# VARIABILITY, CHARACTER ASSOCIATION AND GENETIC DIVERGENCE STUDIES IN INDIAN MUSTARD

**[*Brassica juncea* (L.) Czern and Coss.]**

**Thesis**
**Submitted to the**

**Acharya Narendra Deva University of Agriculture & Technology**
**Ayodhya – 224229, Uttar Pradesh, India**

**By**

***Amarjeet Patel***

**I.D. No. A-11106/19**

**IN PARTIAL FULFILLMENT OF THE**
**REQUIREMENTS FOR THE DEGREE OF**

## Master of Science
## in
## Agriculture

**(Genetics and Plant Breeding)**

**July, 2021**

# CERTIFICATE-I

This is to certify that the thesis entitled "**Variability, character association and genetic divergence studies in Indian mustard (*Brassica* juncea L. Czern and Coss.)**" submitted in partial fulfillment of the requirements for the degree of **Master of Science (Agriculture)** with major in **Genetics & Plant Breeding** of the College of Agriculture. Post Graduate Studies, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya is a record of *bonafide* research carried out by **Mr. Amarjeet Patel, Id. No. A-11106/19** under my supervision and no part of the thesis has been submitted for any other degree.

The assistance and help received during the course of this investigation have been acknowledged.

Kumarganj, Ayodhya
July, 2021

**(O. P. Verma)**
**Chairman**
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# CERTIFICATE-II

We, the undersigned, member of advisory committee of **Mr. Amarjeet Patel, Id. No. A-11106/19** a candidate for the degree of Master of Science (Agriculture)" with major in **Genetics & Plant Breeding** agree that the thesis entitled "**Variability, Character Association and Genetic divergence studies in Indian mustard (*Brassica juncea* L. Czern and Coss.)**" may be submitted in partial fulfillment of the requirements for the degree.

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# CERTIFICATE-III

## DECLARATION FOR ANTI-PLAIGRISM

I **Amarjeet Patel** Id. No. **A -11106/19** certify that the thesis entitled **"Variability, character association and genetic divergence studies in Indian mustard (*Brassica juncea* L. Czern and Coss.)"** submitted in partial fulfillment of the requirements for the degree of **M.Sc. (Ag.)** in **Genetics & Plant Breeding** to the College of **Agriculture**, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.) is original work and has similarities with published work not more than minor similarities as per the UGC (Promotion of Academic Integrity and Prevention of Plagiarism in Higher Educational Institutions) Regulations, 2018, adopted by the university.

I declare that I have faithfully acknowledged, given credit to and referred to the research workers wherever their works have been cited in the text and body of the thesis. I further certify that I have not willfully lifted up some others' work, para, text, data, results etc. reported in the journals, books, magazines, reports, dissertations, thesis etc., or available at web-sites and included them in this thesis and cited as my own work.

Amarjeet

**Place:** Kumarganj, Ayodhya **(Signature of the candidate)**
**Date:**

## CERTIFICATE FROM THE MAJOR ADVISOR

This is to certify that the above statement made by the candidate is correct to the best of my knowledge.

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*Kumarganj, Ayodhya* *(Amarjeet Patel)*
*2021* *Author*

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## LIST OF SYMBOLS AND ABBREVIATIONS:

| | |
|---|---|
| % | Per cent |
| & | and |
| / | Per |
| @ | at the rate of |
| CD | Critical difference |
| Cv | Cultivar |
| $D^2$ | Generalized distance |
| *et. al.* | et. alia |
| ECV | Environmental Coefficient Variation |
| etc. | and so on |
| Fig. | Figure |
| GA | Genetic Advance |
| Ha | Hectare |
| $h^2$ BS | Broad Sense Heritability |
| i.e., | that is |
| ICARDA | International Centre For Agriculture In Dry Areas |
| g | gram |
| GAM | Genetic Advance Per Mean |
| GCV | Genotypic Coefficient variation |

| | | |
|---|---|---|
| GV | : | Genotypic Variance |
| $m^2$ | : | meter-square |
| mm | : | millimetre |
| Min | : | Minimum |
| Max | : | Maximum |
| mg | : | Milligram |
| MT | : | Metric tonnes |
| Pp | : | Page number |
| PCV | : | Phenotypic Coefficient variation |
| S.Em± | : | Standard error mean |
| var | : | Variety |
| *viz.*, | : | Namely |
| Wt. | : | Weight |

# Chapter I

# INTRODUCTION

## *CHAPTER-I*

# INTRODUCTION

Oilseed crops have long been a staple of India's agricultural industry. Mustard made from rapeseeds (*Brassica juncea* L.) is a self-pollinated (2n=2x=36) annual oil seed crop of family Brassicaceae. *B. juncea* (L.) Czern and coss. is the scientific biological name of the Indian mustard plant, In the regional Indian languages of India, i.e., in hindi it is called as Rai, Banarasi rai Kalee sarson, in sanskrit it is called as Asuri, Bimbata, Indian mustard (*B. juncea* L.) is a major rabi oilseed crop of the Indian subcontinent occupies more than 80% of the total cultivated area under rapeseed-mustard in the country. The enhancement in production and productivity of the crop assumes significance, not only for farmers view point but also to the edible oil sector, as well as other vertically and horizontally related businesses and stakeholders.

It is an amphidiploid species that originated through the inter-specific hybridization of *Brassica rapa* (2n=20) and *Brassica nigra* (2n=18) (**Nagaharu Us, 1935**). Indian mustard is the second most important oil seed crops of the world as well as India after groundnut (**Syed *et al.* 1994***)*.

With about 3500 species and 350 genera, the Brassicaceae family is one of the most commercially important plant groups (**Warwick *et al.*, 2000**). Mustard or sarson as it is known in hindi has been mentioned in the Ayurvedic Samhitas. There are references to mustard seed in India from a story of Gautama Buddha in fifth century BC. Rapeseed-mustard, an oleiferous Brassica plant, is one of the most economically important agricultural commodities. The words rape and mustard are derived from the Latin word rapum, which means turnip, and the European habit of combining sweet must of old wine with crushed seeds of black mustard [*B. nigra* (L.) Koch] to make a heated paste (**Hemingway 1976).** Since the fifteenth century, Europe has been growing mustard and rapeseed oilseeds. In the Indus Valley in 3000 BC, mustard seed and rapeseed were produced. From China, the Rai was brought to India. Mustard originated in eastern Europe and Cyberia,(**D. Condole 1892)**.

Mustard is said to have originated in China or India, according to Vavilov and Walknish. Rapeseed-mustard is made up of eight distinct species, including rapeseed. Indian Mustard, toria, yellow sarson, brown sarson, gobhi sarson, karan rai, black mustard, and taramira are all grown in 53 different nations. Banarasi Rai's genesis (*B. nigra*) may be

Uracia, and Toria, Rai and brown mustard is Afghanistan and it's neighbouring north western areas of Indian sub-continent (**Synrem *et al.*,2014**).

Brassica species and cultivars are grown as forage and feed crops in many parts of the world. They are commonly farmed as a source of alternative feed. Production of Brassica crops for forage production can occurs in many locations, including soils. Brassica has a high dry matter digestibility of 85 to 95 percent, compared to 70 percent for excellent alfalfa. Brassica leaves contain 18 to 25% crude protein, while the roots contain about 10% crude protein. These leaf and root crops have long been used as nutritional fodder for sheep and cattle due to their high nutritional value. It also enhances soil fertility and extends the grazing season for farmers. It provides good soil cover winter to prevent soil erosion, produces large amount of biomass, suppresses weed and can improve soil tilth with its root system.

The crop Brassica display enormous diversity and are mainly used as sources of oil containing 38 to 42% oil and 24% protein vegetables, condiments, and fodder and rich source of antioxidants like flavonoids, beta carotene lutein and vitamins C&E. Rapeseed-mustard oil is used primarily for edible purposes and principal cooking oil in the mustard growing area of the country. Known for its great taste and subtle flavor, this vegetable oil is the world's second leading source of protein meal. Besides seeds, it is used as condiments. After the oil is extracted, the meal cake is utilized as cow feed and organic manure.

Brassica is high in vitamins and minerals and has a wide range of therapeutic benefits. They are abundant in vitamin C, soluble fibre, and a variety of nutrients with anti-cancer potential. Rapeseed-mustard oil is a vegetable oil prepared by pressing or extraction from crushed rapeseed-mustard. The colour ranges from pale yellow to reddish yellow. One of the most essential vegetable oils is rapeseed-mustard oil. The oil is made from the seeds of numerous Brassica species, and the oil from different species is not differentiated on the market because they all have identical properties. The oil is usually removed by steam distillation of the pressed cake. The Rapeseed oil or the de-fatted cake did not command a premium price in the international market because of the fact that Indian Brassica cultivars do not meet global standards. The problem is primarily due to two elements i.e., erucic acid in the oil and glucosinolates in the de-fatted cake. Oil is used in Northern India for cooking and frying purposes. It is also used in preparation of hair oil and medicines. It has industrial importance in soap making and in mixtures with mineral oil for lubrication and grease for various machines. Young plant tender leaves are eaten as a green vegetable and are high in Sulphur and other minerals. The per capita availability of edible oil is only 11g/day as normal requirement of 30g/day.

Globally, Rapeseed-mustard growing countries of the world are India, Canada, China, European Union, Pakistan, Poland, Bangladesh and Sweden. The predicted global rapeseed-mustard acreage, output, and productivity for 2019-20 respectively, 36.59 million hectares (m ha), 72.37 million tonnes (mt), and 1980 kilogrammes per hectare (kg/ha). India is ranked fourth in terms of acreage (17.19 percent), behind Canada, China, and the European Union, as well as fourth in terms of production, behind the European Union, Canada, and China (8.54 percent). India provides 19.8% and 9.8% of global GDP, respectively. (**DRMR, 2020-21**)

Rapeseed-mustard crops are grown in India under a variety of Agro-climatic circumstances, including irrigated/rainfed, timely/late sown, saline soils, and mixed cropping. Despite the availability of relevant technologies to boost mustard production per unit area, the total farmed area remains unchanged. Oil crops take up a significant amount of land in the United States. Soyabean, groundnut and rapeseed-mustard are the major oilseed crops in India contributing nearly 84% and 88% to its total acreage and production, respectively.

For the 2019-20 crop year, India's rapeseed-mustard production, acreage and productivity is 9.26 million hectares (m ha), 6.12 million hectares (m ha). and 1511 kilogrammes per hectare (kg/ha) were predicted, respectively. Rapeseed mustard is cultivated in Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana and West Bengal and Assam states accounted for 86.29% of area and 88.46% of production in the country. Rajasthan alone contributed 40.74% to the total area and 44.97% to the production. At country level, the acreage of rapeseed-mustard increased by 6.6% yield by 18.1% and production 25.9% respectively. The total availability of edible oil has increased from 230.59 lakh ton (2014-15) to 253.62 lakh ton (2019-20).

In Uttar Pradesh, the estimated area, production and productivity of rapeseed-mustard had 12.25 lakh ha, 17.10 lakh tonnes and 11.85 q/ha, respectively. Rapeseed-mustard is cultivated in Agra, Mathura, Aligarh, Kanpur, Auraiya, Unnao and Hatras. Mathura is the rapeseed-mustard-producing district in terms of area, production, and productivity. The crop improvement in rapeseed-mustard is complex in nature due to a complex nature of inheritance of yield and its attributes. There are evidences of both additive and non-additive types of gene action in inheritance of characters of mustard. Due to its autogamous nature and adequate additive genetic variance, the attempts at improvement have been stressed upon selection and development of pure line. Though a stable and higher seed yield is the objective of crop improvement programme, the oil content is of paramount importance in oil seed crops.

Because yield is the end product of a chain of contributing traits, the response to selection for yield is minimal. As a result, manipulations of key yield-attributing features such as the number of siliquas on the main branch, the number of seeds per siliqua, test weight, plant height, maturity length, and so on should be prioritized. For a breeding effort focused at creating high yielding stable varieties, an understanding of the nature and extent of genetic diversity, as well as genetic gain of the traits, is necessary (**Simmonds, 1983**).

The availability of genetic variation is advantageous for crop improvements. Such types of variability brought about by a group of genes which have a small individual effect, can be studied through quantitative measurement. The genetic facts are inferred from observation on phenotypes. Because phenotype is determined by the interaction of genotype and environment, non-genetic factors have a significant impact on genetic variation. As a result, multiple genetic indices such as heritability, genetic progress, and others must be used to assess exploitable variability. A study like this appears to be critical for planning genetic improvements in Indian mustard.

The study of genetic advance is equally important as it measures the genetic gain based on selection in a particular character. Therefore, for any crop improvement programme through selection, the study of genetic variability and heritability together with genetic advance is necessary.

A number of variables are studied in correlation, which give an idea about indirect selection as well. Indirect selection is equally important in influencing the final product, grain yield in any crop species. For this, path coefficient analysis has emerged as a very strong tool as it determines the direct and indirect causes of association giving the idea of specific forces which act to produce strong correlation and measures relative importance of each causal factor.

**Objective of Investigation:**

The goal of this study is to find out why Indian mustard (*B. juncea*) is one of India's most important oil seed crops. In order to incorporate desirable characters to maximize economic yields, the information on the nature and extent of genetic variability present in the population for desirable traits, their association and relative contribution to yield constitutes the basic requirement. The present study was undertaken to find out genetic variability available, heritability and genetic advance. The association of different characters and their contribution to define seed yield with following objective:

**1.** To study genetic variability for seed yield and its contributing traits,

**2.** to study character association among different characters,

**3.** to find out direct and indirect effects of yield components on seed yield per plant and

**4.** to study the genetic divergence using $D^2$ analysis.

# Chapter II

# REVIEW OF LITERATURE

## *CHAPTER-II*

# REVIEW OF LITERATURE

A wide survey of genetic variability and a clear understanding of genetic makeup of the crop with the help of biometrical tools is indispensable for initiating an effective breeding programmed. As the available literature pertaining to the present study on the mustard (*B. juncea*) is very meager, work done in other allied species are considered and reviewed under the following aspects.

**2.1** Genetic variability
**2.2** Correlation-coefficient
**2.3** Path coefficient analysis
**2.4** Genetic divergence

## 2.1 Genetic variability

Genetic variability is basic to rationale plant breeding. The genetic variability for various characters is subjected to selection for changing the genetic architecture of the plant character and consequently of the as a whole to develop improved genotypes having higher economic yield.

Variability in germplasm is a prerequisite for effectiveness of selection in plant breeding. The progress due to selection in quantitative characters depends primarily on nature and magnitude of genetic variability present in the population to be improved. Variability within a population is of two types, (i) variability due to genotype or heredity and (ii) variability due to environment. Genotypic variance is due to the different genotypic constitution of the individuals in a population. Variability due to the environment or environmental variance, which by definition embraces all variations of non-genetic origin, can have a great variety of cause and its nature depends very much on the character and the organism studied.

Variability is the distinctive feature of living beings and forms the foundation of plant improvement. Thus, variation, as a matter of fact, offers a working bench for selection in crop improvement programme.

**Gupta (1972)** revealed high genotypic and phenotypic coefficients of variation for 1000-seed weight, seed yield per plant, number of pods per plant, flowering time and plant height.

**Yadav (1973)** observed high phenotypic and genotypic coefficient of variation for seed yield per plant, plant height, number of siliquae, length of main shoot and low for oil content.

**Lakra *et al.* (2020)** observed that existence of genetic variability for selection of superior genotypes. For efficient indirect selection of complex characters, it is important to know the association between traits. and results revealed that the number of secondary branches, seed yield per plant and seed yield per plot exhibited high to moderate GCV accompanied with high to moderate PCV indicating that selection may be effective based on these traits.

**Raliya *et al.* (2018)** revealed that mean sum of squares due to genotypes (treatments) were significant for all the traits. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters, the characters including yield/ ha depicted high genotypic and phenotypic coefficient of variation.

**Singh *et at.* (2018)** studied sixty genotypes of Indian mustard, to determine relationships among yield and some yield components using direct selection parameters like variability, for eleven yield and its contributing characters. Analysis of variance for the design of the experiment indicated highly significant differences for all the characters.

**Malik *et al.* (2018)** found that considerable amount of genetic variability on the basis of GCV and PCV estimates for the traits; days to 50% flowering, numbers of primary and secondary branches per plant, length of siliqua, 1000-seed weight, seed yield per plant, biological yield per plant and harvest index were found in thirty-five genotypes of Indian mustard (*Brassica juncea* L. Czern & Coss).

**Chauhan *et al.* (2017)** studied that to assess the nature of variability and association for fatty acid profile, oil, protein and glucosinolate content. Analysis of variance indicated significant differences for all the quality characters investigated. The coefficients of variation at phenotypic level varied from 4% for protein content to 50.9% for oleic acid. The genotypic coefficients of variability were high for oleic, palmitic + stearic, erucic and linolenic acid. Protein and oil content had the least genotypic variation (GCV: 2.6-2.7%).

**Synrem *et al.* (2014)** studied genetic variability in intra specific crosses of Indian mustard (*Brassica juncea* L. Czern and Coss) evaluated genetic variability for nine quantitative characters. And found that analysis of variance showed significant differences among the crosses for all characters under study except for length of siliqua. Maximum genotypic coefficient of variation and phenotypic coefficient of variation was exhibited by number of secondary branches per plant followed by seed yield per plant and number of primary branches per plant.

**Akabari and Niranjana (2015)** observed that higher values of phenotypic coefficient of variation and genotypic coefficient of variation for number of secondary branches per plant, number of siliquas per plant and yield per plant including the existence of higher magnitude of variability among the test genotypes for effective selection in respect of the above characters.

**Shekhawat *et al.* (2014)** Studied 60 genotypes of Indian mustard for 13 different characters revealed considerable variability for all the characters. The eight characters viz., days to 50% flowering, days to maturity, number of secondary branches per plant, length of main branch, number of siliquas per plant, number of seeds per siliqua, test weight and seed yield per plant showed high estimates of genotypic coefficient of variation. Hence selection will be effective for these traits.

**Meena *et al.* (2017)** studied 39 genotypes of Indian mustard including 28 F1 crosses and 11 parental genotypes. Analysis of variance on 12 quantitative characters was carried out which revealed considerable amount of genetic variability in genotypes for all the traits. 1000-seed weight, siliqua length, plant height and number of primary branches / plants indicated the effectiveness of selection for these traits. 1000-seed weight, siliqua length, plant height, main shoot length and days to maturity were positively associated with seed yield; hence the selection for these traits would help in improving the seed yield. revealed high mean performance for seed yield can be advanced for yield improvement and selection of superior genotypes.

**Bibi *et al.* (2016)** studied 10 genotypes of Indian mustard (*B. juncea*) genotypes which were tested in randomized complete block design (RCBD) with three replications. Eight quantitative parameters were observed namely: Days to 50% flowering, days to 70% maturity, plant height, number of primary branches, silique length, number of seeds silique-1, 1000 seed weight and seed yield noted. Highly significant differences ($p < 0.05$) were taken in all characters which illustrated significant variation.

**Sharma *et al.* (2014)** observed that analysis of variance due to treatments were highly significant for all the characters studied. The study on phenotypic coefficient of variation (PCV) high estimates (>20%) was recorded for number of secondary branches per plant, biological yield, seed yield per plant, 1000-seeds weight, Days to 50 %

flowering, harvest index and number of siliquae on main raceme in E1. Biological yield, seed yield per plant, length of main raceme, harvest index and number of primary branches per plant in E2.

**Bind *et al.* (2014)** observed that maximum genetic variability for biological yield per plant and minimum for days to maturity as reflected by genotypic coefficient of variation. All the characters showed positive correlation with seed yield per plant both at phenotypic and genotypic levels except days to 50% flowering and day to maturity. The path coefficient analysis at genotypic level revealed that biological yield per plant have the highest direct positive effect on seed yield per plant followed by harvest index, 1000-seed weight, number of seeds per siliqua and number of primary branches. Highest negative direct effect on seed yield per plant was observed for plant height at phenotypic level.

**Rai *et al.* (2005)** observed higher estimate of phenotypic and genotypic coefficient of variation for 1000-seed weight, seed yield per plant, number of primary brancher, seed per siliqua and number of siliquae on main raceme. Genetic advance in absolute value ranged from 1.4 for number of primary branches to 17.25 for plant height.

**Singh *et al* (2007)** observed higher genotypic coefficient of variation for seed yield per plant (g), secondary branches per plant, primary branches per plant, 1000-seed weight (g), length of main raceme (cm) and seeds per siliqua. However high heritability ($h^2b$) coupled with high genetic advance in percent of mean (Ga) were observed for seed yield per plant, secondary branches per plant and length of main raceme and also considerably high for primary branches per plant,1000-seed weight, siliquae on main raceme, seeds per siliqua and length of main siliqua.

## Correlation Coefficient Analysis:

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the invent into simple from of association. But measure of correlation does not consider dependence of one variable over the other.

For selection purpose phenotypic correlation is of little practical value genotypic and phenotypic correlation between pairs of traits are in the same direction. When estimated separately, genetic correlation provides a measure of genetic association between a means for improving another. Such correlation coefficient provides information by themselves and could be helpful to the breeder, since they are based on transmissible genetic advance.

**Singh** ***et al.*** **(2020)** studies sixty-four genotypes with four checks varieties (Vardan, Ashirwad, Kranti, and Maya). Results revealed that the seed yield plant-1 showed extremely vital and positive correlational statistics with length of main flower cluster, secondary branches plant-1, primary branches plant-1, plant height and siliquae on main flower cluster whereas non-significant positive correlation with remaining characters.

**Lakra** ***et al.*** **(2020)** revealed that seed yield per plot showed positive and significant correlation with days to 50% flowering, days to maturity, number of siliquae per plant, length of siliqua and number of seeds per siliqua.

**Ralia** ***et al.*** **(2018)** found that seed yield per plant was found to be positively correlated with 1000-seed weight, siliqua length, plant height, main shoot length and days to maturity at genotypic level. The magnitude of genotypic correlation coefficients was higher than phenotypic coefficients which indicated inherent association between different traits, and the phenotypic expression of these traits was less under the influence of environment.

**Ray** ***et al.*** **(2019)** studied 19 genotypes of Indian mustard, and evaluated genotypic correlation coefficient between all characters was higher than phenotypic correlation coefficient indicating strong association among the characters genetically, but phenotypic value is lessened by the significant interaction of environment. Days to 50% flowering, plant height, number of siliquas per plant, biological yield per plant and harvest index had significant and positive association with seed yield per plant at genotypic and phenotypic level respectively. Whereas, number of primary branches was observed significant positive correlation at genotypic level.

**Singh** ***et al.*** **(2018)** revealed that high phenotypic coefficient of variation was recorded for seed yield per plant, secondary branches per plant, test weight, primary branches per plant, and length of main raceme and genotypic coefficient of variation was higher for seed yield per plant recorded by secondary branches per plant, test weight, length of main raceme and plant height. The magnitudes of phenotypic coefficient of variation and genotypic coefficient of variation were high for seed yield per plant, test weight, secondary branches per plant and length of main raceme.

**Ompal** ***et al.*** **(2018)** observed the value of correlation coefficient at phenotypic level, grain yield per plant (g) was recorded with highly positive significant correlation with biological yield and some other traits. Traits biological yield per plant was observed with highest direct effect on grain yield in followed by some other traits in both genotypic and phenotypic path analysis. Resultant direct selection for these traits would be effective for further yield improvement in given genotype of Indian mustard.

**Chauhan *et al.* (2017)** studies 40 varieties of rapeseed-mustard to assess the nature of association for fatty acid profile, oil, protein and glucosinolate content. The environmental effects were significant for erucic, oleic acid, glucosinolate and protein content and the influence of environmental factors appeared to be less on other characters. The genotype x environment interactions were non-significant for all the characters, Erucic acid was negatively and significantly correlated with the rest of the fatty acids except linolenic acid. It had positive association with glucosinolate content (r =0.331). Glucosinolate content had negative and significant correlations with oleic (r =-0.536) and eicosenoic acid (r =-0.260)

**Prasad and Patil (2018)** studied 38 genotypes of Indian mustard (*Brassica juncea* L.) each genotype was collected with 16 yield and attributing observations for statistical analysis. The correlation coefficients revealed that, the trait seed yield was positively associated with biological yield, economical yield and oil yield similarly, negatively associated with seeds per silique and oil content. The trait, oil yield registered positively significant association with biological yield, economical yield, seed yield and negative significant association with seeds per silique and oil content.

**Lyngdoh *et al.* (2017)** studied seven genotypes of green mustard (*Brassica juncea*) have been evaluated to determine correlation coefficient. The correlation studies revealed strong positive association of yield with Leaf area index (LAI), dry matter yield, number of leaves per plant at genotypic level, whereas at phenotypic level only dry matter yield showed a significant positive correlation.

**Devi *et al.* (2017)** studied that correlation and revealed that biological yield per plant and siliqua on main raceme exerted high positive significant genotypic correlation with grain yield per plant and secondary branches per plant was found negatively correlated with grain yield per plant. Path analysis revealed that day to 50% flowering showed maximum positive direct effect however the highest indirect effect of this trait was exhibited through biological yield per plant.

**Roy *et al.* (2017)** estimated that forty diverse genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss] were evaluated for seed yield and its yield components (fourteen characters). Both phenotypic and genotypic coefficients of variation were higher for important traits including seed yield per plant, number of pods per plant, leaf area index, secondary branches per plant and total biomass. The correlation study revealed that seed yield per plant was found to be positively and significantly correlated with pod length, number of seeds per pod and oil content while, negative significant association of seed yield was observed with days to first flowering and total biomass.

**Kumar *et al.* (2015)** studied those 30 genotypes of Indian mustard (*Brassica Juncea* L.) were revealed that harvest index and total biological yield per plant exerted high significant positive correlation coefficients with seed yield at both genotypic and phenotypic level. Seed yield is negatively correlated with days to 50 % flowering and days to maturity which promotes early flowering and early maturing genotypes.

**Lodhi *et al.* (2014)** found that seed yield per plant to be positively and significantly correlated with number of primary branches per plant, number of secondary branches per plant, primary branch angle, main shoot length, siliqua length and number of seeds per siliqua, seed yield per plant had negative association with oil content.

**Singh *et al.* (2011)** studied that seed yield had significant positive association with days to 50% flowering, days to maturity, plant height, length of main shoot, number of siliquae on main shoot and 1000-seed weight.

**Singh *et al.* (2011**) seed yield per plant showed positive and significant correlation with plant height, number of seeds per siliquae, 1000-seed weight, oil content, flowering and grain filling stages.

**Sarma *et al.* (2008)** studied largely random mating composites derived from variety-hybrid populations involving toria, yellow sarson and brown sarson of Indian rapeseed subjected to correlation analysis. Secondary branches, total branches and seeds/ siliqua all with moderate heritability showed positive associations with seed yield both at the phenotypic and the additive genetic levels. Index selection for seed yield along with secondary branches and seeds per siliqua would be effective than simple selection for seed yield alone. Moderate and negative additive genetic correlations of harvest index with the developmental characters and important yield component would dispense with the selection for harvest index for yield improvement.

**Kumar *et al.* (1999) observed** correlation coefficient in four *Brassica sp.* of 23 genotypes and found that seed yield was positively correlated with plant height, primary branches per plant, secondary branches per plant, number of siliquae on main raceme, number of siliquae per plant,1000-seed weight and harvest index.

**Mahla *et al.* (2003)** found that the genotypic correlation coefficient was greater than the phenotypic correlation coefficient. Yield per plant was positive- significant correlation with number of primary branches per plant, number of siliquae on main branch, plant height, number of seeds per siliquae and length of main raceme. Oil content was negatively correlated with test weight.

**Rai *et al.* (2017)** observed significant genetic variation for plant height, main shoot length, fruiting zone length, siliqua length, biological yield/plant, harvest index, seed yield/plant, fibre, phenol, days to flowering under normal conditions while plant height, main shoot length, fruiting zone length, siliqua length, seed/siliqua, harvest index, phenol, days to flowering were found to be significant under drought conditions. Seed yield per plant was significantly and positively correlated with plant height, main shoot length, fruiting zone length, siliqua length, seeds/siliquae, biological yield per plant and harvest index.

**Swetha *et. al* (2019)** studied 28 diverse genotypes of Indian mustard *Brassica juncea* (L.) were evaluated for fourteen quantitative traits. For important traits the genotypic and phenotypic variation is higher for harvest index, siliquae length, seed yield per plant and number of secondary branches of plant. The correlation of seed yield per plant shows the positive correlation with siliquae on main shoot, length of main shoot, plant height, 1000 seed weight, harvest index and days to flowering. Path analysis exhibited positive direct effect on seed yield per plant via plant height, siliquae on main shoot, days to flowering, 1000 seed weight, seeds per siliquae, harvest index and oil content.

### Path Coefficient Analysis:

Path coefficient analysis was first developed and described by Wright (1921) as a tool in genetic analysis which partition the association the components on yield and indirect effects on the characters on yield through other components. By path coefficient analysis, correlation coefficients can be partitioned into two components i.e., direct and indirect effects. It helps to elucidate the intrinsic nature of the observed association for complex characters like grain yield.

**Wright (1921)** coined the term path coefficient and gave the theory of path analysis on the basis of standardized partial regression analysis.

**Le (1956)** gave a detailed account of both basic and applied aspect of path coefficient analysis by means of formulating a path diagram of cause effect relationship showing the inter-relationship of variables under study.

**Dewey and Lu (1959)** for the first time applied the technique of path coefficient to plant breeding and reported that it provides important information about the specific forces acting to produce a particular correlation. They partitioned the total correlation coefficient into direct and indirect effect and assigned the values of path coefficient contributing to yield which help to ascertain with much more precision and clarity the complex association in the selection programme

The association between the various characters in a Rapeseed mustard and the direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here.

**Singh *et al.* (2020)** studies sixty-four genotypes with four checks varieties (Vardan, Ashirwad, Kranti, and Maya). Information obtained by this method helps in direct and indirect selection for genetic improvement of yield. Results revealed that the path analysis disclosed that characters viz., seed yield exhibited the highest positive direct impact on length of main flower cluster followed by primary branches plant-1, secondary branches plant-1and plant height. Considering each, the correlation co-efficient and path co-efficient along, length of main flower cluster, number of primary & secondary branches plant-1 and plant height emerged as vital elements of seed yield which should be given due importance during indirect selection criteria.

**Lakra *et al.* (2020)** studied that the seed yield per plant, days to 50% flowering and plant height has positive direct effect on seed yield per plant which suggests that direct selection for these traits can be done for improvement of yield.

**Pandey *et al.* (2019)** identified as plant height and 1000-seed weight important component having high order of direct effect and seedling dry weight via vigour index-II and seedling length via vigour index-II important component having high order of indirect effect on seed yield per plant. The characters identified above as important direct and indirect yield components merit due to consideration in formulating effective selection strategy for developing high yielding mustard genotypes. These components play an important role in a crop for best selecting of genotypes for making rapid improvement in yield and other desirable characters as well as to select the potential parent for hybridization programmes.

**Prasad and Patil (2018)** studied 38 genotypes of Indian mustard (*Brassica juncea* L.) were found that the traits oil yield, number of primary branches per plant and biological yield registered high direct effects and could be employed in direct selection for seed yield due to high direct effects. In selection for oil yield, the traits viz., seed yield, oil content, economical yield and days to 50 per cent flowering can be employed.

**Chauhan *et al.* (2017)** evaluated that 40 varieties of rapeseed-mustard to assess the nature of direct and indirect effects. The negative association of palmitic + stearic, oleic, linoleic, linolenic and eicosanoid with erucic acid was the result of their high to moderate negative direct effects. Although glucosinolate content had very low direct effect (-0.051) on erucic acid but its positive association was the result of its strong positive indirect effect via oleic acid (0.435), which was partially neutralized by negative indirect effects (-0.112) via linolenic acid.

**Kumar *et al.* (2018)** studied 41 exotic lines of Indian mustard (*Brassica juncea* L.) were evaluated path coefficient analysis was carried out using correlation coefficients to know the yield contributing traits having true associations with seed yield. Improvement in seed yield can be achieved by selection using the correlation and path analysis data generated in this study. Total seed yield/ plant was positively correlated with siliqua length. Number of seeds/ plant and test weight had higher phenotypic direct effects on total seed yield/ plant, revealing that indirect selection for these traits would be effective in improving seed yield. The material used in the study is of diverse nature and can be used in the breeding programme for development of improved genotypes in mustard.

**Lyngdoh *et al.* (2017)** studied seven genotypes of green mustard (*Brassca juncea*) have been evaluated to determine the direct and indirect effects on leaf yield have also been studied. The result of path analysis indicated that dry matter yield had maximum direct effect on yield per plant followed by vitamin C content, total chlorophyll content and leaf length. The present study suggested that while selection, emphasis should be given on these characters in selection programme for increasing the yield of green mustard genotypes.

**Rout *et al.* (2017)** studied that high positive and direct influence of harvest index, biological yield, number of siliquae per plant towards seed yield at genotypic level and at phenotypic level path coefficient analysis showed high positive and direct influence of harvest index and biological yield per plant towards seed yield in Indian mustard.

**Kumar *et al.* (2015)** revealed that harvest index showed maximum positive direct effect, followed by total biological yield per plant, days to maturity, siliquae length at the time of maturity and seed yield per plant at both genotypic and phenotypic levels. Based on result it has been concluded that two traits namely harvest index and total biological yield per plant exerted high correlation as well as direct influence on seed yield may be considered for selection and to improve the seed yield of the mustard genotypes.

**Lodhi *et al.* (2014)** revealed that the main shoot length, number of primary branches per plant, number of seeds per siliqua and primary branch angle showed positive direct effect on seed yield per plant. Which suggested that selection for number of primary branches per plant, primary branch angle, main shoot length, number of seeds per siliqua would be quite effective in improving seed yield in Indian mustard.

**Maurya *et al.* (2013)** the genotypic path analysis showed that the maximum direct affect was contributed by days to 50% flowering (0.404) which was followed by plant height (0.226) and number of seeds per siliqua (0.114). Length of siliqua (-0.198) and 1000-seeds weight (-0.139) exhibited high negative direct effects. Whereas indirect highest positive effect was exerted by plant height followed by number of siliquae on main raceme via. days to 50% flowering were the key yield contributing characters under study.

**Gupta *et al.* (2010)** observed direct effect on seed yield followed by biological yield, harvest index, number of siliquae on main axis and days to 50% flowering.

**Singh and Singh *et al.* (2010)** revealed direct effect of secondary branches per plant followed by plant height, seeds per siliqua on seed yield, whereas highest indirect effect was primary branches per plant on seed yield.

**Lal *et al.* (2011)** revealed that the pods per plant, test weight and number of primary branches/plants had direct effect on seed yield, but indirect effect via number of pods per plant and 1000-seed weight on seed yield.

**Tahira *et al.* (2011)** revealed that the flowering, number of siliquae, biological yield, plant height and siliquae length had direct positive contribution toward seed yield per plant.

**Raut *et al.* (2012)** studied path coefficient analysis which indicated that plant height, number of siliquas per plant, dry matter, 1000-seed weight had direct effect on seed yield in mustard.

**Genetic Divergence:**

Genetic diversity is the variation heritable characteristics present in one species or genotype and serves as a way for population to adopt to changing in environments. It is estimated by using $D^2$ and principal component analysis.

Study of genetic diversity is essential for any breeding programme. Genetic diversity is usually thought of as the amount of genetic variability among individuals of a variety, population or species, **(Brown, 1983).** The quantitative assessment of genetic diversity present among population usually helps a plant breeder in choosing desirable parents for breeding programme.

The eco-geographic divergence has often been considered as an index of genetic diversity. In the past due to lack of precise statistical method to estimate genetic divergence isolation was considered as a reasonable index of genetic diversity (**Vavilov, 1951; Mall et al. 1962; Joshi and Dhawan, 1966; Ram and Panwar, 1970**). It was assumed that the genotypes originally from widely separated parts of the world are likely to be genetically different. However, this criterion may not be used in qualifying the degree of divergence between biological populations at the genotypic level.

A number of classificatory analyses have been proposed by different workers to carryout genetic divergence studies. **Anderson (1957)** proposed metro graph and index score method the pattern of morphological variation in crop species.

A statistical procedure ($D^2$) statistic was outlined by **Mahalanobis (1936)** to measure the genetic divergence is a given population. This concept is based on the techniques of utilizing measurement in respect of as aggregate of characters (**Mahalanobis, 1936 and Rao, 1952**). In recent years these techniques have used as a tool for estimating genetic divergence by plant breeders.

**Sokal and Michener (1958)** developed the average linkages clustering techniques and earlier these were called group methods.

Now a day the need of cluster analysis in a natural way is many fields of study. In order to cluster variables, it is necessary to have some numerical similarity measurement to characterize the relationship among the variables. The traditional method for meeting this condition is to generate an association measure for each pairwise combination of variables. In a problem with N variables there are N/2=1/2N (N-1) different pairs. A basic working assumption of all cluster analysis method is that these numerical measure of association of all comparable to each other (**Anderberge, 1973**)

The association measure so obtain may be used to construct a similarity matrix describing the strength of all pair wise relationship among entries in the date set. Non-hierarchical clustering method are designed to cluster data units into a single classification of K cluster, where K either is specified a prior or is determined as part of the clustering method (**Anderson, 1957; Macqueen, 1967; Morrison, 1967; Baele, 1969 and Spark, 1973**).

Non-hierarchical clustering methods may be used with much larger problems than the hierarchical methods because it is not necessary to calculate and store the similarity matrix, it is not even necessary to store the data set. Generally, data units are processed serially and can be read from tape or disc as needed. This characteristic makes it possible, at least in principle, to cluster arbitrarily large collection of data units.

**Kumari and Kumari. (2018)** observed that cluster analysis grouped the genotypes into six clusters and with cluster I having the highest number of genotype (26). The intra-cluster distance was highest in cluster II, whereas the lowest intra-cluster distance was recorded in cluster VI. Inter cluster divergence was highest between clusters III and V. The study revealed that cluster analysis using yield contributing characters for measurement of genetic divergence, and used in subsequent breeding programme.

**Kumar and Panday (2013)** assessed genetic divergence among 46 Indian mustard genotypes, using Mahalnobis $D^2$ statistics for seed yield and its components. The 46 genotypes were grouped into seven clusters based on $D^2$ analysis. Based on cluster distances I and IV were the highest genotype, while the cluster II had lowest genotype. Cluster V and VI showed the greatest genetic difference. Cluster V recorded lowest for plant height with early flowering and maturity.

**Mohan *et al.* (2017)** reported that all the 25 genotypes of Indian mustard were grouped into 6 clusters based on $D^2$ analysis. The cluster-I with 9 strains had maximum genotypes among all the clusters followed by cluster-III, II, IV, V and VI. The inter cluster distance was recorded highest between cluster-III and cluster-IV (90.88). The minimum inter cluster distance was observed between cluster-I and IV (15.38).

**Devi *et al.* (2017)** studies genetic divergence of 45 genotype of Indian mustard for genetic diversity using Mahalnobis method. Revealed that the analysis of variance had the significance differences for 14 characters were examined, the genotypes were grouped into 7 cluster using Tocher's method. Highest genotypes were found in cluster I and lowest in cluster V, VII with single genotype. The inter-cluster distance was highest in cluster V and

VII while the intra-cluster divergence was highest recorded in VI. Selection of diverse genotype containing desirable characters from the cluster.

**Singh *et al.* (2014)** studies genetic diversity analysis for 35 genotypes of Indian mustard (*Brassica juncea* L. Czern & Coss) was carried out by using Mahalanobis D2 analysis. Observed that quality characters genotype was found in IV cluster. Plant height, number of secondary branches per plant and day to 50% flowering which showed maximum value. Cluster III showed the highest mean value for seed yield per plant, number of siliquas per plant. Plant height contributed the highest to the total divergence followed by day to maturity.

**Singh *et al.* (2011)** assessed genetic divergence among 56 genotypes of Indian mustard using non-hierarchical Euclidean cluster analysis for sixteen economic traits and eight quality characters. The study showed grouping of the genotypes into thirteen clusters based on the economic traits.

**Shathi *et al.* (2012)** studied the genetic diversity present among the 25 mustard (Brassica spp. L) genotypes for eleven quantitative characteristics, namely plant height, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, diameter of siliquae, length of siliquae, number of seed per siliquae, 100 seed weight and yield per plant. Cluster analysis was used for grouping the 25 mustards (Brassica sp. L) genotypes into six clusters. The character such as plant height, number of secondary branches per plant, and number of siliquae per plant contributed greatest towards the divergence in the mustard genotypes

**Goyat *et al.* (2012)** studied genetic divergence among 200 elite germplasm accessions of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] using $D^2$ technique. The genotypes were grouped into seven clusters. Based on the inter-cluster distances, clusters I and VI were found to be most divergent followed by clusters IV and VI and clusters I and VII.

**Shekhawat *et al.* (2014)** evaluated that all the 60 genotypes of Indian mustard, to study genetic diversity using Mahalenobis $D^2$ Statistics. The 60-genotype grouped into 13 cluster based on $D^2$ analysis. The maximum inter cluster distance was observed between vi and vii (824.53) and minimum inter cluster distance found between ii and xii (99.24).

**Pandey *et al.* (2014)** studied 45 genotypes of Indian mustard, $D^2$ analysis was conducted to measure the genetic diversity among the genotypes. The 45 genotypes were grouped into 8 cluster using Tocher's method. Intra-cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found between II and III indicating high genetic divergence among genotypes of these groups. The genotypes of cluster II and cluster VIII constitute high cluster mean for different traits along with early maturity. These genotypes may be hybridized in different combination for selection of transgressive segregants for early maturity and better performance for yield.

**Goyal *et al.* (2012)** studied genetic divergence using Mahalnobis D2 statistics in 200 genetically diverse genotypes of Indian mustard. The genotypes were grouped into 7 cluster. The most divergent inter cluster was found in cluster I and VI. These clusters used in crossing programme to evaluate heterotic hybrid.

**Rout *et al.* (2019)** studies genetic divergence analysis was done among 71 genotypes of Indian mustard (*Brassica juncea* L.) revealed that the inter cluster distance was greatest between cluster VII, indicate sufficient breeding programme to increase yield potential from these clusters. And the highest intra-cluster distance was found between VI followed by V, IV and I in cluster. Cluster III showed the maximum seed yield. While the cluster VII showed very low seed yield.

**Monalisa *et al.* (2005)** studies genetic divergence of 19 all India released strains/cultivars of Indian mustard for 9 traits and showed highly significant differences for all traits, indicating a wide range of genetic diversity in the material. Siliqua per plant had the highest contribution toward total genetic divergence, followed by days to maturity and plant height.

**Singh *et al.* (2005)** Genetic divergence analysis was done among 50 genotypes of Indian mustard (*Brassica juncea*). Four genotypes (RAURD-9602, NDR-190, NDYR-23 and NDM-87-1) could not be grouped together and formed separate clusters. The most diverse groups were clusters VII and VIII. The genotypes present in different clusters may be selected for hybridization for exploiting heterosis.

**Goswami and Behl (2006)** studied genetic divergence and the characters contributing to genetic diversity among 43 genotypes of 13 homozygous diverse lines and their 30 F1 hybrids derived from a 10x3 line x tester mating design in Indian mustard using D2 statistics. Based on divergence analysis, the genotypes were grouped into 6 and 15 clusters, respectively. The intra-cluster distances were almost equal and relatively lower than the inter-cluster distances. Days to 50% flowering, days to maturity, plant height, primary branches, secondary branches, main shoot length, siliquae on main shoot, siliquae length, seeds per siliquae, 1000-seed weight, seed-yield per plant and oil content contributed to total divergence in varietal improvement programme.

# Chapter III

# MATERIALS AND METHODS

# MATERIALS AND METHODS

The present investigation entitled **"Variability, character associaciation and genetic divergence studies in Indian Mustard (*Brassica juncea* L. Czern & Coss.)"** was conducted at Genetics & Plant Breeding, Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U. P.) during the Rabi season 2020-21.

Geographically, this place is located in between $24.47^0$ N and $26.56^0$ N latitude, $82.12^0$ and $83.98^0$ E longitude and at an altitude of 113m above from mean sea level in the genetic plains of eastern U.P. This area falls in sub-tropical climatic zone. The climate of district Ayodhya is semi-arid with hot summer and cold winter. The soils of experimental site were sandy loam with normal pH and saline/alkaline with $p^H$ 8.27 and Ec 2.45 $dSm^{-1}$. The annual rainfall is about 1270mm. The meteorological data during the Rabi crop season is presented in Table 3.1.

**Table 3.1 – Meteorological data (weekly average) during the Rabi crop season 2020-21.**

| Weeks 2020-2021 | Standard weeks | Temperature ($^0$C) | | R.H. (%) | Rainfall (mm) | Wind velocity (10feet) | Sunshine (hrs./day) |
|---|---|---|---|---|---|---|---|
| | | Min. Temp. | Max. Temp. | | | | |
| 19 - 25 Nov. | 47 | 9.6 | 25.4 | 63.0 | 0.00 | 1.6 | 7.1 |
| 26 Nov-2 Dec | 48 | 15.6 | 28.0 | 63.6 | 0.00 | 1.4 | 7.4 |
| 3 - 9 Dec. | 49 | 10.0 | 27.3 | 70.4 | 0.00 | 0.6 | 5.2 |
| 10 - 16 Dec. | 50 | 11.0 | 22.7 | 74.2 | 0.00 | 1.5 | 1.8 |
| 17 - 23 Dec. | 51 | 5.1 | 20.5 | 68.3 | 0.00 | 2.2 | 6.0 |
| 24 - 31 Dec. | 52 | 5.1 | 23.0 | 66.8 | 0.00 | 1.7 | 7.0 |
| 1 - 7 Jan. | 1 | 9.5 | 24.2 | 66.4 | 0.00 | 1.4 | 4.9 |
| 8 - 14 Jan. | 2 | 8.8 | 21.3 | 74.1 | 0.00 | 3.9 | 5.8 |
| 15 - 21 Jan. | 3 | 7.4 | 18.5 | 80.2 | 0.00 | 1.8 | 2.8 |
| 22 - 28 Jan. | 4 | 7.0 | 16.8 | 84.4 | 0.00 | 1.3 | 3.7 |
| 29Jan- 4 Feb. | 5 | 5.5 | 21.1 | 71.1 | 0.00 | 1.4 | 4.5 |
| 5 - 11 Feb. | 6 | 9.0 | 25.5 | 67.1 | 0.00 | 2.2 | 6.3 |
| 12 - 18 Feb. | 7 | 9.5 | 27.2 | 68.1 | 0.00 | 1.4 | 6.8 |
| 19 - 25 Feb. | 8 | 11.7 | 28.2 | 66.3 | 0.00 | 1.8 | 7.6 |
| 26Feb- 4 Mar | 9 | 13.2 | 30.2 | 58.8 | 0.00 | 4.8 | 7.0 |
| 5 - 11 Mar. | 10 | 14.2 | 31.8 | 64.3 | 0.00 | 2.9 | 6.6 |
| 12 - 18 Mar. | 11 | 15.2 | 32.3 | 66.4 | 0.00 | 2.9 | 6.2 |
| 19 - 25 Mar. | 12 | 16.5 | 34.6 | 57.0 | 0.00 | 2.7 | 6.8 |

**Source:** Department of Agro-meteorology, at A.N.D. University of Agriculture and Technology Kumarganj, Ayodhya (U.P.)

### 3.2 Experimental materials:

The experimental materials was consist of 40 diverse genotypes of Indian mustard (*Brassica juncea* L.) *viz.* CS 56, MGK 112, PBR 378, NRC HB 101, PUSA MUSTARD 24, KMR 18-3, SHATABDI, PUSA TARAK, PBR 210, NDR 8501, NRC DR 601, SONAKSHI, B.K. 1008, KMR1 8-1, TPM 1, RH 0119, LET 36, PUSA VIJAY, GODAWARI GANGA, BHU RH 0719, KMR 16-1, KMR 17-4, KMR 17-1, ARAVALI, UJM 20, VAIBHAV, UJM 23, UJM 16, URVASHI, MAYA, KMR 19-4, RH 30 R 17-18, ROHINI, KMR 15-1, KMR 19-6, UJM 10, KMR 14-1, KMR 16-5, KMR 16-3, RGN 145) accessions including three checks *viz.,* MAYA, BHU RH 0719 and NDR 8501 of Indian mustard. These genotypes were made available from the Oilseed Section of the Department of Genetics and Plant Breeding at Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya.

**Table 3.2 The details of genotypes under study are given:**

| S. No | Genotype | Source/ Origin |
|---|---|---|
| 1. | CS 56 | CSSRI, Karnal |
| 2. | MGK 112 | NDUAT, Kumarganj, Ayodhya |
| 3. | PBR 378 | RSS, PAU, Bathinda |
| 4. | NRC HB 101 | DRMR, Bharatpur |
| 5. | PUSA MUSTARD 24 | IARI, New Delhi |
| 6. | KMR1 8-3 | CSAUA&T, Kanpur |
| 7. | SHATABDI | PDKV, Akola |
| 8 | PUSA TARAK | IARI, New Delhi |
| 9. | PBR 210 | RSS, PAU Bathinda |
| 10. | NDR 8501 | ANDUA&T Kumarganj, Ayodhya |
| 11. | NRC DR 601 | DRMR, Bharatpur |
| 12. | SONAKSHI | NDUAT, Kumarganj, Ayodhya |
| 13. | B.K. 1008 | NDUAT, Kumarganj, Ayodhya |
| 14. | KMR 18-1 | CSAUA&T, Kanpur |
| 15. | TPM 1 | MPKV, Jalgaon |
| 16. | RH 0119 | DRMR, Bharatpur |
| 17. | LET 36 | IARI, New Delhi |
| 18. | PUSA VIJAY | IARI, New Delhi |

| | | |
|---|---|---|
| **19.** | GODAVARI GANGA | BHU, Banaras |
| **20.** | BHU RH 0749 | BHU, Banaras |
| **21.** | KMR 16-1 | CSAUA&T, Kanpur |
| **22.** | KMR 17-4 | CSAUA&T, Kanpur |
| **23.** | KMR 17-1 | CSAUA&T, Kanpur |
| **24.** | ARAVALI | ARS, ARU, Navgaon |
| **25.** | UJM 20 | SVPUAT, Meerut |
| **26.** | VAIBHAV | CSAUA&T, Kanpur |
| **27.** | UJM 23 | SVPUAT, Meerut |
| **28.** | UJM 16 | SVPUAT, Meerut |
| **29.** | URVASHI | CSAUA&T, Kanpur |
| **30.** | MAYA | CSAUA&T, Kanpur |
| **31.** | KMR 19-4 | CSAUA&T, Kanpur |
| **32.** | RH 30 R 17-18 | BHU, Banaras |
| **33.** | ROHINI | CSAUA&T, Kanpur |
| **34.** | KMR 15-1 | CSAUA&T, Kanpur |
| **35.** | KMR 19-6 | CSAUA&T, Kanpur |
| **36.** | UJM 10 | SVPUAT, Meerut |
| **37.** | KMR 14-1 | CSAUA&T, Kanpur |
| **38.** | KMR 16-5 | CSAUA&T, Kanpur |
| **39.** | KMR 16-3 | CSAUA&T, Kanpur |
| **40.** | RGN 145 | RAU, ARS, Sriganga nagar |

### 3.3 Experimental site:

The present field experiment was carried out at the Research Farm of Genetics and Plant Breeding, Narendra Deva University of Agriculture & Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) during the Rabi crop season 2020-21.

### 3.4 Field plot technique:

The experimental materials were consisting of 40 diverse genotypes of Indian mustard (*Brassica juncea* L.) including 3 checks, considering each genotype to represent one treatment the experiment was laid out in Randomized block design. The experimental field will be divided into three replications of equal size, and each treatment were planted in two rows of 3m length with inter and intra row spacing of 45cm and 15cm, respectively and maintained by proper thinning. The border rows were also planted to neutralizer the border effect. All cultural practices essential for the good crop of mustard were applied for obtaining healthy and competitive crop stand and observation were recorded on five competitive plants from each replication.

### 3.5 Observation recorded:

Five randomly selected competitive plants from each plot genotype for recording observation for all the quantitative characters except days to 50% flowering and days to maturity which were recorded on the plot basis. The data were recorded for the following 12 characters.

#### 1. Days to 50% flowering:

It was recorded as the number of days from date of sowing to the date when 50% of plants flowered on line basis.

#### 2. Days to maturity:

The duration in days from the date of sowing to turning of 75% siliquae of the plants started to yellowness were recorded as days to maturity.

#### 3. Plant height (cm):

The height of the plant was measured in centimeters from the base of plant to the tip of the plant at the time of maturity.

#### 4. Number of primary branches/ plants:

The first order of branches arising from main shoot were counted on each selected plant when the flowering was completed, and considered as number of primary branches.

#### 5. Number of secondary branches/ plants:

The second order of branches arising from primary branches were counted as secondary branches.

#### 6. Length of main raceme (cm):

The length of main raceme of selected plants was measured from the joint of the apex of primary branches to the top of the plant with the help of meter scale and averaged to represent the length of main raceme.

#### 7. Number of siliquae on main raceme:

The total number of siliquae on main raceme were counted from base to apex of the main raceme of selected plants at maturity and averaged to represent number of siliquae on main raceme.

### 8. Number of seeds per siliqua:

Seed per siliquae were counted from five randomly selected plants in each of the five tagged plants and then average was taken.

### 9. 1000-seed weight (g):

One thousand sun dried seeds from the produce of each selected plants were counted and weight in gram with the help of electronic balance.

### 10. Biological yield per plant (g):

Biological yield per plant were recorded in gram by weighting the total biomass of plant before threshing of each plant separately.

### 11. Harvest index (%):

Harvest index is the ratio of seed yield per plant to the biological yield per plant as per method of Donald (1968).

$$\text{Harvest index (\%)} = \frac{\text{Economical yield}}{\text{Biological yield}} \times 10$$

### 12. Seed yield per plant (g):

Seed yield per plant was recorded in gram by weighting the total seeds obtained after threshing of each plant separately.

## 3.6 Statistical analysis:

The experimental data collected in respect of 12 characters on 40 genotypes including 3 checks were compiled by taking the mean value of selected plants in each plot and subjected for following statistical analyses:

1. Analysis of variance (Panse & Sukhatme, 1967)
2. Estimation of coefficient of variation (Burton & De Vane, 1953)
3. Estimation of correlation coefficient (Aljibouri *et al.,* (1958)
4. Path-coefficient analysis (Deway and Lu, 1959)
5. Estimation of genetic divergence ($D^2$) (Mahalanobis, 1936)

### 3.6.1 Analysis of variance:

The mean value of genotype in each replication were used for statistical analysis. The data were analyzed for a randomized block design to test the significance of differences between the genotypes for various characters. The steps involved in the analysis of the randomized block design were as described by Panse and Sukhatme (1969). The following mathematical model was used in the analysis

$Y_{ij} = \mu + t_i + b_j + e_{ij}$

Where,

$i = 1, 2, 3, 4 \ldots\ldots\ldots\ldots t$, number of treatments (t)

$J = 1, 2, 3, 4 \ldots\ldots\ldots r$, number of replications (r)

$Y_{ij}$ = Performance of $i^{th}$ genotype in $j^{th}$ replication

$\mu$ = general mean of the population

$t_i$ = effect of $i^{th}$ treatment

$b_j$ = effect of $j^{th}$ replication

$e_{ij}$ = random error associated with $i^{th}$ treatment and $j^{th}$ block

### 3.6.1 ANOVA:

The partitioning of total variance, due to block, treatments and error and their expectation are given in the Table.

| Source of Variation | Degree of Freedom | Mean squares | F value |
|---|---|---|---|
| **Replication** | r-1 | MSr | MSr/MSe |
| **Treatments** | t-1 | MSt | MSt/MSe |
| **Error** | (r-1) (t-1) | MSe | _ |
| **Total** | r×t-1 | _ | _ |

Where,

r = Number of replications

t = Number of treatments/genotypes

df = Degree of freedom

MSr = Mean square for replication

MSt = Mean square for treatment

MSe = Mean square for error

Genotypic variance ($\sigma^2 g$) = (MSt/MSe)/r

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Error variance ($\sigma^2 e$) = MSe

$$\text{SE of mean } (\pm) = \sqrt{MSe/r}$$

The significance of differences among treatment means was tested by 'F' test at 5% or 1% level of significance. Whenever the 'F' value was found to be significant, critical difference was calculated to test the significance of difference between treatment means as follow:

$$\text{CD} = \text{SEd} \times t_{(5\%)} \text{ at error d.f.}$$

Where,

t = table value of ‘t’ at error d.f.

SEd = standard error of difference between two treatment means

$$\mathbf{SEd} = \sqrt{\mathbf{2MSe/r}}$$

Where,

MSe = Mean sum square of error

r = Number of replications

**3.6.2 Estimation of coefficients of variation:**

Variability for different characters was estimated as suggested by Burton and de Vane (1953). Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were computed follows as:

$$\text{Coefficient of variation (C.V.)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

Where,

$$\text{Standard deviation} = \sqrt{\text{MSe}}$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{ECV (\%)} = \frac{\text{Environmental standard deviation}}{\text{Mean}} \times 100$$

**3.7.3 Estimation of correlation coefficient:**

Correlation was estimated the association between various character-pairs. The correlations at genotypic, phenotypic and environmental levels were estimated from the analysis of variance and covariance as suggested by **Searle (1961).**

**Phenotypic correlation between character x and y**

$$r_{xy}(p) = \frac{\text{Cov.xy (p)}}{\sqrt{\text{Var.x (p)} \times \text{Var.y (p)}}}$$

Where,

$\text{Cov}_{xy}$ (p) = Phenotypic covariance between two characters x and y.

$\text{Var}_x$ (p) = Phenotypic variance for characters x.

$\text{Var}_y$ (p) = Phenotypic variance for characters y.

**Genotypic correlation between character x and y**

$$r_{xy}\,(g) = \frac{\mathbf{Cov.xy\ (g)}}{\sqrt{\mathbf{Var.x\ (g)\times Var.y\ (g)}}}$$

Where,

$Cov_{xy}$ (g) = Ghenotypic covariance between two characters x and y.

$Var_{x}$ (g) = Genotypic variance for characters x.

$Var_{y}$ (g) = Genotypic variance for characters y.

**Environmental correlation between characters x and y**

$$r_{xy}(e) = \frac{Cov.xy\ (e)}{\sqrt{Var.x\ (e)\times Var.y\ (e)}}$$

Where,

$Cov_{xy}$ (e) = Environmental covariance between two characters x and y.

$Var_{x}$ (e) = Environmental variance for characters x.

$Var_{y}$ (e) = Environmental variance for characters y.

The significance of correlation coefficient was tested by compairing the observed value of correlation coefficient with the tabulated value for (n-2) degree of freedom at 5% and 1% probability level. If the observed value is more than the table value, the correlation coefficient is said to be significant.

$$tc = \frac{\mathbf{r\sqrt{n+2}}}{\sqrt{\sqrt{\mathbf{1-r^2}}}}$$

Where,

r = correlation coefficient

n = number of genotypes

tc = t calculated value

**3.7.4 Path coefficient analysis:**

Path coefficient analysis was conducted following procedure suggested by Wright (1921) and as elaborated by Dewey and Lu (1959).

The 12 yield contributing characters were considered in path coefficient analysis to estimate their direct and indirect effect on seed yield. Seed yield was ×assumed to be dependent variable (effect) which is influenced by all the twelve characters, the independent variable (cause), directly as well as indirectly through other characters. The variation in seed yield unexplained by the twelve causes was presumed to be contributed by a residual factor (x) which is uncorrelated with other factors. Path coefficients were estimated by solving the following simultaneous equation indicating the basic relationship between equations used are as follows:

$r_{iy} = P_{iy} + \sum_{j=1}^{12} \mathbf{rij\ Piy}$

for i = 1, 2 3,…………12

for $r_{ij} = 1$

The above equation can be written in the form of matrix.

(A) 12 ×1 = (B) 12 × 1 (C) 12×1

Where,

A is the column vector of correlations $r_{ij}$

B is the correlation matrix of $r_{ij}$, amd

C is the column vector of direct effects, $P_{iy}$

Resudal factor was calculated as follow:

$$Pxy = \sqrt{1 - R^2}$$

Where,

The $r_{ij}$ i.e., $r_{12}$ to $r_{13}$ denote correlations between all possible combination of independent characters and $P_{1y}$ to $P_{12}$ denote direct effects of various characters on characters y.

$r_{iy}$ = Correlation coefficient between $i^{th}$ and yth characters.

$P_{iy}$ = Direct effectsof $i^{th}$ characters on y.

**3.7.5 Estimation of genetic divergence:**

The genetic divergence among 40 genotypes of Indian mustard was estimated using Mahalanobis's $D^2$ statistics (1936) following Rao (1952). The steps of the analysis are as follow:

1. A set of uncorrelated linear combinatin (Y's) was obtained by the pivotal condensation of the common dispersion matrix (Rao, 1952) of a set of correlated variables (X's).
2. Using the relationship between Y's and X's, the mean values of different genotypes for different characters ($X_1$ to $X_{12}$) were transformed into the mean values of aset of uncorrelated linear combination ($Y_1$ to $Y_{12}$).
3. The between $i^{th}$ and $j^{th}$ genotypes for K characters was calculated as:

$\mathbf{D}^2_{ij} = \sum_{t=1}^{K}(\mathbf{Yij} - \mathbf{Yjt})_2$

Where, t=1

The K components was calculated separately and added to get $D^2_{ij}$.

**4.**The K components of $D^2_{ij}$ for each combination was ranked in descending order of magnitude.

**5.** These ranks were added up for each component over all the combination of i$^{th}$ and j$^{th}$, and the rank total were obtained.

**6.** Testing $D^2_{ij}$ as the generalized statistical distance between i$^{th}$ and j$^{th}$ population, the population was grouped into number of clusters on the basis of values. Any two genotypes belonging to the same cluster had the smallest cluster distance. On an average intra cluster distance was less than the inter-cluster distance (Tocher's method).

Inter and intra-cluster distances were calculated by Tocher's method as suggested by Rao (1952) to form the clusters. This criterion was based on the principles that any two populations belonging to the same cluster should at least on the average show smaller $D^2$ than those belonging to different clusters.

# Chapter IV

# RESULTS AND DISCUSSION

*CHAPTER-IV*

# RESULTS AND DISCUSSION

A major effort of a plant breeder is the constant improvement of the best available genotype for further enhancement in their yield potential either directly improvement of various factors which contributes indirectly to high yield. However, in recent days varietal improvement is centered on utilization of limited germplasm in breeding programme.

The present investigation was carried out on forty genotypes including three checks Maya, BHU-RH-0719 and NDR-8501 of Indian mustard (*Brassica juncea* L. Czern and Coss.) grown during 2021-21 in *Rabi* season. The observation recorded on twelve quantitative characters and those were subjected to various statistical analyses. The results obtained in respect of different biometrical analyses in the present study are described under the following sections:

**4.1** Analysis of variance
**4.2** Mean performance of genotypes
**4.3** Coefficient of variability
**4.4** Correlation coefficient
**4.5** Path coefficient analysis
**4.6** Genetic divergence

## 4.1 Analysis of variance

The analysis of variance for the randomized block design used for accommodating forty Indian mustard (*Brassica juncea*) genotypes including three checks was done for different characters studied along with their range and critical differences are presented in (**Table 4.1**). The analysis of variance showed significant difference among the material used in the present investigation for all twelve characters studied *viz*., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, length of main raceme, number of siliquas on main raceme, number of seed per siliquae, test weight, biological yield per plant, harvest index and seed yield per plant indicating wide spectrum of variation among the genotype.

**Table 4.1: Analysis of variance for different characters in Indian mustard germplasm**

| S. No. | Character | Source of variation | | |
|---|---|---|---|---|
| | | Replication | Treatments | Error |
| | **Degree of freedom** | 2 | 39 | 78 |
| **1.** | Days to 50% flowering | 1.01 | 48.64** | 0.88 |
| **2.** | Days to maturity | 2.51 | 18.31** | 1.45 |
| **3.** | Plant height (cm) | 4.80 | 678.31** | 8.24 |
| **4.** | Number of primary branches per plant | 2.62 | 1.24** | 0.22 |
| **5.** | Number of secondary branches per plant | 2.60 | 28.77** | 0.60 |
| **6.** | Length of main raceme (cm) | 2.25 | 157.95** | 2.97 |
| **7.** | Number of siliquae on main raceme | 5.00 | 68.57** | 1.77 |
| **8.** | Number of seed per siliquae | 0.05 | 2.56** | 0.07 |
| **9.** | 1000-seed weight (g) | 0.02 | 0.63** | 0.01 |
| **10.** | Biological yield per plant (g) | 7.33 | 457.80** | 3.04 |
| **11.** | Harvest index (%) | 0.55 | 28.82** | 0.52 |
| **12.** | Seed yield per plant (g) | 0.36 | 38.89** | 0.41 |

*, ** Significant at 5% and 1% probability levels, respectively

Analysis of variance to determine relationships among yield and some yield components using direct selection parameters like variability, for twelve yield and its contributing characters *viz.,* days to 50% flowering, days to maturity, plant height, number of primary branches per plant , number of secondary branches per plant, length of main raceme, number of siliquas on main raceme, number of seed per siliquas, test weight, biological yield per plant, harvest index and seed yield per plant indicated highly significant differences for all the characters found the same results concluded many scientist Singh *et at.* (2018), Sharma *et al.* (2014)

The analysis of variance for genetic variability have also concluded by many scientists like Singh *et at.* (2018) revealed the same result studied sixty genotypes of Indian mustard, to determine relationships among yield and some yield components using direct selection parameters like variability, for eleven yield and its contributing characters.

Analysis of variance for the design of the experiment indicated highly significant differences for all the characters.

### 4.2 Mean performance of parents:

The mean performance, range, PCV, GCV, of forty germplasm for various characters are presented in **Table 4.2.** The range of variation was maximum for plant height followed by biological yield per plant, length of main raceme, siliquae on main raceme and seed yield per plant. While it was observed minimum in case of test weight followed by primary branches per plant, number of seed per siliquae, days to maturity, harvest index and seed yield per plant. Characters wise results are described below:

#### 4.2.1 Days to 50% flowering:

The days to 50% flowering showed variability ranging from 45 days (MGK-112, Shatabdi, Let-36 and PUSA Vijay) to 58.33 days (UJM-10, KMR 14-1 and KMR 16-5), with a general mean value of 50.11 days.

#### 4.2.2 Days to maturity:

The mean for days to maturity amongst the mustard germplasm varied from 117 days (Shatabdi) to 127 days (KMR-16-1), with a general mean value of 122.24 days.

#### 4.2.3 Plant height:

The general mean value for plant height was observed 169.17 cm. The genotype, NRC-DR-601 showed lowest mean value 135.77 cm, while the highest mean value 205.37 cm was observed in KMR-15-1.

#### 4.2.4 Number of primary branches per plant:

The amount of variability for number of primary branches ranged from 3.33 (Pusa mustard-24) to 6.33 (KMR-17-4, PUSA Vijay) branches, while the general mean was 5.20.

#### 4.2.5 Number of secondary branches per plant:

The amount of variability for number of secondary branches per plant ranged from 2.43 (KMR-16-5) to 16.90 branches in (PBR-378), while the general mean was 9.63

#### 4.2.6 Length of main raceme (cm):

The general mean value for length of main raceme was observed 66.39 cm. The genotype PUSA mustard-24 showed lowest mean value was 46.97 cm, while highest mean value (81.97 cm) was registered in case of. Vaibhav

#### 4.2.7 Number of siliquae on main raceme:

The number of siliquae on main raceme ranged from 34.50 (NRC-DR-601) to 60.67 (Vaibhav), with a general mean value of siliquae on main raceme was 46.69.

### 4.2.8 Number of seed per siliquae:

The highest and lowest values for number of seed per siliquae were recorded in case of B. K.-1008 (15.40) and KMR-18-3 (11.87) respectively. The general mean value registered for this trait was 13.90.

### 4.2.9 1000-seed weight (g):

The general mean performance for 1000-seed weight was 5.22 g. The lowest and highest mean performance for test weight was showed by UJM-20 (4.1g) and B.K.-1008 (5.87g) respectively.

### 4.2.10 Biological yield per plant (g):

The biological yield per plant ranged from 33.62 g (Godavari Ganga) to 86.48 g (KMR-19-4), while the general mean was 55.82 g.

### 4.2.11 Harvest Index (%):

The mean value for harvest index amongst the mustard genotype ranged from 17.91% (KMR-17-4) to 29.89% (Maya), with a general mean value of 22.75%.

### 4.2.12 Seed yield per plant:

The general mean for seed yield per plant was 12.75g. The genotype NRC-DR-601 produced the lowest seed yield per plant (7.41g), while the highest seed yield per plant of 24.49g was given by KMR-19-4 genotype.

Seed yield per plant is the main character for the selection. Bibi *et al.* (2016), Meena *et al.* (2017) have also reported similar variability in seed yield per plant, 1000-seed weight, siliqua length, plant height and number of primary branches/plants indicated the effectiveness of selection for these traits. 1000-seed weight, siliqua length, plant height.

**Table 4.2: The most promising genotypes identified for twelve characters**

The genotypes mentioned below showing very high mean performance in desirable direction for various characters may also be used for improving the characters for which they have high mean performance.

| Characters | Genotypes |
|---|---|
| Days to 50% flowering | Shatabdi, PUSA, Vijay, LET 36, MGK 112, PUSA mustard 24 |
| Days to maturity | Shatabdi, RH 0119, PUSA Vijay, Aravalli, CS 56 |
| Plant height (cm) | KMR 15-1, UJM 23, KMR 19-6, BHU RH 0749, Godavari Ganga |
| Number of primary branches per plant | PUSA Vijay, KMR 17-4, Godavari Ganga, UJM 10, PBR 210 |
| Number of secondary branches per plant | PBR 378, PBR 210, Maya, KMR 18-3, Aravalli |
| Length of main raceme (cm) | Vaibhav, KMR 15-1, Sonakshi, Rohini, Maya |
| Number of siliquas on main raceme | Vaibhav, Rohini, PUSA Tark, KMR 19-4, KMR 15-1 |
| Number of seed per siliquas | B.K. 1008, KMR 19-6, KMR 17-4, Aravalli, Sonakshi |
| 1000-seed weight (g) | B.K. 1008, BHU RH 0749, PUSA Tarak, NRC DR 601, KMR 16-3 |
| Biological yield per plant (g) | KMR 19-4, KMR 19-6, MGK 112, KMR 15-1, PUSA mustard 24. |
| Harvest index (%) | Maya, KMR 16-5, KMR 19-4, CS 56, NDR 8501 |
| Seed yield per plant (g) | KMR 19-4, Maya, Vaibhav, MGK 112, Urvashi |

## 4.3 Coefficient of variability:

Table 4.2 presents the estimates of genotypic and phenotypic coefficient of variability for all the twelve characters under study. A comparative study indicates that the magnitude of phenotypic and genotypic coefficients of variation was invariably higher than genotypic variation for all the characters under study. The genotypic coefficient of variation ranged between 1.94 to 31.81 for days to maturity and number of secondary branches per plant, respectively. The phenotypic coefficient of variation ranged between 2.17 to 32.81for days to maturity and harvesting index, respectively.

The highest estimate (>20%) phenotypic coefficient of variability (32.81%) and genotypic coefficient of variability (31.81%) was observed for number of secondary branches per plant followed by seed yield per plant (PCV=28.54%, GCV=28.09%) and biological yield per plant (PCV=22.28%, GCV=22.06%).

The moderate estimate (10 to 20%) phenotypic and genotypic coefficient of variability were recorded for harvest index (PCV=13.87, GCV=3.50%), number of primary branches per plant (PCV=14.38, GCV=11.23%), length of main raceme (PCV=11.13, GCV=10.83%) and number of siliquae on main raceme (PCV=10.41, GCV=10.15%) whereas the low estimate (<10%) phenotypic and genotypic coefficient of variability were observed for plant height (PCV=9.00, GCV=8.83%), Days to 50% flowering (PCV=8.18, GCV=7.96%), test weight (PCV=8.84, GCV=8.74%) number of seed per siliquae (PCV=6.83, GCV=6.54%) and days to maturity (PCV=2.17, GCV=1.94%).

The assessment of existing variability in germplasm collection was done by computing mean, range and coefficient of variability, heritability and genetic advance. The nature of association among different characters was studied along with variability parameters (Burton and de Vane, 1953). For initiating any breeding programme for plant improvement, the one and most important aspect is to look for sufficient genetic variability for various characters of economic importance. Selection which is the basis of every breeding programme operate only on variation which is of genetic nature (Johansen, 1909). A wide range of variability present in any crop always provides the better chances of selecting desired types (Vavilov, 1951).

The success of plant improvement lies in careful management of variability and techniques to be employed in each case will depend upon clear understanding of the extent and nature of variability. According to Fisher (1918), the continuous variation exhibited by quantitative traits with which most of the plant breeders have to deal with, includes the heritable and non-heritable part is mainly due to unknown environment factors. As it is very difficult to assess the genotype directly, it is possible only through the assessment of phenotypic expression (which is an outcome of genotype and environmental interaction) in the existing material. Therefore, the study of phenotypic variability for various traits under investigation is of great importance.

Although screening of the material study under present investigation exhibited (Table 4.1) sufficient variability for all the twelve characters, namely days to 50% flowering, day to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, length of main raceme, number of siliquae on main raceme, number of seed per siliquae, 1000-seed weight, biological yield per plant, harvest index and seed yield per plant. High amount of genetic variability many for of these traits has been reported by Pant and Singh, 2001; Choudhary *et al.* 2003; Singh *et al.* 2004; Rai et al. 2005; Kumar and Mishra, 2006; Satyendra and Mishra, 2007; Nigam *et al.* 2009; Singh and Singh, 2010; Yadava *et al.* 2011.

The genotypic and phenotypic variances are of little meaning as they do not have any clear limit and at the same time the categorization of the genotype variances as low or high is difficult, rendering them unsuitable for comparison of two populations with desired precision when expressed in absolute values. To overcome this difficulty, the genotype and phenotypic coefficient of variation, which are free from the unit of measurement, can be conveniently employed for making comparison between populations and different metric characters of population.

The genotypic and phenotypic variances are of little meaning as they do not have any clear limit or celling and at the same time the categorization of the genotypic variance as low or high is difficult, rendering them unsuitable for comparison of two populations with desired precision when expressed in absolute values. To overcome this difficulty, the genotypic and phenotypic coefficient of variation, which are free from the unit of measurement, can be conveniently employed for making comparison between populations and different metric characters of population. Results from the present study in this context indicated that phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were high (>25%) for biological yield per plant, seed yield per plant, harvest index and 1000 seed weight, moderate (10-25%) for number of primary branches per plant, number of secondary branches per plant, number of siliquae on main shoot, number of siliquae per plant and length of main shoot and low (<10%) for days to 50%

flowering, days to maturity, plant height, number of seed per siliqua and oil content. Further, the present findings showed that estimates of PCV were generally higher than their corresponding GCV for all the character studied. These findings are similar in agreement with earlier reported by Pant and Singh, 2001; Mehla *et al.,* 2003; Kumar and Srivastava, 2004; Rai *et al.,* 2005; Kumar and Mishra, 2006; Kumar *et al.,* 2007; Nigam *et al.,* 2009; Singh and Singh, 2010; Yadava *et al.,* 2011; Yadav *et al.,* 2012. The present study indicated higher contribution of biological yield per plant, seed yield per plant, harvest index and 1000 seed weight towards genetic variability and thereby suggesting that the parents chosen on the basis of these characters may be utilized in the crossing programme for obtaining good transgressive segments.

**Table 4.3: Range, Mean, least significance differences, phenotypic coefficient of variation for 12 characters in Indian mustard**

| Characters | Mean | Range | | Coefficient of variation | | Heritability (%) | GA | GA% mean |
|---|---|---|---|---|---|---|---|---|
| | | Min. | Max | PCV (%) | GCV (%) | | | |
| Day to 50% flowering | 50.11 | 45.00 | 58.33 | 8.18 | 7.96 | 94.76 | 8.00 | 15.97 |
| Day to maturity | 122.24 | 117.00 | 127.00 | 2.17 | 1.94 | 79.51 | 4.35 | 3.56 |
| Plant height (cm) | 169.17 | 135.77 | 205.37 | 9.00 | 8.83 | 96.44 | 30.23 | 17.87 |
| Number of primary branches/plants | 5.20 | 3.33 | 6.33 | 14.38 | 11.23 | 61.01 | 0.94 | 18.07 |
| Number of secondary branches/ plants | 9.63 | 2.43 | 16.90 | 32.81 | 31.81 | 93.97 | 6.12 | 63.52 |
| Length of main raceme (cm) | 66.39 | 46.97 | 81.97 | 11.13 | 10.83 | 94.57 | 14.40 | 21.69 |
| Number of siliquae on main raceme | 46.69 | 34.50 | 60.67 | 10.41 | 10.15 | 95.04 | 9.52 | 20.39 |
| Number ofseed per siliquae | 13.90 | 11.87 | 15.40 | 6.83 | 6.54 | 91.87 | 1.80 | 12.92 |
| Test weight (g) | 5.22 | 4.10 | 5.87 | 8.84 | 8.74 | 97.63 | 0.93 | 17.78 |
| Biological yield / plant (g) | 55.82 | 33.62 | 86.48 | 22.28 | 22.06 | 98.03 | 25.11 | 44.99 |
| Harvest index (%) | 22.75 | 17.91 | 29.89 | 13.87 | 13.50 | 94.76 | 6.16 | 27.07 |
| Seed yield per plant (g) | 12.75 | 7.41 | 24.49 | 28.54 | 28.09 | 96.91 | 7.26 | 56.96 |

## 4.4 Correlation coefficient:

Investigation was carried out with the experimental data to determine the coefficient of correlation at the phenotypic and genotypic levels. The estimate of phenotypic and genotypic correlation coefficients among the different characters of Indian mustard genotypes are presented in the Table 4.4.1 and 4.4.2.

### 4.4.1 Phenotypic correlation coefficient:

Perusal of the table 4.4 showed that the seed yield per plant was positively and significantly correlated with biological yield per plant (0.867), harvest index (0.613), number of secondary branches per plant (0.328) and number of siliquae on main raceme (0.294), while non-significant and positive correlation was noted with length of main raceme (0.169), days to maturity (0.116), plant height (0.059) and number of seed per siliquae (0.055), while negatively and non-significantly correlated with test weight (-0.146) and number of primary branches per plant (-0.088).

Days to 50% flowering exhibited positive and highly significant correlation with days to maturity (0.808), plant height (0.444), number of primary branches per plant (0.262) and length of main raceme (0.260), positive non-significant correlation with seed yield per plant (0.044) while negative highly significantly correlation with number of secondary branches per plant (-0.304) negative non-significant correlation with biological yield per plant (-0.062) and number of seed per siliquae(-0.028) at phenotypic level.

Days to maturity exhibited significant and positive association with plant height (0.348), number of siliquae on main raceme (0.327), length of main raceme (0.302) and number of primary branches per plant (0.245). Positive non-significant correlation was observed with harvest index (0.131), seed yield per plant (0.116) and biological yield per plant (0.072), whereas number of secondary branches per plant (-0.122), number seed per siliquae (-0.112) and test weight (-0.008) was showed non-significant but negative correlation with days to maturity.

Plant height had positively significant correlation with number of siliquae on main raceme (0.540), length of main raceme (0.482), number of primary branches per plant (0.376) and number of seed per siliquae (0.287) non-significant positive correlation was exhibited with biological yield per plant (0.107) and seed yield per plant

(0.059) and negative non-significant correlation was found with number of secondary branches per plant (-0.122), harvest index (-0.055) and test weight (-0.400) was correlated with negative highly significant.

Number of primary branches per plant exhibited positive significant association with length of main raceme (0.362) and number of siliquae on main raceme (0.241). Test weight (0.018) and number of seed per siliquae (0.005) were showed non-significant but positive correlation. Negative non-significant correlation was exhibited with biological yield per plant (-0.154), seed yield per plant (-0.088) and harvest index (-0.003).

Number of secondary branches per plant showed positive significant correlation with seed yield per plant (0.328) biological yield per plant (0.321). Positive non-significant association with harvest index (0.132), test weight (0.057) length of main raceme (0.046) and number of seed per siliquae (0.005), while negative non-significant correlation with number of siliquae on main raceme (-0.048).

Length of main raceme revealed positive significant association with number of siliquae on main raceme (0.726), whereas non-significant positive correlation with seed yield per plant (0.169), number of seed per siliquae (0.062) and harvest index (0.016). and negative non-significant association with test weight (-0.126).

Number of siliquae on main raceme revealed positive significant correlation with seed yield per plant (0.294), biological yield per plant (0.276). Positive non-significant association with harvest index (0.105) and number of seed per siliquae (0.007), whereas negative significant correlation with 1000-seed weight (-0.289).

Number of seeds per siliquae exhibited positive significant correlation with biological yield per plant (0.211). Positive non-significant association with seed yield per plant (0.055) and negative significant correlation with harvest index (-0.231), whereas negative non-significant association with test weight (-0.078).

Biological yield per plant exhibited positive significant correlation with seed yield per plant (0.867) and harvest index had positive non-significant correlation.

Harvest index revealed positive significant correlation with seed yield per plant (0.613).

1000-seed weight revealed negative non-significant association with seed yield per plant (-0.146), biological yield per plant (-0.131) and harvest index (-0.078).

The result obtained from the genotype correlation coefficient for various characters under study are given in Table 4.4. An interpretation of this table is sought in conjunction with the phenotypic correlation coefficient to reveal the fact that values obtained were similar in direction but of a higher magnitude for most of the inter character association.

In the present investigation genotypes correlation, the seed yield was having positively and significantly correlated with biological yield per plant (0.870) followed by harvest index (0.609), number of secondary branches per plant (0.342) and number of siliquae on main raceme, which might be due to linkage of genes determining these characters. These results are in general agreement with the finding of Kardam and Singh (2005), Tusar *et al.* (2006), Sirohi *et al.* (2008), Gangapur *et al.* (2009), Singh and Singh (2010), Singh *et al.* (2011), Kumar *et al.* (2015), Ompal *et al*. (2018), Prasad and Patil (2018)

In the present investigation the correlation coefficient was estimated among twelve characters at phenotypic and genotypic levels. The phenotypic correlation coefficient was in general, observed to be higher than that of genotypic correlation coefficient, indicating the existence of strong influence of environmental factor for the various characters studied as also observed earlier by Kardam and Singh (2005), Singh *et al.* (2018) The magnitudes of phenotypic coefficient of variation and genotypic coefficient of variation were high for seed yield per plant, test weight, secondary branches per plant and length of main raceme.

Positive correlation of seed yield per plant at genotypic and phenotypic levels with days to 50% flowering, days to maturity, plant height, 1000-seed weight was consonance with finding of Ray *et al.* (2019) and Singh *et al.* (2011).

## Table 4.4. Estimate of phenotypic correlation coefficient between twelve characters in forty genotypes of Indian mustard

| Characters | Day to 50% flowering | Day to maturity | Plant height (cm) | Number of primary branches/ plants | Number of secondary branches/ plants | Length of main raceme (cm) | Number of siliquae on main raceme | Number of seed per siliquae | Test weight (g) | Biological yield / plant (g) | Harvest index (%) | Seed yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Day to 50% flowering | 1.000 | 0.808** | 0.444** | 0.262** | -0.304** | 0.260** | 0.266** | -0.028 | -0.201* | -0.062 | 0.222* | 0.044 |
| Day to maturity | | | 0.348** | 0.245** | -0.122 | 0.302** | 0.327** | -0.112 | -0.008 | 0.072 | 0.131 | 0.116 |
| Plant height (cm) | | | | 0.376** | -0.122 | 0.482** | 0.540** | 0.287** | -0.400** | 0.107 | -0.055 | 0.059 |
| Number of primary branches/plants | | | | | 0.070 | 0.362** | 0.241** | 0.005 | 0.018 | -0.154 | -0.003 | -0.088 |
| Number of secondary branches/ plants | | | | | | 0.046 | -0.048 | 0.005 | 0.057 | 0.321** | 0.132 | 0.328** |
| Length of main raceme (cm) | | | | | | | 0.726** | 0.062 | -0.126 | 0.191* | 0.016 | 0.169 |
| Number of siliquae on main raceme | | | | | | | | 0.007 | -0.289** | 0.276** | 0.105 | 0.294** |
| Number of seed per siliquae | | | | | | | | | -0.078 | 0.211* | -0.231* | 0.055 |
| Test weight (g) | | | | | | | | | | -0.131 | -0.078 | -0.146 |
| Biological yield / plant (g) | | | | | | | | | | | 0.155 | 0.867** |
| Harvest index (%) | | | | | | | | | | | | 0.613** |
| Seed yield per plant (g) | | | | | | | | | | | | 1.000 |

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

### 4.5 Path coefficient analysis:

The genotypic and phenotypic correlation coefficients of seed yield per plant with other remaining characters under study were further partitioned into direct and indirect effect using path coefficient analysis and the results obtained at phenotypic level are presented in Table 4.5.

### 4.5.1 Phenotypic path coefficient:

Phenotypic path coefficient analysis showed that biological yield per plant had highest positive direct effect (0.7851) on seed yield per plant followed by harvest index (0.4955). Number of primary branches per plant (0.0487), number of siliquae on main raceme (0.0451), days to maturity (0.0236) and number of seed per siliquae (0.0113) exhibited positive direct effects, and while the other characters like days to 50% flowering (-0.0481) showed highest negative direct effects on seed yield per plant followed by plant height (-0.0250), length of main raceme (-0.0237), test weight (-0.0134) and number of primary branches per plant (-0.0039).

Days to 50% flowering with positive direct effect showed indirect positive effects for days to maturity, number of primary and secondary branches per plant, number of siliquae on main raceme, test weight, and harvest index and negative indirect effect for plant height, length of main raceme, number of seed per siliquae and biological yield per plant. Day to maturity with positive effect exhibited indirect positive effects for number of primary and secondary branches per plant, number of siliquas on main raceme, test weight, biological yield per plant, harvest index and negative indirect effect for days to 50% flowering, plant height, length of main raceme, number of seed per siliquae. Plant height with high positive direct effect revealed indirect positive effect for days to maturity number of primary and secondary branches per plant, number of siliquae on main raceme, number of seed per siliquae, test weight, biological yield per plant and negative indirect effect for days to 50% flowering, length of main raceme, harvest index. Number of primary branches per plant with positive direct effect showed indirect effect for day to maturity, number of siliquae on main raceme, number of seed per siliquas and negative indirect effect for plant height, number of secondary branches per plant, length of main raceme, test weight, biological yield per plant, harvest index. Number of secondary branches per plant with positive direct effect observed indirect positive effect for day to 50% flowering, plant height, number of primary branches per plant, number of seed per siliquae, biological yield per plant, harvest index and negative indirect effect for day to maturity, length of main raceme, number of siliquae on main raceme, and test weight. Length of main raceme with positive direct effect exhibited indirect positive effect for day to maturity, number of primary branches per plant, number of siliquae on main raceme, number of seed per siliquae, test weight, biological yield per plant, harvest index and negative indirect effect for day to 50% flowering, plant height, and number of secondary branches per plant, Number of siliquae on main raceme with positive direct effect showed indirect positive effect for day to maturity, number of primary and secondary branches per plant, number of seed per siliquae, test weight, biological yield per plant, harvest index and negative indirect effect for day to 50% flowering, plant height, length of main raceme. Number of seed per siliqua with positive direct effect revealed indirect positive effect for day to 50% flowering, number of primary and secondary branches per plant, number of siliquae on main raceme, test weight, biological yield per plant and negative indirect effect for day to maturity, plant height, length of main raceme, and harvest index. Test weight with positive direct effect showed indirect positive effect for day to 50% flowering, plant height, number of primary branches per plant, length of main raceme and negative indirect effect for day to maturity, number of secondary branches per plant, number of siliquae on main raceme, number of seed per siliquae, biological yield per plant and harvest index. Biological yield per plant with positive direct effect showed indirect positive effect for day to maturity, number of siliquae on main raceme, number of seed per siliquae, test weight, harvest index and negative indirect effect for plant height, number of primary and secondary branches per plant and length of main raceme. Harvest index with positive direct effect revealed indirect positive effect for day to maturity, plant height, number of siliquae on main raceme, test weight, biological yield per plant and negative indirect effect for day to 50% flowering, number of primary and secondary branches per plant, length of main raceme, and number of seed per siliquae. The remaining characters showed very low indirect effect on seed yield per plant.

Partitioning of the correlation coefficient into direct and indirect effect was done at the genotypic level results is presented in Table 4.5

A critical perusal of result in table revealed that biological yield per plant (0.8012) had the maximum direct positive effect followed by harvest index (0.4932), number of primary branches per plant (0.0828), number of siliquae on main raceme

(0.0556), day to maturity (0.0237) and number of seed per siliquae (0.0194). At genotypic level also the estimate of direct and indirect effect was generally similar to those observed at phenotypic level with little variation in magnitudes. The residual effect observed in phenotypic and genotypic path analysis was 0.00978 and 0.00562.

The result on the phenotypic and genotypic path coefficient exhibited high positive direct contribution of harvest index, number of siliquae per plant, biological yield per plant, 1000-seed weight and number of seed per siliqua towards seed yield. The direct contribution of harvest index, number of siliquae per plant, biological yield per plant and 1000-seed weight with seed yield per plant observed in this study is also in confirmation with the findings of Singh *et al.* (2020); Lakra *et al.* (2020); Pandey *et al*. (2019); Prasad and Patil (2018); Chauhan *et al.* (2017); Kumar *et al.* (2018); Lyngdoh *et al.* (2017); Rout *et al.* (2017); Kumar *et al.* (2015).

## Table 4.5: Direct and indirect effects of twelve phenotypic characters on seed yield per plant in Indian mustard.

| Characters | Day to 50% flowering | Day to maturity | Plant height (cm) | Number of primary branches/ plants | Number of secondary branches/ plants | Length of main raceme (cm) | Number of siliquae on main raceme | Number of seed per siliquae | Test weight (g) | Biological yield / plant (g) | Harvest index (%) | R with Seed yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Day to 50% flowering | **-0.0481** | 0.0191 | -0.0111 | 0.0128 | 0.0012 | -0.0062 | 0.0120 | -0.0003 | 0.0027 | -0.0483 | 0.1102 | 0.044 |
| Day to maturity | -0.0389 | **0.0236** | -0.0087 | 0.0119 | 0.0005 | -0.0072 | 0.0147 | -0.0013 | 0.0001 | 0.0566 | 0.0649 | 0.116 |
| Plant height (cm) | -0.0214 | 0.0082 | **-0.0250** | 0.0183 | 0.0005 | -0.0114 | 0.0244 | 0.0032 | 0.0054 | 0.0838 | -0.0274 | 0.059 |
| Number of primary branches/plants | -0.0126 | 0.0058 | -0.0094 | **0.0487** | -0.0003 | -0.0086 | 0.0109 | 0.0001 | -0.0003 | -0.1206 | -0.0013 | -0.088 |
| Number of secondary branches/ plants | 0.0146 | -0.0029 | 0.0031 | 0.0034 | **-0.0039** | -0.0011 | -0.0022 | 0.0001 | -0.0008 | 0.2522 | 0.0656 | 0.328** |
| Length of main raceme (cm) | -0.0125 | 0.0071 | -0.0121 | 0.0176 | -0.0002 | **-0.0237** | 0.0327 | 0.0007 | 0.0017 | 0.1499 | 0.0078 | 0.169 |
| Number of siliquae on main raceme | -0.0128 | 0.0077 | -0.0135 | 0.0117 | 0.0002 | -0.0172 | **0.0451** | 0.0001 | 0.0039 | 0.2165 | 0.0522 | 0.294** |
| Number of seed per siliquae | 0.0014 | -0.0026 | -0.0072 | 0.0002 | 0.0000 | -0.0015 | 0.0003 | **0.0113** | 0.0010 | 0.1660 | -0.1142 | 0.055 |
| Test weight (g) | 0.0097 | -0.0002 | 0.0100 | 0.0009 | -0.0002 | 0.0030 | -0.0130 | -0.0009 | **-0.0134** | -0.1032 | -0.0388 | -0.146 |
| Biological yield / plant (g) | 0.0030 | 0.0017 | -0.0027 | -0.0075 | -0.0012 | -0.0045 | 0.0124 | 0.0024 | 0.0018 | **0.7851** | 0.0769 | 0.867** |
| Harvest index (%) | -0.0107 | 0.0031 | 0.0014 | -0.0001 | -0.0005 | -0.0004 | 0.0048 | -0.0026 | 0.0011 | 0.1219 | **0.4955** | 0.613** |

Residual effects = 0.00978 Bold values show direct and normal values shows indirect effects

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

**Table 4.6: Direct and indirect effects of twelve genotypic characters on seed yield per plant in Indian mustard.**

| Characters | Day to 50% flowering | Day to maturity | Plant height (cm) | Number of primary branches/ plants | Number of secondary branches/ plants | Length of main raceme (cm) | Number of siliquae on main raceme | Number of seed per siliquae | Test weight (g) | Biological yield / plant (g) | Harvest index (%) | r with Seed yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Day to 50% flowering | **-0.0559** | 0.0203 | -0.0222 | 0.0277 | 0.0050 | -0.0115 | 0.0162 | -0.0003 | 0.0042 | -0.0510 | 0.1138 | 0.0460 |
| Day to maturity | -0.0479 | **0.0237** | -0.0189 | 0.0321 | 0.0021 | -0.0147 | 0.0218 | -0.0023 | 0.0003 | 0.0632 | 0.0776 | 0.1370 |
| Plant height (cm) | -0.0261 | 0.0095 | **-0.0475** | 0.0400 | 0.0020 | -0.0218 | 0.0308 | 0.0060 | 0.0082 | 0.0828 | -0.0320 | 0.0520 |
| Number of primary branches/plants | -0.0187 | 0.0092 | -0.0230 | **0.0828** | -0.0013 | -0.0195 | 0.0166 | -0.0004 | -0.0001 | -0.1578 | -0.0059 | -0.1180 |
| Number of secondary branches/ plants | 0.0185 | -0.0033 | 0.0064 | 0.0072 | **-0.0150** | -0.0025 | -0.0026 | 0.0000 | -0.0013 | 0.2664 | 0.0685 | 0.342** |
| Length of main raceme (cm) | -0.0150 | 0.0082 | -0.0243 | 0.0378 | -0.0009 | **-0.0426** | 0.0419 | 0.0012 | 0.0026 | 0.1576 | 0.0133 | 0.180* |
| Number of siliquae on main raceme | -0.0163 | 0.0093 | -0.0263 | 0.0247 | 0.0007 | -0.0321 | **0.0556** | -0.0001 | 0.0059 | 0.2243 | 0.0553 | 0.301** |
| Number of seed per siliquae | 0.0009 | -0.0029 | -0.0147 | -0.0016 | 0.0000 | -0.0026 | -0.0003 | **0.0194** | 0.0015 | 0.1807 | -0.1142 | 0.0660 |
| Test weight (g) | 0.0117 | -0.0003 | 0.0196 | 0.0005 | -0.0010 | 0.0055 | -0.0165 | -0.0015 | **-0.0199** | -0.1061 | -0.0409 | -0.1490 |
| Biological yield / plant (g) | 0.0036 | 0.0019 | -0.0049 | -0.0163 | -0.0050 | -0.0084 | 0.0156 | 0.0044 | 0.0026 | **0.8012** | 0.0756 | 0.870** |
| Harvest index (%) | -0.0129 | 0.0037 | 0.0031 | -0.0010 | -0.0021 | -0.0011 | 0.0062 | -0.0045 | 0.0017 | 0.1229 | **0.4932** | 0.609** |

Residual effects = 0.00562 Bold value show direct effects and normal values show indirect effects

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

### 4.6 Genetic divergence:

The study of genetic divergence of forty genotypes was done through **Mahalanobis's D$^2$** statistics as described by **Rao (1952)**. The results are being described as fallow.

#### 4.6.1 Distributions of genotypes in different clusters:

The 40 genotypes were grouped into seven clusters (Table 4.6). Cluster V had highest number of genotypes 14 followed by cluster IV, VII, III, VI, II and I which had 8, 6, 5, 3, 2 and 2 genotypes respectively.

#### 4.6.2 Average intra and inter cluster distance:

The intra and inter-cluster distance among different clusters was given in Table (4.6). The intra-cluster D$^2$ values ranged from 1.640 (cluster II) to 2.545 (cluster V). The inter-cluster D$^2$ values indicated that the most diverse groups were VII and II (6.664) followed by VI and I (6.351). The minimum inter-cluster value was found between VI and IV (3.038) indicates that this group is less diverse.

40 varieties of Indian mustard were grouped into seven clusters. The genotypes from one source of origin clustered with the genotypes of other source of origin. This indicated that there was no parallelism between geographical distribution and genetic diversity. Kumar and Panday (2013), Mohan *et al.* (2017), Devi *et al.* (2017), Singh *et al.* (2014), Shekhawat *et al.* (2014) and in case of *Brassica juncea*,) Monalisa *et al.* (2005) in *Brassica campestirs var. toria* also found the similar trend.

#### 4.6.3 Cluster means:

The cluster mean calculated for twelve characters under study have been presented in Table 4.6. Days to 50% flowering showed highest mean for cluster number VI (58.22) and lowest mean for cluster number I (45.83) For days to maturity highest mean for cluster number IV (125.33) and lowest mean for cluster number I (119.50). Plant height exhibited highest mean for cluster number VI (183.57) and lowest mean for cluster number II (139.48). Number of primary branches per plant revealed highest mean for cluster number IV (5.45) and lowest mean for cluster I (3.70). Number of secondary branches per plant exhibited highest mean for cluster number III (14.61) and lowest mean for cluster number VI (5.7). Length of main raceme exhibited highest mean for cluster number VII (72.91) and lowest mean for cluster number I (52.75). Number of siliquae on main raceme showed highest mean for cluster number VII (50.65) and lowest mean for cluster number II (37.57). Number of seed per siliqua showed highest mean for cluster number VII (14.84) and lowest mean for cluster number III (13.12). Test weight exhibited highest mean for cluster number II (5.60) and lowest mean for cluster number VI (4.44). Biological yield per plant showed highest mean for cluster number I (74.26) and lowest mean for cluster number II (36.07). Harvest index showed highest mean for cluster number III (25.17) and lowest mean for cluster number V (20.53). Seed yield per plant exhibited highest mean for cluster number VII (17.11) and lowest mean for cluster number II (8.13).

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combination which may generate the highest possible variability for various traits. Mahalnobis $D^2$ analysis of quantitative traits is a powerful tool for measuring genetic divergence among the material selected even from the same geographical region, reported by Mahalnobis (1936) followed by Rao (1952).

**Table 4.7.1: Clustering pattern of 40 genotypes of Indian mustard on the basis of non- Hierarchical Euclidean cluster analysis:**

| Clusters | No of genotypes | Genotypes |
|---|---|---|
| I | 2 | MGK 112, Pusa mustard 24 |
| II | 2 | NRC HB 101, NRC DR 601 |
| III | 5 | CS 56, PBR 378, KMR 18-3, PBR 210, Maya |
| IV | 8 | NDR 8501, BHU RH 0749, KMR 16-1, Vaibhav, Urvashi, RH 30 R 17-18, Rohini, KMR 16-3 |
| V | 14 | Shatabdi, Pusa Tarak, B.K. 1008, TPM 1, RH 0119, LET 36, Pusa Vijay, Godavari Ganga, KMR 17-4, KMR 17-1, Aravalli, UJM 23, UJM 16, RGN 145 |
| VI | 3 | UJM 10, KMR 14-1, KMR 16-5 |
| VII | 6 | Sonakshi, KMR 18-1, UJM 20, KMR 19-4, KMR 15-1, KMR 19-6 |

**Table 4.7.2: Estimates of average intra and inter-cluster distances for seven clusters in Indian mustard**

| Clusters no. | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| I | **1.233** | 4.594 | 3.950 | 5.577 | 4.720 | 6.351 | 5.181 |
| II | | **1.640** | 4.497 | 5.223 | 3.970 | 6.074 | 6.664 |
| III | | | **2.469** | 3.635 | 3.368 | 5.487 | 3.957 |
| IV | | | | **2.338** | 3.149 | 3.038 | 3.258 |
| V | | | | | **2.545** | 4.041 | 3.509 |
| VI | | | | | | **1.968** | 3.876 |
| VII | | | | | | | **2.489** |

Bold values represent intra-cluster distances.
Normal values represent inter cluster distances.

**Table 4.7.3: Cluster means for different characters in Indian mustard**

| Cluster no. | Day to 50% flowering | Day to maturity | Plant height (cm) | Number of primary branches/plants | Number of secondary branches/ plants | Length of main raceme (cm) | Number of siliquae on main raceme | Number of seed per siliquae | Test weight (g) | Biological yield / plant (g) | Harvest index (%) | Seed yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 45.83 | 119.50 | 153.85 | 3.70 | 7.82 | 52.75 | 40.70 | 13.58 | 5.22 | 74.26 | 23.06 | 16.81 |
| **II** | 48.33 | 120.50 | 139.48 | 4.77 | 6.10 | 54.43 | 37.57 | 13.47 | 5.60 | 36.07 | 22.64 | 8.13 |
| **III** | 47.20 | 120.80 | 153.38 | 5.17 | 14.61 | 62.29 | 44.76 | 13.12 | 5.37 | 58.80 | 25.17 | 14.82 |
| **VI** | 54.33 | 125.33 | 172.38 | 5.45 | 9.40 | 68.87 | 48.90 | 13.20 | 5.44 | 54.75 | 23.94 | 13.15 |
| **V** | 47.90 | 120.74 | 171.51 | 5.30 | 9.05 | 66.99 | 46.47 | 14.21 | 5.25 | 49.30 | 20.53 | 10.06 |
| **VI** | 58.22 | 125.00 | 183.57 | 5.40 | 5.77 | 67.87 | 47.26 | 14.28 | 4.44 | 51.73 | 24.23 | 12.42 |
| **VII** | 50.00 | 122.94 | 180.41 | 5.21 | 10.88 | 72.91 | 50.65 | 14.84 | 4.98 | 72.47 | 23.55 | 17.11 |

# Chapter V

# SUMMARY AND CONCLUSION

# SUMMARY AND CONCLUSION

The present investigation entitled **"Variability, character association and genetic divergence studies in Indian mustard (*Brassica juncea* L. Czern and Coss.)"** was carried out to assess:

**1.** To study genetic variability for seed yield and its contributing traits,

**2.** to study character association among different characters,

**3.** to find out direct and indirect effects of yield components on seed yield per plant and

**4.** to study the genetic divergence using $D^2$ analysis**.**

The experimental material was consisting of forty divers' genotypes including three checks *viz.,* Maya, BHU RH 0749 and NDR 8501. The present investigation was carried out at Students Instructional Farm of Acharya Narendra Deva University of Agriculture & Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) in the Rabi season of 2020-21 following Randomized Block Design. The experimental field was divided into three replications of equal size, and each treatment were planted in two rows of 3m length with inter and intra row spacing of 45cm and 15cm, respectively and maintained by proper thinning. The border rows were also planted to neutralizer the border effect and to obtain a healthy mustard crop, all cultural practices necessary for a productive harvest were used. and competitive crop stand and observation were recorded on five competitive plants from each replication. Five randomly selected competitive plants from each replication genotype for recording observation for twelve quantitative characters except days to 50% flowering and days to maturity which were recorded on the plot basis. The data were recorded for following characters like plant height (cm), number of primary and secondary branches per plant, length of main raceme (cm), siliquae on main raceme, number of seed per siliquae, 1000-seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g).

Under field condition these strains/ varieties were grown and the experimental data recorded were subjected to appropriate statistical and genetic parameters viz., genetic variability, characters association, path coefficient analysis and genetic divergence. The salient findings of this study are summarized as under:

Analysis of variance revealed considerable significant differences among the genotypes for all the characters viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme, number of siliquas on main raceme, number of seed per siliquae, 1000-seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g) indicating wide spectrum of variation among the genotype. A wide range of variation for different characters and comparison of means of germplasm lines using least significant differences, indicated the existence of very high degree of variability for all the characters in the genotype.

Variability studies suggest that all characters are like days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliquae on main raceme, number of seed per siliquae, 1000-seed weight (g), biological yield per plant (g), harvest index (g) and seed yield per plant (g) to respond direct selection is more effective.

The most desirable genotypes for characters other than seed yield per plant were MGK-112, Shatabdi, LET-36 and PUSA Vijay, Shatabdi for early maturity, KMR15-1 for taller plant height, KMR-17-4, PUSA Vijay for primary branches per plant, PBR 378 for secondary branches per plant, Vaibhav for length of main raceme and numbers of siliquas on main raceme, KMR 18-3 number of seed per siliquas, B.K. 1008 for 1000-seed weight, KMR 19-4 for biological yield per plant and seed yield per plant, Maya for harvest index.

On the basis of mean performance for quantitative traits genotypes KMR 19-4 was identified as best performer for seed yield per plant (g), harvest index (%), 1000-seed weight (%), biological yield per plant (g), number of seed per siliquae, number of siliquae on main raceme, length of main raceme, and primary branches per plant.

The most promising lines showing highest seed yield with high mean performance for other yield contributing characters were identified as Maya and Vaibhav. The above-mentioned genotypes also showed high to very high mean performance for several other yield components.

The highest estimate of (>20%) phenotypic coefficient of variability (32.81%) and genotypic coefficient of variability (31.81%) was observed for number of secondary branches per plant followed by seed yield per plant (g) and biological yield per plant (g). The moderate estimate (10 to 20%) phenotypic and genotypic coefficient of variability were recorded for harvest index (%), number of primary branches per plant, length of main raceme and number of siliquae on main raceme. whereas the low estimate (<10%) phenotypic and genotypic coefficient of variability were observed for plant height (cm), days to 50% flowering, 1000-seed weight (g), number of seed per siliquae and days to maturity.

The seed yield per plant, the most economical traits, was positive significant correlated with biological yield per plant, harvest index (%), number of secondary branches per plant, and number of siliquae on main raceme. The characters would be highly effective and efficient in improving respective traits.

The phenotypic path coefficient analysis showed that biological yield per plant (g) had highest positive direct effect on seed yield per plant (g) followed by harvest index (%), number of primary branches per plant, number of siliquae on main raceme, day to maturity and number of seed per siliquae, while the other character like day to 50% flowering showed highest negative direct effect on seed yield per plant followed by plant height, length of main raceme, 1000-seed weight (g), and number of primary branches per plant, suggesting that an increase or decrease in any one of the other characters may directly contributed to seed yield per plant (g) in any direction.

At genotypic level, the genotypic path coefficient analysis showed that biological yield per plant (g) had highest positive direct effect on seed yield per plant (g) followed by harvest index (%), number of primary branches per plant, number of siliquae on main raceme, day to maturity and number of seed per siliquae. While the other characters like day to 50% flowering exhibited highest negative direct effect on seed yield per plant (g) followed by plant height (cm), length of main raceme, 1000 weight and number of secondary branches per plant.

The non-hierarchical Euclidean cluster analysis forty genotypes were grouped into 7 clusters. This indicated that the existence of high degree of genetic diversity in germplasm evaluated in the present study. In this condition cluster V contained highest number of genotypes (14) followed by clusters IV, VII, III VI, II, and I which had 8,6,5,3,2 and 2 genotypes respectively.

Divergence study suggested that crosses involving genotypes like NDR 8501, BHU RH 0749, PUSA Tarek, PUSA Vijay, Godavari Ganga, and Vaibhav for getting desired segregant from breeding point of view.

The inter-cluster divergence values indicated that the most diverse groups were VII and II (6.664) followed by VI and I (6.351). The minimum inter-cluster values were found between VI and IV (3.038) indicates that this group is less diverse. However, out of seven clusters in intra-cluster, the most diverse groups were V and V (2.545) followed by III and III (2.469). The less diverse intra-cluster values were found between I and I (1.233).

Hence, the above diverse Indian mustard genotypes may be exploited in hybridization programme to increase the production and productivity of mustard crop. However, in recent days, varietal improvement is centered on utilization of limited genotypes in breeding programme.

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# LITERATURE CITED

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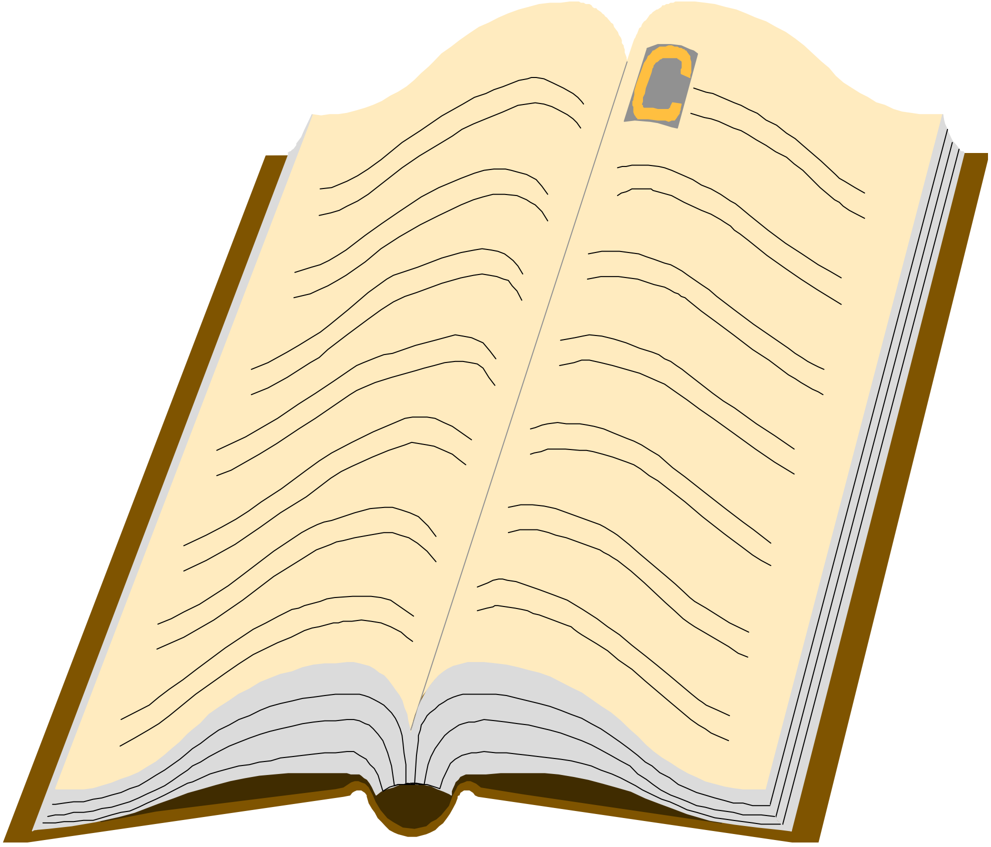

# APPENDICES

# Appendix

## Mean performance

| s.no | Genotypes | Day to 50% flowering | Day to maturity | Plant height (cm) | Number of primary branches/plant | Number of secondary branches/ plant | Length of main raceme (cm) | Number of siliquae on main raceme | Number ofseed per siliquae | Test weight (g) | Biological yield / plant (g) | Harvest index (%) | Seed yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | CS -56 | 46.00 | 119.33 | 153.40 | 5.37 | 10.17 | 56.10 | 44.23 | 14.09 | 5.27 | 59.62 | 27.44 | 16.38 |
| 2 | MGK - 112 | 45.67 | 119.67 | 146.57 | 4.07 | 9.20 | 58.53 | 40.17 | 13.57 | 5.10 | 75.11 | 22.47 | 16.90 |
| 3 | PBR - 378 | 47.33 | 121.00 | 149.17 | 4.23 | 16.90 | 57.87 | 42.80 | 13.70 | 5.27 | 50.40 | 23.92 | 12.06 |
| 4 | NRC-HB-101 | 50.33 | 120.33 | 143.20 | 4.60 | 7.50 | 60.00 | 40.63 | 13.40 | 5.37 | 34.87 | 25.40 | 8.86 |
| 5 | Pusa Mustard -24 | 46.00 | 119.33 | 161.13 | 3.33 | 6.43 | 46.97 | 41.23 | 13.60 | 5.33 | 73.40 | 23.65 | 16.72 |
| 6 | KMR- 18 -3 | 46.33 | 121.33 | 140.83 | 4.53 | 14.47 | 64.80 | 47.67 | 11.87 | 5.53 | 59.85 | 19.92 | 11.96 |
| 7 | Shatabdi | 45.00 | 117.00 | 153.00 | 4.37 | 6.87 | 67.90 | 45.27 | 14.33 | 5.23 | 56.74 | 18.90 | 10.73 |
| 8 | Pusa tarak | 48.00 | 121.33 | 183.03 | 5.03 | 6.23 | 70.73 | 54.63 | 14.33 | 5.80 | 47.63 | 20.67 | 9.88 |
| 9 | PBR - 210 | 48.33 | 121.00 | 156.20 | 5.93 | 16.60 | 59.67 | 42.73 | 14.00 | 5.57 | 66.15 | 24.70 | 16.34 |
| 10 | NDR - 8501 | 53.33 | 123.33 | 174.83 | 4.97 | 11.93 | 65.27 | 46.17 | 13.77 | 5.37 | 53.67 | 27.40 | 14.71 |
| 11 | NRC -DR -601 | 46.33 | 120.67 | 135.77 | 4.93 | 4.70 | 48.87 | 34.50 | 13.53 | 5.83 | 37.27 | 19.88 | 7.41 |
| 12 | Sonakshi | 47.67 | 123.33 | 167.90 | 5.37 | 11.40 | 78.23 | 49.77 | 15.20 | 5.53 | 69.73 | 20.28 | 14.14 |
| 13 | B. K.- 1008 | 48.67 | 123.00 | 169.33 | 4.73 | 12.27 | 67.20 | 41.33 | 15.40 | 5.87 | 65.49 | 18.92 | 12.39 |
| 14 | KMR- 18 -1 | 47.67 | 122.33 | 166.63 | 4.73 | 12.23 | 71.37 | 46.10 | 14.93 | 5.33 | 61.83 | 26.43 | 16.35 |
| 15 | TPM - 1 | 47.00 | 120.33 | 165.13 | 5.73 | 7.57 | 62.03 | 43.13 | 14.00 | 5.53 | 55.35 | 22.94 | 12.70 |
| 16 | RH - 0119 | 46.33 | 118.00 | 171.27 | 4.83 | 9.10 | 64.37 | 45.83 | 14.33 | 4.97 | 49.00 | 21.94 | 10.75 |
| 17 | LET -36 | 45.67 | 120.67 | 167.03 | 5.37 | 11.47 | 72.33 | 44.53 | 14.00 | 5.50 | 59.33 | 20.24 | 12.01 |
| 18 | Pusa Vijay | 45.33 | 118.67 | 177.83 | 6.33 | 11.37 | 68.80 | 46.53 | 13.93 | 4.83 | 46.13 | 18.34 | 8.46 |
| 19 | Godavari Ganga | 48.67 | 120.67 | 185.27 | 6.30 | 10.60 | 66.87 | 44.03 | 14.10 | 5.77 | 33.62 | 23.62 | 7.94 |
| 20 | BHU -RH -0749 | 53.33 | 125.33 | 185.40 | 5.77 | 8.67 | 66.10 | 45.37 | 13.67 | 5.87 | 45.07 | 20.29 | 9.15 |
| 21 | KMR -16 -1 | 55.67 | 127.00 | 160.77 | 5.20 | 8.00 | 60.97 | 46.50 | 13.00 | 5.63 | 43.83 | 24.71 | 10.83 |
| 22 | KMR -17 -4 | 51.33 | 124.00 | 170.73 | 6.33 | 7.67 | 66.50 | 48.67 | 15.33 | 5.57 | 44.50 | 17.91 | 7.96 |
| 23 | KMR -17 -1 | 47.33 | 120.67 | 159.23 | 4.53 | 6.83 | 70.10 | 47.80 | 13.67 | 5.13 | 40.69 | 22.50 | 9.16 |
| 24 | Aravali | 45.67 | 118.67 | 166.90 | 4.97 | 12.70 | 63.67 | 49.00 | 15.27 | 4.67 | 50.57 | 21.50 | 10.88 |
| 25 | UJM -20 | 48.67 | 123.33 | 175.23 | 5.03 | 12.10 | 67.33 | 48.47 | 14.00 | 4.10 | 66.13 | 24.01 | 15.88 |
| 26 | Vaibhav | 53.00 | 125.00 | 163.20 | 5.57 | 6.90 | 81.97 | 60.67 | 12.20 | 5.23 | 65.73 | 26.32 | 17.28 |
| 27 | UJM -23 | 50.67 | 122.67 | 189.20 | 5.13 | 10.70 | 59.83 | 45.00 | 14.43 | 4.47 | 55.88 | 18.25 | 10.20 |
| 28 | UJM - 16 | 48.00 | 122.67 | 183.83 | 5.20 | 6.87 | 65.87 | 51.77 | 12.10 | 4.57 | 42.47 | 20.08 | 8.54 |
| 29 | Urvashi | 54.00 | 126.00 | 162.60 | 5.67 | 11.20 | 66.63 | 44.93 | 13.13 | 5.57 | 69.22 | 24.00 | 16.62 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 30 | Maya | 48.00 | 121.33 | 167.30 | 5.80 | 14.93 | 73.03 | 46.37 | 11.97 | 5.23 | 58.00 | 29.89 | 17.35 |
| 31 | KMR - 19-4 | 51.00 | 123.33 | 178.60 | 5.57 | 11.83 | 69.97 | 54.50 | 15.07 | 5.03 | 86.48 | 28.31 | 24.49 |
| 32 | RH-30 -R -17 -18 | 52.67 | 125.67 | 171.17 | 5.50 | 9.73 | 68.77 | 47.03 | 12.77 | 5.67 | 57.52 | 20.12 | 11.58 |
| 33 | Rohini | 55.33 | 126.00 | 184.90 | 5.87 | 9.40 | 75.73 | 54.63 | 13.20 | 5.00 | 53.93 | 23.94 | 12.91 |
| 34 | KMR -15 -1 | 50.67 | 121.33 | 205.37 | 5.50 | 9.57 | 81.47 | 53.77 | 14.47 | 4.77 | 73.84 | 22.87 | 16.90 |
| 35 | KMR -19 -6 | 54.33 | 124.00 | 188.73 | 5.07 | 8.17 | 69.07 | 51.30 | 15.37 | 5.13 | 76.82 | 19.37 | 14.90 |
| 36 | UJM -10 | 58.33 | 124.33 | 184.03 | 6.17 | 7.60 | 67.07 | 45.33 | 13.77 | 4.13 | 51.73 | 20.97 | 10.85 |
| 37 | KMR -14 -1 | 58.00 | 125.67 | 182.37 | 4.73 | 7.27 | 72.17 | 50.23 | 15.13 | 4.53 | 58.45 | 23.26 | 13.60 |
| 38 | KMR -16 -5 | 58.33 | 125.00 | 184.30 | 5.30 | 2.43 | 64.37 | 46.20 | 13.93 | 4.67 | 45.02 | 28.46 | 12.82 |
| 39 | KMR - 16 -3 | 57.33 | 124.33 | 176.20 | 5.07 | 9.33 | 65.53 | 45.90 | 13.90 | 5.20 | 49.00 | 24.72 | 12.11 |
| 40 | RGN -145 | 53.00 | 122.00 | 159.37 | 5.37 | 6.43 | 71.60 | 43.00 | 13.70 | 5.53 | 42.83 | 21.61 | 9.25 |
| | Mean | **50.11** | **122.24** | **169.17** | **5.20** | **9.63** | **66.39** | **46.69** | **13.90** | **5.22** | **55.82** | **22.75** | **12.75** |
| | Max | 45.00 | 117.00 | 135.77 | 3.33 | 2.43 | 46.97 | 34.50 | 11.87 | 4.10 | 33.62 | 17.91 | 7.41 |
| | Min | 58.33 | 127.00 | 205.37 | 6.33 | 16.90 | 81.97 | 60.67 | 15.40 | 5.87 | 86.48 | 29.89 | 24.49 |
| | SE(d) | 0.77 | 0.98 | 2.34 | 0.38 | 0.63 | 1.41 | 0.88 | 0.22 | 0.06 | 1.42 | 0.59 | 0.52 |
| | C.D. at 5% | 1.53 | 1.96 | 4.68 | 0.76 | 1.26 | 2.81 | 1.76 | 0.44 | 0.12 | 2.84 | 1.18 | 1.04 |
| | C.V. (%) | 1.87 | 0.99 | 1.70 | 8.98 | 8.06 | 2.59 | 2.32 | 1.95 | 1.36 | 3.12 | 3.17 | 5.02 |

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# ABSTRACT

The present investigation entitled **"Variability, characters association and genetic divergence studies in Indian mustard (*Brassica juncea* L. Czern and Coss.)"** involving 40 genotypes was undertaken to examine the (i) variability for seed yield and its contributing traits, (ii) character association among different characters, (iii) direct and indirect effects of yield components on seed yield per plant and (iv) genetic divergence using $D^2$ analysis in the Indian mustard genotypes. The experiment was conducted at Students Instructional Research Farm at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during rabi, 2020-21. All the 40 Indian mustard genotypes were tested in Randomized Block Design with three replications. Observations were recorded on 12 quantitative characters namely, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliquae on main raceme, number of seeds per siliqua, 1000-seed weight (g), harvest index (%) and seed yield per plant (g). Analysis of variance observed substantial amount of variability among the genotypes for all the characters, under study, found wide spectrum of variability among the genotypes. Phenotypic correlation was of higher magnitude as compare to their corresponding genotypic correlation. Among genotypes correlation the seed yield was having positively and significantly correlated with biological yield per plant (0.870) followed by harvest index (0.609), number of secondary branches per plant (0.342) and number of siliquae on main raceme. While positive non-significant correlation with days to maturity (0.132) followed by number of seed per siliquae (0.066) plant height (0.052) and days to 50% flowering (0.046). As a result, any selection based on these characters will increase the performance and quality of Indian mustard. Path coefficient analysis showed that biological yield per plant, harvest index, number of primary branches per plant, number of siliquae on main raceme, days to maturity and number seed per siliquae were the most important character, controlling positive directly to seed yield. Mahalnobis $D^2$ genetic divergence the non-hierarchical Euclidean cluster analysis grouped 40 genotypes into 7 clusters. These indicated the existence of high degree of genetic diversity in the germplasm. The highest number of genotypes appeared in cluster V which contained 14 genotypes followed by cluster IV, VII, III, VI, II, and I which contained 8,6,5,3,2, and 2 genotypes respectively. The inter-cluster divergence values indicated that the most diverse groups were VII and II (6.664) followed by VI and I (6.351). The minimum inter-cluster values were found between VI and IV (3.038) indicates that this group is less diverse. However, out of seven cluster in intra-cluster, the most diverse groups were V and V (2.545) followed by III and III (2.469). The less diverse intra-cluster values were found between I and I (1.233). Hence, the above diverse Indian mustard genotype may be exploited in hybridization programme for getting desired segregants from breeding point of view, and to increase the production and productivity of this crop.

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**मेजर:** आनुवंशिकी और पादप प्रजनन **विभाग:** आनुवंशिकी और पादप प्रजनन
**माइनर:** जैव प्रौद्योगिकी
**थीसिस शीर्षक:** "भारतीय सरसों में परिवर्तनशीलता, चरित्र संघ और आनुवंशिक विचलन अध्ययन (ब्रैसिका जंसिया एल. सीजर्न एंड कॉस।)"
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## सारांश

40 जीनोटाइप वाले भारतीय सरसों में परिवर्तनशीलता, चरित्र संघ और आनुवंशिक विचलन अध्ययन (ब्रैसिका जंसिया एल. सीजर्न एंड कॉस।)" शीर्षक वाली वर्तमान जांच (i) बीज उपज और इसके योगदान लक्षणों के लिए परिवर्तनशीलता की जांच करने के लिए की गई थी, (ii) विभिन्न लक्षणों के बीच चरित्र संबंध, (iii) प्रति पौधे बीज उपज पर उपज घटकों के प्रत्यक्ष और अप्रत्यक्ष प्रभाव और (iv) भारतीय सरसों के जीनोटाइप में डी$^2$ विश्लेषण का उपयोग करके आनुवंशिक विचलन प्रयोग आचार्य नरेंद्र देव कृषि और प्रौद्योगिकी विश्वविद्यालय, कुमारगंज, अयोध्या (यू.पी.) में रबी, 2020-21 के दौरान छात्र निर्देशात्मक अनुसंधान फार्म में आयोजित किया गया था। सभी ४० भारतीय सरसों के जीनोटाइप का तीन प्रतिकृतियों के साथ यादृच्छिक ब्लॉक डिजाइन में परीक्षण किया गया था। प्रेक्षणों को 12 मात्रात्मक लक्षणों पर दर्ज किया गया था, जैसे दिन से 50% फूल, परिपक्वता के दिन, पौधे की ऊंचाई (सेमी), प्रति पौधे प्राथमिक शाखाओं की संख्या, प्रति पौधे माध्यमिक शाखाओं की संख्या, मुख्य दौड़ की लंबाई (सेमी), फली की संख्या मुख्य पुष्प-गुच्छ पर, प्रति फली बीजों की संख्या, 1000-बीज भार (g), फसल सूचकांक (%) और प्रति पौधा बीज उपज (g)। विचरण के विश्लेषण में सभी वर्णों के जीनोटाइप के बीच पर्याप्त मात्रा में परिवर्तनशीलता देखी गई, अध्ययन के तहत, जीनोटाइप के बीच परिवर्तनशीलता का व्यापक वर्णक्रम पाया गया। फिनोटिपिक सहसंबंध उनके संबंधित जीनोटिपिक सहसंबंध की तुलना में उच्च परिमाण का था। जीनोटाइप सहसंबंध के बीच बीज की उपज प्रति पौधे जैविक उपज (0.870) के साथ सकारात्मक और महत्वपूर्ण रूप से सहसंबद्ध थी, इसके बाद फसल सूचकांक (0.609), प्रति पौधे माध्यमिक शाखाओं की संख्या (0.342) और मुख्य पुष्प-गुच्छ पर फली की संख्या थी। जबकि परिपक्वता के दिनों (0.132) के साथ सकारात्मक गैर-महत्वपूर्ण सहसंबंध, इसके बाद बीज की संख्या प्रति फली (0.066) पौधे की ऊंचाई (0.052) और दिनों से 50% फूल (0.046) तक। नतीजतन, इन पात्रों के आधार पर किसी भी चयन से भारतीय सरसों के प्रदर्शन और गुणवत्ता में वृद्धि होगी। पथ गुणांक विश्लेषण से पता चला है कि प्रति पौधा जैविक उपज, फसल सूचकांक, प्रति पौधे प्राथमिक शाखाओं की संख्या, मुख्य नस्ल पर फलियो की संख्या, परिपक्वता के दिन और प्रति फली बीज संख्या सबसे महत्वपूर्ण चरित्र थे, जो सीधे बीज उपज को सकारात्मक नियंत्रित करते थे। महलनोबिस डी$^2$ आनुवंशिक विचलन गैर-पदानुक्रमित यूक्लिडियन क्लस्टर विश्लेषण ने 40 जीनोटाइप को 7 समूहों में समूहीकृत किया। ये जर्मप्लाज्म में उच्च स्तर की आनुवंशिक विविधता के अस्तित्व का संकेत देते हैं। क्लस्टर पांच में सबसे अधिक जीनोटाइप दिखाई दिए, जिसमें 14 जीनोटाइप थे, उसके बाद क्लस्टर चार, सात, तीन, छह, दो और एक थे, जिसमें क्रमशः 8,6,5,3,2 और 2 जीनोटाइप थे। अंतर-क्लस्टर विचलन मूल्यों ने संकेत दिया कि सबसे विविध समूह सात और दो (6.664) और उसके बाद छह और एक (6.351) थे। छह और चार (3.038) के बीच न्यूनतम अंतर-क्लस्टर मान पाए गए, यह दर्शाता है कि यह समूह कम विविध है। हालांकि, इंट्रा-क्लस्टर में सात

क्लस्टर में से, सबसे विविध समूह पांच और पांच (2.545) थे, जिसके बाद तीन और तीन (2.469) थे। एक और एक (1.233) के बीच कम विविध इंट्रा-क्लस्टर मान पाए गए। इसलिए, उपरोक्त विविध भारतीय सरसों के जीनोटाइप का उपयोग संकरण कार्यक्रम में प्रजनन के दृष्टिकोण से वांछित अलगाव प्राप्त करने और इस फसल के उत्पादन और उत्पादकता को बढ़ाने के लिए किया जा सकता है।

(O. P. Verma)
Chairman

(ओ. पी. वर्मा)
**सलाहकार**

अमरजीत पटेल

(अमरजीत पटेल)
**लेखक**

# PERSONAL PROFILE

**Name** : **Amarjeet Patel**

**Father's Name** : Devnarayan Patel

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**Marital Status** : Unmarried

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**Academic Credentials**

| **Class** | **Board / Univ.** | **Subject** | **Year** | **Division** | **Percentage** |
|---|---|---|---|---|---|
| High School | U. P. Board | Science | 2012 | First | 82.5 |
| Intermediate | U. P. Board | Agriculture | 2014 | First | 79.0 |
| B.Sc. (Ag.) | Udai Pratap College, Varanasi, U.P. | Agriculture | 2019 | First | 74.0 |
| M.Sc. (Ag.) | A.N.D.U.A & T. Kumarganj, Ayodhya, U.P. | Genetics and Plant Breeding | 2021 | (Appearing) | - |

**Scholarship/ Fellowship / Research Experience and Extra Curricular Activities**

## DECLARATION

*I hereby declare that all the information furnished above is true to the best of my knowledge & belief; documentary evidences will support them as and when required.*

Amarjeet

**Date:** 30/08/2021
**Place:** A.N.D.U.A & T, Kumarganj, Ayodhya.

***(Amarjeet Patel)***