of main raceme exhibited positive significant correlation with plant height (0.673), number of primary branches per plant (0.487), number of secondary branches per plant (0.522), number of siliquae on main raceme (0.802), number of siliquae per plant (0.773), average seeds per siliquae (0.514), 1000 grain weight (0.675), oil content (0.709) and seed yield per plant (0.485) while it showed negative and non-significant correlation with days to maturity (-0.137). while it showed negative and significant correlation with days to 50% flowering (-0.238).

Plant height (cm):

Plant height showed significant and positive correlation with length of main raceme (0.673), number of primary branches per plant (0.601), number of secondary branches per plant (0.749), number of siliquae on main raceme (0.572), number of siliquae per plant (0.446), average seeds per siliquae (0.386), 1000 grain weight (0.432), oil content (0.457) and seed yield per plant (0.651) while, positive and non-

significant correlation with days to 50% flowering (0.080).

Number of primary branches per plant:

Number of primary branches per plant showed significant and positive correlation for length of main raceme (0.487), plant height (0.601), number of secondary branches per plant (0.813), number of siliquae on main raceme (0.742), number of siliquae per plant (0.470), average seeds per siliquae (0.797), 1000 grain weight (0.645), oil content (0.480) and seed yield per plant (0.586).while days of 50% flowering showed negative and non significant (0.115) and days to maturity showed negative significant(-0.576)

Number of secondary branches per plant:

Number of secondary branches per plant exhibited significant and positive correlation with length of main raceme (0.522), plant height (0.749), number of primary branches per plant (0.813), number of siliquae on main raceme (0.779), number of siliquae per plant (0.543), average seeds per siliquae (0.826), 1000 grain weight (0.700), oil content (0.267) and seed yield per plant (0.826), while negative non -significant correlation with days to maturity (- 0.491).

Number of siliquae on main raceme:

Number of siliquae on main raceme exhibited significant and positive correlation with length of main raceme (0.802), plant height (0.572), number of primary branches (0.742), number of secondary branches (0.749), number of siliquae per plant (0.860), average seeds per siliquae (0.791), 1000 grain weight (0.866), oil content (0.669) and seed yield per plant (0.625). while days of 50% flowering and days to maturity showed negative and non significant .

Number of siliquae per plant:

Number of siliquae per plant exhibited significant and positive correlation with length of main raceme (0.773), plant height (0.446), number of primary branches (0.470), number of secondary branches (0.543), number of siliquae on main raceme (0.860), average seeds per siliquae (0.791), 1000 grain weight (0.866), oil content (0.669)

seed yield per plant (0.530), while negative significant correlation with days to maturity (-0.303).

Average seeds per siliquae:

Average seeds per siliquae exhibited significant and positive correlation with length of main raceme (0.514), plant height (0.386), number of primary branches (0.797), number of secondary branches (0.826), number of siliquae on main raceme (0.791), number of siliquae per plant (0.587), 1000 grain weight (0.822), oil content (0.566) and seed yield per plant (0.630), while negative significant correlation with days to maturity (-0.625), days to 50% flowering (-0.289).

1000 seed weight (g):

1000 seed weight exhibited significant and positive correlation with length of main raceme (0.675), plant height (0.432), number of primary branches (0.645), number of secondary branches (0.700), number of siliquae on main raceme (0.866), number of siliquae per plant (0.822), average seeds per siliquae (0.742), oil content (0.535) and seed yield per plant (0.504) while negative significant correlation with days to maturity (-0.407), days to 50% flowering (-0.288).

Oil content (%):

Oil content showed significant and positive correlation with length of main raceme (0.709), plant height (0.457), number of primary branches (0.480), number of secondary branches (0.267), number of siliquae on main raceme (0.669), number of siliquae per plant (0.566), average seeds per siliquae (0.535), 1000 grain weight (0.463) and seed yield per plant (0.409) while negative significant correlation with days to 50% flowering (-0.462), and negative non-significant correlation with days to maturity (-0.136).

Seed yield per plant (g):

Seed yield per plant exhibited significant and positive correlation with length of main raceme (0.485), plant height (0.651), number of primary branches (0.586), number of secondary branches (0.826), number of siliquae on main raceme (0.625), number of siliquae per plant (0.530), average seeds per siliquae (0.630), 1000 grain weight (0.504) and oil content (0.409). and negative non-significant correlation with days to maturity (-0.254) positive non-significant correlation with days to 50% flowering (0.155).

Phenotypic correlation coefficient:

Days to 50% flowering:

Days to 50% flowering exhibited positive phenotypic correlation with days to maturity (0.048), plant height (0.082), number of secondary branches (0.061), seed yield per plant (0.123) while negative significant correlation with number of siliquae per plant (-0.240), 1000 grain weight (-0.443), oil content (-0.394) Days to 50% flowering exhibited negative non significant length of main raceme (-0.215), number of primary branches (-0.075),

Days to maturity:

Days to maturity exhibited negative significant correlation with, number of primary branches (-0.466) and 1000 grain weight (-0.339), plant height (-0.279), number of secondary branches (-0.396), number of siliquae on main raceme (-0.270), number of siliquae per plant (-0.161) average seeds per siliquae (-0.398), 1000 grain weight (-0.339), and seed yield per plant (-0.194) while some exhibit negative non significant length of main raceme (-0.115). Days to 50% flowering exhibited positive non- significant correlation.

Length of main raceme (cm):

Length of main raceme exhibited positive significant correlation with plant height (0.639), number of primary branches per plant (0.439), number of secondary branches per plant (0.409), number of siliquae on main raceme (0.771), number of siliquae per plant (0.756), average seeds per siliquae (0.414), 1000 grain weight (0.623), oil content (0.655) and seed yield per plant (0.473) while it showed negative and non-significant correlation with days to 50% flowering (-0.215) and days to maturity (-0.115).

Plant height (cm):

Plant height showed significant and positive correlation with length of main raceme (0.439), number of primary branches per plant (0.535), number of secondary branches per plant (0.628), number of siliquae on main raceme (0.556), number of siliquae per plant (0.437), average seeds per siliquae (0.313), 1000 grain weight (0.407), oil content (0.426) and seed yield per plant (0.606) while negative and non-significant correlation with days to maturity (0.131).

Number of primary branches:

Number of primary branches per plant showed significant and positive correlation for characters valued length of main raceme (0.439), plant height (0.535), number of secondary branches per plant (0.612), number of siliquae on main raceme (0.671), number of siliquae per plant (0.434), average seeds per siliquae (0.643), 1000 grain weight (0.578), oil content (0.426) and seed

yield per plant (0.517).

Number of secondary branches per plant:

Number of secondary branches per plant exhibited significant and positive correlation with length of main raceme (0.771), plant height (0.409), number of primary branches per plant (0.612), number of siliquae on main raceme (0.630), number of siliquae per plant (0.445), average seeds per siliquae (0.511), 1000 grain weight (0.562), oil content (0.210) and seed yield per plant (0.631), while negative significant correlation with days to maturity(-0.396) and positive non significant days to 50% flowering (0.061) and.

Number of siliquae on main raceme:

Number of siliquae on main raceme exhibited significant and positive correlation with characters length of main raceme (0.771), plant height (0.556), number of primary branches (0.671), number of secondary branches (0.630), number of siliquae per plant (0.887), average seeds per siliquae (0.677), 1000 grain weight (0.822), oil content (0.634) and seed yield per plant (0.594) while negative non-significant correlation with days to maturity (-0.161) negative significant days to 50% flowering (-0.250)

Table 19(b): Phenotypic correlation coefficient among the seed yield and it's contributing characters for 12 characters in Indian mustard

Parent/Hybrids	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yeild per plant (g)
Days to 50% flowering	1.000	0.048	-0.215	0.082	-0.075	0.061	-0.240*	-0.250*	-0.116	-0.243*	-0.394**	0.123
Days to maturity			-0.115	-0.279*	-0.466**	-0.396**	-0.270*	-0.161	-0.398**	-0.339**	-0.119	-0.194
Length of main raceme (cm)				0.639**	0.439**	0.409**	0.771**	0.756**	0.414**	0.623**	0.655**	0.473**
Plant height (cm)					0.535**	0.628**	0.556**	0.437**	0.313**	0.407**	0.426**	0.606**
Number of primary branches						0.612**	0.671**	0.434**	0.643**	0.578**	0.426**	0.517**
Number of secondary branches							0.630**	0.445**	0.511**	0.562**	0.210	0.631**
Noof siliquae on main raceme								0.847**	0.677**	0.822**	0.634**	0.594**
Number of siliquae/plant									0.493**	0.789**	0.534**	0.504**
Average seeds per siliquae										0.598**	0.429**	0.498**
1000 grain weight (g)											0.439**	0.443* *

Oil content (%)													0.382*
Seed yeild per plant (g)													1.000

***Significant at 5% level; **Significant at 1% level**

Number of siliquae per plant:

Number of siliquae on per plant exhibited significant and positive correlation with all the characters except days to maturity valued days to 50% flowering (0.334), length of main raceme (0.761), plant height (0.799), number of primary branches (0.737), number of secondary branches (0.645), number of siliquae on main raceme (0.756), average seeds per siliquae (0.637), 1000 grain weight (0.784), oil content (0.318) and seed yield per plant (0.733) while negative non-significant correlation with days to maturity (-0.161).

Average seeds per siliquae:

Average seeds per siliquae exhibited significant and positive correlation with characters length of main raceme (0.414), plant height (0.313), number of primary branches (0.643), number of secondary branches (0.511), number of siliquae on main raceme (0.677), number of siliquae per plant (0.493), 1000 grain weight (0.598), oil content (0.429) and seed yield per plant (0.498), while negative significant correlation with days to maturity (-0.398) and negative and non-significant correlation with 50% flowering (-0.116).

1000 seed weight (g):

1000 seed weight exhibited significant and positive correlation with all the characters valued length of main raceme (0.623), plant height (0.407), number of primary branches (0.578), number of secondary branches (0.562), number of siliquae on main raceme (0.822), number of siliquae per plant (0.789), average seeds per siliquae (0.598), oil content (0.439) and seed yield per plant (0.443).

Oil content (%):

Oil content showed significant and positive correlation with length of main raceme (0.655), plant height (0.426), number of primary branches (0.426), number of secondary branches (0.210), number of siliquae on main raceme (0.634), number of siliquae per plant (0.534), average seeds per siliquae (0.429), 1000 grain weight (0.439) and seed yield per plant (0.443). while negative significant correlation with days to 50% flowering (-0.394) and negative non-significant correlation with days to maturity (-0.119).

Seed yield per plant (g):

Seed yield per plant exhibited significant and positive correlation with all the characters

valued length of main raceme (0.473), plant height (0.606), number of primary branches (0.517), number of secondary branches (0.631), number of siliquae on main raceme (0.594), number of siliquae per plant (0.504), average seeds per siliquae (0.498), 1000 grain weight (0.443) and oil content (0.382).

d. Path coefficient analysis:

Path coefficient analysis was done to resolve the direct and indirect effects of different characters on seed yield and depicted in **Table 20(a)** & **Table 20(b)**.

Genotypic path coefficient analysis:

On portioning the genotypic coefficient, it was observed that the highest positive and direct effect on seed yield per plant was exerted by Average seeds per siliquae (1.0346), followed by plant height (0.7927), number of siliquae per plant (0.4399), days to maturity (0.4247), oil content (0.0343), days to 50% flowering (0.2420). while negative and direct effects on length of main raceme (-0.4714), number of secondary branches per plant (-0.1099), number of primary branches (-0.1249) seed yield per plant were exerted by number of secondary branches per plant (-0.163), number of siliquae on main raceme (0.2721), 1000 grain weight (-0.0300).

Days to 50% flowering:

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by days to 50% flowering via plant height (0.0637), days to maturity (0.284) number of siliquae on main raceme (0.0721), length of main raceme (0.1120), 1000 grain weight (0.0086), number of primary branches (0.148) and. while negative and indirect effect on seed yield per plant were exerted by number of secondary branches (-0.01228), days to 50% flowering via oil content (-0.158), average seeds per siliquae (-0.0158).

Days to maturity:

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by days to maturity via days to 50% flowering (0.0165), number of siliquae per plant (0.065), number of siliquae on main raceme (0.061), length of main raceme

(0.0644), 1000 grain weight(0.0122) and number of secondary branches (0.0540), and number of primary branches (0.0746), number of siliquae on main raceme (0.0823), while negative and indirect effect on seed yield per plant were exerted by days to maturity via number of siliquae per plant (-0.0816), oil content (-0.0047), average seeds per siliquae (-0.06466).

Length of main raceme (cm):

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant was exerted by length of main raceme via plantheight (0.5338), number of siliquae per plant (0.3402), average seeds per siliquae (0.5317), and oil content (0.0243) while negative and indirect effect on seed yield per plant were exertedby days to maturity (-0.0538), number of secondary branches (-0.0573), number of primary branches (-0.0630) 1000 grain weight (0.0202) days to maturity (-0.0568), number of siliquae on main raceme (0.2183).

Plant height (cm):

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant was exerted by plant height via number of siliquae per plant (0.463), plant height (1.169), number of siliquae on main raceme (0.242), length of mainraceme (0.154), days to 50% flowering (0.0195), 1000 grain weight (0.026) and oil content (0.016) while negative and indirect effect on seed yield per plant were exertedby number of secondary branches (-0.153), number of primary branches (-0.423) and average seeds per siliquae (-0.549).

Table 20(a): Direct & indirect effect of 12 characters on seed yield of Indian mustard as independent variable at genotypic level

Parent/Hybrids	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yield per plant (g)
Days to 50% flowering	0.2420	0.0284	0.1120	0.0637	0.0148	-0.0128	0.0721	-0.1272	-0.2311	0.0086	-0.0158	0.155
Days to maturity	0.0165	0.4157	0.0644	-0.2405	0.0746	0.0540	0.0823	-0.0816	-0.6466	0.0122	-0.0047	-0.254*
Length of main raceme (cm)	-0.0575	-0.0568	-0.4714	0.5338	-0.0630	-0.0573	-0.2183	0.3402	0.5317	-0.0202	0.0243	0.485**
Plant height (cm)	0.0195	-0.1261	-0.3174	0.7927	-0.0777	-0.0823	-0.1556	0.1961	0.3991	-0.0129	0.0157	0.651**
Number of primary branches	-0.0277	-0.2396	-0.2296	0.4761	-0.1294	-0.0893	-0.2019	0.2065	0.8240	-0.0193	0.0165	0.586**
Number of secondary branches	0.0282	-0.2042	-0.2460	0.5935	-0.1052	-0.1099	-0.2121	0.2388	0.8544	-0.0210	0.0092	0.826**
Noof siliquae on main raceme	-0.0642	-0.1258	-0.3782	0.4534	-0.0960	-0.0856	-0.2721	0.3785	0.8180	-0.0260	0.0230	0.625**
Number of siliquae/plant	-0.0700	-0.0772	-0.3645	0.3534	-0.0608	-0.0596	-0.2341	0.4399	0.6077	-0.0246	0.0194	0.530**
Average seeds per siliquae	-0.0541	-0.2598	-0.2422	0.3058	-0.1031	-0.0907	-0.2151	0.2584	1.0346	-0.0222	0.0183	0.630**
1000 grain weight (g)	-0.0697	-0.1692	-0.3182	0.3423	-0.0835	-0.0770	-0.2357	0.3615	0.7678	-0.0300	0.0159	0.504**

Oil content (%)	-0.1117	-0.0566	-0.3340	0.3621	-0.0621	-0.0294	-0.1821	0.2489	0.5533	-0.0139	0.0343	0.409**
------------------------	---------	---------	---------	--------	---------	---------	---------	--------	--------	---------	---------------	---------

R Square = 1.0555, Residual Effect= SQRT (1- 1.0555)
Bold values shows direct & normal values shows indirect effects

Number of primary branches:

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant was exerted by number of primary branches via plant height (0.4761), number of siliquae per plant (0.2065), oil content (0.0165) average seeds per siliquae (0.8240).

while negative and indirect effect on seed yield per plant were exerted by 1000 grain weight (-0.0193), days to maturity (-0.2396), days to 50% flowering (0.0277), number of secondary branches (-0.0893), number of secondary branches (-0.0893).

Number of secondary branches:

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant was exerted by number of secondary branches via plant height (0.5935), number of siliquae per plant (0.2388), and oil content (0.826), days to 50% flowering (0.0282), average seeds per siliquae (0.8544) while negative and indirect effect on seed yield per plant were exerted by number of siliquae on main raceme (-0.2121), length of main raceme (0.2460), days to maturity (-0.2042), 1000 grain weight (-0.0210), number of primary branches (-0.1050)

Number of siliquae on main raceme:

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by number of number of siliquae on main raceme via plant height (0.4534), number of siliquae per plant (0.3785), oil content (0.0230) average seeds per siliquae (0.8180). while negative and indirect effect on seed yield per plant were exerted by days to maturity (-0.1258), number of secondary branches (-0.0856), length of main raceme (-0.3782), days to 50% flowering (-0.642), 1000 grain weight (0.0260) and number of primary branches (-0.0960)

Number of siliquae per plant:

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by number of number of per plant via number of siliquae per plant (0.4399), average seeds per siliquae (-0.6077) oil content (0.0194, plant height (0.3058), while negative and indirect effect on seed yield per plant were exerted by days to maturity (-0.0772), length of main raceme (-0.3645), days to 50% flowering (-0.0700), number of secondary branches (-0.0596), number of primary branches (-0.0608).

Average seeds per siliquae:

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by average seeds per siliquae via plant height (0.3058), number of siliquae per plant (0.2584), oil content(0.183) while negative and indirect effect on seed yield per plant were exerted by days to maturity (-0.2598), main raceme (0.2422), number of secondary branches (-0.0907), number of primary branches (-0.1031).

1000 grain weight (g):

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by 1000 grain weight via plant height (0.3423), number of siliquae per plant (0.3615), average seeds per siliquae (0.7678), oil content (0.0159) while negative and indirect effect on seed yield per plant were exerted by number of secondary branches (-0.0770), days to maturity (-0.1692), number of primary branches (-0.0835), days to 50% flowering (-0.0697), length of main raceme (-0.3182).

Oil content (%):

On portioning the genotypic correlation, it was observed that positive and indirect effect on seed yield per plant was exerted by oil content via plant height (0.3621), number of siliquae per plant (0.2489 average seeds per siliquae (0.5533) while negative and indirect effect on seed yield per plant were exerted by number of secondary branches (-0.0294), days to 50% flowering (-0.1117), and number of primary branches (-0.0621)), number of siliquae on main raceme (-0.1821), length of main raceme (0.3344), days to maturity (0.0566) and 1000 grain weight(0.0139).

Phenotypic path coefficient analysis:

On portioning the phenotypic coefficient, it was observed that the highest positive and direct effect on seed yield per plant was exerted by number of siliquae per plant (0.3307), length of main raceme(0.309) followed by number of secondary branches per plant (0.3280), plant height (0.2690), average seeds per siliquae(0.1981), days to 50% flowering (0.1790). oil content (0.1615), days to maturity (0.1056), number of primary branches (0.0500) and number of siliquae on main raceme (0.0106).

Days to 50% flowering:

On portioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by days to 50% flowering via days to maturity

(0.0051), plant height (0.0221), 1000 grain weight (0.0409), length of main raceme (0.0313 and while negative and indirect effect on seed yield per plant were exerted by days to 50% flowering via oil content (-0.0635), number of primary branches(-0.0038) number of siliquae per plant (-0.0828)), average seeds per siliquae (-0.0230).

Days to maturity:

On portioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by days to maturity via length of main raceme (0.0167), 1000 grain weight (0.0572), days to 50% flowering (0.0086) while oil content (-0.0193), plant height (-0.0750), average seeds per siliquae (-0.0778), number of primary branches (0.0233), number of siliquae per pant (-0.532) and number of secondary branches(-0.1298) showed negative indirect effect.

Length of main raceme (cm):

On portioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant was exerted by length of main raceme via plant height (0.1720), number of siliquae per pant (0.2499), number of secondary branches per plant (0.1342), number of primary branches per plant (0.0219), average seeds per siliquae (0.0821), days to maturity (0.010), oil content (0.1058) and number of siliquae on main raceme (0.0082). 1000 grain weight (0.051).

Table 20(b): Direct & indirect effect of 12 characters on seed yield of Indian mustard as independent variable at phenotypic level

Parent/Hybrids	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant	Average seeds per siliquae	1000 grain weight (g)	Oil content (%)	Seed yield per plant (g)
Days to 50% flowering	0.1790	0.0051	0.0313	0.0221	-0.0038	0.0201	-0.0026	-0.0828	-0.0230	0.0409	-0.0635	0.123
Days to maturity	0.0086	0.1056	0.0167	-0.0750	-0.0233	-0.1298	-0.0029	-0.0532	-0.0788	0.0572	-0.0193	-0.194
Length of main raceme (cm)	-0.0384	-0.0121	-0.1457	0.1720	0.0219	0.1342	0.0082	0.2499	0.0821	-0.1050	0.1058	0.473**
Plant height (cm)	0.0147	-0.0294	-0.0931	0.2690	0.0267	0.2059	0.0059	0.1445	0.0619	-0.0686	0.0687	0.606**
Number of primary branches	-0.0134	-0.0492	-0.0640	0.1440	0.0500	0.2008	0.0071	0.1435	0.1273	-0.0974	0.0688	0.517**
Number of secondary branches	0.0110	-0.0418	-0.0596	0.1689	0.0306	0.3280	0.0067	0.1472	0.1013	-0.0948	0.0339	0.631**
Noof siliquae on main raceme	-0.0431	-0.0285	-0.1123	0.1495	0.0335	0.2066	0.0106	0.2800	0.1341	-0.1385	0.1023	0.594**
Number of siliquae/plant	-0.0448	-0.0170	-0.1101	0.1176	0.0217	0.1460	0.0090	0.3307	0.0977	-0.1330	0.0863	0.504**
Average seeds per siliquae	-0.0208	-0.0420	-0.0604	0.0841	0.0321	0.1677	0.0072	0.1631	0.1981	-0.1009	0.0693	0.498**
1000 grain weight (g)	-0.0434	-0.0358	-0.0907	0.1095	0.0289	0.1844	0.0087	0.2608	0.1185	-0.1686	0.0710	0.443**
Oil content (%)	-0.0705	-0.0126	-0.0954	0.1145	0.0213	0.0689	0.0067	0.1767	0.0850	-0.0741	0.1615	0.382**

Resi-0.0413

***, ** significant at 5% and 1% level, respectively**

Bold values show direct and normal values shows indirect effect

Plant height (cm):

On partitioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by plant height via number of siliquae per plant (0.1445), number of secondary branches (0.2059), days to 50% flowering (0.0147), number of primary branches (0.0267), average seeds per siliquae (0.0619), oil content (0.0687). while negative and indirect effect on length of main raceme (-0.931), days to maturity (-0.0294) 1000 grain weight (-0.0686).

Number of primary branches:

On partitioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by number of primary branches via plant height (0.1440), number of siliquae per plant (0.1435), number of secondary branches (0.2008), average seeds per siliquae (0.01273), number of primary branches (0.0500), oil content (0.0688), number of siliquae on main raceme (0.0071) while negative and indirect effect on length of main raceme (-0.0640), days to maturity (-0.0492), 1000 grain weight (-0.0974), days to 50% flowering (-0.0134).

Number of secondary branches:

On partitioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by number of secondary branches via plant height (0.1689), number of siliquae per plant (0.1472), number of primary branches (0.0306), average seeds per siliquae (0.1013), oil content (0.0339) days to 50% flowering (0.0110). Number of siliquae on main raceme (0.0067). while negative and indirect effect on days to maturity (-0.0418), length of main raceme (0.0596), 1000 grain weight (-0.948),

Number of siliquae on main raceme:

On partitioning the phenotypic path coefficient, it was observed that positive and indirect effect on seed yield per plant were exerted by number of number of siliquae on main raceme via plant height (0.1495), number of siliquae per plant (0.2800), number of secondary branches (0.2066), number of primary branches (0.0335), average seeds per siliquae (0.0134) and oil content (0.1023). while negative and indirect effect on length of main raceme (-0.1123), 1000 grain weight (-0.1385), days to maturity (-0.0285) days to 50% flowering (-0.0431).

Number of siliquae per plant:

On partitioning the phenotypic correlation, it was observed that positive and indirect

effect on seed yield per plant were exerted by number of number of siliquae per plant via plant height (0.1176), 1000 grain weight (0.065), number of secondary branches (0.1460), number of primary branches (0.0217), average seeds per siliquae (0.0977), days to maturity (0.009), oil content (0.0863) and number of siliquae on main raceme (0.0090). while negative and indirect effect on length of main raceme (-0.1101), 1000 grain weight (-0.1330), days to maturity (-0.0170) days to 50% flowering (-0.0448).

Average seeds per siliquae:

On portioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by average seeds per siliquae via plant height (0.0841), number of siliquae per plant (0.1631), number of secondary branches (0.1677), 1000 grain weight (0.041), number of primary branches (0.0321), oil content (0.0693) and number of siliquae on main raceme(0.0072) while days to maturity (-0.0420) days to 50% flowering (-0.0208) length of main raceme (-0.0604), 1000 grain weight (-0.1009), showed negative indirect effect.

1000 seed weight (g):

On portioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted 1000 grain weight by via plant height (0.1095), number of siliquae per plant (0.2608), number of primary branches (0.0289), number of secondary branches (0.1844), days to maturity (0.037), average seeds per siliquae (0.036), number of secondary branches (0.034), oil content (0.0710) and number of siliquae on main raceme (0.0087). while days to maturity (-0.0358) days to 50% flowering (-0.0434) length of main raceme (-0.0907), 1000 grain weight (-0.1686), showed negative indirect effect.

Oil content (%):

On portioning the phenotypic correlation, it was observed that positive and indirect effect on seed yield per plant were exerted by oil content via plant height (0.1145), number of siliquae per plant (0.1767), number of secondary branches (0.0689), number of primary branches (0.0213), average seeds per siliquae (0.0850) and number of siliquae on main raceme (0.0067) while days to maturity (-0.0126), 50% flowering (-0.0705) length of main raceme (-0.0954), 1000 grain weight (-0.0741), showed negative indirect effect. showed negative indirect effect.

The residual effect of path analysis was positive which indicates that some important

yield contributing characters either genotypically or phenotypically have been left out. It is advised that they should be incorporated for study along with the attributes contributing for high yield potential.

Chapter 5

DISCUSSION

Plant breeders are always challenged with the goal of developing mustard genotypes with better yield and improved oil quality to meet the demands of an ever-increasing population. The current study used various diallel cross analysis approaches

to calculate the **nature and magnitude of genetic variability, gene action, degree of dominance, combining abilities, heterosis, heritability, genetic advance, correlation coefficients,** and **path analysis** for twelve traits associated with yield and its contributing characters in Indian mustard.

For the formulation of an efficient breeding strategy, knowledge of gene action governing polygenically inherited economic qualities to be incorporated in an ideotype is required. **Hayman (1954 a and b,)** and **Jinks (1955)** proposed the Diallel mating design, which has the obvious benefit of providing precise genetic information in early generations when compared to other designs. Several researchers have employed this approach, including **Arifullah et al. (2012), Chaurasiya et al. (2018), and Ashish et al. (2021)**. It is therefore essential to examine novel strains in order to obtain information on their genetic makeup before incorporating them into a hybridization strategy.

The genetic analysis in this study was approached by diallel mating between 7 parents and their 21 F₁s (excluding reciprocals) utilizing **Hayman (1954 a) and Griffing's (1956) method II and model I**. A diallel analysis is based on various assumptions, as stated by: normal diploid segregation,

- (i) normal diploid segregation,
- (ii) lack of maternal effects,
- (iii) absence of multiple alleles,
- (iv) homozygous parents,
- (v) absence of linkage,
- (vi) absence of epistasis, and
- (vii) random mating.

Indian mustard is an often-cross pollinated crop. The genotypes included in this study were maintained through selfing for several years, implying homozygous diploid segregation. Though cytoplasmic inheritance has not been observed on Indian mustard, some degree of reciprocal differences are possible. However, partial failure to satisfy this criterion does not appear to induce significant bias in the study. As a result, the first three assumptions are achieved. **Hayman (1954)** introduced the t^2 test to assess the validity of the other three hypothesis. The non-significant t^2 test scores indicate the consistency of the assumptions behind the current diallel analysis. All features had non-significant t^2 values.

Gilbert (1958) proposed that such assumptions as absence of epistasis, lack of multiple alleles, and equal gene distribution are only postulated to maintain a simple working hypothesis. Two alternative methodologies were used to conduct the genetic analysis in this study. **Griffing's (1956, b)** approach uses the notion of general and specialised combining abilities to identify

superior parents and combinations based on their average performance in specific combinations. It also offers a genetic explanation of general and specific combining ability variances in terms of additive or non-additive gene actions. The other approaches used were **Hayman's (1954 a, 1954 b)** variance components analysis, which is in addition to the preceding information on the distribution of positive and negative genes, as well as the ratio of dominant and recessive alleles in parents.

NATURE & MAGNITUDE OF GENETIC VARIABILITY:

The crucial requirement for enhancing populations through the use of hybridization program is population diversity and variability. Plant breeders can use genetic variability to produce noble plant gene combinations and crop varieties that are more suited to the demands of the human race.

In the current study, the parents and F₁s displayed a wide range of variety as measured by mean, range, and variance values for all 12 traits. Considering the findings of the analysis of variance revealed that there was considerable variability for yield and yield attributes among the parents and crosses, it may be speculated that not only were the parents diverse, but substantial variation could be created in the future generation of their crosses. Furthermore, for all parameters investigated, highly significant differences were found between parents and crossings, indicating the presence of diversity among the crosses. Similar results were reported by **Sohan and Nutan (2010)**, **Iqbal et al. (2015)**, **Tiwari et al. (2019)** and **Prasad et al. (2021)** in their experiments which are in

parity with our findings.

COMPONENTS OF GENETIC VARIANCE & NATURE OF GENE ACTION:

Gene action refers to the behaviour or mode of expression of genes in a genetic population. Knowledge of gene action aids in the selection of parents for hybridization program as well as the selection of breeding strategies. Genetic variation can be divided into three categories:

1. additive or fixable variance arising from the average effects of genes.
2. dominance variance arising from intra-allelic interaction of the genes.
3. epistatic variance arising from the inter-allelic interaction of genes.

Testing the validity of diallel assumption **Mather (1956)** further divided epistatic variance into

1. additive × additive
2. additive × dominance
3. dominance × dominance

The estimation of b , SE , $b-0/SE(b)$, $1-b/SE(b)$ and t^2 are presented in **table 9**. Non-significant

value of regression coefficient from unity suggested the absence of gene interaction for all of the characters. The regression coefficient did not deviate significantly from unity for days to 50% flowering, Number of siliquae/plant, verage seeds per siliquae indicating the involvement of additive gene action. Similar results were found by many workers viz., **Arifullah et al. (2012)**, **Chaurasiya et al. (2018)** and **Yadav et al. (2020)** in their experiments which are in parity with our findings.

The estimates of components of variation along with their standard errors and related statistics are presented in **Table 11**.

Additive genetic variance (D): The estimates of additive components were highly significant for all the characters except number of secondary branches. Additive variance is fixable and selection for these traits will be effective.

Dominance variances (H₁ and H₂) values were significant and higher than additive variance for all the characters except days to 50% flowering. It is the measure of non-additive gene action, which is not fixable and can be utilized for heterosis breeding. The components of a H₁ and H₂ indicated that there was pre-dominance of dominant gene action for all traits.

Similar results for additive gene action as well as dominance gene action were observed by **Dholu et al. (2014)** and **Meena et al. (2017)** and **Yadav et al. (2020)**.

Relative magnitude of \hat{H}_1 component was higher than that of \hat{D} component for most the traits under study except days to 50% flowering indicating the role of both additive and dominance gene action with prevalence of dominant gene action. However, the non-additive component was more prominent than additive component for all the traits based on average degree of dominance (more than unity for almost all traits). Similar results were found by **Sohan and Nutan (2010)**, **Kumari et al. (2018)** and **Gadi et al. (2020)**.

The values of \hat{E} component were positive for all the characters. The estimated values of F component were found positively non-significant for 1000 grain weight (g), days to 50% flowering, main raceme length (cm) seed yield per plant. The positive value indicates the frequent involvement of dominant genes for its expression.

The ratio of mean degree of dominance $(\hat{H}_1 / \hat{D}_1)^{0.5}$ revealed over dominance for

the characters such as days to maturity, length of main raceme (cm), plant height (cm), number of primary branches, number of secondary branches, average seeds per siliquae number of siliquae on main raceme, number of siliquae per plant, oil content (%) and seed yield per plant while the characters which showed partial dominance are days to 50% flowering.

Favorable situation of preponderance of dominant alleles for characters are days to 50% flowering, main raceme length (cm), days to maturity, 1000 seed weight (g), seed yield per plant (g) from proportion of dominant and recessive effects in parents i.e. $[(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}/(4\hat{D}\hat{H}_1)^{0.5} - F]$ reflects that dominant alleles were more frequent as compare with recessive and simple selection may helps to breeder for better improvement for the character under consideration. This would be more helpful in getting the higher gain for direct selection in the advanced generations. **Hayman (1954)** also suggested that the combinations of either positive or negative genes, or a complementary gene interaction, or simply correlated gene distribution might seriously inflate the mean degree of dominance.

The proportion of genes with positive and negative effects ($\hat{H}_2 / 4\hat{H}_1$) were near or equal to its theoretical value (0.25) for most of the traits except, days to maturity which had values less than theoretically value (0.25). It indicated that the genes governing the remaining these were asymmetrically distributed.

Ratio of ($\hat{H}_2 / 4\hat{H}_1$) was less than unity for days to maturity. which revealed the presence of only one gene group was responsible for inheritance of this characters while the remaining characters which showed the ratio more than one indicated that these characters were governed by more than one major gene group. Similar results were found by many workers viz, **Chaurasiya et al. (2018)** and **Yadav et al. (2020)**.

COMBINING ABILITY ANALYSIS:

Combining ability refers to the capacity or ability of a genotype to transmit superior performance to its crosses. The study of combining ability aids in the selection of the finest combiners and allows for the application of these combiners in hybridization programs. Specific combining ability (sca) is caused by non-allelic gene interaction, whereas general combining ability (gca) is caused by additive gene action and additive

× additive interaction. The variance in general combining ability has been associated with additive gene activity, while the variance specific combining ability has been associated with non-additive gene action (**Sprague and Tatum, 1942; Griffing, 1956**).

Highly significant variances for both general and specific combining abilities for all the characters were found which indicated the importance of both additive and non-additive gene

effects. The values of gca and sca ratio estimates were observed more than unity for traits except oil content. All characters showed non-significant gca and sca variances which indicated the less importance of both additive and non-additive gene action. Additive gene action can be utilized for selection of superior parent while non-additive gene action utilized for heterosis breeding.

General combining ability (GCA) effect

The gca effects of various characters and their mean values of parents (**Table 13**) indicated that there was a close relationship between parental mean performance and gca effects for almost all the characters. The promising combiners based on significant *per se* performance and gca effects (**Table 14**) for oil content were AZAD MAHAK, LAHAR while for 50% flowering were NARENDRA AGETI RAI-4, NDR8501. The promising combiners based on significant *per se* performance and gca effects for days to maturity: LAHAR, NRCDR-2; for plant height: AZAD MAHAK, NRCDR-2; for raceme length: NRCDR-2, AZAD MAHAK; for number of primary branches per plant: AZAD MAHAK; for number of secondary branches per plant NARENDRA AGETI RAI-4; for number of siliquae on main raceme: NRCDR-2 and AZAD MAHAK; for number of siliquae per plant AZAD MAHAK, NRCDR-2; for average seeds per siliquae: AZAD MAHAK, NARENDRA AGETI RAI-4 ; for 1000-seed weight AZAD MAHAK, LAHAR; for seed yield per plant: AZAD MAHAK, NDR8501 Similar results were found by many workers viz, **Mahak et al. (2008) and Yadav et al. (2020)**.

The parents discussed above had high general combining ability and thus had fixable component of effects like additive and additive \times additive epistasis. These could be successfully used for improving particular character for which improvement was desired. These parents might be utilized for producing the inter-mating population in order to get desirable recombinants.

Specific combining ability (SCA) effect

On the basis of sca effects and *per se* performance of crosses were presented in **Table 15 & 16** and discussed below:

On the basis of sca effect good cross combination were found for oil content %: NARENDRA AGETI RAI-4 \times AZAD MAHAK; for seed yield per plant- NARENDRA AGETI RAI-4 \times NARENDRA AGETI RAI-8; for days to maturity- NARENDRA AGETI RAI-8 \times JAGRATI; for main raceme length- NARENDRA AGETI RAI-4 \times NDR8501; for plant height- LAHAR \times NDR8501; for number of secondary branches per plant NARENDRA AGETI RAI-4 \times NARENDRA AGETI RAI-8; for number of siliquae per plant- LAHAR \times AZAD MAHAK; for average seeds per siliquae- NARENDRA AGETI RAI-4 \times NDR8501.

The parents AZAD MAHAK and NARENDRA AGETI RAI-4 were good general

combiners for a number of traits especially for oil content (%) and seed yield per plant (g). Crosses NARENDRA AGETI RAI-4× AZAD MAHAK high sca effect for oil content (%) whereas - NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8 showed high sca effect for seed yield per plant (g) hence, they may be used further in hybridization program. Similar results were found by the studies conducted by **Singh *et al.* (2010)**, **Meena *et al.* (2017)**, and **Kaur *et al.* (2019b)**.

HETEROISIS:

The term “heterosis” accounts for an increase or decrease in performance of F1 to their parents. Heterosis, also known as hybrid vigour, is the increase in size, vigour, or production of a hybrid plant over its parents' average or mean. The heterosis evaluated through standard checks is quite important in practise. Heterosis breeding is vital in crop improvement programmes to increase productivity. Knowing the magnitude and direction of heterosis is the most critical step towards using it. **Fonesca and Patterson (1968)** coined the term “heterobeltiosis” as superior performance of heterozygote in relation to better parent. It indicates the presence of an overdominance type of gene action in the manifestation of various traits. Heterosis over better parent and economic parent has been computed (**Table 17**) for the traits under investigation in order to find potential hybrids over better parent and economic parent that may be commercially useful.

Heterosis for days to 50% flowering: All 21 crosses showed negative significant heterosis over better parent in the desirable direction. Out of 21 crosses only 18 cross showed negative and significant heterosis and 3 showed negative non-significant heterosis over economic parent in desirable direction. For length of main raceme, Out of 21 crosses 8 crosses were positive significant heterosis over economic parent in desirable direction. For plant height Three crosses out of 21 crosses showed negative significant heterosis over economic parent in desirable direction. For number of primary branches per plant: Out of 21 crosses only two cross showed positive significant heterosis over economic parent in desirable direction. For number of secondary branches: Out of 21 crosses 5 crosses showed positive significant heterosis over economic parent in desirable direction. For number of siliquae on main raceme: Out of 21 crosses showed positive significant heterosis over economic parent in desirable direction. For number of siliquae per plant:

Out of 21 crosses 15 crosses showed positive significant heterosis over better parent in desirable direction. For average seeds per siliquae: Only one cross out of 21 crosses show positive significant heterosis over economic parents in desirable direction. For 1000 seed weight (g): Seven crosses out of 21 crosses show positive significant heterosis over better parents in desirable direction. For oil content (%): Nine crosses of total 21 crosses were found to have positive and significant heterosis over better parent in desirable direction. For seed yield per plant (g): Six crosses out of 21 crosses showed positive significant heterosis over economic parent

in desirable direction. Hybrids NARENDRA AGETI RAI-4 x JAGRATI showed high heterosis over economic parent for seed yield per plant. NARENDRA AGETI RAI-8 x NDR8501, NARENDRA AGETI RAI-8 x NDR8501 showed high heterosis over better parent for oil content (%). In Indian mustard, heterosis is a complex phenomenon that is determined by the balance of additive, dominance, and their interacting components, as well as the distribution of genes in parental lines. In the current study, positive and significant results suggested that the parent had an over-dominance influence. Similar findings were also reported by **Sabhagnia *et al.* (2010)**, **Gami *et al.* (2013)**, **Malviya *et al.* (2019)** and **Kumar *et al.* (2021)**.

HERITABILITY:

Heritability is the ratio of genotypic variance to the phenotypic variance (broad sense) or ratio of additive variance to the phenotypic variance (narrow sense). Heritability is a measure of the transmissibility of traits from parents to offspring that assists breeders in transmitting traits from genotypes. The population's amenability to selection is determined by heritable variability in parents. The genetic advance has no independent identity; rather, it is based on heritability where character is to be developed.

The selection parameters heritability in broad sense, genetic advance & genetic advance in percent over mean for 12 characters were estimated with the help of statistical and biometrical methods. The values of these parameters are shown in **Table 18** for all the 12 characters which were studied are namely; Number of secondary branches per plant, days to 50% flowering, number of siliquae on main raceme, number of siliquae per plant, length of main raceme, plant height, oil content and 1000 grain weight recorded high values for heritability. Similar findings were also reported by **Sohan and Nutan (2010)** and **Chawla *et al.* (2016)**.

The genetic advance in percent over mean was estimated for all the 12 characters as follows: Low estimates of GAM was exhibited by 1000 grain weight, number of primary branches, average seeds per siliquae. length of main raceme, seed yield per plant (g) showed moderate GAM while Number of primary branches per plant exhibited high genetic advance mean. Character namely, number of siliquae per plant showed high genetic advance in percent mean along with heritability which indicates these characters were least influenced environment and $G \times E$ interaction. Only heritable component of total variation is important from the breeding point of view. These results were in parity with the results of **Meena *et al.* (2017)**, **Chaurasiya *et al.* (2018)** and **Gadi *et al.* (2020)**.

Correlation Coefficient Analysis:

Correlation is the parameter to establish the relationship between two variables which examines the suitability of the characters for direct selection being yield is a complex attribute. The correlation study assists in improving one character without compromising relationships with other characteristics, for which genotypic correlation estimation is essential. The correlation coefficient is calculated primarily to determine the relationship between various traits for indirect selection. As a result, understanding the genetic relationship that exists between yield and its components is essential for improving the efficiency of the selection program. Genotypic and phenotypic correlations were investigated in all conceivable combinations of 12 yield and component characteristics.

In the present investigation, it was observed that the genotypic correlation coefficient was higher in magnitude than their corresponding phenotypic correlation coefficient for all the characters.

The genotypic correlation coefficient of seed yield per plant (g) exhibited significant and positive correlation with all the characters except days to maturity. Oil content showed significant and positive correlation with length of main raceme, height, number of primary branches, number of secondary branches, number of siliquae on main raceme, number of siliquae per plant, average seeds per siliquae, 1000 grain weight and seed yield per plant.

While Days to 50% flowering showed positive correlation with days to maturity, plant height, number of secondary branches, seed yield per plant. and days to maturity showed negative non-significant correlation. These results were in parity with the results of **Kumar and Pandey (2014) and Bind *et al.* (2014)**.

Seed yield per plant exhibited positive significant phenotypic correlation with all the characters except days to maturity which showed negative non-significant correlation. Oil content showed significant and positive correlation with length of main raceme, plant height, number of primary branches, number of secondary branches. While Days to 50% flowering exhibited positive phenotypic correlation with days to maturity, plant height, number of secondary branches, seed yield per plant. These results were in parity of the findings of **Vaghela *et al.* (2011), Ali *et al.* (2015) and Kumar *et al.* (2014)**.

PATH COEFFICIENT ANALYSIS:

Path coefficient analysis is simply a standardized partial regression coefficient which splits the genotypic correlation into the measures of direct and indirect effects. The total correlation coefficient between yield and its component characters may sometime be misleading, as it may be an over or underestimate of its association with other characters. In these cases, direct selection based on correlated coefficient needs to be split into direct and indirect effects using path coefficient analysis. The correlation and path coefficient together can provide a clearer

understanding of the cause-and-effect relationship between different pairs of characters since several characteristics can have an impact on an individual attribute. The following general suggestions made by **Singhand Chaudhary (1977)** may be kept in mind while interpreting the findings of path analysis. A direct selection strategy based on this attribute will be successful if the correlation coefficient between a causative factor and the effect is almost equivalent to that of its direct effect. We eliminate the character from the selection if the correlation coefficient and direct effect are both negative.

Phenotypic path analysis values revealed that positive and indirect effect on seed yield per plant was exerted by all the traits. The residual effect of path analysis was positive which indicates that some important yield contributing characters either genotypically or phenotypically have been left out. It is advised that they should be incorporated for study along with the attributes contributing for high yield potential. The present finding reflected the positive association between seed yield and all traits contributing to combined traits **Lodhi et al. (2014)**, **Roy et al. (2018)**, **Tripathi et al. (2020)** and **Lavanya et al. (2022)**.

BREEDING METHODS:

On the basis of the results which are discussed in the light of literatures available, simple recurrent selection followed by progeny selection will be more appropriate for improvement of yield and its component. The crosses showed significant sca effect in desirable direction can be handled carefully to isolate transgressive segregation for better exploitation of genetic potential as a variety. The economic combination showed positive and significant heterosis can be handled carefully in such a way that the exploitation of both additive and non-additive gene in fruitful yield could be utilized. The whole genetic material can be put into central gene pool for selection in the future.

Chapter 6

SUMMARY & CONCLUSION

The present investigation entitled "**Genetic studies on yield and its attributing traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]**" was carried out to collect the information about the nature and magnitude of gene action for yield and its contributing characters based on seven parents and their all possible combinations excluding reciprocals evaluated in a replicated traits at Oilseeds Research Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during Rabi 2023-24. The information on heritability, Genetic advance, association of characters and their direct and indirect contribution on seed yield; the heterotic performance of crosses based on economic parent were also collected. The details of these criterion are described and discussed in the light of relevant literatures in systematic manner previously in respective chapters.

The following is a summary of the investigation's main findings:

Twelve traits were observed in all of the parents and their crosses, including days to 50% flowering, days to maturity, length of the main raceme (cm), plant height (cm), number of primary branches, number of secondary branches, number of siliquae on the main raceme, number of siliquae per plant, average seeds per siliquae, 1000 grain weight(g), oil content (%), and seed yield per plant (g). Twelve characters' worth of data from five plants, that were selected at random in each replication of the parents and their crossings were submitted to various statistical and biometrical analyses in accordance with conventional practices.

The analysis of variance showed that all of the characters' treatments varied significantly. For all the features, the Parents, F₁s and Parents vs. F₁s were also significant, demonstrating a wide range of variability across the genotypes and their crossings.

For most of the characters magnitude of dominance component (\hat{H}_1 & \hat{H}_2) was higher than the additive component (\hat{D}) based on F₁s generation except for days to 50% flowering. The

positive and significant values of environmental component was found for all the characters.

The proportion of genes with positive and negative effects ($\hat{H}_2/4\hat{H}_1$) was almost equal or near to its theoretical value i.e.; 0.25 in F_1 s generation for most of the characters, indicating symmetrical distribution of positive and negative alleles among parents for most of the characters. except for days to 50% flowering, Length of main raceme (cm) Plant height (cm), number of primary branches, Number of secondary branches 1000 grain weight, oil content (%) and seed yield per plant which indicated values less than its theoretical value indicating the asymmetrical distribution of genes among the parents for these characters.

The observed estimates of average degree of dominance $(\hat{H} / \hat{D})^{0.5}$ were more

than one for the characters for days to maturity, length of main raceme (cm), plant height (cm), number of primary branches, number of secondary branches, average seeds per siliquae number of siliquae on main raceme, number of siliquae per plant, oil content (%) and seed yield per plant indicating the expression over dominance for these traits. However, for days to 50% flowering, it was partial dominance.

Analysis of Variance for combining ability revealed the significant values for both gca & sca various for all the characters. The estimated values of variance due to general combining ability (gca) were higher than the specific combining ability (sca) variance for most of the characters except no of siliquae per plant. It indicated these characters are under the control of additive gene action.

The parents namely, AZAD MAHAK, LAHAR were best general combiners for oil content & seed yield per plant. The crosses namely, NARENDRA AGETI RAI-4 × NARENDRA AGETI RAI-8 were best specific combiners for seed yield per plant while NARENDRA AGETI RAI-4 × AZAD MAHAK was desirable combination for oil content.

Hybrids NARENDRA AGETI RAI-4 x JAGRATI showed high heterosis over economic parent for seed yield per plant. While NARENDRA AGETI RAI-8 x NDR8501, NARENDRA AGETI RAI-8 x NDR8501 showed high heterosis over better parent for oil content (%).

Number of primary branches per plant showed high genetic advance in percent over mean, while plant height (cm) showed moderate genetic advance in percent over mean indicating scope for selecting promising lines for further evaluation in combining ability. High heritability coupled with high genetic advance in percent over mean indicates that there exists influence of additive gene action on these characters and hence may prove useful for effective selection.

Genotypic and phenotypic correlation coefficients & path coefficient analysis for 12 characters in all possible combinations were computed. Significant positive correlation coefficient values were found in seed yield per plant with all the traits.

On partitioning the phenotypic path coefficient, it was observed that the highest positive and direct effect on seed yield per plant was exerted by Average seeds per siliquae followed by plant height, number of siliquae per plant, days to maturity, oil content, days to 50% flowering.

Conclusion:

In general, both additive and non-additive type of gene actions were observed in the population for all the 12 characters. Therefore, to harvest maximum yield potential, a certain degree of heterozygosity should be maintained in a population. Wide range of genetic variability and significant variances were observed for all the characters among all genotypes suggesting that, it could be helpful in isolation of better germplasms. The parents AZAD MAHAK, LAHAR were

good general combiners for a number of traits especially for oil content (%) and seed yield per plant (g). NARENDRA AGETI RAI-4×AZAD MAHAK showed high sca effect for oil content (%) whereas NARENDRA AGETI RAI-4× NARENDRA AGETI RAI-8 showed high sca effect for seed yield per plant (g) hence, they may be used further in hybridization programme.

Genotypic correlation coefficient was higher in magnitude than their corresponding phenotypic correlation coefficient for all the characters. Significant positive correlations were found in seed yield per plant with all the characters except days to maturity.

Phenotypic path analysis values revealed that positive and direct effect on seed yield per plant was exerted by by number of siliquae per plant, followed by number of secondary branches per plant, plant height, average seeds per siliquae, days to 50% flowering . oil content, days to maturity, number of primary branches and number of siliquae on main raceme. Thus, the selection pressure on these traits may lead to overall increase in the yield.

BIBLIOGRAPHY

Adhikari, S., Pathak, S., Joshi, D., Pant, U., Singh, A.K. and Bhajan, R. (2017). Heterosis Analysis for Seed Yield and Other Component Traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Int. J. Curr. Microbiol. App. Sci.*, **6**(10): 1157-1162.

Aher, C.D., Chinchane, V.N., Shelke, L.T., Borgaonkar, S.B. and Gaikwad, A.R. (2009a). Genetic study in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *International Journal of Plant Sciences* (Muzaffarnagar), **4**(1): 83-85.

Aher, C.D., Shelke, L.T., Chinchane, V.N., Borgaonkar, S.B. and Gaikwad, A.R. (2009b). Heterosis for yield and yield components in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *International Journal of Plant Sciences*, **4**(1): 30-32.

Akabari VR, Niranjana M.(2015) Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *International J Agril. Sci.* 2015;11(1):35-39.

Aksel, R., Johnson, L.P.V., 1963 Analysis of a diallel cross: a worked example. *Advent Front Plant Sci.* 2: 37–53

Al-Jioubouri HA, Miller PA, Robinson HF., 1958 Genotypic and environmental variance and covariance in an upland cotton cross of inter-specific origin. *Agron. J.* 1958;50:633-637.

Alie, F. A., Singh, T., Tariq, J. & Sharma, P. K. (2009) Genetic diversity analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Progressive Agriculture-an International Journal*,**9**: 50-53.

Allard, R.W. (1960). Principles of Plant Breeding. John Wiley and Sons, New York. P.85.

E&S DIVISION DA&FW ministry of agriculture and farmer welfare government of india.

Arifullah, M., Munir, M., Mahmood, A. and Khan, S., 2012. Combining ability analysis of some yield attributes in Indian mustard (*Brassica juncea* L.). *Pak J Agric Res*, 25(2).

Ashish, A., Chauhan, M.P., Verma, S.P. and Mishra, S.,(2021). Assessing Gene Action for Yield and its Contributing Traits in Indian Mustard (*Brassica juncea* L.) under timely and late sown conditions. *J. of AgriSearch*, 6: 50-53.

Awasthi D, Tiwari VK, Kandalkar VS. Evaluation of heritability and genetic advance for morphological traits of Indian mustard germplasms. *Current Journal of Applied Science and Technology*. 2020;39(21):39-47.

Awnish Kumar, Ravi Shankar Singh, Chandan Kishore (2021). Heterosis and combining ability for important quantitative traits in *Brassica juncea* L. under late sown conditions. *The Pharma Innovation Journal* 2021; 10(10): 379-385.

Banga, S.S. (2005). Hybrid development in Rapeseed-mustard. *In: Kumar, A; Chauhan, J.S. and Chattopadhyay, C. (Ed.).* Proceedings of Winter School on Advances in Rapeseed-mustard Research Technology for sustainable Production of oilseeds. NRC on Rapeseed-mustard, Sewar, Bharatpur: 46-52.

Barfa, D., Tripathi, M.K., Kandalkar, V.S., Gupta, J.C. and Kumar, G., 2017. Heterosis and combining ability analysis for seed yield in Indian mustard [*Brassica Juncea* (L.) Czern & Coss.]. *Ecology, Environment and Conservation*, 23, pp.75-83.

Barupal, H.L., Sharma, A.K., Shekhawat, H.S., Kumar, P. and Kumar, M. (2017). Heterosis Studies in Indian mustard [*Brassica Juncea*]. *International Journal of Agriculture Innovations and Research* Volume 5, Issue 6, ISSN (Online): 2319-1473.

Beena, N., Vandana, K. and Sheetal, B. (2005). Heterosis studies in mustard. *Journal of Phytological Research*, 18(2): 231-233.

Bind, D., Singh, D. and Dwivedi, V.K., 2014. Genetic variability and character association in Indian mustard [*Brassica juncea* (L) Czerns & Coss]. *Agricultural Science Digest-A Research Journal*, 34(3), pp.183-188.

Briggle, L.W. (1963). Heterosis in wheat a review. *Crop sci.* 3: 407-412.

Castle, W. E., 1921. An improved method of estimating the number of genetic factors concerned in cases of blending inheritance. *Science* **54**: 223

Chandrabhas Nishad, Dr. JL Salam, Shailja Singh and Dr. DP Singh (2022) Studies of genetic variability in Indian mustard (*Brassica juncea* L. Czern and Coss). *The Pharma Innovation J.* 2022; 11(2): 261-263.

Chaturvedi, V.D., Maurya, K.N., Upadhyay, D.K., Singh, P.K. and Chaubey, S., 2021. Genetic diversity for yield and its contributing components in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *J. Pharm. Innov*, 10, pp.748-754.

Chaurasia, R.K. and Bhajan, R. (2014). Heterosis and combining ability studies in Indian mustard (*Brassica juncea* L.). *Trends in Biosciences*, 7(22): 3687-3690.

Chaurasiya, J.P., Singh, M., Yadav, R.K. and Singh, L., 2018. Heterosis and combining ability analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss.). *Journal of Pharmacognosy and Phytochemistry*, 7(2), pp.604-609.

Chawla, V., Priyanka, Dipti, (2016). Correlation and path coefficient analysis for yields contributing parameters in Indian mustard, *American J. of pharmitch research*, 6(2):666-675.

Collins, G.N. (1921) Dominance and the vigour of first generation hybrids. *Amer. Mat.*, 55: 116-133.

Comstock, R.R. and Robinson, H.F. (1952). Genetic parameters, their estimation and significance. *Proc. Sixth International Grassland Congress*, 1: 284-291.

Coughtrey, A. and Mather, K., 1970. Interaction and gene association and dispersion in diallel crosses where gene frequencies are unequal. *Heredity*. 25(1):79-88.

Crumpacker, D. W. and Allard, R. W. (1962). A diallel cross analysis of heading date in wheat. *Hilgardia*. 32: 275- 318.

Darwin, C.R. (1876). The Effects of Cross and Self-fertilization in the Vegetable Kingdom, John Murray.

Devi, B., 2018. Correlation and path analysis in Indian mustard (*Brassica juncea* L.) in agroclimatic conditions of Jhansi (UP). *Journal of Pharmacognosy and Phytochemistry*, 7(1), pp.1678-1681.

Dewey, D.R. and Lu. K.H.,(1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy J.* **51**: 515-518.

Dey S.S., Singh N., Bhatia R., Parkash C., Chandel C. (2014). Genetic combining ability and heterosis for important vitamins and antioxidant pigments in cauliflower (*Brassica oleracea* var. *botrytis* L.). *Euphytica* **195**(2): 169-181.

Dey, S.S., Sharma, S.R., Bhatia, R., Parkash, C. and Barwal, R.N. (2011). Superior CMS (*Ogura*) lines with better combining ability improve yield and maturity in cauliflower (*Brassica oleracea* var. *botrytis*). *Euphytica* **182**(2): 187.

Dhaliwal, L.S., Bajaj, R.K., Dhillon, S.K. and Raheja, R.K. (2006). Genetic analysis for fatty acids across environments in sunflower (*Helianthus annuus* L.). *Journal of Research*, **43**(3): 169-172.

Dhawan, N.L and Singh, J. (1961). Flint x dent maize hybrids gives increased yield. *Curr. Sci.*, **30**: 233-234.

Dholu, V.K., Sasidharan, N., Suthar, K., Bhusan, B. and Patel, J.N. (2014). Heterosis and combining ability analysis in Indian mustard, *Brassica juncea* (L.) Czern & Coss. *International Journal of Agricultural Sciences*, **10**(1): 102-107.

Dixit, S., Kumar, K. and Chauhan, V.S. (2005). Heterosis in Indian mustard [*Brassica juncea* (L.) czern and coss.]. *Agricultural Science Digest*, **25**(1): 19-22.

East, E.M. (1908). Inbreeding in corn. In Reports of the Connecticut Agricultural Experiment Station for Years 1907–1908: 419–428.

East, E.M. (1936). Heterosis. *Genetics*, **21**: 375-397.

East, E.M. and Hayes, H.K. (1912). Heterozygosis in evolution and in Plant Breeding. *Bur. Plant Indust. Bull.*, USDA. No.23.

Fisher R. A. and Yates F. (1938). Statistical Tables for Biological, Agricultural and Medical Research London, UK, Oliver and Boyd.

Fisher, R. A. (1930). The Genetical Theory of Natural Selection. Clarendon, Oxford.

FISHER, R. A.,(1918) The correlation between relatives on the supposition of Mendelian inheritance. *Trans, Roy. Soc. Edinburgh* 52: 3M33.

Fonesca, S. and Patterson, F.L. (1968). Hybrid vigour in seven parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop science*, **8**: 85-88.

Gadi, J., Chakraborty, N. R., and Imam, Z. (2020) To Study the Genetic Variability, Heritability and Genetic Advance for Different Quantitative Characters in Indian

Mustard (*Brassica juncea* L. Czern & Coss). International J. of Current Microbiology and Applied Sciences ISSN: 2319-7706 Volume 9 Number 10 (2020).

Gami, R.A. and Chauhan, R.M. (2013). Heterosis and combining ability analysis for seed yield and its attributes in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Indian Journal of Agricultural Research*, **47**(6): 535-539.

Gangapur, D.R., Prakash, B.G., Salimath, P.M., Ravikumar, R.L. and Rao, M.S.L., 2009. Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern and Coss). *Karnataka Journal of Agricultural Sciences*, **22**(5), pp.971-977.

Genter, G.F. and Alexander, M.N. (1962). Comparative performance of S1 progenies and test crosses of corn. *Crop Science*, **2**: 416-419.

Ghosh, S.K., Gulati, S.C. and Raman, R., (2002). Combining ability and heterosis for seed yield and its components in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *The Indian Journal of Genetics and Plant Breeding*, **62**(1): 29-33.

Gilbert N.E.G. (1958) Diallel cross in plant breeding. *Heredity* **12**: 477-492.

Gopalan.C., Rama Sastri. B. V. and Balasubramanian, S.2007. (Revised and Updated by Rao, B.S.N, Deosthale Y.G. and Pant, K.C.) Nutritive Value of Indian Foods, published by National Institute of Nutrition (NIN), Indian Council of Medical Research.

Goswami, P.K., Thakral, N.K., Behl, R. K. and Kumar, R. (2004). Heterosis breeding in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Brassica*, **6**(1/2): 47-51.

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, **9**: 463-493.

Griffing, B. (1956a). A generalised treatment of the use of diallel crosses in quantitative inheritance. *Heredity* **10**:31-50.

Griffing, B. (1956b). Concept of general and specific combining ability in relation to diallel crossing systems. *Austral. J. Biol. Sci.* **9**:463-493.

GRIFFING, J. B., (1950) Analysis of quantitative gene action by constant parent regressions and related techniques. *Genetics* **36**: 303-321.

Gupta, P., Chaudhary, H.B. and Lal, S.K. (2010). Heterosis and combining ability analysis for yield and its components in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Frontiers of Agriculture in China*, **4**(3): 299-307.

Gupta, V.P., Sekhon, M.S. and Satija, D.R. (1991). Studies on genetic diversity, heterosis and combining ability in Indian mustard [*Brassica juncea*

(L.)Czern & Coss]. *The Indian Journal of Genetics and Plant Breeding*, **51**(4): 448-453.

Hallauer A.R., Miranda J.B. (1988). Testers and combining ability, in Quantitative genetics in maize breeding. In: Hallauer AR, Miranda JB (eds.), Iowa State University Press, Ames, USA, 267-298.

Hayman BI, Mather K. (1955). The description of genetic interactions in continuous variation. *J. of Biometrics*. 11:69-82.

Hayman, B. I. (1954a). The analysis of variance of diallel tables. *Biometrics* 10:235-244.

Hayman, B. I. (1954b). The theory and analysis of diallel crosses. *Genetics* 39:789-809.

Hayman, (1954) The theory and analysis of diallel crosses *Genetics*. 39: 789-809. Hybridization between transgenic *Brassica napus* L. and its wild relatives: *Brassica rapa* L., *Raphanus raphanistrum* L., *Sinapis arvensis* L. and *Erucastrum gallicum* (Willd.) O. E. Schulz. 107: 528-39.

Iqbal, A. M., Shikari, A. B., Ashaq, H., & Dar, Z. A. (2015). Genetic variability *Brassica rapa* var. Brown sarson for maturity, yield and yield attributing traits. *Environmental and Ecology*, 33(1 A), 267-270.

Jat, R.S., Singh, V.V., Sharma, P. and Rai, P.K. (2019). Oilseed brassica in India: Demand, supply, policy perspective and future potential. *OCL*, **26**: 8.

Jinks (1955) A survey of the genetical basis of heterosis in a variety of diallelcrosses. *Heredity* 9: 223-238.

Jinks J. L., Jones R. M., (1958). Estimation of the components of heterosis. *Genetics* 43: 223–234.

Jinks, J. L. (1954). The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genetics* 39:767-788.

JINKS, J. L., and B. I. HAYMAN, (1953) The analysis of diallel crosses. *Maize Genetics Coop. News Letter* 27: 48-54.

Jones, D.F. (1917). Dominance of linked factors as a means of accounting for heterosis. *Genetics*, **2**: 466-479.

K Lavanya, Dr. T Srikanth and Dr. D Padmaja (2022) Correlation and path coefficient analysis among yield and yield contributing traits in Indian mustard (*Brassica juncea* L.). *The Pharma Innovation J.* 2022; **11**(2): 2926-2928.

Kapadia, V.N., Sasidharan, N. and Parmar, D.J., 2021. Genetic consequence through combining abilities for yield and its components traits of Brassica species. *Journal of Pharmacognosy and Phytochemistry*, 10(1), pp.690-698.

Kaur, R., Kumar, R., Kaur, S., Singh, H. and Singh, I. (2019b). Combining ability analysis for yield and yield attributes in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Electronic*

Kempthorne, O. (1957). An introduction to genetic statistics. John Wiley and Sons, Inc.; New York.

Kulembeka HP, Ferguson M, Herselman L, Kanju E, Mkamilo G, et al. (2012) Diallel analysis of field resistance to brown streak disease in cassava (*Manihot esculenta* Crantz) landraces from Tanzania. *Euphytica* 187(2): 277-288.

Kumar B, Pandey A. Association analysis of yield and its components in Indian mustard (Brassica juncea L. Czern and Coss). Environment and Ecology. 2014;32(4B):1778-1783.

Kumar P.R. 2001. Rapeseed-mustard. In: Breeding field crops, Chopra V.L. (ed.). Oxford-IBH publication. 394- 432 pp.

Kumar, A., Tiwari, R., Pandey, P. and Kumar, K. (2017). Research Article Studies on combining ability and heterosis using cytoplasmic male sterility system in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Electronic Journal of Plant Breeding*, 8(1): 51-58.

Kumar, B., Pandey, A. and Kumari, A. (2018). Heterosis and combining ability of F1 and F2 generations of Indian mustard for seed yield and its attributes. *Journal of Oilseed Brassica*, 9(1): 33-39.

Kumar, D. and Rathore, N. (2004). Comparative studies on combining ability and heterosis for yield and yield components in Indian mustard, [*Brassica juncea* (L.) Czern & Coss.] on normal and saline soils. *Journal of Oilseeds Research*. 21(1): 24–27.

Kumar, P., Lamba, A., Yadav, R.K., Singh, L. and Singh, M. (2013). Analysis of yield and its components based on heterosis and combining ability in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *The bioscan*, 8(4): 1497-1502.

Kumari, A. and Kumari, V., 2018. Studies on genetic diversity in Indian mustard (*Brassica juncea* Czern & Coss) for morphological characters under changed climate in midhills of Himalayas. *Pharma Innov. J*, 7, pp.290-296.

Kumawat, S., Sharma, A.K., Shekhawat, K., Kumar, A. and Kumawat, P., 2022. Association of Heterosis and Heterobeltiosis for Yield and its Contributing Traits in Indian Mustard (*Brassica juncea* L. Czern & Coss). *International Journal of Plant & Soil Science*, 34(19), pp.75-80.

Lal, M., Singh, D.P. and Bagadi, D.L., 2011. Combining Ability Analysis for Seed Yield and Its Components in Indian Mustard [*Brassica Juncea* (L) Czern &Coss]. *Agricultural Science Digest–A Research Journal*, 31(1), pp.35-37.

Lenka, D. And Mishra, B. (1973). Path coefficient analysis of yield in rice varieties. *Indian J. of Agri. Sci.* 43: 376-379.

Lodhi, B., Thakral, N.K., Avtar, R. and Singh, A. 2014. Genetic variability, association and path analysis in Indian mustard (*Brassica juncea* L.). *J. Oil. Brass.*, 5(1): 26–31.

Lohia, R.S., Singh, R.K. and Mahak, S., 2013. Studies on genetic variability, heritability and character association in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Progressive Research*, 8(1), pp.75-77.

Mahak, S., Bashrat, A.M., Lokendra, S., Brahm, S. and Dixit, R.K. (2008). Studies on combining ability for oil content, seed yield and its contributing characters in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Progressive Research*, 3(2): 147-150.

Mahto, J.L. and Haider, Z.A. (2006). Heterosis in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Journal of Tropical Agriculture*, 42: 39-41.

Malviya, N., Kumar, K. and Upadhyay, D.K. (2019). Combining ability and heterosis for seed yield, its component traits and oil content in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *J. of Pharmacognosy and Phytochemistry*, 8(3): 696-699.

Mariani, C; De Benckeleer, M.; Truettner, J. Leemans, J. and Goldberg, R. (1990). Introduction of male sterility in plants by a chimeric ribonuclease gene. *Nature*, 347: 737-741.

Mariani, C.; De Greff, W.; De Blok, M.; De Benckeleer, M; Gossele, Y. and Leemans, J. (1991). Genetic analysis of engineered male sterility in oilseed rape. *In: Proc. 6th Int. Rapeseed Cong.*, Saskatoon: 352-357.

Maurya JS, Mohammadi K, Talebi R., 2013 Interrelationships and genetic analysis of seed yield and morphological traits in mini core collection of Iranian

landraces, breeding lines and improved Indian mustard (*Brassica juncea*) cultivars. *Genetika*. 2013;47(2):383-393.

Meena, C.P., Chauhan, J.S., Singh, M., Singh, K.H., Meena, M.L., and Rathore, S.S., (2014), Analysis of genetic parameters and correlations for physiological and quality characters in Indian mustard [*Brassica juncea* (L.) Czern.& Coss.], *Indian J. Genetics*, 74(4): 514-517.

Meena, H.S., Kumar, A., Meena, S.K.P., Ram, B., Sharma, A., Singh, V.V. and Singh, D. (2017). Line x tester analysis for combining ability and heterosis in Indian mustard (*Brassica juncea*). *Journal of Oilseed Brassica*,1(1): 18-26.

Meena, H.S., Kumar, A., Ram, B., Singh, V.V., Meena, P.D., Singh, B.K. and Singh, D. (2015). Combining ability and heterosis for seed yield and its components in Indian mustard (*Brassicajuncea* L.). *Journal of Agricultural Science and Technology*,17: 1861-1871.

Misra, A.K., Chattopadhyaya, C., Kumar, A., Singh, S.K. and Verma, S.K., 2010. Evaluation of exotic germplasm of Indian mustard (*Brassica juncea*) for economic traits. *Indian Journal of Plant Genetic Resources*, 23(01), pp.10-14.

Mizushima U and Tsunoda S (1967). A plant exploration in Brassica and allied genera 17249-71.

Moll, R.H. and Stuber, C.W., (1974). Quantitative genetics empirical results revant to Plant Breeding. *Advent Agronomy*. 20: 277-313.

Moll, R.H., Lonquist, J.H., Fortuna, J.V. and Johnson, E.C. (1965). Heterosis and genetic diversity in varietal crosses of maize. *Crop Sci.*, 2: 197-198.

Mothilal, A., Murlidharan, V. and Mannivannan, N. (2007). Combining ability for yield and its components in groundnut (*Arachis hypogea* L.). *J. Oilseeds Res.*, 24(1): 12-15.

Nagaharu, U. (1935). Genome analysis in Brassica with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. *Japan J. Bot.*, 7: 389–452.

Nagendra Maurya, Singh AK, Singh SK., 2013 Path coefficient analysis in Indian mustard (*Brassica juncea* L.). *Advances in Plant Sci*. 2013;26(1):273-274.

Nair, B., Kalamkar, V., Budhanwar, P.D. and Suryapujary, S.M. (2007).
Studies on heterosis in mustard (*Brassica juncea* L.). *J. Phytological-Res.*, **20**(2): 287-
291.

NASRIN, S., 2008. *HETEROISIS AND COMBINING ABILITY ANALYSIS IN INDIAN MUSTARD (Brassica juncea L.)* (Doctoral dissertation, DEPARTMENT OF GENETICS AND PLANT BREEDING, SHER-E-BANGLA AGRICULTURAL UNIVERSITY, DHAKA, BANGLADESH).

Noshin, M., Iqbal, G., Hassan, R., Ahmad, D. and Khan, S.U. (2007). Combining ability analysis for yield and its components in brown mustard. *Sarhad J. Agri.* **23**(3): 617-622.

Oakey H., Verbyla A., Pitchford W., Cullis B., Kuchel H. (2006). Joint modelling of additive and non-additive genetic line effects in single field trials. *Theoretical and Applied Genetics***113**(5): 809-819.

Olsson. G. Owson, G. And Hagberg, A. (1960). Species cross within the genus Brassica. 46: 351-386.

Pandey, S.Y.A., 2018. Inter relationship and path analysis for seed yield in Indian mustard [Brassica juncea (L.) Czern and Coss].

Panse, V. G. and Sukhatme, P. V. (1967). Statistical Methods of Agricultural Workers. 2nd Endorsement, ICAR Publication, New Delhi, India. : 381

Panse, V.G. and Sukhatme, P.V., (1985). Statistical methods for Agricultural

Parmar, A.S.; Jaimini, S.N. and Ram, B. (2011). Combining ability analysis for seed yield and its components over environments in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica*, **2**(2): 61-66.

Patel, A., Prajapati, K.P., Patel, P.J., Shah, S.K. and Patel, P.S. (2016). Genetic studies of yield and quality traits in Indian mustard (*Brassica juncea*). *Journal of Oilseed Brassica*,**1**(1): 289-295.

Patel, A.M., Prajapati, D.B. and Patel, D.G. (2012). Heterosis and combining ability studies in Indian mustard (*Brassica juncea* L.) *Ind. J. Sci. Res. and Tech.* **1**(1): 38-40.

Patel, D.A., Patel, D.K., Patel, J.R., Prajapati, K.P., Patel, P.J. and Patel, A.B., 2021. Exploitation of heterosis for seed yield and its contributing traits in cms based hybrids of Indian mustard [Brassica juncea (L.) czern and coss]. *International Journal of Bio-resource and Stress Management*, **12**(5), pp.552-563.

Prajapati, K.P., Patel, A.M., Khule, A.A. and Patel, L.P., 2014. Combining ability analysis for seed yield and its attributes in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *J Oilseeds Res*, 31, pp.70-72.

Prasad, D., Yadav, R. K., Singh, M., Shweta and Jaiswal, A. (2021) Genetic variability, heritability and genetic advance for quantitative traits in Indian mustard (*Brassica juncea* L. Czern and Coss.). *The Pharma Innovation J.* 2021; 10(12): 2627-2630.

Raliya B, Kumar K, Ramesh, Pukhraj, Meena HS, Mundiyyara R., 2018 Genetic variability and character association in Indian mustard (*B. juncea* L.). *International Journal of Agricultural Sciences.* **2018**;10:5993-5996.

Research Workers. III edition, ICAR, New Delhi.

Rich, TCG. 1991. Crucifers of Great Britain and Ireland. Botanical Society of the British Isles, London. 336 pp.

Rickey, F.D. (1945). Bruce's explanation of Hybrid vigour. *J. Hered.*, **36**: 243-244.

Robinson H. F., Comstock R. E. and Harvey P. H. (1949). Estimates of heritability and the degree of dominance in corn. 41: 353-359.

Rout, S., Kerkhi, S.A. and Chauhan, C., 2018. Character association and path analysis among yield components in Indian Mustard [*Brassica juncea* (L.) Czern and Coss]. *International Journal of Current Microbiology and Applied Sciences*, 7(1), pp.50-55.

Roy, R. K., Kumar, A., Kumar, S., Kumar, A., & Kumar, R. R. (2018). Correlation and path analysis in Indian mustard (*Brassica juncea* (L.) Czern and Coss) under late sown condition. *Environment and Ecology*, **36**(1A), 247-254.

Sabaghnia, N., Dehghani, H., Alizadeh, B., Mohghaddam, M., (2010). Heterosis and combining ability analysis for oil yield and its components in rapeseed A. *J. Crop Sci.* 4(6):390-397.

Sahib, S.F. (2019). Genetic Analysis of Indian mustard for Yield by Calculating Heterosis and Combining Ability.

Sarkar B. and Singh, J.N. (2001). Combining ability analysis and reciprocal cross effects in Indian mustard (*Brassica juncea*). *Indian J. Agric. Sci.* **71**(7): 493-496.

Sharma, S.P. and Sharma, G.S. (2003). Study of heterosis under moisture stress and irrigated condition for grain yield and oil yield in mustard hybrids. *Bhartiya Krishi Anusandhan Patrika*, **18**(3/4): 119-123.

Sheoran, R.K., Yadav, I.S., Singh, A. and Singh, R. (2000). Combining ability analysis for various characters in brown sarson (*Brassica campestris* L.). *Cereal Research Communications*: 81-86.

Shrimali, T.M., Chauhan, R.M., Gami, R.A. and Patel, P.T., 2017. Components of genetic variation and graphical analysis (Wr-Vr) in indian mustard (*Brassica juncea* L. Czern & Coss.). *International Journal of Current Microbiology and Applied*, 6(2), pp.535-545.

Shull, G.H. (1908). The composition of field of maize. *Am. Breed. Assn Rep.*, 4: 296–301

Shull, G.H. (1911a). Experiments with maize. *Bot. Gaz.*, 52: 480-485.

Shull, G.H. (1911b). The genotypes of maize. *Amer. Nat.*, 45: 234-252.

Shull, G.H. (1914) Development of the heterosis concept. In: J.W. Gowen (Ed.) *Heterosis*, IOWA State College Press, Ames, IA.; 49-65.

Singh, A., Avtar, R., Singh, D., Sangwan, O., Thakral, N.K., Malik, V.S., Goyat, B. and Dalal, U. (2013). Combining ability analysis for seed yield and component traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Research in Plant Biology*, 3(2).

Singh, A.K., Singh, B. and Sachan, J.N. (2003). Diallel analysis for combining ability for yield and its component including oil content in Indian mustard. *J. Oilseeds Res.*, 20(2): 269-271.

Singh, D., Arya, R.K., Chandra, N., Niwas, R. and Salisbury, P. (2016). Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern & Coss.). *Journal of Oilseed Brassica*, 1(1): 19-22.

Singh, I., Kumar, R., Kaur, S., Singh, H. and Kaur, R., 2019. Combining ability studies using diallel mating design in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Indian Journal of Agricultural Research*, 53(3), pp.366-369.

Singh, J. 2020. Correlation and path studies for seed yield and its attributing traits in Indian mustard (*Brassica juncea* L. Czern & Coss). *Int.J.Curr.Microbiol.App.Sci.*9(9):620-626.

Singh, M. and Singh, R. K. (1984). A comparison of different methods of half-diallel analysis. *Theor. Appl. Genet.*, **67**: 323-326.

Singh, M., Avtar, R., Kumar, N., Punia, R., Pal, A., Lakra, N., Kumari, N., Kumar, D., Naruka, A., Bishnoi, M. and Khedwal, R.S., 2022. Genetic analysis for

resistance to sclerotinia stem rot, yield and its component traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss.]. *Plants*, 11(5), p.671.

Singh, M., Singh, L. and Srivastava, S.B.L. (2010). Combining ability analysis in Indian mustard (*Brassica juncea* L. Czern & Coss). *Journal of Oilseed Brassica*, 1(1): 23-27.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical methods in Quantitative Genetic Analysis. Kalyani Publ., New Delhi.

Singh, S., Saroj, R., Soumya S.L., Sankar, S.M., Chaudhary, R., Yashpal, Saini, N., Vasudev, S. and Yadava, D.K., 2021. Unravelling the relationship between seed yield and yield-related traits in a diversity panel of *Brassica juncea* using multi-traits mixed model. *Frontiers in Plant Science*, 12, p.651936.

Singh, S.K. (2007). Heterosis for seed yield and yield contributing traits in mustard (*B. juncea* L. Czern & Coss). In Proceedings the 12th International Rapeseed Congress (Vol. 1: 52-54).

Singh, S.K., Haider, Z.A. and Ram, S. (2005). Combining ability and heterosis for seed yield and its components in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences* (India).

Sohan, R., Nutan, V. (2010). Genetic variability for yield and yield components in Indian mustard (*Brassica juncea* L.). *J. of Oilseeds Research*, 27(2),170-171.

Sprague GF, Tatum LA (1942). General versus specific combining ability in single crosses of corn. *Journal of the American Society of Agronomy*, 34: 923-932.

Srivastava, K. and Sinha, B., 2020. EXPRESSION OF HETEROSIS FOR YIELD AND ITS COMPONENTS IN INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN & COSS) UNDER TIMELY SOWN IRRIGATED CONDITIONS. *Plant Archives* (09725210), 20(2).

Thanmichon, S., Ullah, Z. and Baruah, P.K. (2018). Combining ability and heterobeltiosis for yield and yield-attributing traits in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica*; 132-138.

Tiwari V.K. (2019). Morphological parameters in breeding for higher seed yield in Indian mustard [*Brassica juncea* (L.) Czern. & Coss., Electronic J. of Plant Breeding, 10(1):187-195.

Tomar, A., Singh, M. and Singh, S. K. (2015). Genetic analysis of yield and its components based on heterotic response and combining ability parameters in Indian mustard [*Brassica juncea* (L.) Czern and Coss.] *Prog. Agric.*, **15**(1): 85-91.

Topal A, Aydın C, Akgun N, Babaoglu M (2004). Diallel cross analysis in durum wheat (*Triticum durum* Desf.): identification of best parents for some kernel physical features. *Field Crops Research*, **87**: 1-12.

Tripathi, N., Kumar, K., Tiwari, R. and Verma, O.P. (2020). Correlation and path coefficient analysis for seed yield, its component and oil content in Indian mustard (*Brassica juncea* L. Czern & Coss) under normal and saline/ alkaline condition. *J. Pharmac. and Phyto.* 9 (5), 2846- 2850.

Vaghela, P.O., Thakkar, H.S., Bhadauria, H.S., Sutariya, D.A., Parmar, S.K. and Prajapati, D.V. (2011). Heterosis and Combining Ability for Yield and its Component Traits in Indian mustard (*Brassica juncea*). *J. Oilseed Brassica*, **2**: 39–43.

Vaishnava, A., Sachan, J.N. and Tewari, S.K. (2006). Genetic divergence for important quantitative traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Agricultural Science Digest*, **26**(4): 269-272.

Verma, O.P., Kushwaha, G.D. and Singh, H.P. (2000). Heterosis in relation to genetic diversity in Indian mustard. *Cruciferae Newsletter*, (22): 93-94.

Verma, O.P., Yadav, R., Kumar, K., Singh, R., Maurya, K.N. and Ranjana. (2011). Combining ability and heterosis for seed yield and its components in Indian mustard (*Brassica juncea*). *Plant Arch.*, **11**: 863–865.

Vineet, K., Pant, D.P., Usha, P. and Verma, J.S., 2016. Combining ability and heterosis for seed yield and its components in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Environment and Ecology*, **34**(3B), pp.1382-1388.

Warwick SI, Simard MJ, Légère A, Beckie HJ, Braun L, Zhu B,(2001).
Warwick, SI, Francis, A. and Al-Shehbaz, I.A. 2006. Brassicaceae: species checklist and database on CD-Rom. *Pl. Syst. Evol.* **259**: 249–258.

Wolko, J., A. Dobrzycka, J. Bocianowski and I. Bartkowiak-Broda (2019). Estimation of heterosis for yield-related traits for single cross and three-way cross hybrids of oilseed rape (*Brassica napus* L.). *Euphytica*, **215**(10), 156-164.

Wright, S. (1921). Correlation and causation. *J. of Agri. Research.* 20: 557-587.

Wright, S. (1952). The genetics of quantitative variability. In Reeve, E. C. R., and Waddington, C. H. (eds.), Quantitative Inheritance, HMSO, London, pp. 5-41.

Yadav, C.B., Chauhan, Y.S. and Kumar, K. (2004). Combining ability analysis using CMS system in Indian mustard. *Ann. Pl. Physiol.*, **18**(2): 171-175.

Yadav, R.K. and Yadav R.G. 2020. Genetic variability and path coefficient analysis for seed yield and its related attributes in Indian mustard (*Brassica juncea* L. Czern & Coss) under late shown condition. *Prog. Agri.* 20 (1 and 2), 117-122.

Yadav, S. and Pandey, A. 2018. Inter relationship and path analysis for seed yield in Indian mustard (*Brassica juncea* L. Czern & Coss). *The Pha. Inno.* 7(10):152-156.

Yadav, V.N., Singh, M., Yadav, R.K., Singh, H.C., Maurya, A.K., Singh, A.K. and Singh, S.G., 2020. Genetics of seed yield in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] under late sown environment. *Journal of Pharmacognosy and Phytochemistry*, 9(4), pp.249-254.

Yadava, D.K., Giri, S.C., Vignesh, M., Vasudev, S., Kumar Yadav, A., Dass, B., Singh, R., Singh, N., Mohapatra, T. and Prabhu, K.V. (2012a). Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences*, **81**(8): 712.

Yadava, D.K., Singh, N., Vasudev, S., Singh, R., Singh, S., Giri, S.C., Dwivedi, V.K. and Prabhu, K.V. (2012b). Combining ability and heterobeltiosis for yield and yield-contributing traits in Indian mustard (*Brassica juncea*). *Indian J. Agri. Sci.*, **82**(7): 563-567.

YATES, F. (1947) Analysis of data from all possible reciprocal crosses between a set of parental lines. *Heredity.* **1**: 287-301.

Index: Mean performance of Seven Parents and 21 Different Crosses in Indian mustard

Var	Parent/Hybrids	Days to 50% flowering	Days to maturity	Length of main raceme (cm)	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of siliquae on main raceme	Number of siliquae/plant
	Parents								
1	LAHAR	63.67	131.67	77.07	183.83	8.80	16.87	58.07	409.6
2	NRCDR-2	64.33	135.33	84.50	183.60	8.40	18.33	70.67	488.3
3	NARENDRA AGETI RAI-4	68.00	133.67	66.47	180.10	8.47	18.13	54.13	417.0
4	NRENDRA AGETI RAI-8	62.67	133.33	71.40	179.03	8.40	17.87	61.13	425.1
5	NDR8501	65.33	133.00	72.87	178.20	9.60	17.80	67.80	438.1
6	JAGRATI	56.67	134.00	71.33	168.40	8.13	16.40	61.93	432.1
7	AZAD MAHAK	64.67	119.33	85.27	188.40	11.80	18.73	77.40	491.3
	Mean	63.62	131.48	75.56	180.22	9.09	17.73	64.45	443.1
	Min	56.67	119.33	66.47	168.40	8.13	16.40	54.13	409.6
	Max	68.00	135.33	85.27	188.40	11.80	18.73	77.40	491.3
8	LAHAR X NRCDR-2	61.00	130.67	86.40	202.73	12.67	19.37	75.67	495.0
9	LAHAR x NARENDRA AGETI RAI-4	64.67	128.67	78.40	200.53	9.33	18.63	61.40	422.4
10	LAHAR x NARENDRA AGETI RAI-8	60.33	128.00	81.53	195.47	10.20	18.50	65.47	429.2
11	LAHAR X NDR8501	62.00	132.33	80.27	186.33	11.93	17.92	68.57	465.4
12	LAHAR x JAGRATI	60.00	129.00	81.40	186.07	9.00	17.53	65.30	442.6
13	LAHAR x AZAD MAHAK	60.67	131.00	87.40	200.55	10.60	19.63	74.53	495.5
14	NRCDR-2 x NARENDRA AGETI RAI-4	65.33	129.00	82.47	190.43	9.20	19.60	72.43	497.6
15	NRCDR-2 x NARENDRA AGETI RAI-8	61.00	131.00	85.40	199.50	10.87	18.53	74.33	490.6
16	NRCDR-2 x NDR8501	61.67	130.00	85.33	198.47	9.67	19.47	77.60	503.0
17	NRCDR-2 x JAGRATI	60.00	130.00	86.43	184.40	8.93	18.47	71.77	492.5
18	NRCDR-2 x AZAD MAHAHA	62.00	131.00	87.13	200.33	11.80	20.57	88.33	510.4
19	NARENDRA AGETI RAI-4 x NARENDRA AGETI RAI-8	63.33	120.33	75.53	201.53	12.67	21.63	70.50	446.4
20	NARENDRA AGETI RAI-4 x NDR8501	65.33	125.67	86.13	201.40	11.93	20.53	74.27	455.8
21	NARENDRA AGETI RAI-4 x JAGRATI	63.67	121.33	72.87	182.60	12.55	19.36	69.63	450.6
22	NARENDRA AGETI RAI-4 x AZAD MAHAK	60.33	124.00	89.40	203.27	13.33	21.97	88.53	498.6

23	NARENDRA AGETI RAI-8 x NDR8501	60.33	125.00	78.33	196.47	10.40	18.63	70.43	474.0
24	NARENDRA AGETI RAI-8 x JAGRATI	58.67	120.67	79.27	180.53	9.63	17.90	67.43	471.2
25	NARENDRA AGETI RAI-8 x AZAD MAHAK	62.33	125.00	85.27	200.13	12.53	19.60	76.80	495.6
26	NDR8501 x JAGRATI	59.00	126.67	74.07	180.53	10.60	19.60	70.63	478.2
27	NDR8501 x AZAD MAHAK	61.00	130.33	86.49	189.47	12.93	20.57	80.27	475.3
28	JAGRATI x AZAD MAHAK	58.33	128.00	85.53	189.47	12.53	18.97	81.63	496.4
	mean F1	61.48	127.51	82.62	193.82	11.11	19.38	73.60	475.5
	min	58.33	120.33	72.87	180.53	8.93	17.53	61.40	422.4
	max	65.33	132.33	89.40	203.27	13.33	21.97	88.53	510.4
	mean	62.01	128.50	80.86	190.42	10.60	18.97	71.31	467.4
	min	56.67	119.33	66.47	168.40	8.13	16.40	54.13	409.6
	max	68.00	135.33	89.40	203.27	13.33	21.97	88.53	510.4
	SE(d)	0.95	1.71	1.13	1.21	0.57	0.66	0.95	2.6
	C.D.	1.90	3.45	2.27	2.44	1.15	1.34	1.92	5.2
	C.V.	1.87	1.63	1.71	0.78	6.60	4.29	1.64	0.6