GENETIC ANALYSIS OF YIELD TRAITS IN INDIAN MUSTARD [*Brassica juncea* (L.) Czern. & Coss.]

by
Lalita Kumari
J-21-M-826

A thesis submitted to
Faculty of Agriculture
in partial fulfillment of requirements
for the degree of

MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)

Division of Plant Breeding and Genetics
Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu,
Main Campus, Chatha, Jammu 180009

2023

CERTIFICATE - I

This is to certify that the thesis entitled **"Genetic analysis of yield traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]"** submitted in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture (Genetics and Plant Breeding)** to the Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, is original work and has similarities with published work not more than minor similarities as per UGC norms of 2018 adopted by the University. Further, the level of minor similarities has been declared after checking the manuscript with **URKUND** software provided by the University.

The work has been carried out by **Ms. Lalita Kumari**, under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma. It is further certified that help and assistance received during the course of thesis investigation have been duly acknowledged.

Sunil Kumar Rai

Dr. S.K. Rai
Associate Professor cum Senior Scientist, PBG
(Major Advisor)

Place: Jammu
Date: 25-08-23

Lalita Kumari 25/8/2023

Head of the Division

Dean, FoA
SKUAST-J
Chatha

CERTIFICATE-II

We, the members of Advisory committee of **Ms. Lalita Kumari,** Registration No. **J-21-M-826**, a candidate for the degree of **Master of Science in Agriculture (Genetics and Plant Breeding)**, have gone through the manuscript of thesis entitled **"Genetic analysis of yield traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]"** and recommend that it may be submitted by the student in partial fulfillment of the requirements for the degree.

Dr. S.K. Rai
Associate Professor cum Senior Scientist
Major Advisor &
Chairman Advisory Committee

Place: Jammu
Date: 25-08-23

Advisory Committee Members

1. Dr. Bupesh Kumar
   Associate Professor
   Division of PBG

   25/08/2023

2. Dr. A.K. Singh
   Professor
   School of Biotechnology

3. Dr. Sanjeev Kumar
   Associate Professor
   Division of Vegetable Science
   (Dean's Nominee)

CERTIFICATE-III

This is to certify that the thesis entitled "**Genetic analysis of yield traits in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]**" submitted by **Ms. Lalita Kumari**, Registration No. **J-21-M-826**, to the Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture (Genetics and Plant Breeding)**, was examined and approved by the advisory committee and external examiner on **12-10-2023**.

External Examiner

Dr. S.K. Gupta
Ex. Prof. & Head (PBG)
Director Edu. SKUAST- Jammu

Dr. S.K. Rai
Associate Professor cum Senior Scientist
(Major Advisor)

Head
Division of Plant Breeding and Genetics

Dean
Faculty of Agriculture
SKUAST-Jammu

ACKNOWLEDGEMENTS

All praise for the, "ALMIGHTY GOD" who is the only supreme Authority. Every tiny or massive entity moves with His permission. Countless thanks to Him for accrediting me to accomplish this important task with in this specified time. In view of his saying: "He who does not thank to people is not thankful to GOD"

I am highly obliged in paying deepest gratitude to ***Dr. S.K. Rai, Associate Professor cum Senior Scientist (Plant breeding and Genetics)*** *and Major Advisor, for his constant inspiration, encouragement and guidance throughout my research work. I consider myself fortunate enough that he has given a decisive turn and boost to my career, and helped me to my best potential, and remained a belief in me that I could successfully achieve this milestone. I could not have imagined having a better advisor for my P.G study.*

Besides my advisor, I would like to extend my deepest gratitude to ***Dr. Tuhina Dey (Professor and Head, Division of Plant breeding and Genetics)*** *and members of my Advisory Committee,* ***Dr. Bupesh Kumar (Associate Professor, Division of Plant breeding and Genetics); Dr. A.K. Singh (Professor, School of Biotechnology)*** *for their insight comments and encouragement, and long discussions that helped me sort out the technical details of my work but also for their hard question which incented me to widen my research from various perspectives.*

I most great fully acknowledge my indebtedness to, ***Dr. Sanjeev Kumar (Associate Professor, Division of Vegetable Science) and Dean's Nominee*** *for their scholarly, scientific discussions and generous advices when needed and helping me to understand and enrich my ideas during the entire period of my research work. I will also express my sincere thanks to faculty members of Division of Plant breeding and Genetics,* ***Dr. R.S. Sudan, Dr. Praveen Singh, Dr. S.C. Kashyap and Dr. Sanjeev Kumar*** *for their kind assistance, support, and motivation all throughout the entire study. I am also grateful to* ***Dr. V.B. Singh, Dr. Rajan Slalia, and Dr. M.K. Pandey*** *for their guidance whereever possible.*

I shall fail in my duty, if I don't thank the non-teaching staff of my department ***Mr. Naresh Choudhary, Mr. Rahul, Mr. Parveen, Mr. Darshan, Mr. Latif, Mr. Vijay and Mr. Zakir*** *for their help and assistance during the present study.*

The Words are inadequate to express my heartful thanks to my collegues, juniors and seniors ***Mr. K. Priyatham, Mr. Shivam Raina, Mr. Danish Mushtaq, Mrs. Surbhi Kohli, Ms. Shruhti K., Ms. Ragini Padha, Ms. Sehroz Sharif, Ms. Binnat ul Mukhtar, Ms. Mahapara Bashir, Mr. Malik Mehraj u Din, Mr. Rahul Saini, Ms. Divya Sharma.***

It Is with my personal touch and emotions that I aeize this opportunity to express my heartfelt and affectionate gratitude to my parents and family members who were always been in my heart and thought. I am greatfully indebted to my beloved godly parents ***Sh. Bishan lal*** *and* ***Smt. Kanta Bhagat****, who always been an ideal and touch bearer to me. The eternal blessings, affection and love of my brothers* ***Pankaj Kumar and Dheeraj Kumar***

None is forgotten but everyone is not included

Date: 21-11-23

Place :- Jammu

Lalita

Lalita Kumari

ABSTRACT

Title of the thesis	:	**Genetic analysis of yield traits in Indian mustard [*Brassica juncea* (L.) Czern. &Coss.]**
Name of the student	:	Lalita Kumari
Registration No.	:	J-21-M-826
Major Subject	:	Genetics and Plant Breeding
Name and Designation of Major Advisor	:	Dr. S.K. Rai, Associate Professor cum Senior scientist (Division of Plant Breeding and Genetics)
Degree to be awarded		Master of Science in Genetics and Plant Breeding
Year of award of Degree		2023
Name of the University		Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu

ABSTRACT

The study titled "Genetic analysis of yield traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]" was conducted during the *Rabi* seasons of 2021-22 and 2022-23 at the experimental farm of the division of Plant Breeding and Genetics, as well as the molecular laboratory of the division of Plant Breeding and Genetics at SKUAST, Jammu. Analysis of variance revealed significant differences among the 40 advanced breeding lines/ genotypes across two seasons for all studied traits. Highest GCV and PCV, high heritability and genetic advance as percentage of mean was recorded for seed yield per plant and number of secondary branches per plant in both the seasons. Highest divergence occurred between cluster IV (DRMR-4005, Kranti & RH-1209) and cluster V (PM-195) followed by cluster II (PM-125) and IV (DRMR-4005, Kranti & RH-1209). Seed yield per plant contributed maximum to the diversity followed by main shoot length and siliqua length. The genotypes under study were also characterized for genetic diversity with the help of 10 SSR markers. Among them, 4 were polymorphic, with the PIC value ranging from 0.44 - 0.75. The Jaccard's similarity coefficient also diversified the genotypes into 5 clusters with cluster II carrying only two genotypes i.e., RSPR-01 and RH-406. The examination of both morphological and molecular aspects has unveiled a noteworthy extent of genetic diversity within advanced breeding lines/ genotypes which can be used as parents in further breeding programmes.

Keywords: Indian mustard, D^2, divergence, molecular characterization, SSR, polymorphic.

Signature of Major Advisor

Signature of the Student

LIST OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

ABBREVIATIONS

Abbreviation		Terminology
%	:	Percentage
*	:	Significant at 5% level
**	:	Significant at 1% level
µl	:	Micro litre
µM	:	Micro molar
^{0}C	:	Degree Celsius
^{0}N	:	Degree North
ANOVA	:	Analysis of variance
bp	:	Base pair
cm	:	Centimetre
CV	:	Coefficient of variation
d.f	:	Degree of freedom
dd	:	Double distilled
DNA	:	Deoxyribonucleic acid
EDTA	:	Ethylene Diamine Tetra Acetic Acid
et al.	:	Et alia meaning ‘and others’
F	:	Filial
fig.	:	Figure
g	:	Gram
GAM	:	Genetic Advance as per cent of mean
GCV	:	Genotypic coefficient of variation
$h^2_{(bs)}$	:	Broad sense heritability
ha	:	Hectare
HI	:	Harvest index
Hr	:	Hour
Kg	:	Kilo gram

M	:	Molar
m^2	:	Meter square
mA	:	Milli ampere
MAS	:	Marker Assisted Selection
mg	:	Milli gram
Min.	:	Minute
ml	:	Millilitre
PCV	:	Phenotypic coefficient of variation
PH	:	Plant height
Rnase	:	Ribonuclease Enzyme
S.No.	:	Serial number
S1	:	Season first
S2	:	Season second

CHAPTER 1

INTRODUCTION

India stands as the largest agrarian subcontinent, supporting 26 percent of the world's agricultural population with only 12 percent of arable land. It also ranks as the fifth-largest vegetable oil economy, contributing 7.4 percent to oilseed production, 5.8 percent to oil production, and 6.1 percent to oil meal production. Furthermore, it accounts for 9.3 percent of global edible oil consumption. Oilseeds, a crucial sector in India's agricultural economy, follow cereals in significance, having grown at a consistent rate of 4.1 percent annually over the past three decades. Notably, oilseed brassica encompasses 23.5 percent of the country's oilseed-growing area and contributes 24.2 percent to its overall oilseed production. Globally, the estimated metrics for rapeseed-mustard cultivation comprise 41.95 million hectares of land, 88.35 million tonnes of production, and a yield of 2110 kg/ha. Despite being the world's third-largest oilseed brassica producer (11.3 percent), after Canada and China, India relies on imports to satisfy 57 percent of its domestic edible oil demands, securing its place as the seventh-largest global importer of edible oils. Within India, rapeseed-mustard is cultivated across 7.99 million hectares, yielding 11.96 million tonnes, with a productivity rate of 1497 kg/ha. In the region of Jammu and Kashmir, it spans 140 thousand hectares, yielding 1120 thousand quintals, and achieving a productivity rate of 800 kg/ha (Anonymous 2021-22).

Brassica juncea, denoted as AA BB (with a chromosome count of n=18), is an amphidiploid member of the Brassicaceae family resulting from the hybridization of Brassica nigra (BB, n=8) and Brassica campestris (AA, n=10). Commonly known as Indian mustard, this upright plant features fibrous roots and reaches heights of 90 to 200 cm. Its actinomorphic, bisexual, and fully whorled yellow flowers are predominantly self-pollinated, although a surge in honey bee populations has led to cross-pollination levels of five to thirty percent. The plant yields siliquae as fruits, while its inflorescence adopts an elongated raceme form, marked by immature flowers at the apex and an infinitely developing axis. The leaves exhibit a combination of glabrous and hairy textures. Mustard is widely cultivated across most Indian states, with Rajasthan, Uttar Pradesh, Haryana, Madhya Pradesh, and Gujarat standing out as pivotal contributors, collectively responsible for over 80 percent of the nation's land usage and yield. Renowned for its therapeutic attributes, Brassica is a rich source of vitamins, minerals, soluble fiber, and vitamin C. In Northern India, its oil finds application in frying, cooking, pickles, and chutneys, alongside medicinal uses, particularly in Ayurveda. The plant serves as

an alternate feed crop and fodder, adaptable to various climates and soils, boasting high dry matter digestibility (85-95 percent). Its nutrient density makes it an excellent option for grazing, generating substantial biomass, weed control, and soil improvement through its root system, while also offering winter soil cover to prevent erosion. The industrial utility of Brassica includes soap production, grease, and lubricant formulations for diverse equipment. The tender leaves of young plants, known as "sag," are consumed as nutrient-rich greens, providing sulfur and other essential elements for diets.

Yield is a critical agronomic trait that directly impacts crop productivity and economic viability. In Indian mustard, yield traits encompass a range of characteristics, including seed yield per plant, seed weight, pod length, plant height, flowering time, and branching patterns. Understanding the genetic basis and regulatory mechanisms governing these traits is fundamental to developing high-yielding and resilient cultivars. This research endeavors to unravel the intricacies of yield-related traits in Indian mustard through the integration of morphological and molecular analysis. Morphological analysis involves the observation and measurement of morphological traits, while molecular analysis explores the underlying genetic and molecular mechanisms that govern these traits. This combined approach offers a holistic understanding of the genetic diversity and regulatory pathways influencing yield, laying the foundation for targeted breeding and crop improvement strategies.

Morphological analysis involves the detailed observation and quantification of visible plant traits at various growth stages. Researchers carefully assess the phenotypic variation of yield-related traits in diverse Indian mustard germplasm, representing different ecotypes, landraces, and improved cultivars. By comparing and contrasting these variations, breeders gain insights into the genetic diversity present within the crop. Through morphological analysis, researchers identify the traits most strongly correlated with higher yield and adaptability to specific environments. These observations serve as valuable indicators for selecting superior genotypes and directing breeding efforts towards developing cultivars with desired characteristics.

On the other hand, molecular analysis complements morphological studies by delving into the genetic and molecular mechanisms underlying yield traits in Indian mustard. Through molecular analysis, researchers aim to decipher the genetic mechanisms responsible for important yield traits such as seed yield, oil content, flowering time, and resistance to biotic and abiotic stresses. This analysis involves the examination of specific genes and their

expression patterns, as well as the identification of genetic markers associated with desirable traits. By understanding the molecular basis of yield traits, researchers can unravel the underlying genetic diversity in Indian mustard populations, leading to the development of robust breeding approaches for enhancing crop productivity and resilience. This not only ensures a sustainable supply of mustard-based products but also contributes to food security and economic prosperity for farmers and stakeholders in the agricultural sector.

Combining morphological and molecular data constitutes a potent approach for deciphering the intricate genetic makeup underlying yield traits. By linking specific genetic markers with observable phenotypes, researchers can elucidate the underlying genetic networks and signaling pathways regulating yield-related traits. Integrative approaches provide a comprehensive view of how genetic variations influence yield, enabling breeders to make more informed decisions during the selection and breeding process. Moreover, understanding the molecular basis of yield traits facilitates the development of diagnostic molecular tools for marker-assisted selection (MAS) and gene editing techniques, accelerating crop improvement efforts. The outcomes of this integrated analysis have profound implications for the advancement of Indian mustard agriculture. The identification of genetic markers associated with high yield and stress tolerance can significantly expedite the breeding of improved cultivars tailored to specific agro-climatic conditions. Additionally, the development of genetically enhanced cultivars can bolster food security, promote sustainable agriculture, and alleviate the environmental impact of crop production.

The knowledge gained from this research extends beyond Indian mustard and holds value for other economically important crops within the Brassicaceae family, including rapeseed, cabbage, and cauliflower. By understanding the genetic underpinnings of yield traits in Indian mustard, researchers can transfer this knowledge to improve other related crops, further contributing to global food security.

In conclusion, the integrated approach of morphological and molecular analysis of crop productivity characteristics in Indian mustard represents a vital avenue for crop improvement and sustainable agricultural development. This research aims to unlock the genetic secrets behind yield performance, empowering breeders to create cultivars that exhibit elevated yields with enhanced resilience and nutritional value. Ultimately, the findings of this study have far-reaching implications for addressing food security challenges and fostering a more sustainable future for agriculture.

Considering the diverse factors mentioned earlier, following are the objectives of this study:

- To estimate genetic variation components among advanced breeding lines.
- To study polymorphism using molecular markers.

CHAPTER 2

REVIEW OF LITERATURE

This present investigation entitled **"Genetic analysis of yield traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]"**, was conducted to estimate components of genetic variation and to study the genetic polymorphism using molecular markers. Related and useful literature available on the above title highlights various aspects and methods of crop improvement through genetic analysis both at molecular and morphological level are here as under:

Morphological Characterization

Ahmad *et al.* (2009), conducted a study for examination of thirty Indian mustard genotypes resulted in their classification into seven distinct clusters. Notably, the highest value within clusters surfaced in cluster II, closely trailed by cluster VI. Regarding inter-cluster differences, the greatest D^2 value was observed between cluster III and IV, followed by the comparison between clusters III and II. Analyzing cluster means across 16 characteristics, cluster III exhibited the highest mean values for nine traits. However, the utmost mean values for total leaves per plant, harvest index, and plant height were documented in clusters VII, II, and V, respectively.

Doddabhimappa *et al*. (2010) employed D^2 statistics across two distinct conditions, resulting in the classification of these genotypes into seven clusters. Strikingly, the distribution of genotypes across clusters remained consistent between the two conditions. The study's findings underscored that clusters demonstrating elevated mean values for a majority of the favorable traits in both conditions present potential targets for crossbreeding, aiming to harness heterosis effects.

Singh *et al*. (2010) conducted an evaluation that resulted in the identification of eight distinct clusters. Among these, clusters V and VIII emerged as notably divergent, showcasing elevated seed yield performance, as well as significant contributions from associated traits and a high oil content. The potential for obtaining superior segregants and promising recombinants is anticipated to be heightened through the incorporation of genotypes from these clusters within hybridization initiatives.

Yadava *et al*. (2011) scrutinized thirty established Indian mustard varieties. Through an analysis of variance encompassing 14 quantitative traits, along with a comprehensive evaluation across various environments, the study highlighted traits with both substantial heritability and noteworthy genetic advancement, specifically emphasizing the significance of 1000-seed weight as a viable parameter for indirect selection to enhance seed yield.

Kumar *et al*. (2013) highlighted significant findings related to Indian mustard. Notably, they identified a considerable contribution from the additive genetic component, particularly evident in traits like main shoot length, siliquae on the main raceme, siliqua length, as well as palmitic, oleic, and linolenic acid levels, all exhibiting pronounced variation ranges. The study underscored the combination of high heritability and substantial genetic advancement under selection, specifically noting the potential for leveraging these attributes in early segregating generations to enhance both yield and quality of Indian mustard. Of the eight clusters analyzed, clusters VII and VIII demonstrated the maximum divergence, presenting mono-genotype clusters. The authors suggested that this divergence could be harnessed through inter-varietal hybridization to capitalize on the substantial genetic diversity present between these clusters.

Lodhi *et al*. conducted an assessment of the genetic variability within a collection of ninety Indian mustard genotypes, focusing on fifteen distinct traits. This investigation facilitated the classification of all these genotypes into a total of nine discrete clusters. Noteworthy among these was cluster I, comprising the largest number at 20 genotypes, succeeded by cluster II with 18 genotypes, and cluster III with 15 genotypes. Moreover, clusters IV, V, VI, VII, VIII, and IX accommodated 10, 8, 7, 7, 3, and 2 genotypes respectively. Notably, cluster V exhibited the most pronounced intra-cluster distance of 5.69, while the highest inter-cluster distance was observed between clusters VIII and IX, measuring 9.76.

Singh *et al*. (2013) brought to light significant genetic variation within a collection of fifty Indian mustard genotypes. The examination of both the GCV and PCV indicated greater values for traits such as the secondary branches/plant and the yield of seeds per plant, across different environments. Furthermore, noteworthy heritability was identified in both environments for traits encompassing days to first flowering, siliqua length, and the yield of seeds per plant. High genetic advance values were observed for characteristics including plant height, number of siliquae on the main shoot, and seed yield per plant, consistently across both environments. Notably, the GAM was prominent for traits like yield of seeds per plant, 1000-seed weight, the secondary branches in a plant, and siliqua length.

Iqbal *et al.* (2014) undertook research to determine the genetic variability and diversity among different mustard genotypes. Analysis of variance demonstrated significant variations for all the traits examined among the genotypes. Further, genotypes were grouped into four clusters. The cluster III had higher intra cluster distance and the highest inter-cluster distance was noted between genotypes belonging to clusters I and IV, followed by clusters III and IV.

Shekhawat *et al*. (2014) unveiled their findings in 60 Indian mustard genotypes. The most extensive inter-cluster distance (D2) was discerned between clusters VI and VII, registering at 824.53, while it was low between clusters XII and II, recording 99.24. Cluster VIII demonstrated favorable attributes concerning days to 50 percent flowering, days to maturity, and the length of the main branch. In contrast, cluster VII exhibited peak values for both the number of primary branches and the number of siliquae in a plant. For noteworthy traits such as test weight and plant height, cluster IX emerged as the most favorable cluster.

Hasan *et al.* (2015) investigated different accessions of *Brassica juncea*. Ten genotypes of *Brassica juncea* were sown to evaluate the components of variability (genotypic and phenotypic), heritability ($h^2_{B.S}$). High heritability ($h^2_{B.S}$) was calculated for seeds plant^{-1} and plant height. Maximum Genotypic and Phenotypic Coefficient of Variation for silique plant-1 (21.60 and 23.32 percent) respectively.

Bibi *et al.* (2016) studied eight quantitative parameters of *Brassica juncea*. All the characters studied were significantly different which illustrated significant variation. The high heritability in conjunction with substantial genetic advance was noted in plant height, siliqua length and yield of seeds which gave the evidence that the traits were under the control of additive gene action which would be more valuable in predicting the gain under selection than heritability alone, while others exhibited variable trends.

Singh et al. (2016) collected 33 genotypes of Indian mustard and found that seed yield, 1000 seed weight, number of secondary branches, number of seeds per siliqua, number of primary branches, plant height, siliqua length, and number of siliquae on the main raceme were the maximum contributors to genetic diversity among the genotypes. The genotypes from cluster V had short stature, earliest days to 50 percent flowering and maturity, while cluster VIII had the highest siliqua length, 1000 seed weight, number of seeds per siliqua, and seed yield (kg/ha), along with high values for number of primary and secondary branches, main raceme length, and oil content. Clusters V and VIII were among the most divergent clusters and could be further used in hybridization programs.

Uzair *et al.* (2016) conducted an experiment in *Brassica juncea* genotypes with ten genotypes and eight quantitative parameters were observed. Extremely substantial changes remained taken in all characters which demonstrated substantial difference. High heritability coupled with substantial genetic progress was observed in traits such as plant height, siliqua length, and seed yield. While days taken to flowering, days taken to maturity, number of branches per plant, number of seeds per siliqua and 1000 seed weight revealed capricious trends.

Verma *et al*. (2016) evaluated eighty advanced progenies varieties of mustard. Analysis of variance indicated significant variability among progenies for all the characters studied except primary branches in a plant. Magnitude of high GCV and PCV (>30 percent) were observed for seed yield per plant, harvest index and water use efficiency. The magnitude of moderate heritability was (>50 percent) observed in each characters studied. The genetic advance ranged from 88.0 percent (water use efficiency) to 6.1 percent (low oil content).

Devi *et al*. (2017) executed an experiment involving 45 Indian mustard genotypes, during which data was meticulously collected across 14 distinct agro-morphological traits. Subsequent Analysis of Variance unveiled marked distinctions among the study material. The varieties were effectively categorized into seven distinct clusters, with cluster I accommodating the highest number of genotypes, closely followed by cluster III. Notably, cluster IV displayed the greatest intra-cluster distance, with cluster VI coming next (measuring 844.27), while the most extensive inter-cluster distance was observed between cluster V and VII, registering at a substantial 7273.53.

Kumar *et al.* (2017) assessed in 41 lines of Indian mustard for genetic divergence. Nine characters were taken which enabled grouping of all the genotypes into seven clusters. Cluster means for different clusters and inter cluster distances were used to judge the importance of different clusters in the improvement programme.

Tiwari *et al*. (2017), found higher heritability combined with elevated genetic advancement is observed among different genotypes concerning Traits such as the number of primary branches, secondary branches, siliquae per plant, seeds per siliqua, harvest index, and 1000-seed weight. This implies that these characteristics are less affected by environmental factors because of the influence of additive gene mechanisms in their manifestation, ultimately rendering the selection process more effective.

Kumar *et al*. (2018) investigated the genetic diversity pattern in thirty-one genotypes of Indian mustard, for fifteen morphological traits in two consecutive years. Genotypes were classified into four major groups ranging from 28 genotypes in Cluster I, while cluster II, III and IV had one genotype each. The intra- cluster distance was comparable for cluster I, while for clusters II, III and IV, intra cluster distance was zero. The highest inter-cluster distance was observed between clusters II and III, with the second most distinct clusters being III and IV. Among the traits, 1000- seed weight paid maximum to genetic divergence followed by days to flower initiation and siliqua length.

Maurya *et al*. (2018) conducted a comprehensive experiment aimed at evaluating the genetic variability present among fifty genotypic accessions of Indian mustard. Through meticulous analysis of variance, the study highlighted remarkably significant disparities across all assessed traits. This observation indicates that PCV exceeded the GCV, although this distinction was relatively modest. Notably, heightened GCV values emerged for traits encompassing 1000-seed weight, biological yield, secondary branches, and seed yield. The study further identified traits displaying elevated heritability coupled with notable genetic advance as a percentage of the mean, along with substantial GCV, totaling six characteristics. This observation underlined that heritability primarily stems from additive gene effects, suggesting the potential efficacy of selection strategies and the prospect of predicting gains under selection.

Prasad *et al*. (2018) evaluated 38 Indian mustard genotypes and records were made regarding 16 characters. The GCV, heritability, GAM was high for secondary branches per plant, racemes per plant, economical yield, biological yield, harvest index, seed yield and oil yield. The traits, plant height, secondary branches per plant, racemes per plant, siliqua length, test weight, economical yield, biological yield, seed yield and oil yield registered high heritability indicating less influence of the environment and possibility of rapid improvement.

Rout *et al.* (2018) tested for thirty eighty genotypes of Indian mustard. Data was collected for twelve traits. Genotypes were grouped into seven clusters. Maximum average intra cluster divergence value was found for cluster VII and minimum intra cluster divergence value was found for cluster V. The highest inter-cluster D^2 value was noted between cluster VII and VI, while the lowest inter-cluster distance was seen between cluster II and cluster I. Based on the larger intra cluster distance value, the crosses could be made among the genotypes.

Rout *et al*. (2018) tested thirty eighty genotypes of Indian mustard. Genetic divergence grouped genotypes into seven clusters. Maximum average intra cluster divergence value was found for cluster VII and minimum intra cluster divergence value was found for cluster V. Maximum inter cluster D^2 value was recorded between cluster VII and VI whereas minimum inter cluster distance was observed between cluster II and cluster I. Further crosses could be made among diverse genotypes for obtaining useful progenies.

Jat *et al*. (2019) conducted an investigation involving twenty Indian mustard genotypes, meticulously examining thirteen distinct traits. Through analysis of variance, the study illuminated notable distinctions among genotypes across all the evaluated traits. Traits such as seed yield per plant (g), number of siliquae per plant, days to 50 percent flowering, and siliqua length (cm) exhibited high heritability paired with substantial genetic advance, suggesting their responsiveness to selection. The findings indicated that select genotypes displayed elevated heritability in seed yield, implying their potential for favorable outcomes through selection.

Pal *et al.* (2019) assessed PCV and GCV, heritability, genetic advance (GA), for thirteen characters in seven genotypes of Indian mustard (*Brassica juncea* L.) were investigated for seed yield and its yield-contributing features. Genetic variation showed that environmental influences were a substantial factor in all of the variables evaluated where PCV was greater than GCV. For seed yield per plant, seeds per siliqua, siliqua length, and secondary branches per plant, strong heritability together with high genetic advance as a percentage of mean were reported, showing the breeding improvement through direct selection. Additionally, oil content had a mean value of 37.62 and a range of 35.25 to 40.33.

Patel *et al*. (2019) undertook an evaluation encompassing sixty diverse mustard genotypes. The Analysis of Variance unveiled highly significant differences across all traits, highlighting the existence of extensive genetic variability within the studied genetic pool. Notably, PCV exceeded GCV for all observed characteristics. Traits like 1000-seed weight, oil content, days to flowering, and seed yield exhibited elevated heritability values. Remarkably, the highest genetic advance value (as a percentage mean) was recorded for seed yield per plant.

Ray *et al*. (2019) performed a thorough assessment encompassing nineteen genotypes of Indian mustard, encompassing observations across twelve distinct traits. The analysis of variance unveiled noteworthy distinctions among the characteristics, except for siliqua length and volumetric seed weight. Among these traits, the highest mean was recorded for the number of siliquae, succeeded by plant height and days to maturity. The number of secondary branches,

siliquae per plant, and seed yield showcased the most elevated levels of both PCV and GCV. Similarly, notable heritability and substantial genetic advancement were observed in traits including the secondary branches, siliquae per plant, seed yield per plant, and biological yield, as indicated by Ray *et al*. (2019).

Rout *et al*. (2019) conducted research involving seventy-one genotypes of Indian mustard, significant discrepancies in yield and associated traits were detected among all the genotypes. The investigation uncovered high heritability and considerable genetic progress for attributes spanning height up to the first fruiting branch, primary branches, secondary branches per plant, siliquae per plant, and 1000-seed weight.

Rout *et al*. (2019) conducted an investigation involving thirty-eight varieties of Indian mustard, unveiling significant variability through analysis of variance across all characters. Various traits displayed moderate values of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), with minimal disparities between GCV and PCV values for all attributes. Traits such as the primary branches per plant, secondary branches per plant, siliquae per plant, seeds per siliqua, biological yield per plant, harvest index, seed yield, and 1000-seed weight exhibited high heritability, accompanied by notable genetic advancement as a percentage of the mean.

Swetha *et al*. (2019), twenty-eight diverse varieties of mustard were assessed for fourteen quantitative traits, revealing heightened genotypic and phenotypic variation in harvest index, length of siliqua, yield of seeds in a plant, and the secondary branches in a plant. Attributes including harvest index, siliqua length, days to 50 percent flowering, seeds per siliqua, and the number of secondary branches per plant demonstrated substantial heritability and significant genetic advancement.

Akoju *et al*. (2020) evaluated Indian mustard genotypes and found highly significant mean sum of squares due to genotypes for all characters. Traits like the number of siliquae per plant and secondary branches per plant demonstrated high GCV and PCV values. While 1000-seed weight and siliqua length exhibited high heritability, days to 50 percent flowering and days to physiological maturity showed moderate heritability, and limited potential for improvement through selection was indicated by high heritability estimates coupled with low genetic advancement as a percent of the mean for siliqua length and 1000-seed weight.

Gadi *et al*. (2020) examined thirty-six diverse genotypes of Indian mustard across ten quantitative traits, revealing moderate GCV and high PCV for most characters, with the exception of the number of seeds per siliqua displaying low PCV. Notably, high heritability paired with genetic advancement as a percentage of the mean was evident for days to maturity, followed by days to 50 percent flowering and test weight, signifying effective selection strategies for enhancing seed yield in this population.

Kumar *et al*. (2020), fifty-five Indian mustard accessions were assessed, revealing a trend where PCV was slightly higher than GCV, albeit with a marginal difference. Traits like siliquae per plant, secondary branches per plant, seed yield per plant, and siliquae on the main shoot exhibited elevated GCV values. Notably, attributes including plant height, secondary branches per plant, main shoot length, test weight, siliquae per plant, siliquae on the main shoot, and seed yield per plant displayed high heritability, coupled with genetic advance as a percentage of the mean. This pattern suggests that heritability is influenced by additive gene effects, implying the efficacy of selection strategies and predictive gains under selection.

Lakra *et al*. (2020) examined thirty Indian mustard genotypes to ascertain the presence of genetic variability. Their findings highlighted that parameter such as number of secondary branches, seed yield per plant, and seed yield per plot exhibited notable to moderate Genotypic Coefficient of Variation (GCV), accompanied by high to moderate Phenotypic Coefficient of Variation (PCV), suggesting the potential effectiveness of selection based on these traits. Additionally, the study identified high to moderate heritability alongside significant genetic advance for traits encompassing number of secondary branches and number of siliquae per plant.

Yadav *et al*. (2020) conducted an assessment involving 40 Indian mustard accessions, evaluating 12 quantitative traits. Notably, high values of PCV, followed closely through GCV, were most prominent for harvest index, with thousand seed weight coming next. The study revealed maximum heritability estimates translating into substantial GAM for most traits, barring days to fifty percent flowering and days to maturity. Genotypes were subsequently categorized into seven clusters, with the largest inter-cluster distance found between clusters III and II, and the smallest between clusters VII and VI, suggesting that hybridization between genotypes with greater inter-cluster separation could lead to the most productive heterotic crosses. In a parallel study,

Kumar *et al*. (2021) assessed 25 Indian mustard genotypes across nine agro-morphological traits. Notably, seed yield demonstrated higher heritability coupled with greater genetic advancement as percentage mean, followed by the number of secondary branches and test weight, underscoring their utility for selecting superior genotypes.

Mohan *et al*. (2021) conducted an analysis of variance, uncovering significant differences among genotypes for all characters except the number of seeds per siliquae. Maximum PCV was observed for traits such as number of secondary branches per plant, 1000-seed weight, length of the main raceme, number of primary branches per plant, seed yield per plant, and number of seeds per siliqua, while minimum PCV was noted for days to 50 percent flowering, harvest index, number of siliquae per plant, plant height, days to maturity, biological yield per plant, and oil content.

Patel *et al*. (2021), forty-five Indian mustard genotypes were assessed, with the Analysis of Variance revealing significant differences across all eighteen examined traits. Notably, a minimal difference existed between genotypic and phenotypic variances. Traits including number of branches per plant, seed yield per plant, myristic acid, palmitic acid, and stearic acid displayed high values of GCV and PCV, indicating substantial potential variability for these traits. Furthermore, high heritability estimates coupled with significant genetic advance were observed for multiple traits, underscoring the influence of additive gene action on their expression.

Pradhan *et al*. (2021) evaluated twenty-four Indian mustard genotypes, where analysis of variance highlighted significant distinctions among all 24 genotypes across all assessed characters. Most traits exhibited elevated values of PCV and GCV, particularly traits such as seed yield per plant, number of secondary branches per plant, and number of siliquae per plant. This study also demonstrated high heritability paired with substantial genetic advance as a percentage of the mean, particularly for traits including number of siliquae per plant, number of primary and secondary branches per plant, plant height, 1000 seed weight, siliqua length, and seed yield per plant, signifying the prominent role of additive gene action in their expression.

Priyanka *et al*. (2021) conducted a study involving twenty Indian mustard genotypes, revealing significant distinctions for all examined characters through ANOVA. PCV surpassed GCV for all traits. Notably, traits like secondary branches in a plant, test weight and plant height displayed both high heritability and substantial genetic advance. The genotypes were

subsequently categorized into five clusters, with the largest inter-cluster D^2 value (70.90) noted between cluster IV and cluster V, and the smallest inter-cluster distance (11.68) identified between cluster II and cluster III. Intra-cluster divergence ranged from 20.93 for cluster I to 24.93 for cluster V.

Saroj *et al*. (2021) embarked on a comprehensive study involving 289 diverse Indian mustard accessions from four continents, evaluating 20 traits across two seasons. The analysis unveiled significant genetic variance for each trait in both individual and pooled analyses. Traits encompassing flowering characteristics, plant height, seed size, and yield of seeds per plant displayed high heritability, alongside notable GAM and GCV, hinting at the potential for enhanced genetic gain through selection in subsequent generations.

Yadav *et al*. (2021) conducted a study focusing on 50 Indian mustard genotypes, analyzing fourteen quantitative traits. The analysis of variance revealed significant ratios for all traits, while high Genetic Coefficient of Variation (GCV) and PCV were noted for attributes including First basal branch, Seed yield per plant (g), thousand seed weight, Fruiting zone length, and Seeds per siliqua. Traits such yield of seeds in a plant, 1000 seed weight, fruiting zone length, days taken for initial flowering, and first basal branch displayed both higher heritability and increased genetic advance.

Anjali *et al*. (2022), 45 genotypes were evaluated for 12 characters, indicating high GCV and PCV for number of secondary branches per plant, grain yield per plant, and number of primary branches per plant. The study also identified high heritability and genetic advance for various characters, suggesting the potential for direct genotype selection based on these attributes to enhance *Brassica juncea* genotypes.

Nishad *et al*. (2022) assessed 20 different Indian mustard genotypes for 20 characters, revealing large variability through significant analysis of variance and identifying high to moderate GCV and PCV estimates for traits like number of siliquae per plant, harvest index, seed yield per plant, and number of secondary branches per plant. Additionally, high heritability and genetic advance as a percentage of the mean were observed for traits such as number of siliquae per plant, harvest index, seed yield per plant, and number of secondary branches per plant. Also, oil content ranged from 36.97 to 42.17 with a mean of 40.03.

Singh *et al*. (2022) with 40 genotypes, thirteen characters were investigated, and all characters exhibited highly significant variance. Traits like primary branches per plant, 1000-

seed weight, number of seeds per siliqua, and seed yield per plant showed elevated GCV and PCV values. Notably, higher heritability was observed for all characters except biological yield per plant, while higher genetic advance was noted for the number of siliquae per plant. Highest GCV and PCV values were recorded for 1000-seed weight, followed by biological yield, seed yield per plant, and harvest index, all crucial for hybridization programs.

Tarkeshwar *et al*. (2022) explored sixty Indian mustard genotypes, categorizing them into six clusters based on diversity in seed yield and its component traits. Cluster I and IV contained the highest number of genotypes (13 each), while the lowest number was found in cluster III (6 genotypes). Inter-cluster D2 values highlighted the most diverse groups as III & II and cluster III & I, suggesting these clusters' genotypes could serve as donors for trait improvement.

Vanukuri *et al*. (2022), 21 genotypes were investigated for 14 traits, with analysis of variance indicating significant genotypic influence on all characters. PCV surpassing GCV suggested environmental impact on genotypes. High heritability coupled with substantial genetic advance was observed for eleven characters, and the genotypes were grouped into six clusters, with maximum inter-cluster D2 value between clusters II and V, implying their potential utilization in successful breeding programs.

Molecular characterization

Vinu *et al.* (2013) evaluated the genetic diversity among 44 Indian mustard genotypes including varieties agro-climatic zones of India and few exotic genotypes. Out of the 143 primers tested, 134 reported polymorphism and a total of 355 alleles were amplified. Dendrograms based on Jaccard’s similarity coefficients and Manhattan dissimilarity coefficients were generated and genotypes were grouped into four clusters based on genetic distances which independently, discriminated the genotypes effectively as per their pedigree and origin. Hence, for diversity studies SSR markers are the stronger tools in discriminating *B. juncea* genotypes.

Prajapat *et al.* (2014) evaluated 30 *Brassica* diverse genotypes belonging to four cultivated species was assessed using 24 SSR markers. With a 72 percent polymorphism, a total of 84 alleles varied from 1 to 8 (BRMS 14) with a mean of 2.79 alleles were observed. Nine, out of 24 SSRs produced 100 percent polymorphism. The amplicon size ranged from 99bp (BRMS-26) to 383bp (BRMS-31). The PIC ranged from 0.79 (BRMS-31) to 0.12

(BRMS-003). In four clusters, all 30 accessions were grouped into their respective clusters and can be employed to discriminate between the species.

Singh *et al.* (2016) analysed 45 Indian mustard genotypes for genetic diversity using SSR markers. Of the nine SSR primers used, eight showed polymorphism. Total number of amplified alleles was 23 with one to four total alleles per primer while up to three polymorphic alleles per primer. The range of amplified fragments varied from 112 bp to 930 bp. PIC value varied from 0.022 (O110-A03a) to 0.346 (Ra02-E01a) with an average of 0.121. Similarity coefficients ranged from 0.167 to 1.00 with an average of 0.584 among the tested genotypes. The lowest similarity coefficient (0.167) was found between PR 08-13 and PR 08-5 exhibiting maximum diversity between them.

Manoj MS *et al*. (2019) Molecular diversity analysis of 38 Indian mustard genotypes was carried out employing 18 Simple Sequence Repeats (SSR) These SSRs grouped the genotypes into five major clusters at similarity coefficient of 0.001, with cluster I consisted of 13 genotypes, cluster II and cluster II had six genotypes each. While cluster IV and V consisted of nine and four genotypes.

Baghel *et al.* (2020) categorized of 48 mustard (*Brassica spp*.) genotypes by employing 20 SSR markers out of which seven furnished adequate variations among diverse genotypes. In total 50 percent polymorphism was detected. Major group restrained 48 genotypes that divided into three major groups, first main group 'I' contained 17 genotypes, second chief group 'II' hold 24 genotypes and third core group 'III' included 7 genotypes. Polymorphic information content 7 SSR markers revealed highest PIC value (0.6851) for OI10-CO 5 having 8 alleles whereas, the lowest PIC (0.4038) was examined for SR-7223.

Rajpoot *et al.* (2020) studied, genetic diversity in forty advanced breeding lines and eight cultivars of Indian mustard using morphological traits and SSR markers. Total 50 SSR markers were used out of which 7 SSR markers were highly polymorphic between all the germplasms of mustard. Number of alleles ranged from 3 to 4, and PIC value for markers ranged from 0.65 to 0.59 with mean PIC value 0.61indicating high genetic diversity in the studied plant material.

Singh *et al.* (2020) Ninety-five diverse genotypes of *B. juncea*. Out of 70 SSR markers, 44 were found to be polymorphic which amplified 157 alleles in 95 different genotypes with mean value of 3.57 alleles per locus and 0.48 of average polymorphic information content

(PIC). The expected heterozygosity (He) and observed heterozygosity (Ho) values were 0.54 and 0.81, respectively. Jaccard's dissimilarity coefficient ranged from 0.137 to 0.77. Based on dissimilarity coefficient, M 13 and RC 47 were the most diverse genotypes (0.77).

Rajpoot *et al.* (2022) investigated in forty advanced breeding lines along with eight cultivars of Indian mustard employing different morphological parameters as well as 50 SSR molecular markers out of which 7 SSR molecular markers were found to be highly polymorphic between all the genotypes of mustard. The similarity coefficient arrayed between 0.00 to 0.91. Number of alleles ranged from 3 to 4 and PIC value for markers ranged between 0.65 to 0.59 with a mean worth of 0.61 demonstrating high genetic diversity in the studied genetic stock.

Sharma *et al*. (2022) investigated 145 Indian mustard advanced breeding lines /genotypes accessions using 11 agro-morphological traits and 235 SSR primer pairs, out of which 182 SSRs resulted in polymorphic amplicons. Allele number varied from 2 to 7 with 3.97 average number of alleles per SSR marker. PIC value varied from 0.03 (SJ1668I) to 0.71 (EJU4) with an average value of 0.39 per SSR marker. Cluster analysis grouped all 145 accessions into two major clusters each, respectively and further into three subpopulations with varying degrees of admixture genotypes.

Singh *et al.* (2022) endeavors 88 genotypes of Indian mustard using 59 genomic SSR markers, and their genetic liaison was explored which detected 209 repeatable alleles in a size range of 50-1000 bp. The average PIC value from all the polymorphic primers were 0.49 respectively. All the 88 genotypes were grouped into four distinct clusters with three subpopulations were predicted indicating the presence of considerable genetic diversity among the Indian mustard genotypes for future breeding programmes.

Singh *et al.* (2022) evaluated 87 Indian mustard varieties using 200 genomic-SSR markers and 174 SSRs generating polymorphic products. A total of 552 alleles were obtained and allele number varied from 2–6 with an average number of 3.17 alleles per SSR marker. PIC value ranged from 0.10 (BrgMS841) to 0.68 (BrgMS519) with 0.39 as mean PIC value. Further, dendrogram and population structure analysis divided all the 87 varieties into two major groups/subpopulations which will assist in formulating future breeding strategies in Indian mustard.

Singh *et al.* (2022) evaluated the polymorphic potential of 350 SSR out of which 310 SSRs produced polymorphic amplicons. The allele number varied from 2 to 7 with 3.22 average

number of alleles per locus. PIC value ranged from 0.24 (Ol09A01) to 0.75 (nia-m141a) with an average PIC value of 0.40 per locus. Dendrogram grouped all the 46 genotypes into two main clusters, while structure analysis formed three subpopulations having admixture of alleles.

Shrivastav *et al.* (2023) evaluated 77 microsatellite markers to assess the genetic diversity of 75 Indian mustard genotypes out of which 21 SSRs exhibiting polymorphic amplicons. A total of 99 alleles, ranging from 3 to 5 with an average of 4.71 alleles per SSR marker were obtained. The average polymorphic information content (PIC) value was 0.67 and ranged between 0.43 (ENA28F) and 0.76 (gi258660710gbGT071338.1). The dendrogram grouped the 75 genotypes into three main clusters or subpopulations.

CHAPTER 3

MATERIAL AND METHODS

With a view of obtaining precision in the results, the materials and techniques adopted for the study was considered as the most important one. A detailed account of the material employed and methods followed during the course of investigation is described in this chapter.

3.1 Experimental Site:

The field experiment was conducted in the experimental area of division of Plant Breeding and Genetics. While molecular work was done in molecular biology laboratory in the division of Plant Breeding and Genetics under Sher-e-Kashmir University of Agricultural Sciences and Technology. It is situated between 32º39'N & 74º47'E respectively.

3.2 Experimental Material and Design:

The experimental material includes 40 genotypes of Indian mustard, were brought from different sources (Table 3.1). The experiment was sown in a plot size of $3m^2$ at both the locations using Randomized Complete Block Design (RCBD) with three replications. The line-to-line distance was maintained 45 cm and plant to plant distance was kept at 10 cm. The normal recommended doses of fertilizer were applied as per package and practices of SKUAST- Jammu. Experiment for two consecutive seasons at experimental area of division of Plant Breeding and Genetics SKUAST- Jammu provided us reliable data on various morphological traits.

Table 3.1: Genotypes along with pedigree used in investigation

S.No.	Genotypes	Pedigree	Source
1.	RSPR-03	Kranti x Pusa bold	SKUAST-Jammu
2.	PM-21	Pusa bold x Zem-2	RRS, Bawal
3.	RSPR-01	B. Juncea x D. muralis	SKUAST, Jammu
4.	RH-1209	RH-0555 x RH-04301B	CCSHAU, Hisar
5.	PM-195	NPJ-102 x Pusa Jagannath	IARI, Delhi
6.	JM-12-6	RSPR-01 x Kranti	SKUAST, Jammu

7.	PM-25	SEJ-8 x Pusa Jagannath	IARI, Delhi
8.	RB-77	RH-819 x RH-8814	IARI, Delhi
9.	PM-28	SEJ 8 x Pusa Jagannath	IARI, Delhi
10.	DRMRIJ-15-85	(EC 39288 x PCR11) x (B33 x Sanjucta Asch)	DRMR, Bharatpur
11.	RSPR-69	RLM-198 x Varuna	SKUAST, Jammu
12.	RB-50	Laxmi x RH-9617	RRS, Bawal
13.	RH-819	Prakesh x Bulk pollen	CCSHAU, Hisar
14.	SKJM-5	RSPR-03 x Kranti	SKUAST, Jammu
15.	Tawari	Local collection	Ayodhya
16.	DRMRIJ-31	HB9908 x HB9916	DRMR, Bharatpur
17.	JD-6	Pusa Bold x Glossy	IARI, New Delhi
18.	RLC-3	JM-06003 X JM-06020	PAU, Ludhiana
19.	RH-406	RH-6908 x RH-8812	CCSHAU, Hisar, Haryana
20.	PM-125	-	IARI, Delhi
21.	LES-39	Pusa Basanti x Zem1	IARI, Delhi
22.	RH-725	RH-781 x RH-9617	CCSHAU, Hisar, Haryana
23.	DRMR-1059	-	DRMR, Bharatpur
24.	RH-0923	RH-0115 x JMM-937	CCSHAU, Hisar, Haryana
25.	CN-105364	-	AICRP, R&M, Jammu
26.	DRMR-4005	SEJ-2 x K 28	DRMR, Bharatpur
27.	Kranti	Selection from varuna	CSAUA&T, Kanpur
28.	NC-37362	-	AICRP, R&M, Jammu
29.	DRMR-61-59	-	DRMR, Bharatpur
30.	DRMR-15-5	Choupka x PWR	DRMR, Bharatpur
31.	DRMR-541-44	-	DRMR, Bharatpur
32.	DRMR-12-48	OJR 2 x ZEM-2	DRMR, Bharatpur

33.	DRMR-541-46	-	DRMR,Bharatpur
34.	RB-69	-	RRS, Bawal
35.	DRMRIJ-A-35	-	DRMR, Bharatpur
36.	RB-55	Selection from RB-2001	RRS, Bawal
37.	TN-3	-	BARC, Mumbai
38.	RL-1359	RLM514 x Varuna	PAU, Ludhaina
39.	JM-14-2	RSPR x Urvashi	SKUAST, Jammu
40.	DRMRIJ-12-40	Zem-2 x JGM-1-11	DRMR, Bharatpur

3.3 Observations recorded

The morphological observations recorded for the different traits in two different seasons are:

3.3.1 Days to initial flowering

Number of days from date of sowing to the date of first flowering. The average number of days for initial flowering was calculated for each genotype.

3.3.2 Days to 50 percent flowering

Number of days from date of sowing to the date when 50 percent plants in each genotype flowered in the experimental field. The average number of days for 50 percent flowering was calculated for each genotype.

3.3.3 Number of primary branches per plant

Primary branches are the branches which extends first from the main branch of the plant. Number of primary branches are counted and average data of each genotype was calculated.

3.3.4 Number of secondary branches per plant

Secondary branches are the branches which extends from the primary branches are counted and average of each genotype was noted.

3.3.5 Main shoot length (cm)

Main shoot length is measured from the base of the plant to the length where first primary branch originates.

3.3.6 Number of siliquae on main shoot

Total number of siliquae on the main shoot was counted and average number for each genotype was calculated.

3.3.7 Siliqua length (cm)

Length of siliqua was measured from the base to the top of siliqua excluding pedicle and tip (beak) of the siliqua.

3.3.8 Number of seeds per siliqua

Total number of seeds per siliqua was counted for each genotype by randomly selecting five siliquae for each replication and average number of seeds per siliqua was calculated.

3.3.9 Plant height (cm)

Plant height was measured from the base of plant to tip of the plant in centi-meters when physiological maturity was achieved.

3.3.10 Days to maturity

Days to maturity was calculated by counting number of days from the day of sowing to the date when physiological maturity has been achieved.

3.3.11 Seed yield per plant (g)

Seed yield per plant was calculated by counting total weight of the seeds obtained from randomly selected five plants from each genotype in all the replications and calculated their average at 8-10 percent moisture content.

3.3.12 Test weight (g)

Test weight is measured by manually counting 1000 seeds of each genotype and followed by weighing their weight.

3.3.13 Harvest index (percent)

Harvest index is calculated on the basis of biological and economical yield and is calculated as the ratio of economical yield to biological yield as determined by the formula given by Singh and Stoskoff (1971).

$$\text{Harvest Index (percent)} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.3.14 Oil Content

A seed sample was collected from the overall yield of chosen plants within each specific plot. The measurement of oil content was conducted using the Newport Analyzer-4000, a device founded on the principles of Nuclear Magnetic Resonance (NMR). The resulting oil content measurements were documented as percentages. Oil content has been measured at ICAR- Directorate of Rapeseed Mustard Research - Bharatpur

3.4 Statistical analysis

The collected data for various observations were used for statistical analysis using Windostat 9.30 version.

3.4.1 Analysis of variance

The analysis of variance (ANOVA) was carried out for yield and its attributes.

The model mentioned below was applied to accomplish the variance analysis.

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

Where,

Y_{ij} = Yield (performance of i^{th} entry in j^{th} replication)

μ = General mean effect

t_i= Effect of the i^{th} replication (i=1,2,….v)

b_j = Effect of j^{th} replication (j=1,2,…v)

e_{ij} = Random error.

Table 3.2: Analysis of variance

Sources of variation	Degree of freedom (d.f)	Mean sum of squares (MSS)	"F" calculated
Replication	r	M_r	M_r/M_e
Genotype	g	M_g	M_g/M_e
Error	(r-1) (g-1)	M_e	
Total	(rg-1)		

Where, r and g are the numbers of replications and genotypes, respectively

σ_r^2 = Mean sum of square of replication

σ_g^2 = Mean sum of squares of genotype

σ_e^2 = Error mean sum of squares

M_r, M_t, M_e = Mean sum of squares owing to replications, treatments, and error, respectively

Mean sum of square attributable to genotypes were compared to variance owing to error using F-test at five percent and one percent significance levels, with V_1=(g-1) and V_2=(g-1)(r-1) degree of freedom, where V_2 reflects the degree of lower value of variance.

3.4.2. Pooled analysis of variance:

The pooled analysis of variance for all the thirteen traits were carried out and presented in Table 3.3

Table 3.3: Pooled analysis of variance

Source	d.f	Sum of squares	Mean sum of squares	Exp. mean sum of squares
Genotype	(t-1)	SS_g	MS_g	$\sigma_e^2+r\sigma_{ge}^2+re\sigma_g^2$
Environment	(e-1)	SS_e	MS_e	$\sigma_e^2+r\sigma_{ge}^2+rg\sigma_e^2$
Genotype x Environment	(t-1) (e-1)	$SS_{g\times e}$	MS_{ge}	$\sigma_e^2+r\sigma_{ge}^2$
Pooled Error	(m	SS_{pe}	MS_{pe}	σ_e^2
Total	r(ge-1)			

Where,

t = Number of genotypes

r = Number of replications

e = Number of seasons

m = Degrees of freedom pooled associated to error over seasons i.e., : e(r-1)(g-1)

σ_e^2= Variance due to pooled error

σ_g^2 = Variance due to genotypes

σ_e^2 = Variance due to seasons

σ_{ge}^2 = Variance due to interactions between genotype and seasons

Estimation of pooled error

The pooled error was deduced by using the below mentioned formula:

$$\text{Pooled error} = \frac{(e_1-1)\,(\text{M.S.error } e_1)+\ldots+(e_n-1)(\text{M.S.error } e_n)}{(e_1-1)+\ldots+(e_n-1)}$$

Where,

$e_1 - 1$ = Degree of freedom associated to error within E-I.

M.S. error e_1 = Mean sum of square owing to error within E-I

$e_n - 1$ = Degree of freedom associated to error within EI .

M.S. error e_n= Mean sum of square owing to error within En.

The F-test was employed to determine whether or not the interaction of genotypes with varied environments was significant. We came to the conclusion that there was a genotype x environment interaction for all twelve traits and continued on to compute phenotypic stability.

3.5 Estimation of genetic components of variation

3.5.1 Mean:

Mean value for each character was numerated by dividing the total values with the relative number of observations.

$$\text{Mean: } \frac{\sum X}{N}$$

Where,

$\sum X$= Sum of the observations and

N = Count of the observations

3.5.2 Coefficient of variation (C.V.):

The coefficient of variation is a relative measure of dispersion that expresses the standard deviation as a percentage of the mean.

$$\text{CV (percent)} = \sqrt{\frac{MSe}{\bar{X}}} \times 100$$

Where,

MS_e = Error variance

$\bar{X}$= Mean of grand total

3.5.3 Components of variation

Using the appropriate mean sum of squares from the ANOVA table (Johnson *et al*. 1955), the genotypic and phenotypic variances was interpreted in the following way.

Environmental variance $\sigma_e^2 = M_e$

$$\text{Genotypic variance } \sigma_g^2 = \frac{Mg\text{-}Me}{r}$$

Phenotypic variance $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

3.5.4 Estimation of genetic variability parameters

Phenotypic and Genotypic Coefficient of Variation

Phenotypic and genotypic coefficient of variation were computed as per Burton and Devane *et al*. (1953).

3.5.4.1 Phenotypic coefficient of variation (PCV):

The phenotypic coefficient of variation quantifies the variability of a trait in a population, encompassing both genetic and environmental influences.

$$PCV = \frac{\sigma_p^2}{\bar{X}} X\ 100$$

Where,

σ_p^2 = Phenotype variance and,

$\bar{X}$ = Mean of character

3.5.4.2 Genotypic coefficient of variation (GCV):

The genotypic coefficient of variation assesses the genetic diversity of a trait within a population.

$$GCV = \frac{\sigma_g^2}{\bar{X}} X\ 100$$

Where,

σ_g^2 = Genotype variance and,

$\bar{X}$ = Mean of character

3.5.5 Estimation of Heritability h² (bs)

Heritability ($h^2_{(b.s.)}$) in the broad sense was calculated as per the formula given by Allard *et al*. (1960).

$$\text{Heritability } (h^2_{(b.s.)}) = \frac{\sigma g2}{\sigma p2}$$

Where,

$h^2_{(b.s.)}$ = heritability in broad sense

Vg is the variance attributed to genotype that is σ_g^2

Vp is the variance attributed to phenotype that is σ_p^2

As suggested by Johnson *et al.* (1955) $h^2_{(b.s.)}$ estimates were categorized as:

Low: 0-30 per cent

Moderate: 30-60 per cent

High: 60 per cent and above

3.5.6 Genetic advance

The anticipated genetic advance, which was assessed using a formula purposed by Johnson *et al*. (1955), was described as the variation between the mean of descendants of chosen individuals and the base population.

$$G.A.= k\times h^2_{(b.s.)} \times \sigma_p$$

Where,

G.A. = Expected genetic advance

k = Selection differential which is 2.06 at 5 percent selection intensity

σ_p = Standard deviation due to phenotype

$h^2_{(b.s.)}$ = Heritability in broad sense

3.5.7 Genetic Advance (G.A.) as per cent of Mean (GAM)

$$GAM= \frac{G.A}{X} X\ 100$$

Genetic advance as per cent of mean was categorized as given below as suggested by Johnson *et al*. (1955).

Low: 0 – 10 per cent

Moderate: 10.1 – 20 per cent

High: > 20.1 per cent

The observations recorded for the morphological traits were subjected to statistical analysis.

3.6 Molecular Method

3.6.1 Isolation of Genomic DNA [Doyle and Doyle *et al*. (1987)]

1) Isolation of the genomic DNA were carried out by CTAB method of DNA isolation.
2) Fresh leaves of 10-20 days old (1-2 g) population were used.

3) Leaves and seeds were taken to molecular biology laboratory at the time of their respective extraction and grinded into fine powder in liquid nitrogen using mortar and pestle.

4) Fine powder is transferred to 2ml micro-centrifuge tubes and 800 µL of prewarmed CTAB buffer was added to it.

5) After mixing it well, the tubes were incubated in water bath at 60ºC for 1hr. with continuous shaking after every 10 minutes.

6) After incubation, DNA samples were cooled to room temperature.

7) Equal volume of Chloroform: Isoamyl alcohol (24:1) were added to it.

8) Mix it well by gently inverting the tubes for 10-15 minutes.

9) Centrifuge the tubes at 10,000 rpm for 10 min at 4ºC.

10) Take out the supernatant in another micro-centrifuge tubes and discard the rest.

11) Add 800 µL of Phenol: Chloroform: Isoamyl alcohol (PCI) 25:24:1 and mix it well by gentle shaking. 12) Again, centrifuge the tubes at 10,000 rpm for 10 min at 4ºC.

13) Take out the supernatant to 1.5 µL micro-centrifuge tubes and add 600 µL of chilled isopropanol.

14) Mix it well by gently inverting the tubes and kept them on -20ºC for overnight precipitation.

15) Take out the samples and centrifuge at 6000 rpm at 4ºC for 6 min.

16) Discard the supernatant gently without disturbing the palette.

17) Wash the palette with 800 µL of 70 percent ethanol at 4000 rpm for 4 min.

18) Air dried the palette and then dissolve in 100 µL of Tris- acetate- EDTA (TAE) buffer and store it at 4ºC for further use

3.6.2 Purification of DNA

1) RNAase (2 µL) was added to each DNA tube and incubated for 1 hour at 37°C in water bath.

2) Add 800 µL of Phenol: Chloroform: Isoamyl alcohol (PCI) 25:24:1 and mix it well by gentle shaking for 5-10 min.

3) Again, centrifuge the tubes at 10,000 rpm for 10 min at 4ºC.

4) Take out the supernatant to 1.5 µL micro-centrifuge tubes and add 600 µL of chilled isopropanol.

5) DNA pellet so obtained, washed with 800 µL of 70 percent ethanol at 4000 rpm for 4 min.

6) The supernatant consisting of ethanol was discarded and the pellet so obtained was air-dried.

7) After air- drying, the DNA pellet was dissolved in 100 µL (leaves) 300 µL (seeds) of Tris- acetate- EDTA (TAE) buffer and stored at 4°C for further use.

3.6.3 Quality check of DNA

Genomic DNA quality was checked using Nanodrop method and horizontal electrophoresis with 0.8 percent agarose gel.

- **Nanodrop method:** To quantify DNA Nanodrop spectrophotometer was used. A set of the instrument blank with Diethyl Pyro carbonate (DEPC) water was used. Then put 2µl of DNA sample into the receiving fibre of the instrument, there after source fibre brought in contact with the end of receiving fibre and then reading was taken (concentration (ng/µl) at OD 260/280 value of the sample). If the OD value lies between1.8-2.0, means the DNA is pure. If the OD value lies above 2, then this means RNA contamination and if it is below 1.8 then it indicates protein contamination.
- **Agarose gel electrophoresis:**

1) Agarose powder of 1.2 g was dissolved in150 mL of 1× TBE buffer and then heated in microwave oven until it got clear and transparent solution.

2) Allow it to cool for 1 minute, 6µL of ethidium bromide (EtBr) was added and stirred to mix it well. 26 3) The agarose solution was poured gently in the casting tray with pre fixed two combs and already enclosed with tape. Allowed it to solidify for 7-10 minutes at room temperature.

4) Remove the combs and set the tray inside the electrophoresis unit.

5) To each well add 2-4 µL of DNA mixed with 4µL of DNA loading dye.

6) The electrophoresis was performed at 100 V and 90 mA current for 50 minutes. Then 0.8 percent gel was viewed in the Gel Documentation System.

3.6.4 Primers for PCR Amplification

A set of 21 SSRs markers mentioned below were selected for amplification of genomic DNA.

3.6.5 Method for preparation of primers

1) To obtain a concentration of 100 µM for each lyophilized primers, these were dissolved in nuclease free water at the volume mentioned on the technical data sheet.

2) Working solution was prepared out the stock solution by adding 10 µL of stock solution and further diluting it with 90 µL of nuclease free or double distilled water and then stored at -20ºC

3.6.6 Amplification of genomic DNA –

Amplification of genomic DNA was carried out using thermo-cycler machine through polymerase chain reaction (PCR). Various components were used for PCR in 0.2ml PCR tubes with total reaction volume of 15µL.

Table 3.4: Components used in PCR reaction

S. no.	Reagents	Concentration	Quantity (µL)
1.	PCR Buffer	5 X	3.0
2.	dNTPs	0.25 Mm	0.3
3.	$MgCl_2$	2.00 mM	1.2
4.	Forward primer	10 µM	0.3
5.	Reverse primer	10 µM	0.3
6.	Taq DNA Polymerase	0.75 U	0.15
7.	Template DNA	~50 ng/µl	1.0
8.	Nuclease free water		8.75
Total Volume			**15.0**

Table 3.5: PCR program different SSR Primers steps

Steps	**Temperature (ºC)**	**Duration**
Initial denaturation	95	5 min
Denaturation	95	30 sec
Annealing	50-55	30 sec
Initial elongation	72	30 sec
Elongation	72	7 min
Hold	15	Infinite
Number of cycles		**35**

PCR amplified SSR products were separated on 3 percent agarose gel in 1X TBE 1 hour 30 minutes at 120 volts as described in section. Gels were visualized under UV and photographed by using UVP gel documentation system.

Table 3.6: List of SSR markers used for molecular study

S. No.	Primer Name	Primer Sequence Forward (F)-(5'-3') Reverse (R)-(3'-5')	Annealing temperature (°C)
1.	A02_18870790	F-5'TACACCGTCTGATTCCATCT3' R-3'GCCTGACTGCTGCTACTAAC5'	55
2.	Na10-D07	F-5'CTACTTTGATGGACACTTGCC3' R-3'TCTGAAGTTGATTAGTCGGTCC5'	61
3.	A03_3174449	F-5'AAAGAAGAGCTTTGAAGAGGA3' R-3'TTGATTCACAACACACATACC5'	55
4.	A09_27227566	F-5'GGGAGTGAAATGAAGAGAAGA3' R-3'GCTTCACAGCTGTTTAATCTC5'	55
5.	Ni4-F11	F-5'CGTAAGTTTCAATTGTCAACGG3' R-3'TCGTACGAAACAATCAACGG5'	58
6.	Ni2-H06	F-5'CATCAGATCCGACGAAATCC3' R-3'TCCTTTGGACTGTGAAAAACG5'	60
7.	A05_25290881	F-5'ATAAAGATTTGATGGGAGGAG3' R-3'GGTGGAGGAGGATAGTTGTAG5'	55
8.	Ni2-C09	F-5'ACGGAAGAAATCCAACCTCG3' R-3'TATGCTTGGAAATGGTTTGG5	58
9.	Ni3-C08	F-5'CCCTAACACGGTGTCAACAG3' R-3'GGCAGAATCATCGAGAGGTC5'	62
10.	Ni3-C05	F-5'TTTCGTGCTTTGGTGTGAAG3' R-3'TCCCCAAATCGAACCATAAG	58

3.7 Marker analysis:

Based on the allele size the genetic profile of 40 mustard advanced breeding lines/ genotypes was scored using polymorphic SSR markers. The observations were recorded for major allele frequency, polymorphism information content (PIC) by using Cervus 3.0.3 and the dendrogram was constructed using NTSYS software.

CHAPTER 4

RESULTS

Present study entitled, "Genetic analysis of yield traits in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]", was carried out during *Rabi* 2021-22 and 2022-23 in which forty lines of Indian mustard were evaluated on morphological and molecular basis. The results obtained have been presented under following headings:

4.1 Analysis of variance

4.2 Mean performance of advanced breeding lines/ genotypes

4.3 Estimation of PCV, GCV, heritability, and genetic advance

4.4 Genetic diversity analysis

4.5 Molecular analysis of genotypes

4.1 Analysis of variance

The data obtained for each of the thirteen characters from 40 genotypes evaluated in three replications in *Rabi* 2021-22 and *Rabi* 2022-23 are depicted in Table 4.1 and Table 4.2. The results of the variance analysis demonstrated noteworthy significance at the 1 percent level for the mean sum of squares attributed to genotypes across all the examined traits except days to maturity, which exhibited significance at the 5 percent level during both the seasons. Likewise, a combined analysis of variance for all genotype traits exhibited notable significance at the 1 percent level.

4.2 Mean performance and range of genotypes

Average performance of genotypes for thirteen morphological characters of two seasons i.e., *Rabi* 2021-22 & 2022-23 are discussed below:

4.2.1 Days to initial flowering:

The number of days taken to initial flowering ranged from 42 to 57.33 days in year 2021-22 with a mean of 50.25 days. The genotype PM-21 recorded the minimum days taken to initial flowering (42 days), while RB-77 AND JD-6 took maximum days taken to initial flowering (57.33 days).

In year 2022-23, number of days taken to initial flowering ranged from 38.67 to 56 days with a mean of 48.02 days. The genotype PM-21 recorded the minimum days taken to initial flowering (38.67 days), while JD-6 took maximum days taken to initial flowering (56 days).

On the basis of mean of two-year data, number of days taken to initial flowering ranged from 40.67 to 57 days with a mean of 49.46 days. The genotype PM-21 recorded minimum days taken initial flowering (40.67 days), while genotype JD-6 recorded maximum taken to initial flowering (57 days).

4.2.2 Days to 50 percent flowering:

During 2021-22, number of days taken to 50 percent flowering ranged from 46 to 61.33 days, yielding an average of 54.09 days. Notably, the genotype which exhibited minimum days to 50 percent flowering was PM-21 (46 days), while JD-6 recorded maximum days to 50% flowering (61.33 days).

Similarly, in the subsequent year, 2022-23, number of days to 50 percent flowering ranged from 43.67 to 59.33 days, with an average of 51.98 days. Here, PM-125 demonstrated minimum days to 50% flowering (43.67 days), while JD-6 recorded maximum days to 50% flowering (59.33 days).

When considering the cumulative data across the two years, number of days to 50 percent flowering ranged from 45.67 to 60.67 days, with an average of 53.38 days. Remarkably, PM-21 and JD-6 exhibited minimum days to 50 percent flowering (45.67 days each), while JD-6 recorded maximum days to 50% flowering (60.67 days).

4.2.3 Number of primary branches per plant:

In year 2021-22, number of primary branches ranged from 7.44 to 3.44 with a general mean of 4.97. The lowest number of primary branches were recorded by DRMR-15-5 (3.44) while, the highest number of primary branches were present in genotype TN-3 (7.44).

In year 2022-23, number of primary branches showed the mean of 6.33 with the range of 4.77 to 8.88. The lowest number of primary branches were recorded in PM-125 (4.77) while, the highest number of primary branches were recorded in DRMR-4005 (8.88).

Table 4.1: Analysis of variances for different characters in Indian mustard (*Rabi* 2021-22 and 2022-23)

Source	Degree of freedom	Days to initial flowering	Days to 50% flowering	Number of primary branches per plant	Number of secondary branches per plant	Main shoot length(cm)	Number of siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Plant height (cm)	Days to maturity	Seed yield per plant (g)	Test weight (g)	Harvest index (%)
Replication	**2**	2.80	4.23	0.30	0.58	5.31	20.97	0.12	1.23	26.38	13.73	0.84	0.26	0.55
Genotypes	**39**	52.56**	55.97**	2.85**	17.11**	394.39**	134.36**	1.21**	7.36**	1743.14**	61.55*	24.69**	1.18**	11.46**
Error	**78**	7.66	10.91	0.15	0.29	16.98	13.85	0.05	1.06	104.47	33.22	0.42	0.13	1.10

Source	Degree of freedom	Days to initial flowering	Days to 50% flowering	Number of primary branches per plant	Number of secondary branches per plant	Main shoot length(cm)	Number of siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Plant height (cm)	Days to maturity	Seed yield per plant (g)	Test weight (g)	Harvest index (%)
Replication	**2**	1.51	1.16	0.49	1.22	49.72	46.58	0.03	2.25	534.95	2.17	1.41	0.17	3.73
Genotypes	**39**	62.67**	60.14**	2.76**	47.58**	367.22**	112.96**	0.48**	5.63**	1709.99**	66.64*	36.26**	1.68**	14.31**
Error	**78**	7.77	10.40	0.24	0.61	16.11	17.21	0.06	1.56	187.32	35.96	0.71	0.07	2.09

Table 4.2: Analysis of variances for different characters in Indian mustard (Pooled)

Source	Degree of freedom	Days to initial flowering	Days to 50% flowering	Number of primary branches per plant	Number of secondary branches per plant	Main shoot length(cm)	Number of siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Plant height (cm)	Days to maturity	Seed yield per plant (g)	Test weight (g)	Harvest index (%)
Replication	**2**	1.11	1.73	0.07	0.28	6.96	3.07	0.07	1.49	262.58	1.7	0.86	0.01	0.38
Genotypes	**39**	56.83**	56.78**	1.80**	26.82**	351.85**	103.49**	0.52**	3.98**	993.9**	62.77**	29.35**	1.28**	12.26**
Error	**78**	3.76	5.06	0.12	0.18	8.62	10.69	0.03	0.71	173.62	18.63	0.31	0.05	0.82

**, * represents significance level at 1 % and 5 % respectively

Table 4.3: Mean performance of various genotypes for different traits in Indian mustard (*Rabi* 2021-22, 2022-23 & pooled)

Genotypes	Days to initial flowering			Days to 50% flowering			No. of primary branches/ plant			No. of secondary branches/ plant			Main shoot length (cm)			No. of siliquae on main shoot			Siliqua length (cm)		
	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean
RSPR-03	46.33	44.33	45.67	50.0	48.33	49.33	4.89	5.77	5.33	3.55	6.89	5.22	61.11	73.44	67.28	36.44	46.66	41.55	2.29	3.89	3.09
PM-21	42.0	38.67	40.67	46.0	44.33	45.67	4.0	4.89	4.44	4.77	5.33	5.06	54.22	53.66	53.94	47.33	41.44	44.39	3.72	3.78	3.76
RSPR-01	50.33	48.33	49.67	56.0	53.67	55.33	5.66	7.77	6.72	9.11	15.0	12.06	64.33	70.77	67.55	50.11	53.78	51.94	3.2	3.3	3.25
RH-1209	54.0	51.67	53.0	58.33	56.0	57.67	6.44	7.66	7.06	8.0	14.22	11.11	73.55	72.11	72.83	60.44	53.66	57.06	4.76	4.7	4.73
PM-195	48.33	46.0	47.67	53.0	50.0	51.67	4.22	5.44	4.83	2.11	2.0	2.06	69.44	62.44	65.94	43.88	39.33	41.61	4.23	3.93	4.08
JM-12-6	56.0	53.67	55.0	60.0	58.67	59.67	5.0	5.66	5.33	4.88	5.22	5.05	47.55	55.66	51.61	46.22	41.55	43.89	3.96	4.54	4.25
PM-25	51.0	48.67	49.67	55.0	52.67	54.0	4.55	6.33	5.45	4.22	7.67	5.95	37.55	45.00	41.28	48.11	49.55	48.83	4.29	4.11	4.2
RB-77	57.33	54.0	55.67	57.67	57.67	58.0	5.55	7.44	6.5	7.22	9.88	8.55	44.11	59.0	51.56	45.78	48.89	47.33	3.77	4.52	4.15
PM-28	48.33	46.33	47.67	52.0	50.67	51.67	5.77	6.55	6.16	6.66	10.66	8.67	44.33	53.11	48.72	45.88	56.33	51.11	3.9	4.69	4.3
DRMRIJ-15-85	46.33	45.0	46.0	49.33	48.33	49.33	5.11	6.67	5.89	6.22	11.99	9.11	41.33	44.22	42.78	38.89	40.33	39.61	4.49	3.78	4.14
RSPR-69	56.33	53.0	55.0	60.33	56.67	58.67	4.44	6.77	5.61	7.11	10.33	8.72	45.11	47.44	46.28	45.66	48.44	47.05	3.84	3.68	3.76
RB-50	55.33	54.0	55.0	59.0	57.67	58.67	4.11	6.44	5.28	4.44	9.11	6.78	46.44	61.55	54.0	32.77	37.89	35.33	4.2	4.45	4.33
RH-819	50.0	47.67	49.33	53.33	51.33	52.67	5.66	5.33	5.5	4.0	9.55	6.78	38.22	43.11	40.67	42.33	42.77	42.55	3.08	4.11	3.6
SKJM-5	45.33	43.0	44.33	48.67	46.33	47.67	6.22	5.77	6.0	6.0	5.0	5.5	39.0	44.55	41.78	38.33	41.11	39.72	4.3	3.66	3.98
Tawari	51.33	49.33	51.0	54.67	52.33	53.67	4.33	6.0	5.17	4.89	8.22	6.56	44.44	48.33	46.39	40.0	44.66	42.33	3.36	4.43	3.9
DRMRIJ-31	54.67	53.0	54.0	58.33	57.0	58.33	4.55	5.77	5.16	5.78	8.11	6.95	48.78	56.44	52.61	33.55	36.11	34.83	5.7	4.78	5.24
JD-6	57.33	56.0	57.0	61.33	59.33	60.67	3.89	5.0	4.44	5.66	8.0	6.83	63.22	69.22	66.22	43.89	43.22	43.55	4.2	4.13	4.17
RLC-3	51.0	49.0	50.67	54.67	52.67	54.33	7.11	6.22	6.66	10.33	13.0	11.67	68.11	58.33	63.22	55.55	54.22	54.89	4.7	3.39	4.05
RH-406	45.67	42.67	44.33	49.33	46.67	48.33	4.44	5.44	4.94	3.33	6.33	4.83	46.0	59.22	52.61	36.89	37.44	37.17	4.33	4.06	4.2
PM-125	44.0	40.0	42.33	47.33	43.67	46.0	5.0	4.77	4.89	4.88	4.55	4.72	51.22	52.66	51.94	43.44	49.78	46.61	5.58	4.48	5.03
LES-39	48.67	47.0	48.33	52.33	50.67	52.0	4.44	6.33	5.39	6.33	5.78	6.06	66.11	63.89	65.0	47.89	46.0	46.94	3.53	3.96	3.75
RH-725	43.67	42.33	43.0	47.0	45.67	46.67	4.0	6.89	5.44	4.11	7.11	5.61	33.33	40.0	36.67	40.22	50.44	45.33	4.93	4.77	4.85
DRMR-1059	52.0	51.67	52.0	55.67	54.33	55.67	3.89	6.89	5.39	3.33	9.11	6.22	43.44	55.0	49.22	45.11	37.55	41.33	4.18	4.41	4.29
RH-0123	46.0	40.0	43.67	50.0	45.67	48.0	4.77	4.99	4.89	7.55	6.66	7.11	43.66	48.77	46.22	33.77	38.89	36.33	4.18	4.71	4.44
CN-105364	50.33	47.67	49.33	54.33	52.67	54.0	5.55	6.44	6.0	9.55	13.55	11.55	40.22	49.44	44.83	29.22	30.33	29.77	4.37	4.33	4.35
DRMR-4005	53.33	51.33	52.67	57.0	54.67	56.0	4.77	8.88	6.83	10.77	23.11	16.94	66.22	73.89	70.05	38.44	52.22	45.33	3.88	3.97	3.93
Kranti	54.0	52.0	53.67	61.0	57.67	59.67	5.77	8.44	7.11	11.55	15.0	13.28	47.55	56.99	52.28	40.22	44.33	42.28	4.07	4.0	4.04

NC-37362	53.67	51.67	53.0	58.67	56.0	57.67	6.44	6.33	6.39	12.67	13.66	13.17	30.33	36.0	33.17	28.11	29.89	29.0	3.91	3.63	3.77
DRMR-61-59	53.0	51.33	52.33	57.33	54.67	56.33	4.0	6.33	5.17	6.33	9.55	7.94	66.22	72.11	69.16	42.77	38.22	40.5	3.94	3.61	3.78
DRMR-15-5	43.33	40.67	42.33	47.0	44.33	46.33	3.44	5.77	4.61	5.44	8.22	6.83	44.11	55.88	50.0	33.66	37.77	35.72	3.33	4.24	3.79
DRMR-541-44	52.33	50.33	51.67	56.33	54.33	55.67	3.66	5.66	4.67	8.22	7.44	7.83	44.0	60.88	52.44	39.0	44.0	41.5	3.79	3.84	3.82
DRMR-12-48	48.67	47.33	48.33	51.67	51.0	51.67	5.55	6.11	5.83	7.88	12.66	10.28	60.44	64.78	62.61	40.77	44.0	42.39	4.99	3.91	4.45
DRMR-541-46	46.67	43.33	45.33	50.67	47.0	49.33	4.44	8.0	6.22	6.77	11.88	9.33	48.11	52.89	50.5	40.33	42.66	41.5	4.01	4.31	4.16
RB-69	56.33	54.0	55.67	60.33	58.0	59.33	4.66	5.88	5.28	7.11	10.33	8.72	53.22	65.33	59.28	35.77	45.66	40.72	3.84	4.84	4.35
DRMRIJ-A-35	48.33	47.0	48.0	52.33	51.0	52.0	4.44	6.0	5.22	5.78	11.88	8.83	56.22	63.33	59.78	43.11	43.88	43.5	4.72	4.07	4.4
RB-55	52.0	50.67	51.67	55.0	53.67	54.33	5.55	6.66	6.11	6.78	11.44	9.11	51.44	65.89	58.66	35.33	47.11	41.22	3.78	4.12	3.95
TN-3	52.67	50.0	52.0	57.0	54.0	55.67	7.44	6.66	7.05	9.0	17.22	13.11	42.89	32.66	37.78	48.44	48.89	48.67	4.75	3.99	4.37
RL-1359	51.33	51.0	51.33	55.0	54.67	55.0	3.77	6.55	5.17	8.78	11.33	10.06	27.66	36.66	32.16	37.11	39.66	38.39	4.34	3.78	4.06
JM-14-2	45.33	42.0	44.0	49.67	46.67	48.67	4.77	5.22	5.0	4.33	6.66	5.5	34.89	38.78	36.83	40.33	47.22	43.78	3.78	3.98	3.88
DRMRIJ-12-40	47.33	45.0	46.33	51.0	48.67	50.0	6.55	7.44	7.0	5.77	12.55	9.17	57.33	63.11	60.22	32.89	43.33	38.11	4.16	3.63	3.9
Mean	50.25	48.02	49.46	54.09	51.98	53.38	4.97	6.33	5.65	6.53	9.9	8.22	49.64	55.66	52.65	41.2	43.98	42.59	4.11	4.11	4.11
C.V	5.51	5.81	3.92	6.11	6.2	4.21	7.83	7.79	6.13	8.26	7.9	5.22	8.3	7.21	5.58	9.03	9.43	7.67	5.45	5.85	3.93
CD at 5%	4.5	4.53	3.15	5.37	5.24	3.66	0.63	0.8	0.56	0.88	1.27	0.7	6.7	6.52	4.77	6.05	6.74	5.31	0.36	0.39	0.26
CD at 1%	5.96	6.01	4.18	7.12	6.95	4.85	0.84	1.06	0.75	1.16	1.69	0.92	8.88	8.65	6.33	8.02	8.94	7.05	0.48	0.52	0.35

Genotypes	**Number of seeds per siliqua**			**Plant height (cm)**			**Days to maturity**			**Seed yield per plant (g)**			**Test weight (g)**			**Harvest index (%)**		
	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean
RSPR-03	10.33	13.77	12.06	159.78	225.33	192.56	140.33	137.33	138.833	7.8	9.07	8.44	3.96	4.69	4.33	16.66	17.45	17.06
PM-21	10.55	14.78	12.67	180.33	153.55	166.94	141.33	139.0	140.17	7.48	9.06	8.27	3.85	4.51	4.19	14.96	16.07	15.52
RSPR-01	9.0	13.11	11.06	154.55	170.22	162.39	141.33	141.0	141.17	3.81	5.6	4.7	3.26	2.77	3.02	11.89	12.62	12.26
RH-1209	11.66	15.33	13.5	207.77	169.89	188.83	142.33	136.67	139.50	11.85	15.21	13.54	4.77	5.21	4.99	21.07	23.16	22.12
PM-195	12.66	12.66	12.67	196.33	196.0	196.17	142.0	139.67	140.84	4.16	5.85	5.01	3.65	3.12	3.39	14.56	15.2	14.88
JM-12-6	14.44	15.78	15.11	191.53	139.22	165.38	150.0	145.67	147.84	7.15	6.91	7.03	3.88	3.5	3.69	15.03	15.23	15.13
PM-25	14.88	15.0	14.94	168.55	196.88	182.72	142.33	138.0	140.17	8.29	10.48	9.39	3.92	4.47	4.2	15.34	15.92	15.63
RB-77	11.44	16.89	14.17	173.77	237.11	205.45	137.33	133.33	135.34	8.06	10.39	9.23	3.82	4.25	4.04	17.55	19.06	18.31

PM-28	11.78	12.67	12.23	204.11	215.55	209.83	148.33	143.33	145.83	8.49	12.46	10.47	3.65	3.94	3.8	11.56	16.99	14.28
DRMRIJ-15-85	14.44	12.55	13.5	174.89	202.11	188.5	140.33	136.67	138.50	2.55	3.95	3.25	2.21	2.46	2.34	12.55	12.86	12.71
RSPR-69	13.11	14.33	13.72	197.76	223.66	210.71	151.0	147.67	149.34	3.82	5.02	4.42	3.55	3.84	3.7	13.66	14.54	14.11
RB-50	12.33	15.11	13.72	178.22	198.78	188.5	143.67	141.33	142.5	4.42	4.64	4.53	3.06	3.25	3.16	12.87	13.83	13.35
RH-819	13.44	12.88	13.17	186.11	229.44	207.78	142.33	139.0	140.67	5.57	8.24	6.91	3.85	3.98	3.92	16.09	17.81	16.95
SKJM-5	13.89	14.33	14.11	200.11	234.11	217.11	138.67	135.33	137.01	7.34	7.44	7.39	3.85	3.73	3.79	15.37	15.74	15.56
Tawari	12.89	14.77	13.83	173.22	220.33	196.77	141.0	137.67	139.34	9.25	10.28	9.77	3.69	4.13	3.92	16.88	17.65	17.27
DRMRIJ-31	15.33	15.33	15.34	171.66	183.0	177.33	139.67	136.0	137.83	7.56	8.74	8.15	4.15	4.66	4.41	14.26	15.54	14.9
JD-6	12.89	13.11	13.0	167.66	202.22	184.94	148.67	144.33	146.5	7.30	8.17	7.74	4.67	5.17	4.92	18.32	20.11	19.22
RLC-3	13.55	14.11	13.83	233.55	231.0	232.28	143.0	140.0	141.5	6.15	5.65	5.9	4.85	5.27	5.06	14.88	15.55	15.22
RH-406	12.66	17.55	15.11	170.33	200.77	185.56	137.0	132.67	134.84	6.96	8.41	7.69	3.64	4.15	3.9	15.77	16.17	15.97
PM-125	12.22	12.89	12.56	142.44	216.0	179.22	135.0	130.0	132.5	3.56	3.83	3.7	4.13	4.45	4.29	14.26	14.65	14.46
LES-39	16.11	14.89	15.5	231.0	225.33	228.17	137.67	133.67	135.67	6.25	6.64	6.45	4.34	4.7	4.52	15.76	16.58	16.17
RH-725	13.11	14.11	13.61	201.0	215.33	208.16	136.0	132.0	134.0	7.86	9.16	8.51	3.71	3.87	3.8	14.86	16.86	15.86
DRMR-1059	11.55	14.44	13.0	159.66	214.77	187.223	142.67	139.33	141.0	7.18	8.24	7.71	4.47	4.95	4.71	14.23	16.0	15.12
RH-0123	11.66	15.44	13.55	196.77	163.67	180.22	134.67	130.67	132.67	3.86	4.26	4.06	3.96	3.74	3.85	15.27	15.44	15.35
CN-105364	10.89	12.66	11.78	175.89	207.0	191.443	139.33	139.33	139.34	4.15	4.86	4.50	5.13	3.28	4.21	12.34	12.97	12.66
DRMR-4005	14.44	14.55	14.5	208.0	226.0	217.003	139.67	139.67	139.67	13.58	16.68	15.13	3.96	4.23	4.1	17.13	17.84	17.48
Kranti	12.33	14.89	13.61	198.88	208.55	203.72	153.0	149.67	151.33	14.36	18.06	16.21	4.53	4.73	4.63	16.35	17.78	17.07
NC-37362	11.44	13.22	12.33	219.89	231.22	225.56	136.67	132.0	134.34	5.06	5.64	5.35	2.65	2.83	2.74	12.43	13.58	13.0
DRMR-61-59	11.44	14.0	12.72	191.44	188.22	189.833	140.67	136.33	138.5	4.04	4.44	4.24	3.45	3.86	3.66	13.97	14.85	14.41
DRMR-15-5	10.55	13.11	11.83	173.44	227.55	200.5	133.67	129.67	131.67	5.74	6.83	6.29	4.05	4.30	4.18	15.46	16.04	15.76
DRMR-541-44	10.44	13.55	12.0	179.55	235.66	207.61	143.67	138.67	141.17	7.65	8.14	7.9	4.47	4.74	4.61	14.56	16.54	15.55
DRMR-12-48	10.88	13.77	12.33	220.44	221.77	221.11	139.33	134.33	136.84	10.43	9.74	10.09	3.74	3.56	3.65	15.75	16.77	16.27
DRMR-541-46	13.55	14.88	14.22	187.11	211.11	199.11	140.67	135.67	138.17	10.34	7.72	9.04	3.57	3.64	3.61	15.47	16.55	16.01
RB-69	12.77	15.44	14.11	167.22	185.11	176.167	146.67	142.0	144.34	5.59	5.99	5.79	3.46	3.75	3.61	15.37	15.52	15.45
DRMRIJ-A-35	10.66	13.55	12.11	178.55	196.78	187.667	143.33	139.33	141.34	2.86	3.41	3.14	2.78	2.91	2.85	13.44	13.86	13.66
RB-55	10.55	13.22	11.89	159.0	218.33	188.667	145.67	142.33	144.0	4.57	5.34	4.96	3.16	3.53	3.34	13.65	14.34	14.0

TN-3	13.89	10.89	12.39	258.89	207.55	233.223	149.0	145.0	147.0	3.85	4.44	4.15	3.86	3.74	3.8	12.57	13.06	12.82
RL-1359	11.0	11.0	11.0	161.44	177.66	169.557	143.0	139.33	141.17	11.68	13.21	12.45	5.24	5.85	5.55	18.35	20.43	19.39
JM-14-2	11.89	13.77	12.83	182.66	194.55	188.613	142.33	137.67	140.0	6.46	6.87	6.66	4.05	4.35	4.2	16.07	16.08	16.08
DRMRIJ-12-40	12.66	15.55	14.11	163.89	232.11	198	139.33	133.33	136.34	4.36	4.98	4.67	3.51	3.62	3.57	12.79	13.44	13.12
Mean	12.38	14.1	13.24	186.18	205.84	196.01	141.82	138.12	139.97	6.79	7.85	7.32	3.86	4.04	3.96	14.98	16.02	15.5
C.V	8.32	8.87	6.37	5.49	6.65	6.72	4.06	4.34	3.08	9.59	10.71	7.57	9.31	6.36	5.72	7.01	9.03	5.85
CD at 5%	1.67	2.03	1.37	16.61	22.25	21.42	9.37	9.75	7.02	1.06	1.37	1.19	0.58	0.42	0.37	1.71	2.35	1.47
CD at 1%	2.22	2.69	1.82	22.03	29.51	28.41	12.42	12.93	9.3	1.4	1.81	3.14	0.78	0.55	0.49	2.26	3.12	1.96

Table 4.4: Genetic parameters of variation for seed yield and its component traits in Indian mustard (*Rabi* 2021-22, 2022-23 & pooled)

CHARACTERS	GCV			PCV			h^2 (b.s.)			GA			GA (% of mean)		
	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean
Days to initial flowering	7.7	8.91	8.50	9.47	10.63	9.36	66.17	70.19	82.48	6.48	7.38	7.87	12.90	15.38	15.91
Days to 50% flowering	7.16	7.83	7.78	9.41	9.99	8.85	57.91	61.45	77.32	6.08	6.58	7.52	11.23	12.65	14.09
No. of primary branches/plant	19.07	14.46	13.24	20.62	16.43	14.59	85.57	77.5	82.38	1.81	1.66	1.4	36.34	26.23	24.76
No. of secondary branches/plant	36.26	39.95	36.25	37.19	40.72	36.62	95.07	96.23	97.97	4.76	8.0	6.08	72.83	80.73	73.91
Main shoot length (cm)	22.6	19.44	20.32	24.07	20.73	21.07	88.11	87.9	92.99	21.69	20.89	21.25	43.7	37.54	40.36
No. of siliquae on main shoot	15.38	12.85	13.06	17.84	15.94	15.15	74.36	64.97	74.33	11.26	9.38	9.88	27.33	21.33	23.19
Siliqua length (cm)	15.14	9.12	9.87	16.09	10.83	10.62	88.53	70.85	86.33	1.21	0.65	0.78	29.34	15.81	18.89
No. of seeds per siliqua	11.7	8.26	7.88	14.36	12.12	10.14	66.45	46.44	60.48	2.43	1.63	1.67	19.65	11.59	12.63
Plant height (cm)	12.55	10.95	8.44	13.70	12.81	10.79	83.95	73.04	61.16	44.11	39.66	26.64	23.69	19.27	13.59
Days to maturity	2.17	2.32	2.74	4.61	4.92	4.13	22.14	22.14	44.13	2.98	3.1	5.25	2.10	2.24	3.75
Seed yield/ plant (g)	41.91	43.85	42.5	42.99	45.14	43.17	95.02	94.37	96.93	5.71	6.89	6.31	84.16	87.75	86.19
Test weight (g)	15.33	18.12	16.19	17.94	19.2	17.17	73.06	89.03	88.91	1.04	1.42	1.24	26.99	35.21	31.45
Harvest index (%)	12.4	12.6	12.59	14.24	15.5	13.89	75.77	66.08	82.24	3.33	3.38	3.65	22.23	21.10	23.53

Mean of two-years data showed that primary branches among the genotypes ranged from 4.44 to 7.11 with a general mean of 5.65. Maximum number of primary branches were recorded in Kranti (7.11), while minimum number of primary branches recorded in JD-6 (4.44).

4.2.4 Number of secondary Branches per plant:

In year 2021-22, number of secondary branches ranged from 2.11 to 12.66 with a general mean of 6.64. The lowest number of secondary branches were observed in PM-195 (2.11) while, the highest number of secondary branches were observed in NC-37362 (12.67).

In year 2022-23, number of secondary branches showed the mean of 9.9 with the range of 2 to 23.11. PM-195 (2) recorded lowest number of secondary branches while, the highest secondary branches were recorded by genotype DRMR-4005 (23.11).

Mean of two-years data showed that secondary branches among the genotypes ranged from 2.06 to 16.94 with a general mean of 8.22. Maximum number of secondary branches were recorded in DRMR-4005 (12.67), while minimum number of secondary branches were recorded in PM-195 (2.11).

4.2.5 Main shoot length (cm):

In year 2021-22, main shoot length ranges from 27.66 to 73.55 with a general mean of 49.64. The lowest main shoot length was recorded in RL-1359 (27.66) while, the highest main shoot length was recorded in RH-1209 (73.55).

In year 2022-23, main shoot length showed the mean of 55.66 with the range of 32.66 to 73.89. The lowest main shoot length was recorded in TN-3 (32.66) while, the highest main shoot length in DRMR-4005 (73.89).

Mean of two-years data showed that main shoot length ranged from 32.16 to 72.83 with a general mean of 52.65. Minimum data for main shoot length was recorded in RL-1359 (32.16), while maximum data for main shoot length were recorded in RH-1209 (72.83).

4.2.6 Number of siliquae on main shoot:

During the 2021-22 period, the recorded observations for the quantity of siliquae on the main shoot encompassed a range from 28.11 to 60.44, culminating in an overall average of 41.20. Notably, the genotype NC-37362 exhibited the fewest siliquae on the main shoot (28.11), while conversely, the genotype RH-1209 showcased the highest count (60.44).

In the subsequent year, 2022-23, the dataset for the number of siliquae on the main shoot presented a mean of 43.98, encompassing a range from 29.89 to 56.33. Here, the genotype NC-37362 recorded the lowest count (29.89), while the genotype PM-28 displayed the most abundant count of siliquae on the main shoot (56.33).

Upon combining the data over the two-year span, the range for the number of siliquae on the main shoot extended from 29.0 to 57.06, yielding an overall average of 42.59. The minimum count of siliquae on the main shoot was observed in NC-37362 (29.0), in contrast to the maximum count recorded in RH-1209 (57.06).

4.2.7 Siliqua length:

In year 2021-22, the observation data for siliqua length ranges from 2.29 to 5.70 with a general mean of 4.13. The lowest number of siliqua length was recorded for RSPR-03 (2.29) while, the highest siliqua length was recorded by genotype DRMRIJ-31 (5.70).

In year 2022-23, data for siliqua length showed the mean of 4.11 with the range of 3.30 to 4.84. The lowest siliqua length is recorded for genotype recorded RSPR-01 (3.30) while, the highest siliqua length in genotype RB-69 (4.84).

Mean of two-years data showed that siliqua length ranged from 3.09 to 5.24 with a general mean of 4.11. Minimum data siliqua length was recorded in RSPR-03 (3.09), while maximum data for siliqua length was recorded in DRMRIJ-31 (5.24).

4.2.8 Number of seeds per siliqua:

In year 2021-22, the observation data for number of seeds per siliqua ranges from 9.0 to 16.11 with a general mean of 12.38. The lowest number of seeds per siliqua recorded RSPR-01 (9.0) while, the highest number of seeds per siliqua recorded by genotype LES-39 (16.11).

In year 2022-23, data for number of seeds per siliqua showed the mean of 14.10 with the range of 10.89 to 17.55. The lowest number of seeds per siliqua are recorded for genotype recorded TN-3 (10.89) while, the highest number of seeds per siliqua genotypes RH-406 (17.55).

Mean of two-years data showed that number of seeds per siliqua ranged from 11.0 to 15.5 with a general mean of 13.24. Minimum data for number of seeds per siliqua were

recorded in Rl-1359 (11.0), while maximum data for number of seeds per siliqua were recorded in LES-39 (15.5).

4.2.9 Plant height (cm):

Plant height showed the mean of 186.18 cm with the range of 142.44 cm to 258.89 cm in the year 2021-22. The genotype which showed minimum height was PM-125 (142.44 cm) whereas, TN-3 (258.89 cm) showed maximum plant height.

In the year 2022-23, plant height showed the mean of 205.84 cm with the range of 139.22 cm to 237.11 cm. The genotype which showed minimum height was JM-12-6 (139.22 cm) whereas, RB-77 (237.11cm) showed maximum plant height.

Mean of two-years data showed that plant height among the genotypes ranged from 162.39 cm to 233.22 cm with a general mean of 196.01 cm. Minimum plant height was recorded in RSPR-01 (162.39 cm), while maximum plant height was recorded in TN-3 (233.22 cm).

4.2.10 Days to maturity:

In the 2021-22 timeframe, the mean duration for maturity across genotypes ranged from 133.67 to 153.0 days, yielding an overall average of 141.82 days. Notably, the genotype DRMR-15-5 exhibited the swiftest maturity (133.67 days), while the genotype Kranti displayed the lengthiest duration to maturity (153.0 days).

Similarly, during 2022-23, the mean duration for maturity among genotypes spanned from 129.67 to 149.67 days, with a general mean of 138.12 days. Here, the genotype DRMR-15-5 demonstrated the shortest maturity period (129.67 days), whereas RSPR-69 exhibited the longest (147.67 days).

Taking into account the combined data from the two-year period, the span for days to maturity among genotypes ranged from 131.67 to 151.33 days, resulting in an average of 139.97 days. Notably, the genotype DRMR-15-5 again showcased the shortest time to maturity (131.67 days), while the genotype Kranti persisted as the longest (151.33 days).

4.2.11 Seed yield per plant (g):

In the 2021-22 period, the seed yield per plant exhibited a range from 2.55 g to 14.36 g, culminating in an average of 6.79 g. Noteworthy was the fact that the genotype Kranti

showcased the highest seed yield per plant (14.36 g), while conversely, the genotype DRMR-15-85 displayed the lowest seed yield per plant (2.55 g).

Similarly, during 2022-23, the observed seed yield per plant spanned from 3.40 g to 18.06 g, with an overall mean of 7.85 g. Here, the genotype DRMR-A-35 recorded the minimum seed yield per plant (3.40 g), while the genotype Kranti exhibited the maximum (18.06 g).

Upon amalgamating the data across the two-year period, the seed yield per plant among the genotypes extended from 3.14 g to 16.21 g, resulting in a general mean of 7.32 g. It is notable that the genotype Kranti demonstrated the maximum seed yield per plant (16.21 g), in contrast to the minimum observed in DRMRIJ-A-35 (3.14 g).

4.2.12 Test weight (g):

The 1000 seed weight ranged from 2.21 g to 5.24 g with the mean value of 3.86 g in the year 2021-22. The maximum 1000 seed weight was recorded genotype RL-1359 (5.24) while, the genotype DRMRIJ-15-85 (2.21 g) had the minimum 1000 seed weight.

In year 2022-23, 1000 seed weight showed the mean of 4.0 with the range of 2.46 g to 5.85 g. The lowest 1000 seed weight genotype recorded DRMRIJ-15-85 (2.46 g) while, the highest 1000 seed weight genotypes RL-1359 (5.85 g).

Mean of two-years data showed that 1000 seed weight among the genotypes ranged from 2.34 g to 5.55 g with a general mean of 3.96 g. Maximum 1000 seed weight was recorded in RL-1359 (5.55 g), while minimum 1000 seed weight was recorded in DRMRIJ-15-85 (2.34 g).

4.2.13 Harvest index (percent):

The variation harvest index ranged from 11.56 to 21.07 with the average of 14.98 in the year 2021-22. The genotypes PM-28 had the minimum harvest index (11.56) while, the genotype RH-1209 (21.07) had the maximum harvest index.

In year 2017-18, the harvest index ranged from 12.62 to 23.15 with the mean of 16.02. Maximum harvest index was recorded in genotype RH-1209 (23.16) while, minimum harvest index was recorded in genotype RSPR-01 (12.61).

Mean of two-years data showed that harvest index among the genotypes ranged from 12.26 to 22.12 with a general mean of 15.5. Maximum harvest index was recorded in RH-1209 (21.07), while minimum harvest index was recorded in RSPR-01 (12.26).

4.3 Estimation of genetic parameters:

Genetic parameters including PCV, GCV, heritability, genetic advance, and genetic advance as a percentage of the mean were calculated for all the characteristics and are provided in Table 4.4.

4.3.1 Days to initial flowering:

In the year 2021-22, the trait "days to initial flowering" exhibited a low phenotypic coefficient of variation (PCV) of 9.47 and a genotypic coefficient of variation (GCV) of 7.70. The heritability for this trait was high, recorded at 66.17, while the genetic advance was observed to be low at 6.48. The genetic advance as a percentage of the mean was found to be moderately moderate, at 12.9 percent.

Additionally, for the next year, the PCV was noted as moderate (10.63), the GCV was low (8.91), heritability stood at 70.19 with a low genetic advance of 7.38, and the genetic advance as a percent of the mean was estimated to be 15.38, displaying a medium level.

When considering the pooled data, a low PCV (9.36) and GCV (8.50) were evident. High heritability (82.48) was observed, accompanied by a low genetic advance of 7.87, and the genetic advance as a percent of the mean was measured at a medium level of 15.91, all of which are detailed in Table 4.4.

4.3.2 Days to 50 percent flowering:

In the year 2021-22, the trait "days to 50 percent flowering" exhibited a low phenotypic coefficient of variation (PCV) of 9.41 and a genotypic coefficient of variation (GCV) of 7.16. The heritability for this trait was moderate, recorded at 57.91, while the genetic advance was observed to be low at 6.08. The genetic advance as a percentage of the mean was also recorded at a moderate level of 11.23 percent.

Similarly, in the year 2022-23, the PCV was noted as low (9.41) and the GCV was low (7.16). The heritability for this year was found to be at a high level of 61.45, along with a low

value of genetic advance (6.58) and a moderate genetic advance as a percent of the mean (12.65).

When considering the combined data, both PCV (8.85) and GCV (7.78) were low. High heritability (77.32) was again observed, accompanied by a low genetic advance of 7.52, and the genetic advance as a percent of the mean was measured at a medium level of 14.09, as outlined in Table 4.4.

4.3.3 Number of primary branches per plant:

In the year 2021-22, the trait under consideration displayed a moderate genotypic coefficient of variation (GCV) of 19.07, while the phenotypic coefficient of variation (PCV) was found to be high at 20.61. The heritability for this trait was high, recorded at 85.57, and the genetic advance was observed to be low at 1.81. However, the genetic advance as a percentage of the mean was high at 36.34 percent.

In the subsequent year, 2022-23, the PCV was found to be moderate (16.43), and the GCV was also moderate at 14.46. The heritability was high at 77.5, while the genetic advance was low at 1.66. Nonetheless, the genetic advance as a percentage of the mean remained high at 26.23 percent.

When considering the combined data, high PCV (14.59) and moderate GCV (13.24) were found. High heritability (82.38) was again observed, coupled with a low genetic advance of 1.4. Additionally, the genetic advance as a percentage of the mean was found to be high at 24.76 percent, as indicated in Table 4.4.

4.3.4 Number of secondary branches per plant:

In the year 2021-22, the analyzed trait exhibited both a high phenotypic coefficient of variation (PCV) of 37.19 and a high genotypic coefficient of variation (GCV) of 36.26. This trait also demonstrated high heritability, recorded at 95.07, with a low genetic advance of 4.76. Interestingly, the genetic advance as a percentage of the mean was high, reaching 72.83 percent.

Similarly, in the year 2022-23, the trait displayed both a high PCV (40.72) and a high GCV (39.95). Moreover, the heritability remained high at 96.23, while the genetic advance was low at 8.0. Notably, the genetic advance as a percentage of the mean remained high at 80.73 percent.

Table 4.4: Genetic parameters of variation for seed yield and its component traits in Indian mustard (*Rabi* 2021-22, 2022-23 & pooled)

CHARACTERS	GCV			PCV			h^2 (b.s.)			GA			GA (% of mean)		
	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean	21-22	22-23	Mean
Days to initial flowering	7.7	8.91	8.50	9.47	10.63	9.36	66.17	70.19	82.48	6.48	7.38	7.87	12.90	15.38	15.91
Days to 50% flowering	7.16	7.83	7.78	9.41	9.99	8.85	57.91	61.45	77.32	6.08	6.58	7.52	11.23	12.65	14.09
No. of primary branches/plant	19.07	14.46	13.24	20.62	16.43	14.59	85.57	77.5	82.38	1.81	1.66	1.4	36.34	26.23	24.76
No. of secondary branches/plant	36.26	39.95	36.25	37.19	40.72	36.62	95.07	96.23	97.97	4.76	8.0	6.08	72.83	80.73	73.91
Main shoot length (cm)	22.6	19.44	20.32	24.07	20.73	21.07	88.11	87.9	92.99	21.69	20.89	21.25	43.7	37.54	40.36
No. of siliquae on main shoot	15.38	12.85	13.06	17.84	15.94	15.15	74.36	64.97	74.33	11.26	9.38	9.88	27.33	21.33	23.19
Siliqua length (cm)	15.14	9.12	9.87	16.09	10.83	10.62	88.53	70.85	86.33	1.21	0.65	0.78	29.34	15.81	18.89
No. of seeds per siliqua	11.7	8.26	7.88	14.36	12.12	10.14	66.45	46.44	60.48	2.43	1.63	1.67	19.65	11.59	12.63
Plant height (cm)	12.55	10.95	8.44	13.70	12.81	10.79	83.95	73.04	61.16	44.11	39.66	26.64	23.69	19.27	13.59
Days to maturity	2.17	2.32	2.74	4.61	4.92	4.13	22.14	22.14	44.13	2.98	3.1	5.25	2.10	2.24	3.75
Seed yield/ plant (g)	41.91	43.85	42.5	42.99	45.14	43.17	95.02	94.37	96.93	5.71	6.89	6.31	84.16	87.75	86.19
Test weight (g)	15.33	18.12	16.19	17.94	19.2	17.17	73.06	89.03	88.91	1.04	1.42	1.24	26.99	35.21	31.45
Harvest index (%)	12.4	12.6	12.59	14.24	15.5	13.89	75.77	66.08	82.24	3.33	3.38	3.65	22.23	21.10	23.53

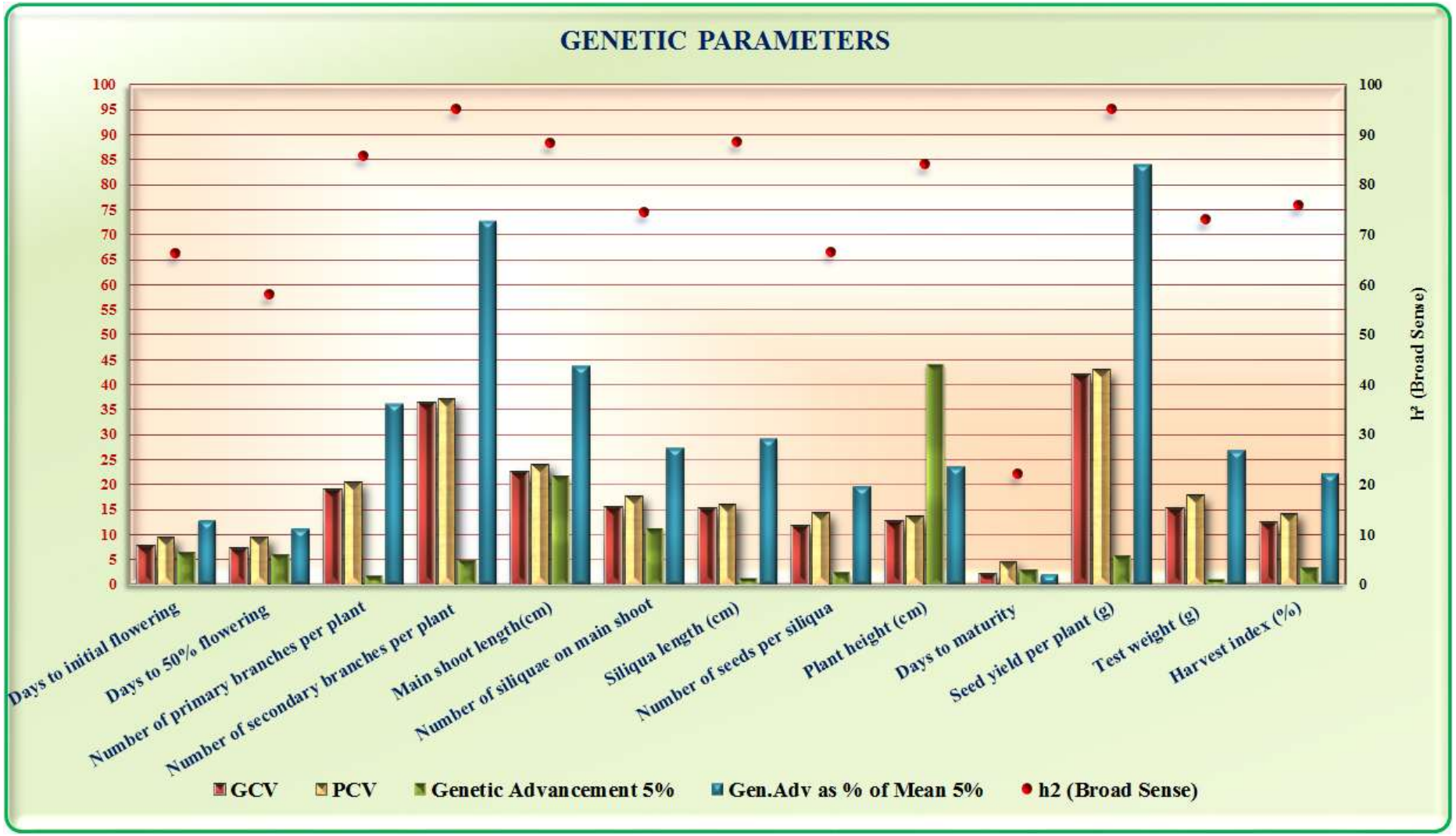

Fig. 4.1 Graphical representation of estimates of genetic parameters for different morphological traits in year 2021-22

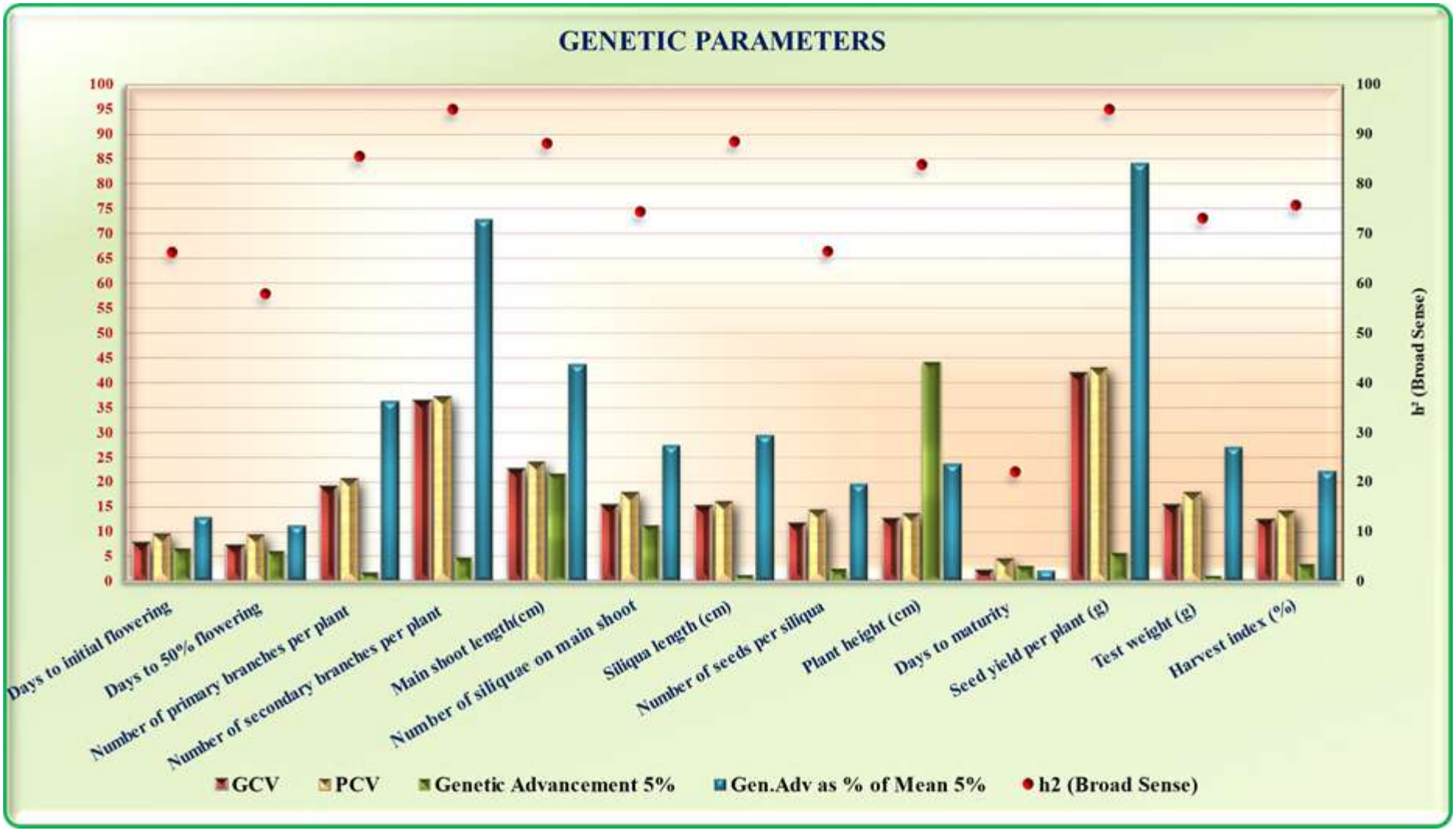

Fig. 4.2 Graphical representation of estimates of genetic parameters for different morphological traits in year 2022-23

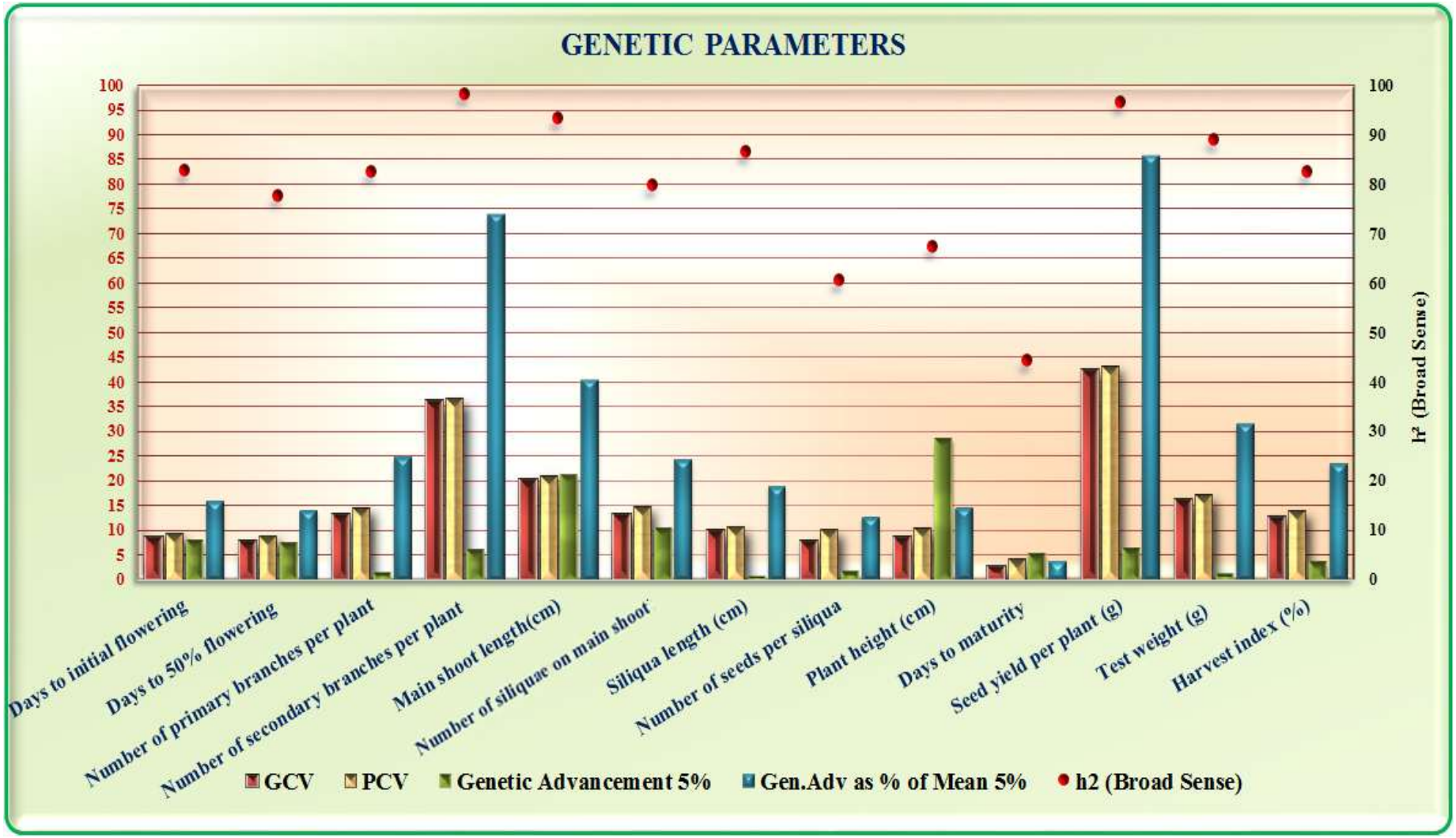

Fig. 4.3 Graphical representation of estimates of genetic parameters for different morphological traits in 2021-22 & 2022-23 (Pooled)

Upon pooling the data, the trait continued to exhibit high PCV (36.62) and GCV (36.65). The heritability was observed to be high at 97.97, while the genetic advance was low at 6.08. The genetic advance as a percentage of the mean was also notably high, recorded at 73.91 percent, as detailed in Table 4.4.

4.3.5 Main shoot length (cm):

For the trait examined, the year 2021-22 revealed a high phenotypic coefficient of variation (PCV) of 24.07 and a high genotypic coefficient of variation (GCV) of 22.60. In contrast, the trait displayed high heritability at 88.11, coupled with a high genetic advance of 21.69. Notably, the genetic advance as a percentage of the mean was substantial, reaching 43.70 percent.

Similarly, in 2022-23, the PCV was high (20.73) and the GCV was moderate (19.43). The trait continued to exhibit high heritability (87.9) and a high genetic advance (20.89), with the genetic advance as a percentage of the mean at 37.54 percent.

On a combined basis, the trait displayed high PCV (21.07) and GCV (20.32). High heritability (92.99) was observed alongside a high genetic advance of 21.25, and the genetic advance as a percentage of the mean was recorded at 40.36 percent, as outlined in Table 4.4.

4.3.6 Number of siliquae on main shoot:

For the trait analyzed, the year 2021-22 showcased a moderate phenotypic coefficient of variation (PCV) of 17.84 and a low genotypic coefficient of variation (GCV) of 15.38. On the other hand, the trait exhibited high heritability at 74.36, coupled with a moderate genetic advance of 11.26. Impressively, the genetic advance as a percentage of the mean was high at 27.33 percent.

Similarly, in 2022-23, the PCV was moderate (15.94) and the GCV was low (12.85). The trait maintained a high heritability (64.97) while the genetic advance was low at 9.38. Nonetheless, the genetic advance as a percentage of the mean remained high at 21.33 percent.

Combining the data, the trait demonstrated a medium PCV (15.15) and GCV (13.06). The heritability continued to be high (74.33), alongside a medium genetic advance of 9.88. The genetic advance as a percentage of the mean was notably high at 23.19 percent, as detailed in Table 4.4.

4.3.7 Siliqua length:

For the trait assessed, the year 2021-22 displayed a moderate phenotypic coefficient of variation (PCV) of 16.09 and a moderate genotypic coefficient of variation (GCV) of 15.13. In the same period, the trait exhibited high heritability at 88.53, accompanied by a low genetic advance of 1.21. Notably, the genetic advance as a percentage of the mean was found to be high at 29.34 percent.

In 2022-23, the PCV was moderate (10.83) and the GCV was low (9.12). Despite this, the trait maintained a high heritability at 70.81, alongside a low genetic advance of 0.65. Additionally, the genetic advance as a percentage of the mean was noted to be at a medium level of 15.81 percent.

Considering the pooled data, the trait displayed a moderate PCV (10.62) and low GCV (9.87). The heritability was moderate (86.33), and the genetic advance remained low at 0.78. The genetic advance as a percentage of the mean was recorded at a moderate level of 18.89 percent, as outlined in Table 4.4.

4.3.8 Number of seeds per siliqua:

For the trait studied, the year 2021-22 revealed a moderate phenotypic coefficient of variation (PCV) of 14.36 and a moderate genotypic coefficient of variation (GCV) of 11.7. Similarly, the trait displayed high heritability at 66.45, along with a low genetic advance of 2.43. Moreover, the genetic advance as a percentage of the mean was found to be moderate at 19.65 percent.

In 2022-23, the PCV was moderate (11.7) and the GCV was low (8.26). In this year, the heritability was at a medium level of 46.44, and the genetic advance was low at 1.63. The genetic advance as a percentage of the mean was noted to be moderate, at 11.59 percent.

When combining the data, the trait demonstrated a moderate PCV (10.14) and low GCV (7.88). The heritability remained high at 60.48, while the genetic advance was low at 1.67. The genetic advance as a percentage of the mean was observed to be at a moderate level of 12.63 percent, as outlined in Table 4.4.

4.3.9 Plant height

For the trait "plant height," in the year 2021-22, a medium phenotypic coefficient of variation (PCV) of 13.7 and a medium genotypic coefficient of variation (GCV) of 12.55 were observed. High heritability was noted at 83.95, accompanied by a high genetic advance of 44.11. Furthermore, the genetic advance as a percentage of the mean was found to be at a moderate level of 23.69 percent.

Similarly, in 2022-23, the PCV was moderate (12.81) and the GCV was recorded at 10.95. In this year, the heritability was at a medium level of 73.04, while the genetic advance was high at 39.66. The genetic advance as a percentage of the mean was observed to be moderate, at 19.3 percent.

Upon considering the pooled data, the trait maintained a moderate PCV (10.79) and a low GCV (8.44). High heritability (61.16) was coupled with a high genetic advance of26.64, and the genetic advance as a percentage of the mean was obtained at 13.59 percent, as outlined in Table 4.4.

4.3.10 Days to maturity

The low PCV (4.61) and GCV (2.17) was obtained whereas, low heritability (22.14) with low genetic advance (2.98) and genetic advance as percent of mean (2.10) was found for the trait in 2021-22.

The low PCV (4.92) and GCV (2.32) was found while low heritability (22.14) with low genetic advance (3.10) and genetic advance as percent of mean (2.24) was obtained in 2022-23.

On the pooled basis, low PCV (4.13) and GCV (2.74) was obtained whereas medium heritability (44.13) and low genetic advance (5.25) and genetic advance as percent of mean (3.75) was recorded.

4.3.11 Seed yield per plant

The high PCV (42.99) with GCV (41.91) was obtained while high heritability (95.02) with low genetic advance (5.71) and high genetic advance as percent of mean (84.16) was obtained in 2021-22.

Similarly, high PCV (45.14) and high GCV (43.85) was obtained while high heritability (94.37) with low genetic advance (6.89) and high genetic advance as percent of mean (87.75) was obtained in 2022-23.

On pooled basis, high PCV and GCV (43.17 and 42.50 resp.) was found for the trait whereas high heritability (96.93) and low genetic advance (6.31) and high genetic advance as a percentage of mean (86.19) was found.

4.3.12 Test weight

For this trait moderate PCV (17.94) with GCV (15.33) was found in 2021-22 with high value of heritability (73.06). Low genetic advance (1.04) and high genetic advance as percent of mean (26.99) was obtained.

In 2022-23 moderate PCV (19.19) with moderate GCV (18.12) was found and high heritability (89.03) and low genetic advance (1.42) and high genetic advance as percent of mean (35.21) was recorded.

On pooled basis, moderate PCV (17.17) with moderate GCV (16.19) was obtained whereas high heritability (88.91) low genetic advance (1.24) and high genetic advance as percent of mean (31.45) was recorded.

4.3.13 Harvest index

Moderate PCV (14.24) with GCV (12.40) were found in 2021-22 with high heritability (75.77). Low genetic advance (3.33) and high genetic advance as percent of mean (22.23).

In 2022-23 moderate PCV (15.5) and GCV (12.60) with high heritability (66.08), low genetic advance (3.38) and high genetic advance as percent of mean (21.1) was found.

Pooled estimation showed moderate PCV (13.89) and low GCV (12.59) was found whereas high heritability (82.24) with low genetic advance (3.65) and moderate genetic advance as percent of mean (23.53) was found for the trait.

4.4 Oil content

Oil content ranged from 34.03 to 42.04. Maximum oil content was recorded in DRMR-541-44 (42.04 percent), while minimum oil content was recorded in PM-21 (34.03 percent) with a mean of 39.02 as mentioned in Table 4.5.

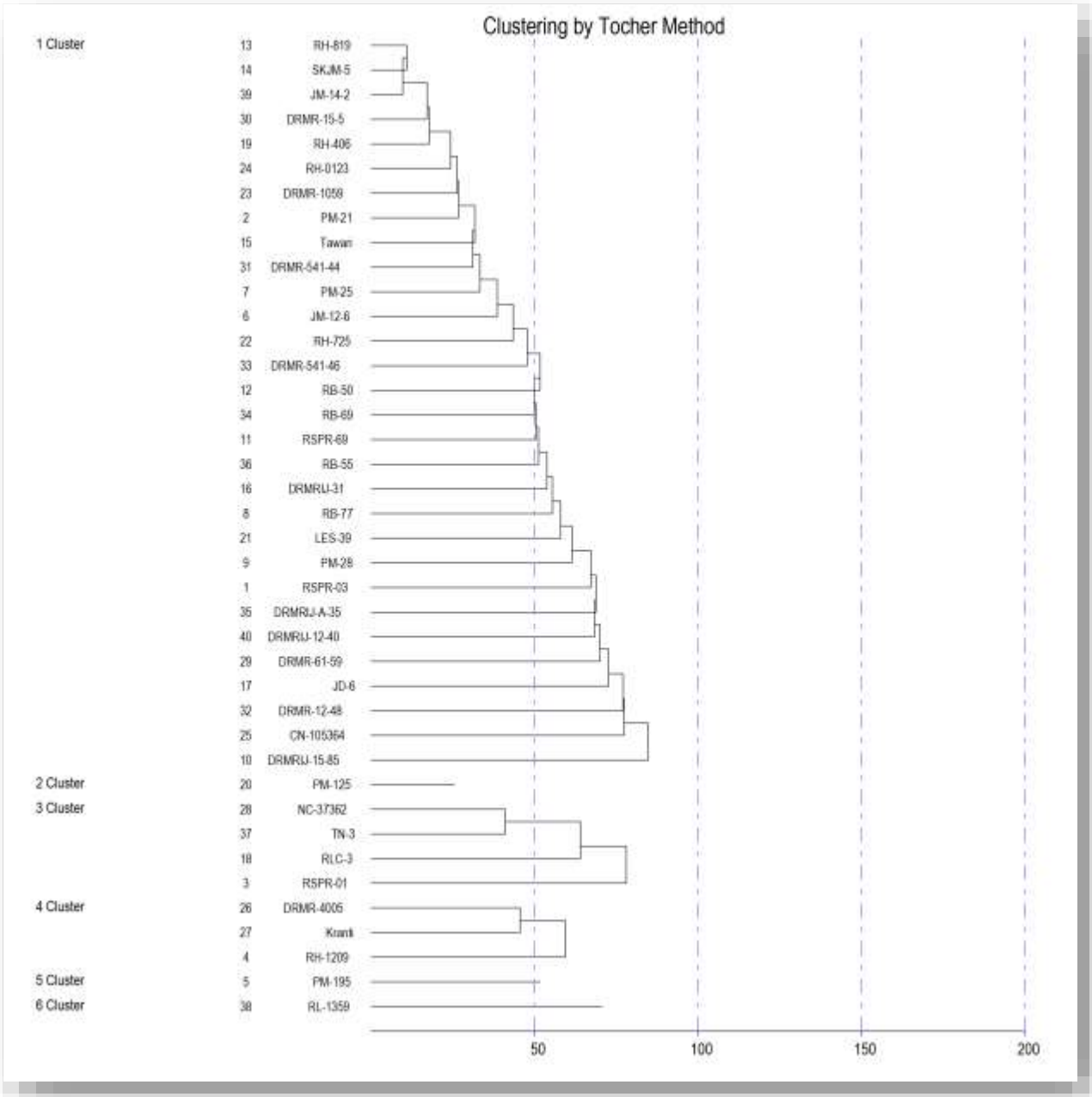

Fig.-4.4: Dendrogram showing clustering of genotypes

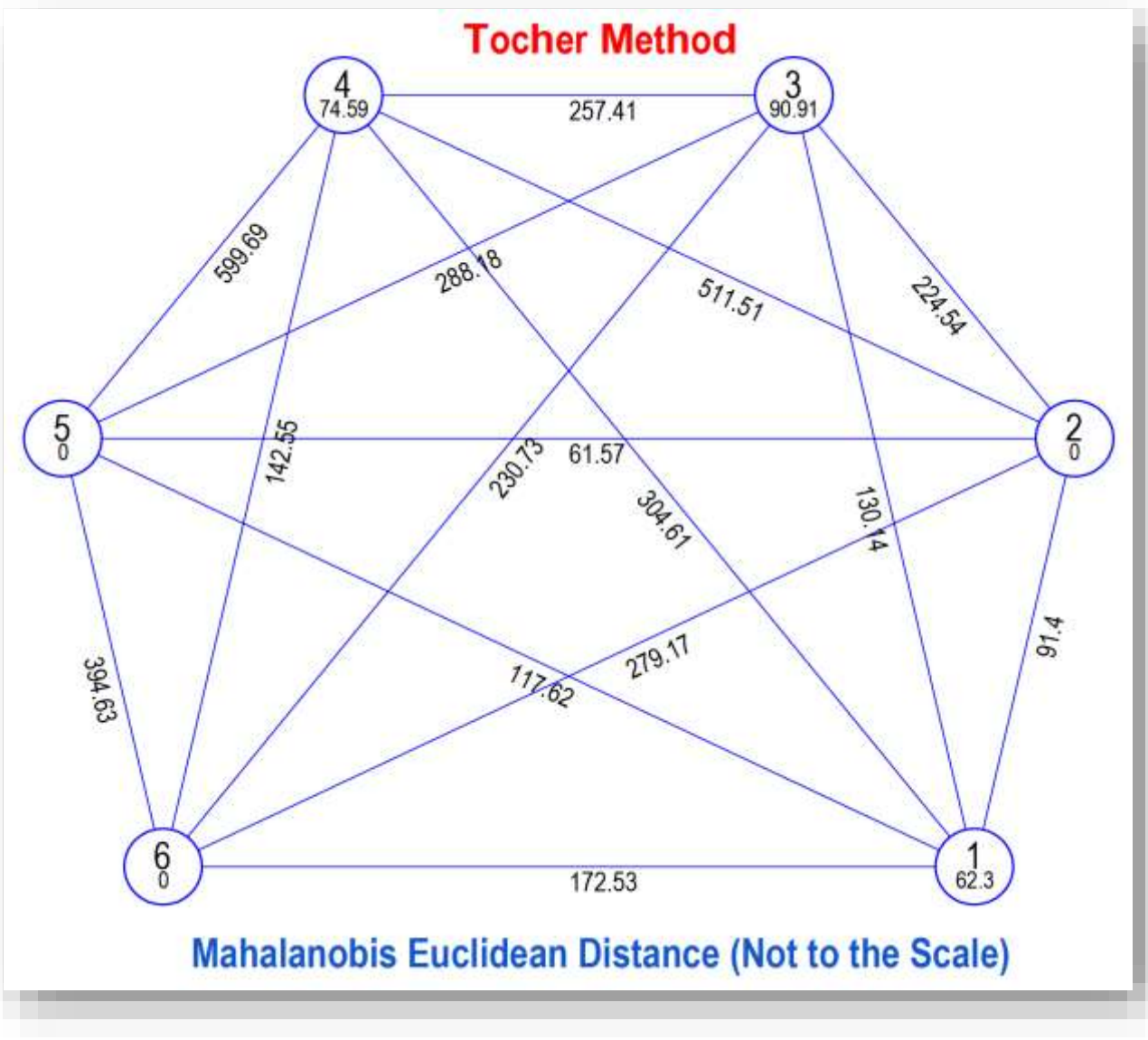

Fig 4.5: Mahalanobis Euclidean distance through tocher method

Table-4.5: Estimates of oil content (%) in top high yielding 40 diverse advanced breeding lines/ genotypes:

S.No.	Genotypes	Oil content (percent)
1.	RSPR-03	34.66
2.	PM-21	34.03
3.	RSPR-01	36.45
4.	RH-1209	39.31
5.	PM-195	38.20
6.	JM-12-6	39.10
7.	PM-25	39.20
8.	RB-77	40.35
9.	PM-28	38.40
10.	DRMRIJ-15-85	38.55
11.	RSPR-69	36.18
12.	RB-50	40.73
13.	RH-819	37.25
14.	SKJM-5	40.86
15.	Tawari	39.40
16.	DRMRIJ-31	36.02
17.	JD-6	39.63
18.	RLC-3	40.10
19.	RH-406	39.68
20.	PM-125	38.50

S.No.	Genotypes	Oil content (percent)
21.	LES-39	40.10
22.	RH-725	39.10
23.	DRMR-1059	40.60
24.	RH-0923	38.68
25.	CN-105364	39.80
26.	DRMR-4005	40.80
27.	Kranti	39.17
28.	NC-37362	39.10
29.	DRMR-61-59	40.10
30.	DRMR-15-5	40.17
31.	DRMR-541-44	42.04
32.	DRMR-12-48	39.80
33.	DRMR-541-46	40.20
34.	RB-69	38.72
35.	DRMRIJ-A-35	40.30
36.	RB-55	40.52
37.	TN-3	39.10
38.	RL-1359	35.95
39.	JM-14-2	39.80
40.	DRMRIJ-12-40	40.20
Mean value		**39.02**

Table 4.6: Distribution of 40 advanced breeding lines/ genotypes into different clusters (Pooled)

Cluster Group	No. of Genotypes	List of Genotypes
Cluster I	30	RH-819, SKJM-5, JM-14-2, DRMR-15-5, RH-406, RH-0123, DRMR-1059, PM-21, Tawari, DRMR-541-44, PM-25, JM-12-6, RH-725, DRMR-541-46, RB-50, RB-69, RSPR-69, RB-55, DRMRIJ-31, RB-77, LES-39, PM-28, RSPR-03, DRMRIJ-A-35, DRMRIJ-12-40, DRMR-61-59, JD-6, DRMR-12-48, CN-105364 & DRMRIJ-15-85
Cluster II	1	PM-125
Cluster III	4	NC-37362, TN-3, RLC-3 & RSPR-01
Cluster IV	3	DRMR-4005, Kranti & RH-1209
Cluster V	1	PM-195
Cluster VI	1	RL-1359

Table-4.7: Cluster mean value of thirteen different characters in mustard advanced breeding lines/ genotypes (Pooled).

	Days to initial flowering	Days to 50% flowering	Number of primary branches	Number of secondary branches	Main shoot length(cm)	Number of siliquae on main shoot	Siliqua length (cm)	Number of seeds per siliqua	Plant height (cm)	Days to maturity	Seed yield per plant (cm)	Test weight (g)	Harvest index (%)
Cluster I	49.08	52.81	5.45	7.36	51.97	41.60	4.11	13.41	194.42	139.66	6.89	3.89	15.38
Cluster II	42.33	46.00	4.89	4.72	51.94	46.61	5.03	12.56	179.22	132.50	3.70	4.29	14.46
Cluster III	51.33	55.75	6.71	12.50	50.43	46.13	3.86	12.40	213.36	141.00	5.03	3.66	13.32
Cluster IV	53.11	57.78	7.00	13.78	65.05	48.22	4.23	13.87	203.18	143.50	14.96	4.57	18.89
Cluster V	47.67	51.67	4.83	2.06	65.94	41.61	4.08	12.67	196.17	140.84	5.01	3.39	14.88
Cluster VI	51.33	55.00	5.17	10.06	32.16	38.39	4.06	11.00	169.56	141.17	12.45	5.55	19.39

Table 4.8: Intra (diagonal) and inter cluster average D^2 distance for different clusters in Indian mustard (Pooled)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	62.30	91.40	130.14	304.61	117.62	172.53
Cluster II		0.00	224.54	511.51	61.57	279.17
Cluster III			90.91	257.41	288.18	230.73
Cluster IV				74.59	599.69	142.55
Cluster V					0.00	394.63
Cluster VI						0.00

Table 4.9: Contribution of individual characters towards divergence (Pooled)

S. No.	Source	Contribution (%)	Times ranked 1st
1	Days to initial flowering	1.67	13
2	Days to 50% flowering	3	23
3	Number of primary branches per plant	1.54	12
4	Number of secondary branches per plant	8.43	66
5	Main shoot length (cm)	12.82	100
6	Number of siliquae on main shoot	7.54	59
7	Siliqua length (cm)	9.32	73
8	Number of seeds per siliqua	1.41	11
9	Plant height (cm)	3.46	27
10	Days to maturity	4.04	31
11	Seed yield per plant (cm)	34.9	272
12	Test weight (g)	7.05	55
13	Harvest index (%)	4.82	38

Table 3.6: List of SSR primers used for molecular study

S. No.	Primer Name	Primer Sequence Forward (F)-(5'-3') Reverse (R)-(3'-5')	Annealing temperature (°C)
1.	A02_18870790	F-5'TACACCGTCTGATTCCATCT3' R-3'GCCTGACTGCTGCTACTAAC5'	55
2.	Na10-D07	F-5'CTACTTTGATGGACACTTGCC3' R-3'TCTGAAGTTGATTAGTCGGTCC5'	61
3.	A03_3174449	F-5'AAAGAAGAGCTTTGAAGAGGA3' R-3'TTGATTCACAACACACATACC5'	55
4.	A09_27227566	F-5'GGGAGTGAAATGAAGAGAAGA3' R-3'GCTTCACAGCTGTTTAATCTC5'	55
5.	Ni4-F11	F-5'CGTAAGTTTCAATTGTCAACGG3' R-3'TCGTACGAAACAATCAACGG5'	58
6.	Ni2-H06	F-5'CATCAGATCCGACGAAATCC3' R-3'TCCTTTGGACTGTGAAAAACG5'	60
7.	A05_25290881	F-5'ATAAAGATTTGATGGGAGGAG3' R-3'GGTGGAGGAGGATAGTTGTAG5'	55
8.	Ni2-C09	F-5'ACGGAAGAAATCCAACCTCG3' R-3'TATGCTTGGAAATGGTTTGG5	58
9.	Ni3-C08	F-5'CCCTAACACGGTGTCAACAG3' R-3'GGCAGAATCATCGAGAGGTC5'	62
10.	Ni3-C05	F-5'TTTCGTGCTTTGGTGTGAAG3' R-3'TCCCCAAATCGAACCATAAG	58

Table 4.10: Representation of Polymorphic primers, their number of alleles identified & Polymorphism Information Content

S.No.	Marker Name	No. of different alleles	Polymorphism Information content (PIC)
1.	**A02-12270790**	2.000	0.44
2.	**Na10 Do-7**	2.000	0.75
3.	**A09-3174449**	2.000	0.61
4.	**A05-25290221**	2.000	0.44

4.5 Genetic diversity analysis:

Data were collected from 40 genotypes of mustard, encompassing thirteen distinct traits: Days to initial flowering, Days to 50 percent flowering, Number of primary branches per plant, Number of secondary branches per plant, Main shoot length (cm), Number of siliquae on main shoot, Siliqua length (cm), Number of seeds per siliqua, Plant height (cm), Days to maturity, Seed yield per plant (g), Test weight (g), and Harvest index (percent). These traits were scrutinized to uncover the genetic divergence among the genotypes. The quantitative assessment of this genetic divergence was executed utilizing the Mahalanobis D^2 statistic, which encompassed both yield and its contributing attributes. The findings derived from this study are presented subsequently, organized into the following sections.

4.5.1 Generalized Distance (D^2):

The Mahalanobis D^2 statistic was employed to evaluate the genetic diversity among the 40 genotypes, leading to the formation of six distinct clusters based on their genetic divergence, as detailed in Table 4.13. Among the six clusters, cluster I was the most extensive, encompassing thirty genotypes, while cluster III followed with four genotypes and cluster IV comprising three genotypes. Conversely, clusters II, V, and VI were smaller in size, each accommodating only one genotype as mentioned in Table 4.6.

4.5.2 Maximum and minimum values of various clusters for different characters:

Maximum mean values for days to initial flowering, days to 50 percent flowering, number of primary branches per plant, number of secondary branches per plant, number of siliquae on main shoot, number of seeds per siliqua, days to maturity, seed yield per plant were found in cluster IV, maximum mean value for siliqua length was found in cluster II, maximum mean value for plant height was found in cluster III, maximum mean value for main shoot length was found in cluster V, while mean value for Test weight and harvest index was found in cluster VI.

Minimum value for days to initial flowering, days to 50 percent flowering, days to maturity and test weight were found in cluster II, Similarly, minimum value for main shoot length, number of siliquae on main shoot, number of seeds per siliqua, plant height were found in cluster VI. Minimum values for siliqua length and harvest index were found in cluster III and minimum values for number of primary branches per plant, number of secondary branches per plant and test weight in cluster V as depicted in Table 4.7

4.5.3 Average Intra and Inter Cluster Distance

The average values for intra and inter-cluster Mahalanobis D^2 values are presented in Table 4.15. The intra-cluster D^2 values ranged from 0.00 (in clusters II, V, and VI) to 90.91 (in cluster III). The inter-cluster D^2 values among the six clusters revealed the highest divergence between cluster IV and cluster V (599.69), followed by cluster II and cluster IV (511.51), cluster V and cluster VI (394.63), Cluster I and cluster IV, cluster III and cluster V (288.18), cluster II and cluster VI (279.17), cluster III and cluster IV (257.41), cluster III and cluster VI (230.73).

Conversely, the lowest divergence was observed between cluster II and cluster V (61.57), followed by cluster I and cluster II (91.40), cluster I and cluster V (117.62), cluster I and cluster III (130.14), cluster IV and cluster VI (142.55), and cluster II and cluster III (224.54) as shown in Table-4.8.

4.5.4: Relative Contribution of Characters towards Diversity

Data presented in Table-4.9 showed that the character seed yield per plant contributed maximum (34.9 percent) to the diversity followed by main shoot length (12.82), siliqua length (9.32), number of secondary branches per plant (8.43), number of siliquae on main shoot (7.54), test weight (7.05), harvest index (4.82), days to maturity (4.04), plant height (3.46), days to 50 percent flowering (3.0), days to initial flowering (1.67), number of primary branches (1.54), number of seeds per siliqua (1.41).

4.6 Molecular polymorphism in advanced breeding lines/ genotypes lines of *Brassica juncea*

To detect polymorphism in advanced breeding lines/ genotypes lines of Indian Mustard through molecular markers, SSR were used in the present investigation. 40 different lines were used for their molecular characterization. Genetic diversity was checked among these lines using agarose gel with the help of 10 PCR based SSR primers.

4.6.1 Primer based amplification:

A total set of 10 SSR primers were used, out of which five were found to be polymorphic, namely, A02-12270790, Na10 Do-7, A09-3174449, A05-25290221.

4.6.2 Polymorphism information content (PIC):

Polymorphic information content (PIC) determines the discriminatory power of a locus as it consider the number of alleles expressed as well as their relative frequency. PIC value of each SSR primer is presented in Table 4.10. The PIC values were ranged from 0.44 to 0.75 with an average value of 0.56. The higher PIC value was exhibited by Na10 Do-7 (0.75) followed by A09-3174449 (0.61), A02-12270790 (0.44), A05-25290221 (0.44).

4.6.3 Number of different alleles:

Among all the 4 primers which were polymorphic, scoring data of the amplified product showed that all four primers viz., A02-12270790, Na10 Do-7, A09-3174449, A05-25290221 showed two different type of alleles per locus as presented in table 4.10.

4.6.4 Cluster analysis using SSR markers:

The molecular data attained from 40 diverse lines of *Brassica juncea* with SSR markers were analyzed with Un-weighted Paired Group Method on Arithmetic averages (UPGMA) by using NTSYS software and a dendrogram was constructed from genetic similarity coefficients to explain genetic relationships among these 40 diverse lines. Forty lines were grouped into five major clusters. Cluster I contains twenty seven genotypes i.e. RSPR-03, PM-21, RH-1209, PM-195, PM-25, PM-20, DRMRIJ-15-25, RB-50, RH-719, DRMRIJ-31, JD-6, RLC-3, PM-125, LES-39, RH-725, RH-0923, CN-105364, DRMR-4005, Kranti, DRMR-15-5, DRMR-541-44, DRMR-541-46, RB-69, DRMRIJ-A-35, TN-3, RL-1359, JM-14-2, cluster II contains 2 genotypes i.e. RSPR-01 and RH-406, cluster III contains three genotypes i.e. JM-12-6, SKJM-5, DRMR-61-59, cluster IV contains four genotypes i.e. RB-77, RSPR-69, DRMRIJ-12-40, DRMRIJ-12-48, cluster V contains four genotypes i.e. Tawari, DRMR-1059, NC-37362, RB-55.

Table 4.10: Representation of Polymorphic primers, their number of alleles identified & Polymorphism Information Content

S.No.	Marker Name	No. of different alleles	Polymorphism Information content (PIC)
1.	**A02-12270790**	2.000	0.44
2.	**Na10 Do-7**	2.000	0.75
3.	**A09-3174449**	2.000	0.61
4.	**A05-25290221**	2.000	0.44

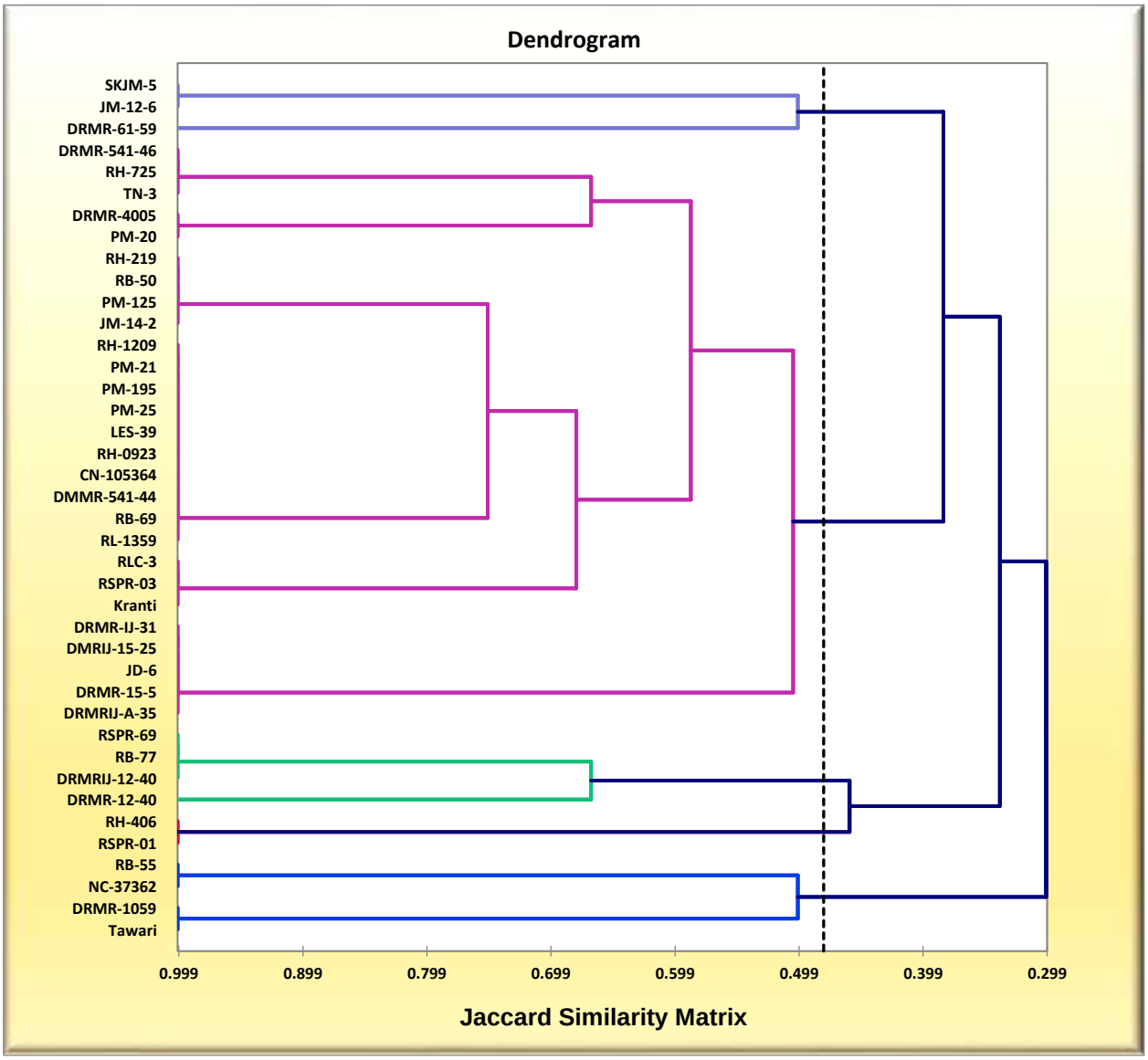

Fig 4.6: Jaccard similarity matrix

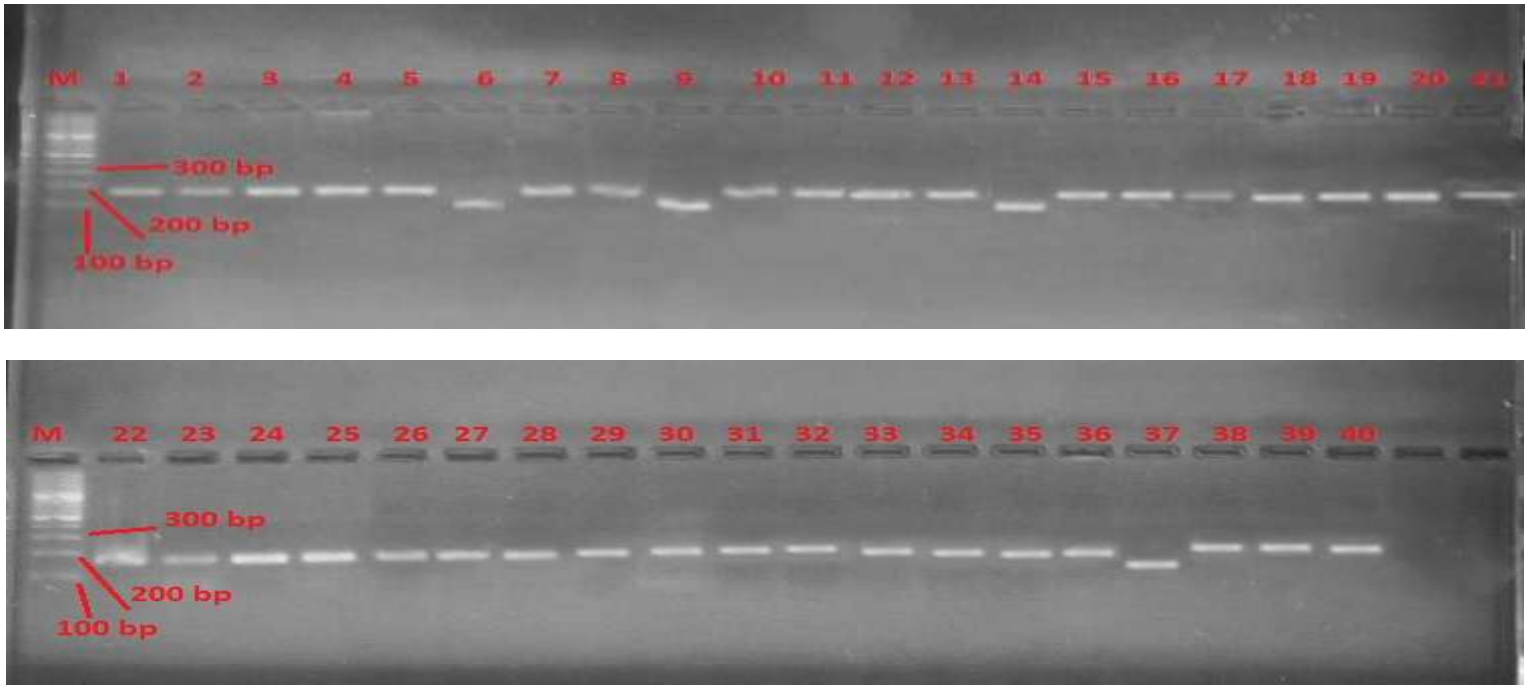

Plate 1 : Amplified PCR products obtained with SSR primer A02-12270790 compared with 100 bp ladder [M: marker (DNA Ladder of 100-1000 bp)], with 40 diverse lines of Indian mustard

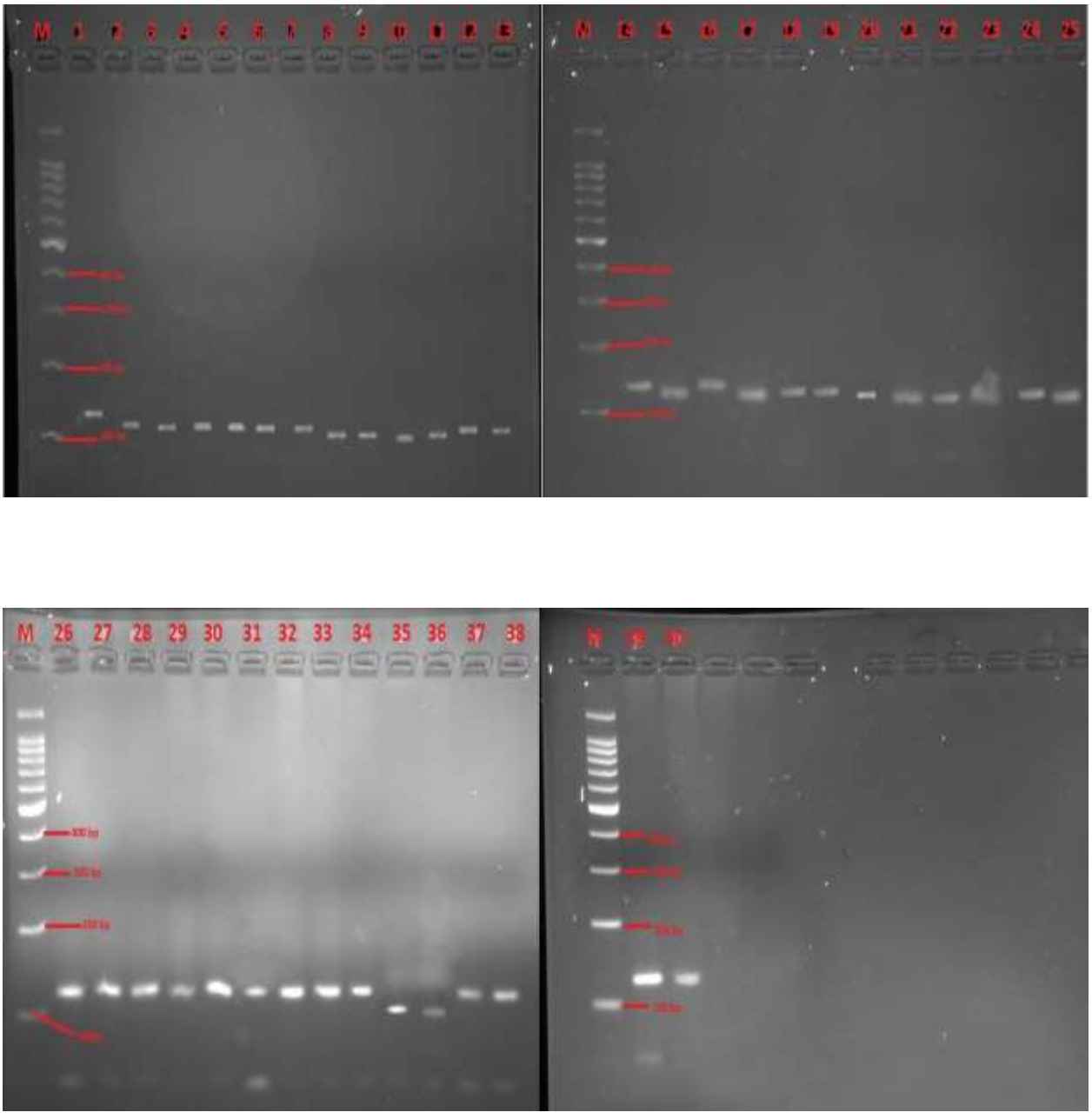

Plate 2: Amplified PCR products obtained with SSR primer Na10 Do-7 compared with 100 bp ladder [M: marker (DNA Ladder of 100-1000 bp)], with 40 diverse lines of Indian mustard

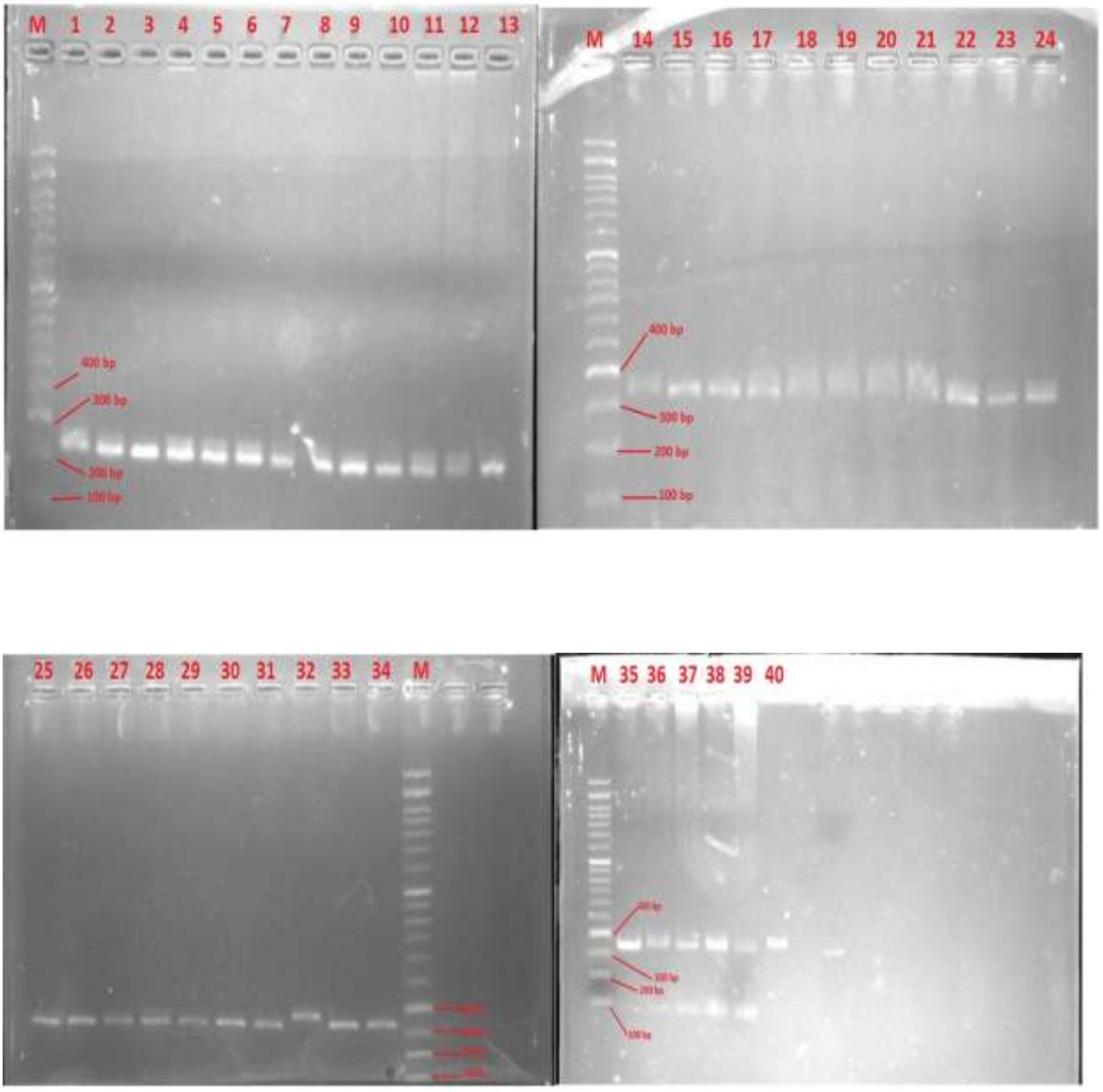

Plate 3: Amplified PCR products obtained with SSR primer A09-3174449 compared with 100 bp ladder [M: marker (DNA Ladder of 100-1000 bp)], with 40 diverse lines of Indian mustard

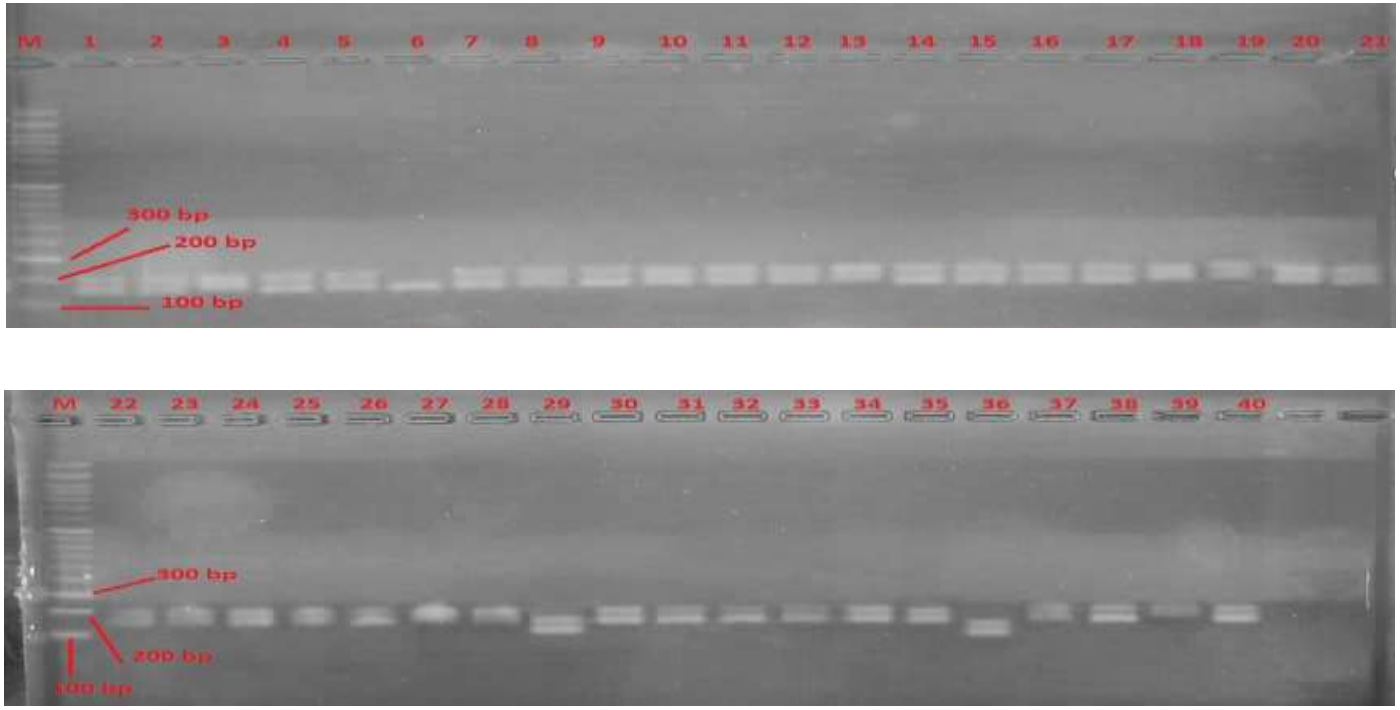

Plate 4: Amplified PCR products obtained with SSR primer A05-25290221 compared with 100 bp ladder [M: marker (DNA Ladder of 100-1000 bp)], with 40 diverse lines of Indian mustard

Plate 5: Pictures showing experimental field at different stages and work at molecular biology laboratory

CHAPTER 5

DISCUSSION

Indian mustard (*Brassica juncea* (L.) Czern. & Coss.) holds a significant place as both an oilseed crop and a source of valuable nutrients. The seeds of Indian mustard are rich in oil content, making them a crucial source of edible oil. This oil is renowned for its nutritional qualities, particularly its high content of essential fatty acids with balanced ratio of omega-3 and omega-6 fatty acids, vitamin E and many other essential nutrients that can contribute to a well-rounded and healthy diet.

Varieties play a pivotal role in plant breeding, serving as the tangible outcomes of breeding efforts and representing the culmination of genetic improvement. Improved variety is the first and most important requirement for initiation and accelerated crop production program. By selecting and crossbreeding plants with favorable traits, breeders create new varieties that excel in crucial aspects that collectively boost yield potential. The study of genetic parameters is crucial in plant breeding as it provides essential insights into the inheritance patterns and potential for trait improvement. By understanding parameters like heritability, genetic variance, and genotype-environment interactions, breeders can select superior parent plants, predict trait expression, and design effective breeding strategies. This knowledge enables the development of new varieties with improved yield, and other desirable traits. Additionally, it aids in optimizing resource allocation and selection efforts, resulting in more efficient and successful plant breeding programs. On the other hand, diversity studies hold critical importance in elevating crop yield by analyzing and harnessing the genetic diversity within a species, breeders can identify valuable traits that enhance yield potential. Diverse genetic backgrounds provide access to variations in various morphological traits that can be incorporated into breeding programs to create high-yielding varieties. This approach, ultimately leads to improved crop productivity and global food security. Similarly, SSR (Simple Sequence Repeat) marker-based molecular studies play a pivotal role in exploring genetic diversity within plant breeding. These markers provide a reliable and cost-effective method to analyze genetic variations at the molecular level. By assessing the presence and distribution of SSRs across plant genomes, breeders can precisely quantify genetic diversity, determine relatedness between individuals, and identify unique traits for targeted selection. SSR markers facilitate the identification of diverse parent plants for crossbreeding, leading to the development of novel varieties with improved yield. This molecular approach accelerates

the breeding process by allowing breeders to make informed decisions based on data-driven insights, ultimately resulting in the creation of high-performing crops that contribute to increased agricultural productivity.

In present study 40 diverse advanced breeding lines/ genotypes of Indian mustard were evaluated morphologically and simultaneously genetic polymorphism was determined in 40 genotypes using microsatellite markers. Results obtained in the present study entitled "Genetic analysis of yield traits in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]" have been discussed citing relevant literature and explanations as follows:

5.1 Analysis of Variance:

This method assesses plant variations, identifies trait differences for informed breeding selections, and dissects genetic and environmental contributions. It's a crucial tool for designing effective breeding strategies, optimizing programs, and enhancing agricultural productivity.

In present study, analysis of variance revealed that all the characters under consideration had significant differences among the studied genotypes in both the seasons i.e., *Rabi* 2021-22 & 2022-23. The presence of a significant amount of genetic variations among lines may be due to inherent variations in the parents being hybridized. Similar results were also reported previously by Akoju *et al*., 2020 and Pradhan *et al*. 2021.

5.2 Estimation of genetic parameters:

5.2.1 Genetic and phenotypic coefficient of variation:

Genotypic and phenotypic coefficients of variation play a crucial role in evaluating the variability of traits within a population. The GCV serves as a quantification of the genetic diversity inherent in a group of plants, showcasing the potential for enhancement through selective breeding practices. Conversely, the PCV encapsulates both genetic and environmental influences on traits. These coefficients are instrumental in identifying traits primarily governed by genetics, aiding in focusing on those with higher heritability during the selection process. By comparing GCV and PCV, breeders can pinpoint reliable indicators of genetic potential, thereby facilitating more precise selections for creating superior plant varieties endowed with desired traits.

Notably, the phenotypic coefficient of variation (PCV) exceeded the corresponding genotypic coefficient of variation (GCV) across all observed characteristics. This outcome is

consistent with findings from Shekhawat *et al*., (2014); Patel *et al*., (2019), and Yadav *et al*. (2021).

During *Rabi* 2021-22, both high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were exhibited by seed yield per plant, secondary branches per plant, and main shoot length. Also, for number of primary branches per plant substantial PCA was detected during this season. Similarly, during *Rabi* 2022-23, high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were reported for seed yield per plant and secondary branches per plant. High PCV was also reported for main shoot length during the same season. These outcomes align with findings from Anjali *et al*., (2022), and Vanukuri *et al*. (2022). Likewise, Rout *et al*., (2019) and Kumar *et al*. (2020) also reported akin results, particularly concerning the heightened genetic and phenotypic coefficients of variation in main shoot length.

Moderate estimations of the coefficient of variation, encompassing both phenotypic (PCV) and genotypic (GCV) aspects, were marked across several attributes. These attributes included the number of siliquae on the main shoot, test weight, siliqua length, plant height, number of seeds per siliqua, and harvest index. In the *Rabi* season of 2021-22, a moderate genotypic coefficient of variation was also evident for the number of primary branches per plant. Similarly, during the *Rabi* season of 2022-23, moderate values of both PCV and GCV were identified for test weight, number of primary branches per plant, number of siliquae on the main shoot, harvest index, and plant height. Furthermore, attributes such as siliqua length, number of seeds per siliqua, and days to initial flowering displayed moderate phenotypic coefficient of variation values. During this season, a moderate genotypic coefficient of variation was determined for main shoot length. These outcomes are in line with analogous findings documented by Maurya *et al*., (2018); Ray *et al*., (2019) and Rout *et al*. (2019). Additionally, for traits showcasing moderate PCV in terms of days to initial flowering, days to 50 percent flowering, and plant height, consistent results were identified in investigations conducted by Rout *et al*., (2019); Kumar *et al*., (2020) and Lakra *et al*. (2020)

In contrast, the *Rabi* season of 2021-22 displayed diminished values for both phenotypic and genotypic coefficients of variation in terms of days to maturity, days to 50 percent flowering, and days to initial flowering. Likewise, the *Rabi* season of 2022-23 also demonstrated reduced phenotypic and genotypic coefficients of variation for days to maturity, and days to 50 percent flowering accompanied by low genotypic coefficients of variation

specifically for days to initial flowering. These findings harmonize with discoveries by Verma *et al*., (2016); Mohan *et al*., (2017); Maurya *et al*., (2018); Rout *et al*., (2019); Swetha *et al*., (2019); Kumar *et al*., (2020) and Nishad *et al*. (2022)

5.2.2 Heritability:

Heritability is of paramount importance in plant breeding as it quantifies the proportion of phenotypic variation in a trait that is attributed to genetic factors. A high heritability indicates that the trait's expression is strongly influenced by genetics, making it a reliable target for selective breeding. Plant breeders prioritize traits with high heritability because they are more likely to be passed on to the next generation with minimal influence from environmental factors. This knowledge enables breeders to focus their efforts on traits that can be efficiently improved through controlled crosses and selection, ultimately leading to the development of plant varieties with enhanced characteristics and desired traits. In current context, heritability estimates ranged from 22.14 to 95.02 in *Rabi* 2021-22 and 22.14 to 94.37 in *Rabi* 2022-23.

During the *Rabi* season of 2021-22, an array of traits exhibited notably high and high estimates of broad sense heritability. These traits encompassed seed yield per plant, secondary branch count per plant, harvest index, primary branch count per plant, siliqua length, main shoot length, plant height, seeds per siliqua count, test weight, siliquae count on the main shoot, and days to initial flowering. Similarly, in the *Rabi* season of 2022-23, elevated heritability was observable in traits like seed yield per plant, secondary branch count per plant, main shoot length, test weight, siliqua length, primary branch count per plant, siliquae count on the main shoot, days to initial flowering, plant height and harvest index. These findings imply a reasonable level of variation within these traits, indicating the potential for selection based on them. Corresponding conclusions have been documented by Kumar *et al*., (2013); Shekhawat *et al*., (2014); Singh *et al*., (2016); Uzair *et al*., (2016); Tiwari *et al*., (2017); Patel *et al*., (2019); Ray *et al*., (2019) and Anjali *et al*. (2022)

Additionally, medium estimates of broad sense heritability were found for number of seeds per siliqua, and days to 50 percent flowering in the *Rabi* season of 2022-23. Also estimates of days to 50 percent flowering were reported in *Rabi* season of 2021-22. Similar findings were reported by Gadi *et al*., (2020) and Lakra *et al*. (2020).

Low heritability was found in days to maturity in both the seasons i.e., *Rabi* 2021-22 & *Rabi* 2022-23. Prasad *et al*., 2018 and Yadav *et al*. 2020.

5.2.3 Genetic advance as a percentage of mean

Genetic advance is a critical parameter in plant breeding that assesses the potential progress achievable through selection. It represents the anticipated increase in mean performance of a trait in the next generation due to selective breeding. By calculating genetic advance, breeders can gauge the effectiveness of their selection methods and choose the most promising individuals for further propagation. This parameter guides breeders in identifying genotypes with the highest genetic potential for desired traits, accelerating the process of developing improved plant varieties. Genetic advance serves as a valuable tool in making informed decisions to maximize the efficiency and success of plant breeding programs, ultimately contributing to the advancement of agricultural productivity and quality.

In the *Rabi* season of 2021-22, a substantial genetic advance as a percentage of the mean (GAM) was observed across a range of traits. These traits encompassed seed yield per plant, secondary branch count per plant, main shoot length, primary branch count per plant, siliqua length, test weight, siliquae count on the main shoot, harvest index, and plant height. Similarly, during the *Rabi* season of 2022-23, notable genetic advance percentages were noted for seed yield per plant, secondary branch count per plant, main shoot length, test weight, harvest index, primary branch count per plant, and siliquae count on the main shoot. These findings correspond to analogous results documented by Verma *et al*., (2016); Anjali *et al*., (2022) and Nishad *et al*. (2022)

In the *Rabi* season of 2021-22, moderate values of genetic advance as a percentage of the mean were observed for traits such as seeds per siliqua count, days to 50 percent flowering and days to initial flowering. In contrast, during the *Rabi* season of 2022-23, genetic advance as a percentage of the mean was evident for traits including plant height, siliqua length, days to initial flowering, seeds per siliqua count, and days to 50 percent flowering. These outcomes correspond with findings documented by Patel *et al*., (2019); Ray *et al*., (2019); Lakra *et al*., (2020), and Nishad *et al*. (2022), particularly in relation to siliqua length and days to 50 percent flowering.

Low values of genetic advance as a percentage of mean were observed in days to maturity in *Rabi* 2021-22 and *Rabi* 2022-23. Similar results were documented by Patel *et al*., 2019; Lakra *et al*., 2020 and Vanukuri and Pandey *et al*. 2022

5.2.4 High heritability and genetic advance as a percentage of mean:

This combination of factors is ideal for breeding programs. It allows breeders to target specific traits with confidence, knowing that the improvements made in the selected individuals will have a significant impact on the population as a whole. This scenario maximizes the efficiency of selective breeding efforts and helps achieve the breeding objectives more effectively.

During the *Rabi* season of 2021-22, traits such as seed yield per plant, secondary branch count per plant, harvest index, primary branch count per plant, siliqua length, main shoot length, plant height, seeds per siliqua count, test weight, and siliquae count on the main shoot exhibited a conjunction of high heritability and genetic advance. Similarly, in the *Rabi* season of 2022-23, high heritability combined with genetic advance was observed for Seed yield per plant, secondary branch count per plant, main shoot length, test weight, primary branch count per plant, siliquae count on the main shoot, and harvest index. These findings harmonize with outcomes detailed by Kumar *et al*., (2013); Akbari *et al*., (2015) and Pradhan *et al*. (2021).

5.3 Oil content

Oil content ranged from 34.03 to 42.04. Maximum oil content was recorded in DRMR-541-44 (42.04 percent), while oil content was recorded in PM-21 (34.03 percent) with a mean of 39.02. Similar results for oil content were found by Pal *et al.,* (2019), and Nishad *et al.* (2022).

5.4 Genetic diversity analysis

Study of genetic divergence among the genotypes is important and effective tool for breeding program. Mahalanobis D^2 analysis is a vital technique in plant breeding for quantifying genetic distances and trait variability among plant populations. It facilitates the identification of genetically diverse parents for crossbreeding, helping to enhance offspring vigor and trait improvement. By prioritizing traits with high Mahalanobis distances, breeders can focus on those with the greatest potential impact. The analysis aids in evaluating new germplasm, guiding decisions on introducing novel genetic material. Additionally, it supports clustering for targeted trait enhancement and informs the creation of effective selection indices for complex breeding goals. Overall, Mahalanobis D^2 analysis optimizes breeding strategies, promoting the development of improved plant varieties with desired traits.

Assessment of genetic diversity among the 40 genotypes, resulted into formation of six distinct clusters as detailed in Table 4.13. Out of six clusters, cluster I was the most extensive, encompassing thirty genotypes, while cluster III followed with four genotypes and cluster IV comprising three genotypes. Conversely, clusters II, V, and VI were smaller in size, each accommodating only one genotype. Similar results were observed by Tarkeshwar *et al*., 2022 and Vanukuri and Pandey *et al*. 2022.

Maximum mean values for days to initial flowering, days to 50 percent flowering, number of primary branches per plant, number of secondary branches per plant, number of siliquae on main shoot, number of seeds per siliqua, days to maturity, seed yield per plant were found in cluster IV, maximum mean value for siliqua length was found in cluster II, maximum mean value for plant height was found in cluster III, maximum mean value for main shoot length was found in cluster V, while mean value for test weight and harvest index was found in cluster VI. Consequently, the crossing of genotypes from these clusters offers a promising approach to foster variability in these specific traits, paving the way for their systematic enhancement, especially for augmenting seed yield per plant. Analogous outcomes have been reported in Kumar *et al*., (2013); Singh *et al*., (2016), and Priyanka and Pandey *et al*. (2021).

The average values for intra and inter-cluster Mahalanobis D^2 values are presented in Table 4.15. The intra-cluster D^2 values ranged from 0.00 (in clusters II, V, and VI) to 90.91 (in cluster IV). The inter-cluster D^2 values among the six clusters revealed the highest divergence between cluster IV and cluster V (599.69), followed by cluster II and cluster IV (511.51), cluster V and cluster VI (394.63), Cluster I and cluster IV, cluster III and cluster V (288.18), cluster II and cluster VI (279.17), cluster III and cluster IV (257.41), cluster III and cluster VI (230.73). Conversely, the lowest divergence was observed between cluster II and cluster V (61.57), followed by cluster I and cluster II (91.40), cluster I and cluster V (117.62), cluster I and cluster III (130.14), cluster IV and cluster VI (142.55), and cluster II and cluster III (224.54). Similar findings were reported by Doddabhimappa *et al*., (2010); Kumar *et al*., (2013) and Vanukuri and Pandey *et al*. (2022).

Diversity analysis showed that the character seed yield per plant contributed maximum (34.9 percent) to the diversity followed by main shoot length (12.82), siliqua length (9.32), number of secondary branches per plant (8.43), number of siliquae on main shoot (7.54), test weight (7.05), harvest index (4.82), days to maturity (4.04), plant height (3.46), days to 50

percent flowering (3.0), days to initial flowering (1.67), number of primary branches (1.54), number of seeds per siliqua (1.41). Similar results were found in Singh *et al*. 2016.

5.5 Molecular characterization of genotypes

Diversity analysis through molecular characterization using Simple Sequence Repeat (SSR) markers is a vital tool in optimizing yield traits in plant breeding. SSR markers, with their ability to detect variations in repeated DNA sequences, provide a precise means to assess genetic diversity within plant populations. By analyzing these markers, breeders can identify unique genetic signatures associated with superior yield traits. This facilitates the targeted selection of parent plants for crosses, increasing the likelihood of transmitting high-yield genetic factors to the offspring. Through SSR-based diversity analysis, breeders can accelerate the development of new plant varieties with enhanced yield potential, contributing significantly to sustainable agriculture and global food production.

5.5.1 Polymorphism among genotypes using SSR markers:

Genetic polymorphism among individuals arises due to variations in DNA sequences of different genotypes. Effective representation of genetic diversity and discrimination among genotypes is achieved through the presence of higher polymorphic bands of primers (Pradhan *et al*., 2004). Simple sequence repeats (SSRs) or microsatellites are particularly effective due to their locus specificity, ease of use, codominance, and high polymorphism (Landjeva *et al*., 2007; Laido *et al*., 2013).

In this current study, a set of 10 SSR primers were employed to assess the genetic polymorphism among 40 diverse mustard genotypes (*Brassica juncea* L. Czern. & Coss.). Among these primers, 4 were found to be polymorphic: Na10 Do-7 (0.75), A09-3174449 (0.609), A02-12270790 (0.4375), and A05-25290221 (0.4375). The Polymorphism Information Content (PIC) values ranged from 0.75 to 0.4375. Similar findings have been reported by Baghel *et al*., (2020); Rajpoot *et al.,* (2020); Rajpoot *et al.,* (2022); Sharma *et al*., (2022) and Shrivastav *et al*., (2023). Notably, Na10 Do-7 exhibited the highest PIC value (0.75), followed by A09-3174449 (0.609), A02-12270790 (0.4375), and A05-25290221 (0.4375). PIC values serve as an indicator of the discriminatory power of a locus, taking into consideration both the number of alleles present and their relative frequencies. All four polymorphic primers revealed two distinct alleles per locus, consistent with the work of Prajapat *et al.,* (2014), and Singh *et al*. (2022).

Furthermore, the 40 genotypes were grouped into five major clusters: Cluster I encompassed twenty-seven genotypes, including RSPR-03, PM-21, RH-1209, PM-195, PM-25, PM-20, DRMRIJ-15-25, RB-50, RH-719, DRMRIJ-31, JD-6, RLC-3, PM-125, LES-39, RH-725, RH-0923, CN-105364, DRMR-4005, Kranti, DRMR-15-5, DRMR-541-44, DRMR-541-46, RB-69, DRMRIJ-A-35, TN-3, RL-1359, JM-14-2. Cluster II contained 2 genotypes: RSPR-01 and RH-406. Cluster III comprised three genotypes: JM-12-6, SKJM-5, DRMR-61-59. Cluster IV included four genotypes: RB-77, RSPR-69, DRMRIJ-12-40, DRMRIJ-12-48. Lastly, cluster V encompassed four genotypes: Tawari, DRMR-1059, NC-37362, RB-55. These results are in agreement with the findings of Manoj and patil *et al*. (2019).

CHAPTER 6

SUMMARY AND CONCLUSIONS

The current study, **titled "Genetic analysis of yield traits in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]",** was conducted over the *Rabi* seasons of 2021-22 and 2022-23 at the experimental area of the division of Plant Breeding and Genetics, as well as the molecular laboratory of the same division. The primary objectives of this investigation were as follows:

- To estimate components of genetic variation among advanced breeding lines.
- To study polymorphism using molecular markers.

6.1. Summary

A total of 40 diverse lines were subjected to evaluation using a Randomized Complete Block Design (RCBD) with three replications, each occupying a plot size of 3 square meters. Throughout the evaluation, data was meticulously recorded for various traits including days to initial flowering, days to 50 percent flowering, number of primary branches, number of secondary branches, main shoot length, number of siliquae on the main shoot, siliqua length, number of seeds per siliqua, plant height, days to maturity, seed yield per plant, test weight, and harvest index. The summarized outcomes of this evaluation are as follows:

- Analysis of variance for 40 diverse lines evaluated in Randomized Complete Block Design of Indian mustard depicted wide variation for all the 13 traits. The genotypic source of variations for all the characters was significant in both the years at 1 percent level of significance except for days to maturity at 5 percent level of significance in both the seasons i.e., *Rabi* 2021-22 & 2022-23.
- In the *Rabi* season of 2021-22, there were notably high values observed for both phenotypic and genotypic coefficients of variation in traits like Seed yield per plant, number of secondary branches, and main shoot length. Additionally, a high phenotypic coefficient of variation was observed in the number of primary branches per plant in this season. This pattern was also observed in the *Rabi* season of 2022-23, where high phenotypic and genotypic coefficients of variation were evident for seed yield per plant and the number of secondary branches. Furthermore, a high phenotypic coefficient of

variation was noted for main shoot length in this season, indicating that this trait's expression was influenced equally by both genetic and environmental factors.

- In the *Rabi* season of 2021-22, there were moderate values observed for both phenotypic and genotypic coefficients of variation for traits such as the number of siliquae on the main shoot, test weight, siliqua length, plant height, number of seeds per siliqua, and harvest index. Additionally, moderate genotypic coefficient of variance was found for the number of primary branches in this season. Moving to the *Rabi* season of 2022-23, moderate values were observed for both phenotypic and genotypic coefficients of variation in traits including test weight, number of primary branches per plant, number of siliquae on the main shoot, harvest index, and plant height. In this same season, a moderate phenotypic coefficient of variation was found for traits like siliqua length, number of seeds per siliqua, days to initial flowering, and days to 50 percent flowering. Notably, a moderate genotypic coefficient of variance was observed for main shoot length during this season.

- In the *Rabi* season of 2021-22, both phenotypic and genotypic coefficients of variation were low for traits such as days to maturity, days to 50 percent flowering, and days to initial flowering. Similarly, in the *Rabi* season of 2022-23, low values were observed for both phenotypic and genotypic coefficients of variation for days to maturity. Additionally, a low genotypic coefficient of variation was noted for siliqua length, number of seeds per siliqua, days to initial flowering and days to 50 percent flowering during this season.

- In the *Rabi* season of 2021-22, very high and high estimates of broad sense heritability were observed for several traits, including seed yield per plant, number of secondary branches per plant, harvest index, number of primary branches per plant, siliqua length, main shoot length, days to 50 percent flowering, plant height, number of seeds per siliqua, test weight, number of siliquae on main shoot, and days to initial flowering. Similarly, in the *Rabi* season of 2022-23, high heritability was observed for traits such as seed yield per plant, number of secondary branches per plant, main shoot length, test weight, siliqua length, number of primary branches per plant, number of siliquae on main shoot, plant height, and harvest index. These high and reasonable heritability values suggest that these traits have a significant genetic basis, making them suitable for selection in breeding programs.

- Medium estimates of broad sense heritability were found in number of seeds per siliqua, days to initial flowering, days to 50 percent flowering in *Rabi* 2022-23.

- Low heritability was found in days to maturity in both the seasons i.e., *Rabi* 2021-22 & *Rabi* 2022-23.

- In the *Rabi* season of 2021-22, high genetic advance as a percentage of mean was observed for traits such as seed yield per plant, number of secondary branches per plant, main shoot length, number of primary branches per plant, siliqua length, test weight, number of siliquae on main shoot, harvest index, and plant height. Similarly, in the *Rabi* season of 2022-23, high genetic advance as a percentage of mean was observed for seed yield per plant, number of secondary branches per plant, main shoot length, test weight, harvest index, number of primary branches per plant, and number of siliquae on main shoot. These high values of genetic advance as a percentage of mean indicate the potential for substantial improvement in these traits through selection and breeding programs.

- In the *Rabi* season of 2021-22, moderate values of genetic advance as a percentage of mean were observed for traits like days to number of seeds per siliqua, 50 percent flowering and days to initial flowering. In contrast, in the *Rabi* season of 2022-23, genetic advance as a percentage of mean was observed for plant height, siliqua length, days to initial flowering, number of seeds per siliqua, and days to 50 percent flowering. These moderate to high values of genetic advance as a percentage of mean suggest that selection based on these traits could lead to meaningful improvements in the subsequent generations.

- Low values of genetic advance as a percentage of mean were observed in days to maturity in both seasons of *Rabi* 2021-22 and 2022-23.

- Oil content ranged from 34.03 to 42.04. Maximum oil content was recorded in DRMR-541-44 (42.04 percent), while minimum oil content was recorded in PM-21 (34.03 percent) with a mean of 39.02.

- In the present study, 40 genotypes of mustard were grouped into five, six and six different clusters in both seasons of *Rabi* 2021-22 & 2022-23 and pooled respectively.

This indicated the large diversity existing in the mustard genotypes giving the opportunity further improvement in mustard.

- In the *Rabi* season of 2021-22, the highest genetic divergence was observed between cluster III and cluster V, whereas the lowest divergence was noted between cluster V and cluster I. In the *Rabi* season of 2022-23, the maximum divergence was recorded between Cluster III and cluster VI, while the minimum divergence was observed between cluster II and cluster V. When considering the pooled data, the highest divergence occurred between cluster IV and cluster V, followed by cluster II and cluster IV. The lowest divergence was noticed between cluster II and cluster V, followed by cluster I and cluster II.

- Seed yield per plant contributed maximum to the diversity followed by main shoot length. While minimum contribution was recorded by number of seeds per siliqua and number of primary branches per plant.

- Out of 10 microsatellite markers, four were found to be polymorphic, namely, Na10 Do-7 (0.75) followed by A09-3174449 (0.61), A02-12270790 (0.44), A05-25290221 (0.44).

- The PIC values were ranged from 0.44 -0.75. The higher PIC value was exhibited by Na10 Do-7 (0.75) followed by A09-3174449 (0.61), A02-12270790 (0.44), A05-25290221 (0.44). Also, among all the four primers that were polymorphic showed two different alleles per locus.

- Further, 40 genotypes were grouped into five major clusters i.e., Cluster I contains twenty seven genotypes i.e. RSPR-03, PM-21, RH-1209, PM-195, PM-25, PM-20, DRMRIJ-15-25, RB-50, RH-719, DRMRIJ-31, JD-6, RLC-3, PM-125, LES-39, RH-725, RH-0923, CN-105364, DRMR-4005, Kranti, DRMR-15-5, DRMR-541-44, DRMR-541-46, RB-69, DRMRIJ-A-35, TN-3, RL-1359, JM-14-2, cluster II contains 2 genotypes i.e. RSPR-01 and RH-406, cluster III contains three genotypes i.e. JM-12-6, SKJM-5, DRMR-61-59, cluster IV contains four genotypes i.e. RB-77, RSPR-69, DRMRIJ-12-40, DRMRIJ-12-48, cluster V contains four genotypes i.e. Tawari, DRMR-1059, NC-37362, RB-55.

6.2. Conclusion

An experiment was conducted during two consequent seasons i.e., *Rabi* 2021-22 and 2022-23 to study the morphological and molecular diversity among the 40 genotypes of Indian mustard. Highest GCV and PCV, high heritability and genetic advance as percentage of mean was recorded for seed yield per plant and number of secondary branches per plant in both the seasons. Highest divergence occurred between cluster IV (DRMR-4005, Kranti & RH-1209) and cluster V (PM-195) followed by cluster II (PM-125) and IV (DRMR-4005, Kranti & RH-1209). Seed yield per plant contributed maximum to the diversity followed by main shoot length and siliqua length. The genotypes under study were also characterized for genetic diversity with the help of 10 SSR markers. Among these 10 markers, 4 were polymorphic, with the PIC value ranging from 0.44 - 0.75. Jaccard's similarity coefficient also diversified the genotypes into 5 clusters with cluster II carrying only two genotypes i.e., RSPR-01 and RH-406. The examination of both morphological and molecular aspects has unveiled a noteworthy extent of genetic diversity within advanced breeding lines/ genotypes which can be used as parents in further breeding programmes.

6.3 Suggestions for further work

- The study could be expanded by incorporating a greater number of SSR primers to obtain more accurate insights into diversity analysis.
- Diverse parental lines identified in this investigation will provide promising opportunities to serve as valuable assets in the continuation and enhancement of improvement programs focused on Brassica crops, contributing to the robust development and refinement of these agricultural cultivars.
- Additional assessment of other crucial germplasm lines could be initiated to conduct diversity analysis, utilizing the SSR markers that exhibit PIC values exceeding 0.5, as reported.

REFERENCES

Ahmad, A.F., Singh, T. and Sharma, P.K. 2009. Genetic diversity analysis in Indian mustard [*Brassica juncea* (l.) *Czern. & coss.*]. *Progressive Agriculture*, **9**(1): 50-53.

Akoju, S., kumar, B. A., Kuchanur, P. H., Khan, H., and Patil, A. 2020. Genetic Variability, Association and Path Analysis in Indian Mustard [*Brassica juncea* (L.) *Czern. & coss.*] for Yield and its Component Traits. *International Journal on Current Microbiology and Applied Sciences*, **9**(11): 1373- 1384.

Anjali, M.K, Chaudhary, N.K., Ahlawat, S., Kumar, V., Kumar, V., Singh, S., and Mohan, S. 2022. Morphological Evaluation of Variability, Heritability and Genetic Advance in Relation to Seed yield and its Attributing Traits in Indian Mustard [*Brassica juncea* (L.) Czern. and coss.]. *Biological Forum – An International Journal*, **14**(3): 000-000.

Baghel, R., Sharma, A.K., Tiwari, S., Tripathi, M.K. and Tripathi, N. 2020. Genetic diversity analysis of Indian mustard (*Brassica* spp.) germplasm lines using SSR molecular markers. *International Journal Current Microbiology and Applied Sciences*, **9**(12): 137-143.

Bibi T, Rauf S, Mahmood T, Haider Z, Salah, D. 2016. Genetic Variability and Heritability Studies in Relation to Seed Yield and its Component Traits in Mustard (*Brassica juncea* L.). *Academia Journal of Agricultural Research*, **4**(8): 478-482.

Burton, G. H. and Devense, F. R. 1952. Quantitative inheritance in grasses. In *Proceedings of 6th International Grassland Congress*, **1**: 227-283.

Devi, T.R., Devi, N.D., Vivekananda, Y. and Sharma, P.R. 2017. Genetic diversity analysis in Indian mustard (*Brassica juncea* (L.) Czern. and coss.) genotypes using agro-morphological parameters. *Electronic Journal of Plant Breeding*, **8**(3): 749-753.

Doddabhimappa, R., Gangapur, B., Prakash, G. and Hiremath, C.P. 2010. Genetic diversity analysis of Indian mustard (*Brassica juncea* L.). *Electronic Journal of Plant Breeding*, **1**(4): 407-413.

Doyle, J.J. and Doyle, J.L. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*, **19**(1): 11-15.

Gadi, J., Chakraborty, N.R. and Imam, Z. 2020. To Study the genetic variability, heritability and genetic advance for different quantitative characters in Indian mustard (*Brassica juncea* (L.) *Czern. & coss.*). *International Journal of Current Microbiology and applied sciences*, **9**(10): 1557-1563.

Iqbal, S., Hamim, I., Haque, S. and Nath, U.K., 2015. Genetic diversity analysis of mustard (*Brassica* spp.) germplasm using molecular marker for selection of short duration genotypes. *African Journal of Biotechnology*, **14**(17): 1439-1448.

Jat, L., Rai, S.K., Choudhary, J.R., Bawa, V., Bharti, R., Sharma, M. and Sharma, M. 2019. Phenotypic evaluation of genetic diversity of diverse Indian mustard (*Brassica juncea (*L.) Czern. and coss.) genotypes using correlation and path analysis. *International Journal of Bio-resource and Stress Management*, **10**(5): 467-471.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 314-318.

Kalyar, A. and Salim, J., 2015. Genetic evaluation and characterization for yield and related traits in mustard (*Brassica juncea*). *Research Journal of Agriculture and Environmental Management*, **4**(2): 82-87.

Kumar, A., Chauhan, R. and Singh, K.P. 2020. Genetic variability, heritability and genetic advance among Indian mustard (*Brassica juncea*) genotypes. *Annals of Plant and Soil Research*, **22**(1): 92-95.

Kumar, B., Pandey, A. and Singh, S.K. 2013. Genetic diversity for agro-morphological and oil quality traits in Indian mustard (*Brassica juncea* (L.) *Czern. & coss.*). *The Bioscan*, **8**(3): 771-775.

Kumar, H., Kumar, A., Gupta, S., Gupta, V. and Singh, A.K. 2021. Estimation of Genetic Parameters and Character Association in Indian Mustard (*Brassica juncea* L.). *International Journal of Plant & Soil Science*, **33**(19): 145-156.

Kumar, R., Singh, H., Kaur, S., Singh, I. and Kaur, R. 2017. Quantitative analysis for yield and its components in IC lines of Indian mustard [*Brassica juncea* (L.) Czern. and coss.]. *Journal of Pharmacognosy and Phytochemistry*, **6**(5): 2257-2260.

Kumari, A. and Kumari, V. 2018. Studies on genetic diversity in Indian mustard (*Brassica juncea* (l.) *Czern. & coss.*) for morphological characters under changed climate in midhills of Himalayas. *The Pharma Innovation Journal*, **7**: 290-296.

Laido, G., Mangini, G., Taranto, F., Gadaleta, A., Blanco, A., Cattivelli, L., Marone, D., Mastrangelo, A. M., Papa, R. and De Vita, P. 2013. Genetic diversity and population structure of tetraploid wheat (Triticum turgidum L.) estimated by SSR, DArT and pedigree data. *Plos One*, **8**(6): 1-17

Lakra, A., Tantuway, G., Tirkey, A.E. and Srivastava, K. 2020. Genetic variability and trait association studies in Indian mustard (*Brassica juncea* (L.) Czern. & Coss). *International Journal on Current Microbiology and Applied Sciences*, **9**(1): 2556-2563.

Landjeva, S., Korzun, V. and Berner, A. 2007. Molecular markers: actual and potential contributions to wheat genome characterization and breeding. *Euphytica*, **156**(3): 271-296

Lodhi, B., Thakral, N.K., Singh, D., Avtar, R. and Bahadur, R. 2016. Genetic diversity analysis in Indian mustard (*Brassica juncea*). *Journal of Oilseed Brassica*, **1**(2): 57-60.

Manoj MS., Patil, B.R. 2019. Assessment of molecular diversity in Indian mustard [*Brassica juncea* (L.) Czern. and coss.] using SSR markers. *International Journal of Chemical Studies*, **7**(5): 875-878.

Maurya, S.K., Maurya, K.N., Lal, K., Singh, Y., Singh, S., Dixit, B. and Singh, S. 2018. Assessment of Genetic Variability, Heritability and Genetic Advance in Indian Mustard (*Brassica juncea (*L.) *Czern. & coss.*.). *International Journal on Current Microbiology and Applied Sciences*, **7**(11): 13-18.

Mohan, S., Yadav, R.K., Tomar, A. and Singh, M. 2017. Utilization of selection parameters for seed yield and its contributed traits in Indian mustard (*Brassica juncea* (L.) *Czern. & coss.*). *The Pharma Innovation Journal*, **6**(8): 306-309.

Nishad, C., Salam, J.L., Singh, S. and Singh, D.P. 2022. Studies of genetic variability in Indian mustard (*Brassica juncea* (L.) Czern. and coss.). *The Pharma Innovation Journal*, **11**(2): 261-263.

Pal, S., Dubey, N., Avinashe, H., Khan, S. and Reddy, J.P., 2019. Estimation of genetic variability, correlation and path analysis for yield and yield contributing characters in Indian mustard (*Brassica juncea* L.). *Journal of Pharmacognosy and Phytochemistry*, **8**(1S): 102-105.

Patel, J.R., Prajapati, K.P., Patel, P.J., Patel, B.K., Patel, A.M., Jat, A.L. and Desai, A.G. 2019. Genetic variability and character association analysis for seed yield and its attributes in Indian mustard (*Brassica juncea* (L.) Czern. and coss.). *The Pharma Innovation Journal*, **8**(4): 872-876.

Patel, P.B., Patel, P.J., Patel, J.R. and Patel, P.C. 2021. Elucidation of genetic variability and inter-relationship studies for seed yield and quality traits in Indian mustard [*Brassica juncea* (L.) Czern. and coss.]. *Electronic Journal of Plant Breeding*, **12**(2): 589-596.

Pradhan, A., Yan, G. and Plummer, J. A. 2004. Development of DNA fingerprinting keys for the identification of radish cultivars. *Australian Journal of Experimental Agriculture*, **44**(1): 95-102.

Pradhan, A.M., Choudhury, M.R., Sawarkar, A. and Das, S. 2021. Genetic analysis of some genotypes of Indian mustard (*Brassica juncea* L.) for yield and yield attributing traits. *Current Journal of Applied Science and Technology*, **40**(34): 51-60.

Prajapat, P., Sasidharan, N., Kumar, M. and Prajapati, V. 2014. Molecular characterization and genetic diversity analysis in four Brassica species using microsatellite markers. *Bioscan*, **9**(4): 1521-1527.

Prasad, G. and Patil, B.R. 2018. Genetic variability and heritability studies for yield and attributes in Indian mustard. *Journal of Pharmacognosy and Phytochemistry*, **7**(5): 519-522.

Priyanka, N. and Pandey, M.K. 2021. Genetic variability and Genetic diversity study in Indian mustard (*Brassica juncea* L.). *The Pharma Innovation Journal*, **10**(10): 1133-1135.

Rajpoot, N.S., Tripathi, M.K., Tiwari, S., Tomar, R.S. and Kandalkar, V.S. 2020. Characterization of Indian mustard germplasm on the basis of morphological traits and SSR markers. *Current Journal of Applied Science and Technology*, **39**(48): 300-311.

Rajpoot, N.S., Tripathi, M.K., Tiwari, S., Tomar, R.S., Tripathi, N., Sikarwar, R.S. and Tomar, S.S. 2022. Morphological and molecular characterization of Indian mustard germplasm lines. *Research and Development in Science and Technology*, **4**: 151-165.

Ray, J., Singh, O.P., Pathak, V.N. and Verma, S.P., 2019. Assessment of genetic variability, heritability, genetic advance and selection indices for yield contributing traits in Indian mustard [*Brassica juncea*]. *International Journal of Conservation Science*, **7**(4): 1096-1099.

Rout, S., Kerkhi, S.A. and Gupta, A. 2019. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard [*Brassica juncea* (L.) Czern. and coss.]. *Journal of Pharmacognosy and Phytochemistry*, **8**(3): 4119-4123.

Rout, S., Kerkhi, S.A., Chand, P. and Singh, S.K. 2018. Assessment of genetic diversity in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L.). *Journal of Oilseed Brassica*, **9**(1): 49-52.

Rout, S., Sur, B., Sadhu, S., Ghimiray, T.S., Mondal, H.A., Hijam, L., Chakraborty, M. and Roy, S.K. 2019. Trait's association, cause and effect analyses in Indian mustard [*Brassica juncea* (L.) *Czern. & coss.*]. *Electronic Journal of Plant Breeding*, **10**(4): 1482-1494.

Saroj, R., Soumya, S.L., Singh, S., Sankar, S.M., Chaudhary, R., Yashpal, Saini, N., Vasudev, S. and Yadava, D.K. 2021. Unraveling the relationship between seed yield and yield-related traits in a diversity panel of *Brassica juncea* using multi-traits mixed model. *Frontiers in Plant Science*, **12**: 651936.

Sharma, D., Nanjundan, J., Singh, L., Parmar, N., Singh, K.H., Verma, K.S. and Thakur, A.K. 2022. Genetic diversity and population structure analysis in Indian Mustard genotypes using phenotypic traits and SSR markers. *Plant Molecular Biology Reporter*, **40**(3): 579-594.

Shekhawat, N., Jadeja, G.C. and Singh, J., 2014. Genetic variability for yield and its components in Indian mustard (*Brassica juncea* (L.) *Czern. & coss.*). *Electronic Journal of Plant Breeding*, **5**(1): 117-119.

Shrivastav, A., Tripathi, M.K., Tiwari, S., Tripathi, N., Tiwari, P.N., Bimal, S.S., Rajpoot, P. and Chauhan, S. 2023. Evaluation of Genetic Diversity in Indian Mustard (*Brassica juncea*

var. rugosa) employing SSR Molecular Markers. *Plant cell biotechnology and molecular biology*, **24**(3-4): 10-21.

Singh KH, Singh L, Parmar N, Kumar S, Nanjundan J, Singh G. 2022. Molecular characterization and genetic diversity analysis in Indian mustard (*Brassica juncea (*L.) *Czern. & coss.*) varieties using SSR markers. *Plos one*, **17**(8).

Singh, D., Arya, R.K., Chandra, N., Niwas, R. and Salisbury, P. 2016. Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* (L.) *Czern. & coss.*). *Journal of Oilseed Brassica*, **1**(1): 19-22.

Singh, I.D. and Stoskopf, N.C., 1971. Harvest index in cereals. *Agronomy Journal*, **63**(2): 224-226.

Singh, K.H., Singh, L., Parmar, N., Kumar, S., Nanjundan, J., Singh, G. and Thakur, A.K. 2022. Molecular characterization and genetic diversity analysis in Indian mustard (*Brassica juncea* (L.) *Czern. & coss.*) varieties using SSR markers. *Plos one*, **17**(8): 0272914.

Singh, S., Kumar, V., Singh, S.K. and Daneva, V. 2022. Genetic variability, interrelation and path analysis for yield & yield characters in Indian mustard (*Brassica juncea* L.) *Journal of Oilseed Brassica*, **13**(2): 112-118.

Singh, V., Bhajan, R. and Pant, U. 2016. Molecular diversity analysis of Indian mustard genotypes through SSR markers. *Environment and Ecology*, **34**(3): 1212-1217.

Singh, V.K., Avtar, R., Kumari, N., Kumar, R.M. and Khedwal, R.S. 2022. Analysis of genetic structure and diversity in Indian mustard [*Brassica juncea* (L.) *Czern. & coss.*] assessed by SSR MS. *Journal of Animal & Plant Sciences*, **32**(1): 173-185

Swetha, M., Janeja, H.S., Singh, H., Sravani, M., Rajaneesh, K. and Madakemohekar, A.H. 2019. Genetic evaluation of Indian mustard (*Brassica juncea* L.) genotypes for yield and quality parameters. *Plant Archives*, **19**(1): 413-417.

Tarkeshwar, Nath, S., Mishra, G., Chaudhary, A.K., Gupta, R., Gupta, A.K. and Vimal, S.C. 2022. Genetic Diversity Analysis in Indian Mustard [*Brassica juncea* (L.) Czern. and coss.] Genotypes. *Biological Forum – An International Journal*, **14**(2): 1571-1574.

Tiwari, A.K., Singh, S.K., Tomar, A. and Singh, M. 2017. Heritability, genetic advance and correlation coefficient analysis in Indian mustard (*Brassica juncea* (L.) *Czern. & coss.*). *Journal of Pharmacognosy and Phytochemistry*, **6**(1): 356-359.

Uzair, M., Shahzadi, I., Jatoi, G.H., Bibi, T., Rauf, S., Mahmood, T. and Din, S.U. 2016. Genetic variability and heritability studies in relation to seed yield and its components traits in mustard (*Brassica juncea* L.). *Science International*, **28**(4): 4267-4270.

Vanukuri, A.R. and Pandey, M.K. 2022. Genetic variability and genetic diversity studies in Indian mustard (*Brassica juncea* L.). *The Pharma Innovation Journal*, **11**(7): 1357-1360.

Verma, S., Singh, V.V., Meena, M.L., Rathore, S.S., Ram, B., Singh, S., Garg, P., Singh, B.R., Gurjar, N., Ambawat, S. and Singh, D. 2016. Genetic analysis of morphological and physiological traits in Indian mustard (*Brassica juncea* L.). *Journal of Breeding & Genetics*, **48**(4).

Yadav, B.S., Sharma, H.K., Yadav, A.P. and Ram, B. 2021. Correlation and path analysis in Indian mustard (*Brassica juncea* L.) for seed yield and attributing traits. *International Journal on Current Microbiology and Applied Sciences*, **10**(2): 1761-1768

Yadav, V.K., Srivastava, K. K., Mishra, V.K. and Negi, S. 2020. Studies on Genetic Variability, Character Association and Genetic Divergence in Indian Mustard (*Brassica juncea* (L.) Czern. and coss..). *International Journal of Current Microbiology and Applied Sciences,* **10**: 132-143.

Yadava, D.K., Giri, S.C., Vignesh, M., Vasudev, S., Kumar Yadav, A., Dass, B., Singh, R., Singh, N., Mohapatra, T. and Prabhu, K.V. 2011. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences*, **81**(8): 712.

CERTIFICATE – IV

Certified that all necessary corrections as suggested by the external examiner and advisory committee have been duly incorporated in the thesis entitled **"Genetic analysis of yield traits in Indian mustard [*Brassica juncea*(L.) Czern.&Coss.]"**, submitted by Ms. Lalita Kumari, Registration No. **J-21-M-826**.

Dr. S.K. Rai
Associate Professor cum Senior Scientist, PBG
(Major Advisor)

Place: Jammu
Date: 23-11-23

Dr. Tuhina Dey
Head of the Division

VITA

Name of the student	:	Ms. Lalita Kumari
Father's Name	:	Sh. Bishan Lal
Mother's Name	:	Smt. Kanta Bhagat
Nationality	:	Indian
Date of birth	:	03.11.1998
Permanent home address	:	H.No.32A Om nagar udheywalla, near J&K Bank, Patta bohri, Jammu
PIN Code	:	180012

EDUCATIONAL QUALIFICATIONS

Bachelor's degree	:	B.Sc. (Hons.) Agriculture
University and year of award	:	Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu; 2023
OGPA/ % marks	:	7.73/10.00
Master's degree OGPA	:	7.89/10.00