

“CHARACTERIZATION OF INDIAN MUSTARD (*Brassica juncea* L.) GENOTYPES FOR HEAT TOLERANCE AT REPRODUCTIVE STAGE”

AMITA SINGH

Thesis

Master of Science in Agriculture

(Genetics and Plant Breeding)



DEPARTMENT OF GENETICS AND PLANT BREEDING

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RANI LAKSHMI BAI CENTRAL AGRICULTURAL UNIVERSITY

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“CHARACTERIZATION OF INDIAN MUSTARD (*Brassica juncea* L.) GENOTYPES FOR HEAT TOLERANCE AT REPRODUCTIVE STAGE”

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By

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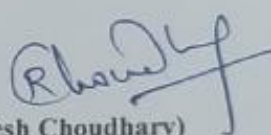
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Certified that Ms. Amita Singh, ID. No. RLBCAU/AG/PG/034/20 has satisfactorily pursued her course of research for not less than IV semesters and that the thesis entitled "Characterization of Indian mustard (*Brassica juncea* L.) genotypes for heat tolerance at reproductive stage" submitted by her to the Rani Lakshmi Bai Central Agricultural University, Jhansi 284003 (U.P.) in partial fulfilment of the requirements for the award of the degree of Master of Science in Agriculture in the subject of Genetics and Plant Breeding is the result of original research work conducted by her under my supervision and is sufficiently of a high standard to warrant its presentation to the examination.

I also certify that the thesis or part thereof has not been previously submitted by her for a degree/diploma of any University.

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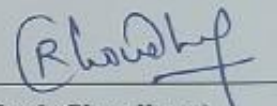
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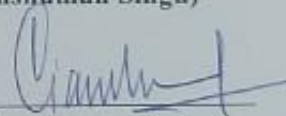
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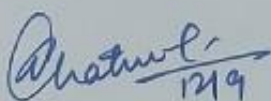
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LIST OF ABBREVIATIONS

S. No.	Symbols	Abbreviations	S. No.	Symbols	Abbreviations
1	%	Per cent	18	TS	Total siliqua per plant
2	/	Per	19	SAM	Siliquea on main shoot
3	<	Less than	20	SSQ	Seeds per siliqua
4	>	more than	21	SW	1000 Seed weight
5	°C	Degrees Celsius	22	YP	Yield per plant
6	ANOVA	Analysis of variance	23	cm	Centimeter
7	T	Timely sown	24	<i>et al.</i>	Co-workers
8	L	Late sown	25	GCV	Genotypic coefficient of variation
9	FW50	Days to 50 percent flowering	26	PCV	Phenotypic coefficient of variation
10	DM	Days to maturity	27	h^2bs	Heritability in broad sense
11	PH	Plant height	28	Ha	Hectare
12	PB	Number of primary branches per plant	29	i.e.	That is
13	SB	Number of secondary branches per plant	30	viz.	namely
14	CC	Chlorophyll content	31	Mha	million hectare
15	LAI	Leaf area index	32	rp	Phenotypic correlation
16	FLU	Chlorophyll fluorescence	33	rg	Genotypic correlation
17	MAL	Main shoot length	34	GAM	Genetic advance as percentage of mean

Chapter 1

INTRODUCTION

Oilseeds are ranked second most important agricultural economy next to cereals in the country and it is growing at a pace of 4.1 % per annum in last three decades. In the country, production of oilseed is 36.56 million tonnes from 28.82 mha acreage with an average productivity of 1269 kg/ha, covering nearly 70 % under rainfed areas. **(Source: Directorate of Oilseeds Development, 2019-20).** India is cultivating nine oilseed crops as primary source of oil under the diverse agro-climatic condition. Among them, oilseed *Brassica* stands second after soybean (44.5%) in terms of area (rapeseed-mustard- 24.98 %) whereas, in production it stands third (27.45 %) after soybean (33.77 %) and groundnut (30.40 %) however, stand first in edible oil production in the country (35.87 %). Globally, India is fifth largest vegetable oil economy accounting 7.4 % oilseeds, 5.8 % oils and 6.1 % oil meal production and 9.3 % of edible oil consumption in the world **(Jat et al., 2019)**. Despite of significant progress achieved in oilseed production; country is still dependent on imported vegetable oil which is 11.2 % of the total world import worth of about **Rs. 1,17,000 crores** in 2020-21 as said by Solvent Extractors Association of India (SEA). Dependency on import has increased mainly due to increasing consumption of edible oils (24.07 million tonnes) against oil production (10.66 million tonnes) due to the rising population and changing life style. The per capita consumption of edible oils has increased from 15.8 kg/head/year during 2012-13 to 19.3 kg/head/year in 2017-18 **(MAFW, 2019)**. The production growth is not in the pace of consumption growth which is resulting in drains of significant quantum of revenue to the foreign countries. So, it is a strong apprehension to the national economy and there is strong need to increase oilseed production and productivity with climate change scenario to become self-sufficient in vegetable oil.

Oilseed *brassica* spp., commonly known as rapeseed-mustard group, plays an important role in the Indian economy by virtue of its different uses like edible oils, vegetables, condiments and animal feed. Out of 37 species in the *Brassica* genus, *B. juncea* (L.) Czern. & Coss., *Brassica rapa* L. syn. *B. campestris*, *B. napus* L. and *B. carinata* A. Braun are four most cultivated species for oilseed and vegetables. Globally, during 2018-19 oilseed brassicas are grown in about 36.59 million hectares area with an annual production of 72.37 million tonnes and with an average productivity of 1980 kg/ha,

making it is the third most important oil crop worldwide after palm oil and soybean. India is second largest rapeseed-mustard cultivating country after china and third in production next to China and Canada. India shared 19.8 and 9.8 % to global acreage and production, respectively (**USDA, 2020**). In India, rapeseed-mustard is cultivated on 6.78 million hectares area with an annual production of 9.12 million tonnes and with an average productivity around 1345 kg/Ha (**Source: DES, DAC& FW, 2019-20**). The top most rapeseed-mustard producing states of the country are Rajasthan (44.56%), Madhya Pradesh (12.97%), Haryana (12.63 %), Uttar Pradesh (9.78%) and West Bengal (7.12 %), respectively (**Source: DES, DAC& FW, 2019-20**). In the Bundelkhand region, Indian mustard is grown over 1.13 lakh hectares area and production is 1.15 lakh tonnes. Mustard productivity in this region is only 1022 kg/ha which is very much lesser than the national average productivity. (**Source: DES, DAC& FW, 2019-20**). *Brassica juncea*, commonly known as Indian mustard is a predominant oilseed crop of India and accounts for more than 90% of acreage among the rapeseed – mustard group of crops. It is also called as rai, sarson, lahi, raya and possesses relatively better level of tolerance for different biotic and abiotic factors.

Indian mustard (*B. juncea* (L.) Czern. & Coss.), is a natural amphidiploid (AABB; $2n=36$) and it has originated from interspecific hybridization events between diploid progenitors, *B. rapa* (AA; $2n=20$) and *B. nigra* (BB; $2n=16$) (**Nagaharu, 1935**). **Burkill (1930), Olsson (1960), Vaughan et al. (1963) and Sun (1970)** hold the view that *B. juncea* originated from several independent hybridizations between wild *B. rapa* and *B. nigra* at multiple places in the Middle East and neighbouring regions where their distributions overlapped. Its main origin is considered to be Central Asia (north western India), China, north eastern India from where it has extended up to Afghanistan via Punjab (Vaughan, 1997). At present, *B. juncea* is a mainly cultivated in tropical and subtropical countries, especially in south-east Asia like India, China, Bangladesh and Pakistan. Indian mustard is an annual herbaceous plant and plants are tall (90-200 cm), erect and heavily branched. Indian mustard is a self-compatible species and predominately self-pollinated crop (**Labana et al. 1992**). However, in some environments out crossing varies from 7.6% to 22% (**Dhillon and Labana, 1988; Ram Bhajan et al.1991; Abhram, 1994**) and bees are primary pollen vector. Mustard flowers are bisexual with four free sepals and four yellow petals, along with two longer and two shorter stamens. The mustard inflorescence is known as raceme and fruit is called siliqua. Oil content in different varieties show slight variation

in percentage and it ranges from 35 to 42 %. The mustard oil is utilized for cooking and preparation of pickles whereas; seeds are used for making paste and sauce. The aroma and pungency in mustard oil is due to presence of sulphur containing glucosinolates. Mustard seed contains protein (26.08 g), fat (36.24 g), minerals (1.6 g), fibres (12.2 g), carbohydrates (28.09 g), energy (508 kcal), calcium (266 mg), magnesium (370 mg) and iron (9.21 mg). The oil possesses erucic acid (38-57%). **(USDA National Nutrient data base)**

Mustard is grown under diverse agro-ecological conditions such as early, timely, late, rainfed, irrigated, sole and or mixed crop with cereals and pulses. Therefore, cultivation of mustard crop is adversely influenced by several biotic (diseases, insects, weeds etc.) and abiotic stresses (heat stress, drought, salinity and alkalinity etc.). It is a cool season crops, hence high temperature stress has detrimental effect both at seedling and flowering or pod filling stage. Whereas, the problem of heat stress at flowering stage is observed in all the major mustard growing countries including China, Australia, Canada and European **(Salisbury and Gurung, 2011)**. In India or Bundelkhand region, delayed sowing of the mustard crop after harvesting of rice, groundnut and cotton exposes to the high temperature stress during reproductive stage **(Chauhan *et al.*, 2009)**; referred as 'terminal heat stress (THS)'. Though, mustard has relative tolerance against biotic and abiotic stresses moreover terminal heat stress not only impaired the seed filling but also leads to an increase in disease incidence and insect-pest infestation, thereby causing lower seed weight and seed yield. **(Tuteja *et al.*, 1996)**. **Sharma and Sardana, 2013** reported mustard yield reduction by 53.10 % and 6.97 % reduction in oil content under terminal heat stress. Under climate change scenario, elevating atmospheric temperature has become major threat to Indian mustard which is directly influences the farm income of the farmers as well as national economy. Intergovernmental panel on climate change (IPCC), 2018 reported the impact of global warming led to increase of 1.5 °C above pre-industrial level due to greenhouse gas emissions worldwide.

Heat stress triggers an array of physiological, biochemical and molecular changes and heat tolerance in crop plants is a developmentally regulated, stage specific phenomena; means tolerance at one stage of plant may not be correlated with tolerance at other stages **(Wahid *et al.*, 2007)**. Therefore, heat tolerance at terminal stage shall be evaluated separately for the assessment, characterization and genetic manipulation of heat tolerance traits. Several high yielding varieties of Indian mustard (Giriraj, RH-725, RH-406, RH-

749, RGN-73, NRCHB-101, Vardan *etc.* have released but they fail to provide optimum yield due to delayed sowing. Therefore, it is imperative to screen the mustard germplasm against the terminal heat stress and diverse thermo-tolerant genotype is the need of time to strengthen resilience under mustard crop improvement programmes. This will help in stabilize the mustard productivity and to meet the national demand of edible oil.

The quantitative assessment of available genetic variability present among selected genotypes is of utmost importance in all the crop improvement programmes. The yield components depend on some physiological and agro-morphological traits. To understand, the physiological basis of yield difference among the genotypes of mustard, it is essential to quantify the components of growth and the variation, if any, may be utilized in crop improvement. The effect of heat stress on seed yield and its contributing traits *viz.*, plant height, main shoot length, number of primary and secondary branches, number of pods on main shoot and seed size, has been well documented (**Morrison and Stewart 2002; Alam *et al.*, 2014; Sharma, 2014 and Sharma and Sardana, 2014**). Yield is a major complex character that is an outcome of interaction of plant characters and plant breeders are seldom interested in one character and therefore, there is the need to examine the relationship among various characters, especially between yield and other morphological traits. Nevertheless, selection for yield via highly correlated characters becomes easy if the contribution of different characters to yield is quantified using path coefficient analysis (**Dewey and Lu, 1959**). Therefore, success of crop improvement program is dependent on highly heritable genotypic variability. So, the extent of genetic variability, heritability, genetic advance and association of seed yield components help in seed yield improvement.

Keeping above facts in mind, this study is designed to assess the genetic variability for terminal heat tolerance in the Indian mustard germplasm with the following objectives:

1. To find out genetic variability and diversity in mustard germplasm based on agro-morphological traits,
2. To estimate the nature of association between yield and its attributing traits and direct and indirect effect of various characters on seed yield and,
3. Phenotyping of Indian mustard genotypes to identify heat tolerance under normal and terminal heat stress environments.

Chapter 2

REVIEW OF LITERATURE

The knowledge about nature and magnitude of genetic variation of breeding material is of prime importance for crop improvement programme of any crop and assessment of genetic variability and divergence is a foremost activity in any breeding programme. It gives opportunities for selection of superior and climate resilient genotypes from diverse germplasm. Yield is a quantitative and complex trait which is determined by the direct and indirect effect of contributing traits and influenced by the environment. Inter-character association studies revealed their direct and indirect effect of yield attributing traits towards crop yield. In view of climate change scenario and global warming, terminal heat tolerant crop varieties are a key requirement for sustainable agriculture. Along with other commercially important crop, mustard is also influenced by terminal heat tolerance therefore; a brief review of the research work carried out in relation with the present investigation in mustard has been presented under the following heads:

2.1 Genetic variability

2.2 Genetic divergence

2.3 Correlation and path analysis

2.4 Heat tolerance

2.1 Genetic variability

Variability refers to the presence of differences among the individuals of plant population. The success of any crop improvement programme is depends upon genetic variability exist in crop. Total variation can be divided into genotypic variation and phenotypic variation. The genotypic variation is heritable part of total variation. The assessment of genetic variation is a pre-requisite for any plant breeding strategies. The estimation of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provides the information on genetic variability. The selection of breeding strategies and theirs effectiveness for crop improvement depends on nature and magnitude of genetic variability. The availability of genetic variability and its assessment is essential for resistance to abiotic and biotic stress. High heritability coupled with high genetic advance for yield attributing traits is an essential requirement for selection of superior parents. Knowledge over heritability with genetic advance is more beneficial in prediction of effect of selection (**Johnson *et al.*, 1955**). Therefore, characterization of genetic

variability along with heritable differences is indispensable for a long term crop improvement programme in any crop. In past, several researchers reported the genetic variation in mustard for yield and its component traits and some of them are reviewed as described below:

Kumar and Singh (2013) evaluated 35 varieties of Indian mustard to study genetic variability for 10 agro-morphological traits. ANOVA revealed that the number of secondary branches per plant, seed yield, harvest index and number of primary branches per plant showed highest genotypic coefficient of variation (GCV). The length of main raceme, length of siliqua and 1000 seed weight showed moderate genotypic coefficient of variation. The oil content and plant height showed low genotypic coefficient of variation.

Shekhawat *et al.*, (2014) carried out an experiment with 60 genotypes of Indian mustard for 13 different characters to study genetic variability. It observed that eight characters viz., days to 50 percent flowering, days to maturity, number of secondary branches per plant, length of main branch, number of siliqua per plant, number of seeds per siliqua, test weight and seed yield per plant showed high estimates of GCV as well as high heritability while number of secondary branches per plant, seed yield per plant and number of siliqua per plant showed high heritability and high expected genetic advance.

Akabari *et al.*, (2015) conducted an experiment on 36 Indian mustard genotypes to estimate genetic variability for yield and other yield contributing traits. Analysis of variation revealed that the all traits under study were observed with significant genotypic variability. The number of secondary branches per plant, number of siliqua per plant and yield per plant had higher value for GCV and PCV both. The number of siliqua per plant, yield per plant, number of seeds per siliqua, length of main branch, days to 50 percent flowering, 1000 seed weight, number of secondary branches per plant, siliqua length, protein content and plant height showed higher heritability which indicated less influence of environment on expression of all these traits.

Prasad and Patil (2018) evaluated Indian mustard genotypes to study genetic variability for yield contributing traits. ANOVA indicated that the number of secondary branches per plant, racemes per plant, economical yield, biological yield, harvest index, seed yield and oil yield showed high genotypic coefficient of variance. High heritability

was found for plant height, secondary branches per plant, racemes per plant, siliqua length, test weight, biological yield, seed yield and oil yield.

Singh *et al.*, (2018) studied 60 germplasm of Indian mustard to assess genetic variability for yield and yield contributing traits. ANOVA revealed that all the characters showed significant variation. Seed yield per plant, number of secondary branches per plant, 1000 seed weight, number of primary branches per plant and length of main raceme had highest PCV and seed yield per plant showed highest GCV followed by number of secondary branches per plant, 1000 seed weight, length of main raceme and plant height. Seed yield per plant, 1000 seed weight, number of secondary branches per plant and length of main raceme showed high both GCV and PCV.

Chaurasiya *et al.*, (2018) evaluated 36 Indian mustard genotypes and observed that number of secondary branches per plant, number of siliqua per plant and yield per plant had higher values of phenotypic co-efficients of variation and genotypic co-efficients of variation whereas, number of siliqua per plant, plant height, length of main axis and yield per plant had high heritability values coupled with high genetic advance.

Tripathi *et al.*, (2019) evaluated 20 genotypes of Indian mustard with four checks for thirteen quantitative traits. High PCV and GCV observed for number of secondary branches per plant, biological yield per plant and seed yield per plant while moderate PCV and GCV was observed in case of number of primary branches per plant, length of main raceme, seeds per siliquae and harvest index. Low PCV and GCV were observed in days to 50 percent flowering, days to maturity and plant height.

Tiwari (2019) carried out an experiment on Indian mustard genotypes to assess genetic variability for yield contributing traits. ANOVA indicated that the number of secondary branches per plant showed highest GCV. Number of secondary branches per plant, number of siliqua per plant, length of siliqua, 1000 seed weight, oil content and seed yield per plant recorded with high GCV and heritability.

Singh *et al.*, (2019) examined 7 germplasm lines of Indian mustard to study genetic variability based on 12 yield contributing traits viz., days to 50 percent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, 1000 seed weight, biological yield per plant, harvest index, oil content and seed yield per plant.

ANOVA revealed that all the characters had significant variation. Primary branches per plant, 1000 seed weight, number of seeds per siliqua and seed yield per plant were recorded with high GCV and PCV.

Khan *et al.*, (2019) studied genetic variability for 13 quantitative traits in 10 Indian mustard lines. ANOVA indicated that all the characters showed highly significant variation. All the characters under study were recorded with high GCV and PCV which indicate that environment had less effect on expression of studied characters. Seed yield per plant, seeds per siliqua, number of secondary branches per plant, siliqua per plant and 1000 seed weight showed high heritability with high genetic advance which indicate that crop improvement can be done through direct selection of these characters.

Srivastava and Srivastava (2019) evaluated 38 genotypes of Indian mustard with check Giriraj to study genetic variability for yield contributing traits. The ANOVA revealed that all characters showed sufficient variation and seed yield per plot recorded with highest performance followed by number of siliqua per plant and plant height. Seeds per siliqua recorded with higher genotypic variation and phenotypic variation. Days to 50 percent flowering, number of siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight, seed yield per plant, seed yield per plot, biological yield and seed yield showed high heritability coupled with high genetic advance which indicating presence of additive gene action so direct selection of these traits help in breeding programme. RGN-73(16.4 q/ha), RGN-298(15.9 q/ha), JD-6(16.2 q/ha), RVM-2 (17.3 q/ha) and RGN-48(15.8 q/ha) were recorded with more yield than Giriraj.

Rout *et al.*, (2019) carried out an experiment with 38 genotypes of Indian mustard to study about variability, heritability and genetic advance of percent of mean. ANOVA revealed that all the characters had substantial amount of variability among the genotypes which indicate wide spectrum of genetic variability among the genotypes. Number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, biological weight per plant, harvest index, seed yield per plant and 1000 seed weight were observed with moderate PCV and GCV. For the traits *viz.*, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, biological yield per plant, harvest index, seed yield per plant and 1000 seed weight, high heritability was coupled with

high genetic advance as per cent of mean. Low difference between PCV and GCV were observed for all the traits under study.

Patel *et al.*, (2021) evaluated 45 genotypes of Indian mustard to study genetic variability for seed yield contributing traits. ANOVA revealed that all the 18 characters under study had significant mean sum of squares which indicate the presence of sufficient level of genetic variability. Number of branches per plant, seed yield per plant, myristic acid, palmitic acid and stearic acid showed high GCV and PCV. The difference between genotypic and phenotypic variation was recorded very low for all characters except days to maturity and plant height which indicated that genotypic variation contributed maximum to total variation which is heritable proportion of the variation. Number of branches per plant, the number of siliquae per plant, seeds per siliqua, length of siliqua, 1000 seed weight, seed yield per plant, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid and glucosinolate showed high heritability coupled with high genetic advance which indicate that additive gene action play predominant role in their expression.

2.2 Genetic divergence

Genetic diversity is the base for crop survival and crop improvement. Genetic diversity in plant genetic resources facilitates plant breeders to develop new and superior cultivars with desirable traits. Genetic diversity in plant genetic resources may include wild species, breeding stocks, related species, mutant lines, absolute cultivar, species genetic stocks, improved strains and primitive cultivars. Genetic diversity provides broad genetic base, more fitness and wide adaptability to a population. In present scenario, breeding for climate resilient crop varieties is becoming more important with changing climate and genetic diversity in crop species may serve as source for development of climate resilient varieties. D^2 statistics is used for assessment of genetic divergence present in crop species. The concept of D^2 statistics was developed by P. C. Mahalanobis in 1928 and its application for plant breeding was suggested by Rao. Through the D^2 values, the genetic diversity is depicted by cluster diagram.

Kumar and Pandey (2013) characterized 46 genotypes of Indian mustard for genetic diversity using Mahalanobis D^2 analysis and grouped total genotypes into 7 clusters. The cluster I and IV was contained maximum genotypes (9) each and cluster II contained minimum two genotypes. Maximum inter-cluster distance was observed between cluster V and VI followed by cluster V and VII and cluster II and VI. More divergent

genotypes were RAURD-166, RAURD-205, RAURD-241, RAURD-32, JD-6, RAURD-168, RAURD-78, RAURD-195, RAURD-246, RAURD-172, RAURD-25 and RAURD-34. The minimum mean value for plant height with early flowering and maturity was recorded for cluster V whereas cluster VI showed maximum value for primary branches per plant, secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, biological yield per plant and seed yield per plant. Cluster VII was superior in length of main raceme, siliqua on main raceme and seed yield per plant and cluster II was superior in siliqua density. More divergent clusters were clusters VI, VII, V and II with high seed yield. Individuals from such clusters can be used to generate more genetic variability.

Singh *et al.*, (2014) studied genetic divergence in 30 Indian mustard genotypes using Mahalanobis D^2 analysis. Based on D^2 values, all genotypes were grouped into 4 clusters. The maximum mean value for plant height (185.73), number of secondary branches per plant (32.55) and days to 50 percent flowering (71.23) was recorded for cluster IV genotypes. The maximum mean value for seed yield per plant (28.36 g), number of pods per plant (728.12) and chlorophyll content (3.60) was observed for cluster III genotypes. The minimum mean value for days to 50 percent flowering (54.00) was observed for cluster II. The main contributor of genetic divergence was plant height followed by days to maturity. Most divergent cluster was clusters I and IV because these showed maximum inter-cluster distance (9.953). The genotypes contained in these diverse clusters can be used in hybridization programme as parents will give high heterotic responses.

Gupta *et al.*, (2015) carried out an experiment on 39 genotypes of Indian mustard to study genetic divergence using D^2 analysis. D^2 analysis revealed that cluster II had maximum 14 genotypes, cluster I had 6 genotypes whereas cluster III, IV and V had minimum number of genotype (1). Maximum intra-cluster distance was observed for cluster III whereas, the minimum intra-cluster distance shown by cluster I. Maximum diversity and superiority in mean performance for most of the characters was observed in cluster III and IV.

Singh *et al.*, (2016) carried out an investigation on 33 genotypes of Indian mustard to study genetic variability and genetic diversity. It was observed that main contributors of genetic diversity were seed yield per plant, 1000 seed weight, number of

primary branches per plant, number of secondary branches per plant, number of seeds per siliquae, siliqua length, plant height and number of silique on main raceme. D^2 analysis revealed that cluster I and IX was having maximum six genotypes each and cluster IV was having only one genotype (JM-016). Clusters IV and VIII had maximum divergence (8.3) followed by cluster IV and VI (7.1), cluster IV and V (7.1) and cluster V and VIII (6.9). Hence, accessions belonging to cluster IV and VIII can be used as parents for hybridization programme for the development of high yielding mustard genotypes. Most divergent genotypes were JM0-16, PCR-7 and RH-8812. Cluster V genotypes had short stature, earliest in days to 50 percent flowering and in maturity. Cluster VIII had highest siliqua length, number of seeds per siliqua, 1000 seed weight, seed yield (kg/ha), high values of number of primary and secondary branches per plant, main raceme length and oil content. The most divergent clusters were cluster V and VIII having high mean values for seed yield and oil content.

Lodhi et al., (2016) conducted detailed morphological study based on quantitative traits to assess genetic diversity using D^2 statistics among 90 Indian mustard genotypes and were grouped into nine clusters. The major contributors for genetic diversity were number of primary branches per plant, number of secondary branches per plant, siliqua angle, siliqua on main shoot, primary branch angle, 1000 seed weight and main shoot length. D^2 statistics revealed that cluster I included maximum 20 genotypes which is followed by cluster II with 18 genotypes, cluster III with 15 genotypes, cluster IV with 10 genotypes, cluster V with 8 genotypes, cluster VI and cluster VII with 7 genotypes in each, cluster VIII with 3 genotypes and cluster IX with 2 genotypes. The cluster VIII and IX (9.76) had maximum inter-cluster distance while cluster V recorded maximum intra-cluster distance (5.69). Considering the genetic distance, they reported the cultivars of cluster VIII and IX are likely to recombine genes for higher yield and its contributing traits as these two clusters contain genetically most distant cultivars.

Mohan et al., (2017) conducted an experiment on 25 genotypes of Indian mustard to assess genetic divergence using D^2 analysis. D^2 analysis grouped all genotypes into 6 clusters. The maximum genotypes were exhibited by cluster I with 9 strains followed by cluster III, II, IV, V and VI. Cluster III and cluster IV showed highest inter-cluster distance (90.88) suggesting that these groups of genotypes are highly divergent from each other. The minimum inter cluster distance (15.38) was recorded between cluster-I and

cluster IV. Study revealed that clusters show genetic divergence for all characters and accessions from these cluster can be hybridize to get more transgressive segregants.

Devi *et al.*, (2017) evaluated 45 genotypes including local cultivars, advanced lines and notified varieties of Indian mustard to study genetic divergence based on 14 different agro-morphological characters *viz.*, days to 50 percent flowering, days to maturity, plant height , number of primary and secondary branches per plant, main shoot length , leaf area index, root width and length ratio, number of siliqua per plant, siliqua length , number of seeds per siliqua, seed yield per plant, 1000 seed weight and oil content using Mahalanobis's D^2 statistics. It was reported that the genotypes under study fell in 7 clusters. The analysis revealed that maximum genotypes (18) were observed in cluster I, cluster III containing 9 genotypes, cluster IV containing 8 genotypes, cluster II containing 6 genotypes, cluster VI containing 2 genotypes while cluster V and VII containing single genotype each. The major contributors for genetic diversity were root width and length ratio, siliquae per plant, main shoot length and 1000 seed weight and their contribution towards genetic divergence were 23%, 21.80%, 21.32% and 20.51%, respectively. Maximum intra-cluster distance was observed for cluster IV (844.272) while cluster V and VII (7273.532) had maximum inter-cluster distance indicating a vast scope of hybridization between the genotypes in order to generate variability.

Kumar *et al.*, (2017) conducted an experiment on 41 accessions of Indian mustard to study genetic divergence using D^2 statistics for 9 characters *viz.*, plant height, number of primary branches per plant, number secondary branches per plant, number of siliquae per plant, siliqua length, number of seeds per siliqua, total number of seeds per plant, total seed yield per plant and test weight. The analysis revealed that all the genotypes were grouped into 7 clusters and cluster I containing 10 lines followed by cluster II containing 7 lines, cluster IV and VI containing 6 lines each, whereas, clusters V, III and VI had 5, 4 and 3 genotypes, respectively. Highest cluster mean value for siliqua length, number of seeds per siliqua, total seed yield per plant and test weight was observed in cluster VII whereas, cluster II had highest cluster mean value for number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant.

Rathod *et al.*, (2017) evaluated 50 genotypes of Indian mustard to study genetic divergence for oil content and seed yield attributes viz., days to 50 percent flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per silique, length of silique, 1000 seed weight, seed yield per plant, biological yield per plant, harvest index and oil content. D^2 statistic grouped 50 genotypes into 9 clusters and cluster II and VI was observed with maximum inter-cluster distance (33.15). The main contributors for genetic diversity were days to maturity, days to 50 percent flowering and 1000 seed weight. Cluster VIII exhibited highest cluster mean value for seed yield per plant, number of primary branches per plant, 1000 seed weight and biological yield per plant along with delayed days to 50 percent flowering and days to maturity, whereas cluster II exhibited highest cluster mean value for number of secondary branches per plant, number of siliquae per plant and oil content. Study revealed that selection based on seed yield per plant, biological yield per plant, harvest index, number of secondary branches per plant and number of siliquae per plant help in crop improvement.

Tudu *et al.*, (2018) carried out an investigation among 30 genotypes of Indian mustard to study genetic divergence based on yield contributing traits using D^2 statistics. The analysis revealed that all genotypes were grouped into seven clusters with cluster I containing maximum genotypes (12 genotypes) followed by cluster III and cluster IV containing 7 genotypes in each, while clusters II, V, VI and VII contained only one genotype in each. Cluster IV was observed with most of the desirable characters viz., number of primary branches per plant and number of secondary branches per plant, plant height, number of silique per plant, 1000 seed weight and seed yield per plant. Maximum divergence contributing traits were days to 50 percent flowering followed by number of secondary branches per plant, silique length, number of seeds per silique and 1000 seed weight. Highest inter cluster distance was observed between cluster IV and VI (16.08) followed by cluster III and VI (13.40) and cluster IV and VII (12.30). Cluster IV and VI genotypes will give maximum heterosis when it is used for crossing because these show maximum divergence.

Nagda *et al.*, (2018) evaluated 36 Mustard genotypes of Indian mustard to assess genetic divergence based on 13 quantitative traits using D^2 statistics. ANOVA revealed that all the traits of different genotypes had significant variation. All genotypes

under this study were grouped into 7 clusters in which cluster I had maximum 13 genotypes followed by cluster II containing 11, cluster IV containing 5 and cluster III containing 4 and cluster V, VI and VII were solitary. Maximum intra cluster distance showed by cluster IV (267.22) followed by cluster III (217.06), cluster II (133.07) and cluster I (92.53). Maximum inter-cluster distance was recorded between cluster VI and cluster VII. The inter-cluster distance was varied from 171.51 to 1645.64. If the cross attempted between genotypes belong to cluster VI and cluster VII would produce transgressive segregates for seed yield.

Tripathi *et al.*, (2019) evaluated 25 genotypes of Indian mustard using D^2 analysis and were grouped into 6 clusters. The cluster I was largest cluster which contains 9 genotypes followed by cluster III (7), cluster II (6) and cluster IV, cluster V and cluster VI contains single genotype in each. The maximum inter cluster distance was observed between cluster III and cluster IV (90.88) which indicate these are most divergent cluster under study. Cluster I and IV had minimum inter cluster distance (15.38) which revealed that these clusters contain closely related genotypes.

Gadi *et al.*, (2020) carried out an investigation on 36 genotypes of Indian mustard to assess genetic divergence based on 10 characters by using D^2 statistics. Analysis revealed that all genotypes were grouped in 11 clusters. The main contributors for genetic diversity were days to maturity (32.50%) followed by days to 50 percent flowering (30.76%), test weight (26.30%), plant height (1.48%), number of seeds per siliqua (1.27%), total number of siliqua per plant (0.63%), seed yield (5.32%), number of siliqua on main shoot (1.27%), harvest index (0.50%) and biological weight (0.23%). Cluster I was largest with 11 genotypes followed by cluster IV with 7 genotypes, cluster II and V with 5 genotypes, cluster VIII with 2 genotype whereas, remaining clusters contain single genotype each. Maximum intra-cluster distance (8.20) was observed for cluster V, while maximum inter-cluster distance was observed between cluster XI and VI (41.82).

Malviya *et al.*, (2021) led an experiment with 15 Indian mustard varieties/strains, 4 testers and 60 F_1 s developed by crossing 15 lines with 4 testers to assess genetic diversity. The D^2 statistics grouped 19 parental lines into five clusters in E1 (timely sown) and E2 (late sown) condition based on D^2 values. In E1, cluster II included maximum 8 genotypes followed by cluster I and IV with four genotypes. In E2, cluster I

included maximum 9 genotypes followed by cluster V which had four genotypes. In E1, most diverse clusters were cluster IV and V with inter-cluster distance of 7169.70 followed by cluster II and V (4829.11) and intra-cluster distance ranged from 0.00 (cluster V) to 581.64 (cluster IV). In E2, most diverse clusters were clusters IV and V with inter-cluster distance of 1894.16 and intra-cluster distance ranged from 0.00 (cluster IV) to 296.03 (cluster V). Based on D^2 values 60 F_1 s were grouped into 8 clusters in E1 and E2. In E1, clusters I and VI were largest having 12 genotypes. The maximum inter-cluster distance was observed between cluster IV and VIII (3554.76) and intra-cluster distance ranged from 111.59 (cluster IV) to 318.07 (cluster II). Whereas, in E2 cluster III was largest having 15 genotypes. The maximum inter-cluster distance (D^2) was observed between cluster V and VIII (43829.30) and intra-cluster distance ranged from 0.00 (cluster V) to 351.31 (cluster VIII).

Genetic divergence for 13 agro-morphological traits among 75 exotic and indigenous lines of Indian mustard was studied by **Lien *et al.*, (2021)**. Based on D^2 values all genotypes were grouped into 15 clusters. Cluster I was largest cluster with 46 genotypes, followed by cluster V containing 8 genotypes, cluster III containing 7 genotypes, cluster XII (3 genotypes) while clusters II, IV, VI, VII, VIII, IX, X, XI, XIII, XIV and XV, contains single genotype in each cluster. The maximum intra-cluster distance (15.51) was recorded for cluster XII whereas, cluster XII and cluster XV showed maximum inter-cluster distance (38.15). The 1000 seed weight (33.26%), days to 50 per cent flowering (26.09%), oil content (23.93%), days to maturity (26.09%) and seed yield per plant were main contributors of genetic divergence. Considering clusters means and genetic distances, crosses between the genotypes of cluster XII and cluster XV will be useful to recombine genes for higher yield as these two clusters contain genetically more divergent genotypes.

2.3 Correlation and path analysis

The term correlation coefficient was given by Karl Pearson in 1902 and denoted by “r”. It is used to measure association between yield and its contributing traits to determine the component trait on which selection can be based for genetic improvement in yield. For a plant breeder, it is essential to know the degree of relationship between yield and its contributing traits to facilitate the improvement in desirable traits. Correlation coefficient provides information on inter-character association of various yield components but when more characters are involved in the association analysis it becomes challenging to

ascertain which trait actually contributes more towards yield. Thus correlation analysis is not enough to give an exact picture of relative importance of direct and indirect influence of each of the component characters on seed yield. Therefore, path coefficient analysis is an ideal way of partitioning correlation coefficients into direct and indirect effects to design effective selection programme for dependent trait. The concept of path analysis was developed in 1921 by Wright but it was used for plant selection suggested by Dewey and Lu in 1959. It gives information about the direct contribution of traits on yield as well as their indirect contribution via other component traits. It helps to direct and indirect selection of superior genotypes from the diverse breeding population.

Singh and Singh (2010) evaluated sixty three F_1 hybrids along with 24 parents to study the genetic variability and genetics of characters contributing to yield and oil content in Indian mustard. Experiment results suggested that seed yield was positively correlated with plant height, number of primary branches per plant, number of secondary branches per plant, siliquae on main raceme, length of main raceme, seeds per siliqua and 1000 seed weight. Path coefficient analysis indicated that positive direct effects were highest for secondary branches per plant followed by plant height, seeds per siliqua on seed yield while number of primary branches per plant had highest indirect effect on seed yield.

Yadava *et al.*, (2011) carried out ANOVA, path coefficient analysis and correlation analysis in 30 released varieties of Indian mustard. They observed that 1000 seed weight was positively correlated with siliqua length and total siliquae per plant, which had higher phenotypic and genotypic direct effect on seed yield per plant. Indirect effect of 1000 seed weight was observed on seed yield per plant.

Singh *et al.*, (2013) led an experiment to study ANOVA, associations study among yield components in 10 early generation (F_3) lines of Indian mustard. The results of study revealed that number of secondary branches per plant and seed yield per plant were highly heritable and coupled with higher genetic advance. Seed yield per plant had positive and significant association with number of secondary branches per plant, number of siliquae on main shoot and total siliquae per plant at both genotypic and phenotypic level. Path coefficient analysis indicated that number of secondary branches per plant, number of siliquae on main shoot and total siliqua per plant had positive and direct effect on seed yield per plant.

Singh *et al.*, (2013) evaluated 50 genotypes of Indian mustard to describe inter character association between seed yield and its attributing traits under timely sown (E1) and late sown (E2) environments. Path coefficient analysis revealed that under timely sown environment (E1) seed yield per plant was positively correlated with main shoot length, siliqua length, number of seeds per siliqua and 1000 seed weight and under late sown environment (E2) seed yield was positively correlated with plant height, main shoot length, number of siliqua on main shoot and 1000 seed weight. Under both environments only days to 50 percent flowering had direct and indirect positive effect on seed yield.

Bind *et al.*, (2014) studied genetic variability, interrelationship and genetic divergence in thirty indigenous collections of Indian mustard for 14 different quantitative characters. All the characters except days to 50 percent flowering and days to maturity had positive phenotypic and genotypic correlation with seed yield per plant. The path coefficient analysis indicated that biological yield per plant had the highest direct positive effect on seed yield per plant followed by harvest index, 1000 seed weight, number of seeds per siliqua, number of primary branches per plant while plant height at phenotypic level had highest negative direct effect on seed yield per plant.

Kumar *et al.*, (2016) carried out an experiment with 12 quantitative traits in 30 Indian mustard germplasm lines to study the correlation and path coefficient analysis. It was observed that harvest index and total biological yield per plant exerted highly significant and positive correlation with seed yield at both genotypic and phenotypic level. Seed yield was negatively correlated with days to 50 percent flowering and days to maturity. Under study it was witnessed that harvest index showed maximum positive direct effect, followed by total biological yield per plant, days to maturity, siliqua length at the time of maturity and seed yield per plant at both genotypic and phenotypic levels through path analysis.

Solanki *et al.*, (2017) carried out an experiment on 220 cultivars of Indian mustard to assess the association between yield and agro-morphological traits. Observation was recorded for ten agro-morphological traits viz., days to 50 percent flowering, plant height, number of primary branches per plant, number of secondary branches per plant, days to maturity, number of seeds per siliqua, 1000 seed weight. Correlation analysis indicated that the seed yield had highly significant positive correlation with plant height, number of siliqua per plant, number of secondary branches per plant and number of

primary branches per plant. Days to 50 percent flowering, length of siliqua and number of seeds per siliqua had non-significant positive correlation with yield per plant at phenotypic level. Seed yield was negatively correlated with plant height, number of primary branches per plant, number of secondary branches per plant, days to maturity, number of siliqua per plant and 1000 seed weight at phenotypic level but correlation was non-significant. Path coefficient analysis indicated that, length of siliqua, days to 50 percent flowering and number of seeds per siliqua showed highest positive direct effect on seed yield. While, 1000 seed weight, number of primary branches per plant, plant height, number of secondary branches per plant and number of siliqua per plant showed negative direct effect on seed yield. Negative indirect effects on seed yield showed by number of primary branches per plant, days to maturity, length of siliqua, days to maturity and 1000 seed weight.

Roy *et al.*, (2018) examined inter character association among 14 agromorphological characters observed in 40 genotypes of Indian mustard under late sown condition. The correlation analysis revealed the significant and positive association of seed yield with pod length, number of seeds per pod and oil content while, negative correlation was observed with days to first flowering and total biomass. Path coefficient analysis indicated that oil content, leaf area index had highest and positive direct effect on seed yield per plant followed by number of seeds per pod and pod length.

Ompal *et al.*, (2018) studied 12 agro-morphological characters viz., days to 50 per cent flowering, plant height, primary branches per plant, secondary branches per plant, days to maturity, siliquae per plant, seeds per siliquae, biological yield per plant, grain yield per plant, harvest index, 1000 seed weight and oil content of 12 varieties of Indian mustard. It was observed that grain yield per plant was highly positive and significantly correlated with biological yield. Path analysis revealed that biological yield per plant had highest direct effect on grain yield.

Devi (2018) evaluated 12 Indian mustard genotypes with 13 quantitative traits for the correlation and path analysis study. Biological yield per plant and siliqua on main raceme had positive and significant correlation with grain yield per plant at genotypic level whereas, secondary branches per plant was negatively correlated with grain yield per plant. Path analysis stated that days to 50 percent flowering showed maximum positive direct

effect however the highest indirect effect of this trait was exhibited through biological yield per plant.

Gupta *et al.*, (2018) carried out an experiment to describe the correlation and path coefficients for yield and yield related traits for 30 genotypes of Indian mustard with 3 checks (Kranti, Vardan and RGN-73) under timely and late sown conditions. Seed yield per plant had significant and positive association under both timely and late sown conditions with biological yield per plant followed by harvest index, silique on main raceme, length of main raceme, 1000 seed weight and secondary branches per plant. Present study revealed that in timely sown, plant height had highly significant and positive association with seed yield per plant. Path analysis indicated that major direct yield component was biological yield per plant followed by harvest index under both timely and late sown conditions. Under timely sown conditions, plant height was indirect yield component and under late sown conditions, secondary branches per plant at genotypic level and plant height at phenotypic level were indirect yield component via biological yield per plant.

Pandey and Yadav (2018) evaluated twenty genotypes of Indian mustard to study correlation and path coefficient analysis between seed yield and yield components. Correlation analysis revealed that the seed yield per plant showed significant and positive correlation with plant height, number of primary branches per plant, number of secondary branches per plant, silique on primary branches, silique on secondary branches, silique on main axis, biological yield per plant and physiological maturity at both genotypic and phenotypic levels. Path coefficient analysis revealed that highest positive direct effect on seed yield showed by number of primary branches per plant and biological yield per plant followed by harvest index, test weight, length of siliqua and silique on primary main axis.

Kumar *et al.*, (2018) conducted an experiment on Indian mustard to assess correlation and path analysis between yield and its contributing traits. Correlation analysis revealed that seed yield per plant was positively and significantly correlated with 1000 seed weight, leaf area index, harvest index, oil content, protein content, biological yield per plant, seeds per silquae, silquae per plant, primary branches per plant and length of main raceme but at phenotypic level seed yield showed negative and significant correlation with days to 50 percent flowering, days to maturity and plant height. A positive direct effect on seed yield at phenotypic level was observed highest by 1000 seed weight followed by

biological yield per plant and leaf area index, while days to 50 percent flowering and primary branches per plant showed negative direct effect on seed yield.

Tantuway *et al.*, (2018) conducted an experiment on thirty genotypes of Indian mustard to describe association between yield and agro-morphological traits. He observed that plant height, number of primary branches per plant, number of secondary branches per plant, length of main raceme and number of siliqua per plant had positive and significant correlation with seed yield per plant at genotypic level. Siliqua length showed significant correlation but in negative direction with seed yield. Path coefficient analysis indicated that plant height, number of secondary branches, siliqua length and seed yield per plant showed positive direct effect on seed yield per hectare.

Pal *et al.*, (2019) carried out an experiment to assess the genetic variation for quantitative traits among 7 genotypes of Indian mustard. The results of this study revealed that seed yield per plant was positively correlated at both genotypic and phenotypic level with secondary branches per plant, siliqua per plant, biological yield per plant, harvest index, days to maturity, 1000 seed weight and oil content. Path coefficient analysis revealed that biological yield per plant had highest positive direct effect on seed yield per plant. A negative direct effect of seeds per siliqua, plant height, days to 50 per cent flowering, days to maturity, secondary branches per plant and oil content were observed for seed yield per plant.

Kumar *et al.*, (2019) assessed correlation and path analysis in F₁ hybrid of Indian mustard to describe association between yield and its contributing traits. It was observed that seed yield per plant was positively correlated with biological yield per plant followed by traits like number of primary branches per plant, plant height, number of secondary branches per plant, siliqua length and number of siliquae per plant at phenotypic level. Path coefficient analysis revealed a high positive direct effect on seed yield by biological yield followed by harvest index, siliqua length, number of primary branches per plant, days to maturity, plant height and number of secondary branches per plant.

Khan *et al.*, (2019) evaluated 10 Indian mustard lines to study correlation and path analysis between seed yield and its attributing traits. Correlation analysis indicated that seed yield per plant had positive and significant association with siliqua per plant,

biological yield per plant, secondary branches per plant and harvest index. Path analysis showed that biological yield per plant and harvest index exerted highest positive direct effect on seed yield per plant.

Srivastava and Srivastava (2019) conducted an experiment on 38 genotypes of Indian mustard with check Giriraj to study association between yield and its contributing traits. It was found that seed yield had positive correlation at genotypic level with plant height, number of secondary branches per plant, number of silique per plant, siliqua length, main raceme length, number of siliqua on main raceme, test weight and biological yield per plot. Path coefficient analysis indicated that plant height, number of primary branches per plant, number of secondary branches per plant, siliqua length, seeds per siliqua, main raceme length, number of siliqua on main raceme and number of siliqua per plant showed positive direct effect on seed yield at phenotypic level.

Ray *et al.*, (2019) conducted an experiment to study correlation and path analysis between yield and its contributing traits among nineteen genotypes of Indian mustard. The seed yield per plant had significant and positive correlation with days to 50 per cent flowering, plant height, number of siliqua per plant, biological yield per plant and harvest index both at genotypic and phenotypic level. Therefore, these traits could be directly used for the improvement of seed yield to develop high yielding mustard cultivar. Number of primary branches per plant showed significant positive correlation with seed yield per plant at genotypic level. Path analysis indicated that seed yield per plant had positive direct effect with days to 50 per cent flowering, number of primary branches per plant, plant height, number of siliqua per plant, biological yield per plant and harvest index.

Dinesh *et al.*, (2020) assessed association between yield and its contributing traits in Indian mustard. Study revealed that seed yield showed positive and significant correlation with days to 50 per cent flowering and number of secondary branches per plant at both genotypic and phenotypic level. Path co-efficient analysis indicated that harvest index percentage showed the highest direct positive effects on seed yield per plant, number of siliqua per plant, number of seeds per siliqua, number of secondary branches per plant and days to maturity.

Chaturvedi *et al.*, (2021) conducted an experiment to study association between different characters of 73 varieties/strains of Indian mustard. Correlation analysis revealed

that seed yield per plant had positive association with number of siliqua on main raceme followed by number of primary branches per plant. Path analysis indicated that seed yield per plant had direct positive effect with number of siliqua followed by number of primary branches per plant while number of seeds per siliqua, test weight and plant height had indirect effect on seed yield. Hence, number of siliqua per plant and number of primary branches per plant should be considered as important criteria for mustard breeding programme to evolve high yielding mustard varieties.

Patel et al., (2021) evaluated 45 genotypes of Indian mustard to gain the knowledge about association between yield and its contributing traits. Seed yield per plant showed positive significant correlation with the number of siliquae per plant, seeds per siliqua and length of siliqua. Path analysis indicated that seed yield per plant had positive direct effect with the number of siliquae per plant and seeds per siliqua. Seed yield per plant had positive indirect effect with the number of branches per plant via the number of siliquae per plant. Based on the investigation, a *Brassica juncea* ideotype should have high number of siliquae per plant and high number of seeds per siliqua and that would enhance the yield in mustard genotypes.

Pandey et al., (2021) conducted an experiment to describe association between seed yield and its components traits among 20 genotypes of Indian mustard. Correlation analysis indicated that seed yield was positively correlated at both genotypic and phenotypic level with days to 50 per cent flowering, plant height, test weight and harvest index while, number of seeds per siliqua was also positively correlated but only at genotypic level. Path coefficient analysis revealed that harvest index (1.277) had highest positive direct effect on seed yield followed by biological yield per plant (0.9511), days to maturity (0.1951) and number of secondary branches (0.1430). Therefore, selection can be practiced effectively on the basis of high harvest index, biological yield per plant, days to maturity and number of secondary branches for the improvement in seed yield of Indian mustard.

Lavanya et al., (2022) evaluated fifty genotypes of Indian mustard to find out association between yield and its contributing characters. At genotypic level, seed yield per plant showed positive and significant correlation with harvest index followed by number of secondary branches per plant and number of siliquae per plant. Path coefficient analysis

indicated that seed yield per plant had direct positive effect with days to maturity, number of secondary branches per plant, number of siliquae per plant, siliqua length, 1000 seed weight, harvest index and oil content both at genotypic and phenotypic level.

2.4 Heat tolerance

Rising temperature is important factor of climate change which is affecting crop productivity around the world. High temperature stress during terminal stage is affecting pollen fertility, flowering and grain filling which is the most sensitive stage of Indian mustard. Heat stress triggers an array of physiological, biochemical and molecular changes. Heat tolerance in crop plants is a developmentally regulated, stage specific phenomenon. Therefore, heat tolerance at terminal stage shall be evaluated separately for the assessment, characterization and genetic manipulation of heat tolerance traits.

Chauhan *et al.*, (2009) evaluated 22 advance breeding lines of Indian mustard to study the effect of terminal heat stress on plant height, number of primary branches per plant, siliquae on main shoot, seeds per siliqua, 1000 seed weight, seed yield, oil and protein content, leaf area index (60 DAS), specific leaf weight (80 DAS), crop growth rate (40-60 DAS), chlorophyll stability index (60 DAS) and harvest index. The genotypes were grown in two environments viz. E1 (timely) and E2 (late). All the characters except chlorophyll stability index and protein content showed significant genotypic difference. All the morpho-physiological characters under study showed highly significant environmental effect. Leaf area index, 1000 seed weight and crop growth rate were observed with significant genotypes x environment interaction. Under E2, crop growth rate, leaf area index, chlorophyll stability index, specific leaf weight and harvest index were observed with reduced by up to 76.2%, 49.4%, 54.2%, 52.1% and 28.9%, respectively. Seeds per siliqua and seed yield per plant were observed with highest reduction by up to 22.2% and 69.2%, respectively. BPR 538-10, NRCDR-2, RH-0216 and NPJ-112 were found terminal heat tolerant genotypes with low heat susceptibility index (HSI) for seed yield per plant 0.33, 0.44, 0.57 and 0.58, respectively. Study revealed that BPR-2, BPR-141, B-205-43 and BPR 540-6 were found as terminal heat tolerant genotypes for multiple characters and these genotypes can be used in breeding programme.

Terminal heat stress studies were carried out in 43 germplasm of Indian mustard by the **Singh *et al.*, (2014)** and effects of heat is observed for transpiration, stress intensity, photosynthesis, stomatal conductance, mean productivity, geometric mean productivity,

yield attributing characters and seed yield. Genotypes, JS-29 and PBR-378 were observed with reduction in photosynthesis by 9.85% and 48.3%, respectively under high terminal heat stress. The genotypes, EJ-20, EJ-22, NDT-05-02 and NPJ-124 were observed with low reduction in seed yield due to earliness at terminal heat stage. While, the genotypes BPR-540-6, BPR-549-9 and BPR-349-9 were recorded < 20% reduction in seed yield and also recorded high 1000 seed weight. Three genotypes viz. BPR-540-6, BPR-549-9 and BPR-349-9 were observed tolerant to terminal heat stress due to less reduction in seed yield, medium transpiration rate and low stress intensity.

Sharma and Sardana (2014) examined 25 Indian mustard genotypes to study the effect of terminal heat stress on yield and its contributing traits under two environments viz., timely and late sown. The study revealed that RGN-152 and RL-2047 showed <30% yield reduction under terminal heat stress. RL-2047 was observed with terminal heat tolerance for seed yield per plant while moderately tolerant for siliqua length, biological yield per plant and seeds per siliqua. The genotype RGN-152 showed terminal heat stress tolerance for biological yield per plant and moderate heat tolerance for siliquae on main shoot and siliqua length. Under timely sown condition, seed yield per plant had positive and significant correlation with heat susceptible index (HSI, $r=0.58$) and negative association with heat tolerance efficiency (HTE, $r=-0.57$). Resistant genotypes showed average heat tolerance efficiency (84.8%) and average heat susceptible index (0.28). Resistant genotypes can be used in crossing programme as suitable donor to develop terminal heat tolerant cultivar.

Sharma (2014) conducted a study on 22 genotypes of Indian mustard to investigate terminal heat stress effect on seed yield, in two environments viz., timely (3rd week of October) and late sown (3rd week of November). The results suggested that all the morphological traits under study had significant genotypic differences. SKM-0149, NPJ-92, PR-2002-8, Varuna, RM-15 and RM-101 showed $\leq 30\%$ seed yield reduction. High heat tolerance efficiency was recorded for cultivars RM-15(99%), RM-101(96%), PR2002-8 (93%) and Varuna (80%) and low HSI was recorded for RM-15(0.01), RM-101(0.09), PR-2002 (0.15) and Varuna (0.42). Varuna, PR-2002-8, RM-15 and RM-101 were identified as tolerant genotypes with average 0.155 heat susceptible index (HSI) and 92 % heat tolerance efficiency (HTE). Study indicated that most important heat resistant parameters was heat

susceptible index (HSI) and heat tolerance efficiency (HTE) to assess terminal heat tolerant genotypes under field conditions.

Singh (2015) carried out an experiment on 22 genotypes of Indian mustard to study genetic variability for physio-biochemical parameters under terminal heat stress conditions. The genotypes, RH-8814, NRCDR-02 and BPR-549-9 as terminal heat tolerant which scored maximum values of relative water content (RWC %), chlorophyll content (mg/g f. wt. leaf tissue), chlorophyll stability index (CSI %) and lesser membrane injury index (MII %) under terminal heat stress over other genotypes. Moderate heat tolerance was observed for NPJ-117, NRCDR-701, RGN-773, RGN-197, NPJ-113, RH-0116 and DRMR-537-40. Study revealed that these genotypes can be used as donor for heat tolerance in crossing programme.

Singh et al., (2015) conducted an experiment on 22 genotypes of Indian mustard to study the effect of terminal heat stress on growth parameters and their association with seed yield under late sown conditions. Study revealed that the specific leaf weight (SLW) and crop growth rate (CGR) were higher for genotypes such as RH-8814, NRCDR-02 and BPR-549-9. The relative growth rate (RGR) was higher for NPJ-117, NPJ-113 and NRCDR-02 genotypes under terminal heat stress conditions at different growth stages and these genotypes were also recorded positive correlation with other growth parameters like, leaf area index (LAI) ($r=0.911$, 0.805 and 0.756 , respectively), SLW ($r=0.556$, 0.814 and 0.742 , respectively) and CGR ($r=0.586$ and 0.863) with seed yield at different growth stages while RGR ($r=0.508$) and NAR ($r=0.458$) had positive correlation with seed yield at 60-80 DAS of growth stage. The study indicated that positive correlation of growth parameters with seed yield is important in reducing heat inducing oxidative injury during post flowering stage.

Ram et al., (2017) conducted an experiment on 53 genotypes with two checks (BPR 543-2 and RH-30) to study heat stress under two conditions viz., normal (maximum temperature 31.0°C at 0-10 cm depth) and heat stress (maximum temperature 40.1°C at 0-10 cm depths). Heat tolerant genotypes were BPR-541-2, BPR-349-9, RGN-48, Urvashi, BPR 605-40, Pusa tarak (EJ 9912-13), BPR-549-2, DRMR-729 and DRMR-1918 with ≤ 0.5 heat susceptibility index (HSI) and $>80\%$ yield stability ratio (YS). Under stress condition, the relative water content was observed with highly significant but negative correlation with excised-leaf water loss ($r=-0.385$). DRMR 541-44 and RGN-48 were

recorded high temperature stress tolerant with high population survival and higher membrane stability index under heat stress. These tolerant genotypes can be used in future breeding programme to develop heat tolerant genotype.

Tripathi *et al.*, (2020) evaluated 12 Indian mustard genotypes to study the effect of terminal heat stress on physiological traits like (chlorophyll content at anthesis and siliquae initiation stage, net photosynthesis rate [(Pn) ($\mu\text{ mol/m}^2\text{/s-1}$)], chlorophyll stability index (CSI %), relative water content (RWC %) and canopy temperature depression (CTD $^{\circ}\text{C}$) at pre-flowering and post-flowering stage). Study revealed that the genotypes, DRMRIJ-16-3, RGN-403 and RH-1556 genotypes were observed with higher net photosynthesis rate (33.5, 33.0 and 32.6, respectively), CSI (0.53, 0.52 and 0.46, respectively), RWC (60.8, 59.7 and 59.1, respectively) and canopy temperature depression (3.5, 3.7 and 3.5, respectively) at post-flowering stage while high chlorophyll content (41.3, 40.6 and 39.2, respectively) observed at siliquae initiation stage. The study revealed that genotypes, DRMRIJ-16-3, RGN-403 and RH-1556 were recorded as tolerant genotypes for terminal heat stress which maintained high values for physiological parameters under stress environment.

Chauhan *et al.*, (2020) characterized 5 genotypes (Pusa Mustard 25, Pusa Mustard 26, BPR-541-4, RH-406 and Urvashi) of Indian mustard to assess the effect of higher temperature on yield and its contributing traits (morphological, physiological and phenological parameters) in 3 different sowing dates viz., October 30 (normal sown; S1), November 18 (late sown; S2) and November 30 (very late sown; S3). Maximum leaf area per plant, number of leaves per plant and leaf dry weight per plant showed when crop sown on November 18 (late sown) and decreased when crop sown on November 30 (very late sown). Differences in these parameters were marginal in normal sown and late sown but higher between late sown and very late sown. Specific leaf area and leaf area ration were maximum at 30 DAS and gradually declined till maturity. Leaf area index was the maximum at 60 DAS while specific leaf weight was the maximum at 90 DAS.

Sandhu *et al.*, (2020) carried out an experiment on 486 Indian mustard lines under late sown condition (terminal heat stress) for 2 years to assess terminal heat stability. Kang -SAS Path computer program was used along with expected genetic advance (GA) at 5% selection intensity to calculate selection indices. Set I include 5 traits (plant height,

number of secondary branches, number of siliquae on main shoot, seed yield, 1000 seed weight), set II include 4 traits (plant height, number of secondary branches, number of siliqua on main shoot, 1000 seed weight), set III include (number of secondary branches, number of siliquae on main shoot, seed yield, 1000 seed weight) and set IV include 3 traits (number of secondary branches, number of siliquae on main shoot, 1000 seed weight). Highest GA (8.612) for five traits viz., plant height, number of secondary branches, number of siliquae on main shoot, seed yield and 1000 seed weight were observed in comparison to other trait combinations. A small difference in GA of set I (8.612; seed yield included) and set II (8.599 seed yield excluded) and selection index efficiency was 131% and 130%, respectively.

Srivastava and Srivastava (2020) carried out an experimentation on 39 genotypes (9 thermo-tolerant lines, 3 high yielding testers and their 27 F₁ hybrids) of Indian mustard (*Brassica juncea*) under 3 dates of sowing (i.e. timely, late and very late sown) at 2 locations to identify tolerant genotypes for terminal heat stress which give high and stable yield under stress conditions. To identify tolerant genotypes, 3 stability parameters (mean, b_i and S^2di) and 8 characters (plant height, primary branches per plant, siliquae per plant, seeds per siliqua, test weight, seed yield per plant, oil content and oil yield) were selected under 6 environments (3 dates of sowing at 2 locations). The genotypes, PM-26, PM-28, RH-406, RGN-229 and BPR-541-4 were recorded as terminal heat tolerant which observed with stable and high seed yield in the heat stress environment ($b_i < 1$, $S^2di = 0$). The hybrid, PM-28 × NRCHB-101 observed as stable genotype for plant height, siliqua per plant, test weight and seed yield per plant. Among the parents, PM-26 was observed stable for primary branches and test weight, JD-6 for plant height, RGN-236 for seeds per siliqua, RH-406 for test weight and Giriraj for oil yield.

Chugh and Sharma (2021) evaluated forty-nine advanced breeding lines of Indian mustard to study association between destructive and non-destructive methods for the evaluation of photosynthetic pigments under two conditions (timely and late sown). The data was recorded by calorimetric method and SPAD (non-destructive) methods for photosynthetic pigments at three crop stages i.e. vegetative, flowering and siliquing and correlation and regression analysis was done. The total chlorophyll (siliquing stage) and SPAD value (flowering stage) showed a significant and strong correlation in timely sown crop. A positive correlation between SPAD value and total chlorophyll content at flowering

stage was observed. Regression analysis revealed that a linear relationship was observed ($R^2 = 0.0362$) at flowering stage while a non-linear relationship was observed at vegetative stage under both sowing condition.

Sharma *et al.*, (2022) carried out an experiment on 145 Indian mustard genotypes to study the effect of terminal heat stress on different agro-morphological traits under late sown condition. Study revealed that all traits showed significant reduction except fruiting zone length and oil content and highest reduction was observed in seed yield per plant (33.92%) followed by 1000 seed weight (21.28%). Association analysis suggested that 1000 seed weight and secondary branches per plant showed positive association with seed yield under late sown conditions. Study revealed that genotypes, DRMR-1154, DRMR-1347 and DRMR-1190 were identified as tolerant to the terminal heat based on heat stress susceptibility index and DRMR-59, DRMR-2094, DRMR-2129, DRMR-2071, DRMR-2136 were identified terminal heat tolerant with high yield based on yield index, yield under stress, geometric mean productivity and stress tolerance indices.

Chapter 3

MATERIALS AND METHODS

The present investigation entitled “**Characterization of Indian mustard (*Brassica juncea* L.) genotypes for heat tolerance at reproductive stage**” was undertaken to evaluate Indian mustard genotypes for genetic variability, association analysis and comparative phenotyping against terminal heat. The materials used and methods employed for the collection, analysis and interpretation of the data have been described as below:

3.1 Experimental Site/Climate/Weather

The experiment was conducted in Block D-3, Seed and Research Farm, Rani Lakshmi Bai Central Agricultural University (RLBCAU), Jhansi during *rabi*, 2021-2022. Geographically, RLBCAU, Jhansi research farm is located between 25°31'02.5"N latitude, 78°33'05.11" E longitude and at an altitude of 271 meters above the mean sea level. The university falls under the sub-tropical climatic zone.

Climate:

Climate of the Bundelkhand region is sub-tropical with cool winter, sweltering summer and semi- humid weather. The average annual rainfall of this region varies from 850-1000 mm. Jhansi had an average temperature of 25.8° C and annual average precipitation of about 870 mm. Jhansi experiences extreme temperature due to its location on a rocky and plateau region. The meteorological data for the cropping season *rabi* 2021-22 is presented in **Table: 3.1** and temperature during reproductive phase is also presented in **Fig. 3.1**.

Table 3.1: The meteorological data for the cropping season *rabi*- 2021-22

Standard meteorological week	Duration	Temperature (°C)		Rainfall (mm)	Relative humidity (%)	
		Max.	Min.		Max.	Min.
46	12- 18 Nov.	27.9	10.6	0	84	50
47	19- 25 Nov.	28.1	12.0	0	85	49
48	26 Nov.- 2 Dec.	27.5	9.3	0	85	57
49	03 - 09 Dec.	24.7	11.2	0	88	56
50	10- 16 Dec.	23.4	7.8	0	89	60
51	17 - 23 Dec.	22.9	4.4	0.0	88	61
52	24- 31 Dec.	22.3	8.4	12.0	90	65

1	01- 07 Jan.	20.9	7.7	18.0	91	71
2	08- 14 Jan.	19.2	10.4	23.8	91	71
3	15- 21 Jan.	18.3	5.8	0.0	91	72
4	22- 28 Jan.	19.9	7.6	3.6	91	71
5	29 Jan. – 04 Feb.	26.4	7.3	0.0	89	59
6	05- 11 Feb.	24	7.5	0.0	88	47
7	12- 18 Feb.	25.8	8	0.0	87	46
8	19- 25 Feb.	28	11.3	0.0	84	46
9	26 Feb. – 04 Mar.	28.5	11.3	0.0	84	45
10	05- 11 Mar.	30	12.6	0.4	81	44
11	12- 18 Mar.	35.2	16	0.0	80	38
12	19- 25 Mar.	38	17.4	0.0	79	38
13	26 Mar. – 01 Apr.	38.8	16.8	0.0	76	34
14	02- 08 Apr.	40.4	17.4	0.0	60	30
15	09- 15 Apr.	42.7	20.4	0.0	53	29
16	16- 22 Apr.	40.5	20.5	0.0	52	29
17	23 - 29 Apr.	42.3	21.3	0.0	49	26

(Source: ICAR-IGFRI, Jhansi)

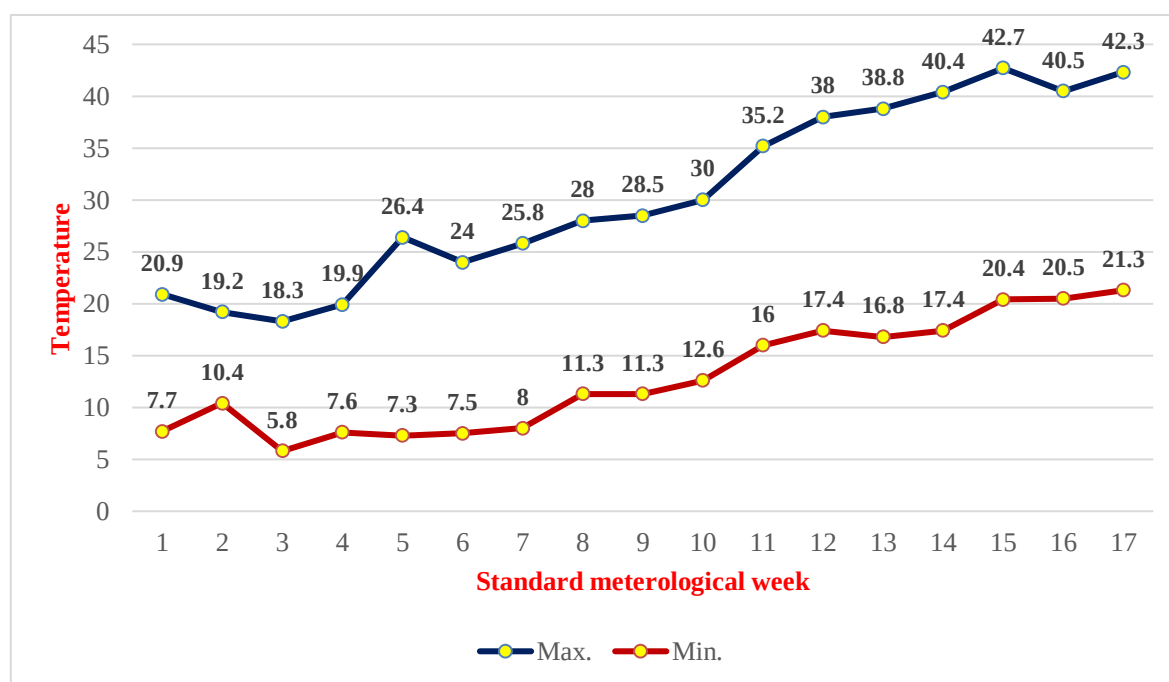


Fig. 3.1 Graphical representation of maximum and minimum temperature during the flowering and reproductive phase of crop (01 January- 29 April, 2022)

3.2 Experimental Materials

The experimental materials used in the present study included a constellation of 200 Indian mustard genotypes along with 7 checks (NRCHB-101, NRCRD-2, Krishna, Pusa agrani (Sej-2), PM-25 (NPJ-112), PM-26 (NPJ-113), Radhika) and Indian mustard germplasms were obtained from ICAR-National Bureau of Plant Genetic Resources, New Delhi and ICAR-Directorate of Rapeseed and Mustard Research, Bharatpur (Rajasthan), the list of genotypes are presented in **Table: 3.2**.

Table: 3.2 List of Indian mustard genotypes raised in present investigation.

S.No.	Accession No.	S.No.	Accession No.	S.No.	Accession No.	S.No.	Accession No.
V1	DRMR - 2	V51	DRMR - 909	V101	RCQR-9901	V151	EC – 766310
V2	DRMR - 8	V52	SITARA SAGAR	V102	RNN - 505	V152	EC – 766296
V3	DRMR - 4	V53	PUSA BAHAR	V103	NDRE - 4	V153	EC – 766292
V4	DRMR - 5	V54	BASANTI	V104	I - 79	V154	EC – 766276
V5	DRMR - 6	V55	RHUR - 2 -1	V105	PCR - 9403	V155	EC – 766278
V6	DRMR - 7	V56	RC -371-1	V106	PM - 67	V156	EC – 766270
V7	DRMR - 9	V57	RC -371	V107	PM -30	V157	EC – 766234
V8	DRMR - 11	V58	RC - 132	V108	CN -101845	V158	EC – 766211
V9	DRMR - 12	V59	RC - 571	V109	IC - 122137	V159	EC – 766207
V10	DRMR - 13	V60	RC - 891-1	V110	IC - 11721	V160	EC – 766557
V11	DRMR - 33	V61	RC - 1271	V111	IC -206741	V161	EC – 766124
V12	DRMR - 46	V62	RC - 1270	V112	IC - 372259	V162	EC – 766060
V13	DRMR - 48	V63	RLC - 3	V113	IC - 341108	V163	EC -766204
V14	DRMR - 136	V64	NC - 37362	V114	IC - 491455	V164	EC – 766487
V15	DRMR - 137	V65	NC - 660	V115	IC - 491175	V165	EC – 766344
V16	DRMR - 138	V66	CN - 105257	V116	IC - 491485	V166	EC – 766200
V17	DRMR - 264	V67	CN - 105312	V117	IC - 531377	V167	EC – 766069
V18	DRMR - 266	V68	CN - 105309	V118	IC -589676	V168	EC – 766576
V19	DRMR - 357	V69	CN - 34005	V119	IC - 589683	V169	EC – 399318
V20	DRMR - 358	V70	CN - 113780	V120	IC - 497904	V170	EC – 399293
V21	DRMR - 359	V71	CN - 34008	V121	IC - 70302	V171	EC – 571648
V22	DRMR - 360	V72	CN - 105364	V122	IC - 491348	V172	EC – 399308
V23	DRMR - 361	V73	CN - 101813	V123	IC - 375924	V173	EC – 399302
V24	DRMR - 362	V74	CN - 105233	V124	IC - 422156	V174	EC – 764501
V25	DRMR - 364	V75	CN - 105379	V125	IC -422172	V175	EC – 766622
V26	DRMR - 574	V76	AJ - 11	V126	IC - 481011	V176	EC – 766325

V27	DRMR - 576	V77	AJ - 3	V127	IC - 73225	V177	EC - 766115
V28	DRMR - 577	V78	DJ - 5	V128	IC - 766313	V178	EC - 766498
V29	DRMR - 578	V79	DJ - 12	V129	IC -766377	V179	EC - 766564
V30	DRMR - 579	V80	DJ - 65	V130	EC -399300	V180	EC -766489
V31	DRMR -582	V81	RJ - 10	V131	EC -766423	V181	EC - 766393
V32	DRMR - 610	V82	DTM - 50	V132	EC -766110	V182	EC - 766470
V33	DRMR - 611	V83	PTJ - 3-89	V133	EC -766234	V183	EC - 766616
V34	DRMR - 624	V84	PTJ - 3-64	V134	EC -766127	V184	EC - 766594
V35	DRMR - 625	V85	NPJ - 161	V135	EC -766134	V185	EC - 766555
V36	DRMR- 626	V86	KDM - 49-1	V136	EC -766136	V186	EC - 766094
V37	DRMR -669	V87	RB - 60	V137	EC -766141	V187	EC - 766312
V38	DRMR - 680	V88	PR - 2001-42	V138	EC - 66431	V188	EC -766095
V39	DRMR - 683	V89	EM - 1	V139	EC -766402	V189	EC - 564649-1
V40	DRMR - 686	V90	GR - 325(EM - 7)	V140	EC -766401	V190	EC - 766207
V41	DRMR - 689	V91	IM - 108	V141	EC -766611	V191	EC - 766322
V42	DRMR - 691	V92	IM - 76	V142	EC -766576	V192	IC - 320378
V43	DRMR -692	V93	IM - 152	V143	EC -766571	V193	IC - 766214
V44	DRMR - 693	V94	IM - 3	V144	EC -766560	V194	IC - 766098
V45	DRMR -710	V95	IM - 170	V145	EC -766391	V195	IC -766029
V46	DRMR - 711	V96	PBR - 97	V146	EC -766381	V196	IC - 766614
V47	DRMR - 726	V97	RE - 44	V147	EC -766335	V197	IC - 766129
V48	DRMR - 731	V98	RGN - 34	V148	IC - 766334	V198	IC - 766299
V49	DRMR - 900	V99	RH - 30	V149	EC -766322	V199	IC - 399318
V50	DRMR - 906	V100	NPJ- 113	V150	EC -766311	V200	IC - 321424

3.3 Experimental details

- Cropping season** *Rabi*, 2021 -2022
- Experimental design** Augmented block design
- Sowing date** 14 November 2021 (Normal Sown)
10 December 2021 (Late Sown)
- Spacing (Row to row and plant to plant)** 30 x 10 cm
- No. of rows per plot** Single row

6.	Row length	4 meter
7.	Number of total genotypes	200
8.	Number of genotypes per block	50 test accessions and 7 Checks
9.	Total number of blocks	04
10.	Number of checks	7 [NRCHB-101, NRC DR-2, Krishna, Pusa Agrani (SEJ-2), PM-25 (NPJ-112), PM-26 (NPJ-113), Radhika (DRMR 2017-15)]

In each accession proper plant stand was maintained by timely thinning and to raise a good crop recommended package of practices for this region were strictly followed.

3.4 Observations to be recorded

In present study, observation on 12 agro-morphological traits and 3 physiological parameters were taken under consideration and the average values of these traits were calculated and used for statistical analysis. The observations were recorded as described below:

Agro-morphological traits

- 3.4.1 **Number of days to 50 percent flowering:** number of days taken from date of sowing to the date at which 50 per cent plants in each genotype-initiated flowering.
- 3.4.2 **Number of days to maturity:** number of days to maturity was taken from date of sowing to the date on which plants reached physiological maturity.
- 3.4.3 **Plant height (cm):** mean length (in centimeters) of the five randomly selected plants from ground level to the tip of the main shoot and recorded at the time of maturity.
- 3.4.4 **Number of primary branches per plant:** at maturity, mean of the number of primary branches of five randomly selected plants.
- 3.4.5 **Number of secondary branches per plant:** at maturity, mean of the number of secondary branches of five randomly selected plants.

3.4.6 Main shoot length (cm): mean of the main shoot length of five randomly selected plants.

3.4.7 Number of siliquae on main shoot: mean of the total siliqua present on the main shoot of five randomly selected plants.

3.4.8 Siliqua length (cm): the length of five siliqua on each plant is taken and then averaged over five randomly selected plants.

3.4.9 Number of siliqua per plant: mean of total siliqua present on the individual plant of five randomly tagged plants.

3.4.10 Number of seeds per siliqua: the number of seeds in five siliquae on each plant is taken and then averaged over randomly selected plants.

3.4.11 Seed yield per plant (g): mean of seed yield from five randomly selected plants.

3.4.12 1000 seed weight (g): mean weight of 1000 seeds from five randomly selected plants.

Physiological traits

3.4.13 Chlorophyll content – The total chlorophyll concentration is measured by non-destructive method using chlorophyll concentration meter (Model- MC-100 make Apogee Instruments) and it is calibrated to measure chlorophyll concentration in leaves with units of μmol of chlorophyll per $\text{m}^2\cdot\text{a}$. Observations were recorded by selecting healthy 3 leaves often randomly tagged plants after 60 days of sowing and then averaged.

3.4.14 Chlorophyll fluorescence - Chlorophyll fluorescence is the one of the most important parameter for plant stress detection. Chlorophyll fluorescence is well proven and it provide reliable, non-destructive information regarding the photosynthetic efficiency and it is an indicator of plant health/stress. Chlorophyll fluorescence (Fv/Fm) was measured with portable handy chlorophyll fluorometer model OS 30 p+ of Opti sciences USA at anthesis stage. Fv/Fm is having a robust capability to measure plant stresses that affects photosystem-II (PSII) and under stress condition like high temperature that affects PSII, measures low Fv/Fm value as compare to normal 0.79 to 0.84. It correlate to carbon assimilation measurement and all samples are compared at the same known dark adapted state by using dark clips for 30 minutes. After dark adaptation of 30 minutes, modulated fluorometer allow the accurate measurement of minimum fluorescence (F_0) that is done by using weak modulated light. In this weak light, photosynthesis process cannot be driven but enough to excite prephotosynthetic antenna and PSII is maximally oxidized. The

maximal fluorescence (Fm) output will be taken under an intense light and under this condition PSII are fully reduced. The fluorescence variable (Fv) is measured by difference between Fm and Fo (Fm-Fo). Ratio of Fv/Fm was used to characterize photochemical efficiency of PSII referred to as maximum PSII photochemical efficiency in a dark adapted state.

3.4.15 Leaf area index – The leaf area index (LAI) was recorded with Sun Scan plant canopy analyzer (SS1-COM) of Delta- T devices Cambridge, United Kingdom system which measures photo synthetically active radiation (PAR) in crop canopies to provide valuable information about leaf area index (LAI). For better accuracy in observation the data was recorded by placing the sensor once above the crop canopy followed by placing it below the crop canopy and observations were recorded for each row between 11:00 A.M. to 2:00 P.M. after 65 days of sowing.

3.5 Statistical Analysis

The data recorded on above traits would be subjected to following statistically analysis by adopting appropriate analysis of variance technique.

3.5.1 Analysis of variance (ANOVA): ANOVA for augmented design is carried out as elaborated by the Federer and Raghavarao (1975) and Peterson (1985) to find out the significant difference between the characters under study. The evaluation of the mustard genotypes during *rabi*, 2021-22 was conducted in an augmented block design under non-stress environment and heat stress environment. For the examination of a high number of accessions/germplasm lines, this design is critical. To construct the design, experimental field is divided into a number of blocks and in each block, test entries are planted only once in this design, with no replication, whereas a set of checks (c) are assigned randomly and repeated in each block to estimate the error mean square and block impact. An equal number of test genotypes were planted in each block to facilitated statistical analysis. In this design the values of genotypic means are adjusted for the block effect, which are measured by the check entries which present in each block. The block size is determined by the number of blocks (b), the number of check entries (c) and the number of test genotypes/entries (v). When the block size is constant the following relationship hold true:

$$N = bc + v = b(c + n) = \text{total number of plots}$$

Where,

b = number of blocks,

v = number of genotypes

$P = c+n$ = number of plots per block

c = number of check varieties

$n = v/b$ number of genotypes per block

The total number of blocks is determined by the need to have at least 10 degree of freedom for error in the analysis of yield data which is given by the following relationship.

$$b > [(10/c-1) + 1]$$

In present investigation 4 blocks were used with seven checks and 200 test entries.

The details of the statistical methods adopted for data analysis are presented below.

Checks	Blocks			Total	Mean
	1	2.....	4		
1.	$X_{1.1}$	$X_{1.2} \dots$	$X_{1.1}$	C_1	X_1
2.	$X_{2.1}$	$X_{2.2} \dots$	$X_{1.1}$	C_2	X_2
3.	$X_{3.1}$	$X_{3.2} \dots$	$X_{3.4}$	C_3	X_3
c.	B_1	B_2	B_4	G	M

Where,

X_{ij} = any observation of i^{th} check in j^{th} block

$B_j = \sum_i^c X_{ij}$ = Sum of all checks in j^{th} block

$C_i = \sum_j^B X_{ij}$ = Sum of any observation of i^{th} check in overall blocks

$G = \sum_j^B X_{ij} = \sum_j^B X_{ij}$ = Grand total of all checks

$X_i = C_i/b = \text{Mean of the } i^{\text{th}} \text{ check}$

$M = \sum X_i = G/b = \text{Sum of all check means}$

$b = \text{number of blocks}$

$c = \text{number of checks}$

Analysis of variance (ANOVA) for Augmented Block Design					
S.No	Source of variation	Degrees of freedom	Sum of Squares (SS)	Mean Sum of Squares (MSS)	Calculated F
1	Blocks	(b-1)	SSB	MSB	MSB/MSE
2	Check	(c-1)	SSC	MSC	MSC/MSE
3	Error	(b-1)(c-1)	SSE	MSE	
	Total	bc-1	SST		

Where,

$$SST = \sum \sum_j X_{ij}^2 - G^2/bc$$

$$SSB = \left(\frac{1}{c}\right) \sum_j B_j^2 - G^2/bc$$

$$SSC = \left(\frac{1}{b}\right) \sum_i C_i^2 - G^2/bc$$

$$MSS = SST - (SSB + SSC)$$

$$MSE = SSE / (b-1)(c-1)$$

Then compute of block effect r_j for each block where $r_j = \left(\frac{1}{c}\right) (B_j - M)$

After this, a table of adjusted yield for all the genotypes was

Where,

$Y_{ij} = \text{Yield of the } i^{\text{th}} \text{ genotype in } j^{\text{th}} \text{ block}$

$Y_i = Y_{ij} - r_j$ = yield of the i^{th} variety adjusted for block differences

Variances for different pair wise comparisons:

1. Difference between two check means = $2MSE/b$
2. Difference between adjusted yield of two genotypes in the same block = $2MSE$
3. Difference between adjusted yield of two genotypes in different blocks

$$= 2MSE \left[1 + \frac{1}{c} \right]$$

4. Difference between adjusted yield of genotypes and check means

$$= 2MSE (b+1) (c+1)/bc$$

Least significant difference values:

1. For two check means = $t_{\alpha} \sqrt{2MSE/b}$
2. For two adjusted genotypes in same block = $t_{\alpha} \sqrt{2MSE}$
3. For two adjusted genotypes in different blocks = $t_{\alpha} \sqrt{2MSE (c + 1)/c}$
4. For an adjusted genotype against check means = $t_{\alpha} \sqrt{2MSE(b + 1)(c + 1)/bc}$

For all L.S.D. the t values are two tail value at α % level of significance and $(b-1)$ $(c-1)$ degrees of freedom.

3.5.2 Estimation of mean: The average value of each character was estimated by dividing sum of the observations by the number of genotypes or corresponding number of observations.

$$\text{Mean (x)} = \sum x_i / N$$

Where, $\sum x_i$ = any observation for i^{th} character

N = total number of observations/genotypes

3.5.3 Range: It was taken as the difference between the highest and lowest mean value for each character.

$$\text{Range} = X_{\text{max.}} - X_{\text{min.}}$$

Where $X_{\max}$ = highest mean value of the character

$X_{\min}$ = lowest mean value of the character

3.5.4 Coefficient of variation (%)

$$CV = \left(\frac{\sqrt{MS_e}}{\bar{X}} \right) \times 100$$

Where, $\bar{X}$ = general mean of character and the Coefficient of variation (CV), being a unitless measurement is a good basis for comparing the extent of variation between different characters with different scales.

The standard error of the difference between any two treatments is expressed by the following formula:

$$SE_d = \sqrt{\frac{2MSe}{r}}$$

Where, MS_e = error mean square and r = number of replications.

The significance of difference among the treatments means was tested by F test at 5% and 1% level of significance. Whenever, the F value was found to be significant; critical difference was calculated to test the significance of difference between any two treatment means as follows:

$$C.D.(at 5\%) = SE_d \times t(5\%) \text{ at error degrees of freedom}$$

3.5.5 Parameters of genetic variability

Different coefficients of variance were computed following **Burton (1952)**.

Phenotypic Coefficient of Variation (PCV %)

$$= \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

Genotypic Coefficient of Variation (GCV %)

$$= \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

According to **Sivasubramanian and Menon (1973)**, the PCV and GCV values were grouped into three categories as mention below.

Low (0-10%)

Moderate (10-20%)

High (20% and above)

Heritability (broad sense)

It is the ratio of genotypic variance to the phenotypic variance

$$h^2_{(b)} = \frac{\sigma^2_g}{\sigma^2_p}$$

Heritability in broad sense ($h^2_{(b)}$) was estimated as the ratio of genotypic variance to phenotypic variance (**Allard 1960**). Where, σ^2_p and σ^2_g are the phenotypic and genotypic variances of the character and $\bar{x}$ is the mean of the character.

According to **Robinson et al. (1949)** the estimates of broad sense heritability were also classified into three categories as presented below.

Low (0-30%)

Moderate (30-60%)

High (60% and above)

Genetic advance as percentage of mean

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection.

$$\text{Genetic advance} = h^2_{(b)} \times \sigma_p \times K$$

Where,

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

σ_p = phenotypic standard deviation

K = selection differential at 5% selection intensity

The value of K (at 5% selection intensity) = 2.06 (**Allard, 1960**).

Genetic advance expressed as per cent of population mean was calculated from the method:

$$\text{Genetic advance as per cent of mean (\%)} = \frac{\text{Genetic advance}}{\text{General mean population (Gm)}} \times 100$$

If the value of genetic advance is high, it shows that the character is governed by additive gene action and selection will be rewarding for improvement of such traits. If the value of genetic advance is low, it indicates that the character is governed by non-additive gene action and heterosis breeding may be useful.

Genetic advance as per cent mean was also classified into three categories shown below as suggested by **Johnson et al. (1955)**.

Low (0-10%)

Moderate (10-20%)

High (20% and above)

3.5.6 Estimation of Correlation Coefficient

Correlation coefficients were computed to determine the association among all the yield and yield contributing traits. The correlation coefficients at genotypic and phenotypic levels were estimated from the analysis of variance and covariance as suggested by **Searle (1961)**. All these calculations were based on the mean values for different characters for each genotype. The formulas used for the estimation of correlation are as follows:

Genotypic correlation coefficient between character X and Y

$$r_{xy(g)} = \frac{\text{Cov}(x, y)_g}{\sqrt{\text{Var}(x)\text{Var}(y)}}$$

Where,

$\text{Cov}(x, y)_g$ = Genotypic variance between character X and Y,

$\text{Var}(x)_g$ = Genotypic variance of character X,

$\text{Var}(y)_g$ = Genotypic variance of character Y.

Phenotypic correlation coefficient between characters X and Y

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

where,

$\text{Cov}(x, y)_p$ = phenotypic covariance between character X and Y

$\text{Var}(x)_p$ = phenotypic variance of character X

$\text{Var}(y)_p$ = phenotypic variance of character Y

Test of significance for correlation coefficient

For testing the significance of correlation coefficient, the t value was calculated as follows

$$t = \frac{r}{\sqrt{1-r^2}} \sqrt{n-2}$$

Where, r is the estimate obtained from n pairs and the ratio is distributed in sampling as t with $(n-2)$ degrees of freedom. The significance for correlation coefficient (r) was tested by comparing observed value of correlation coefficient with tabulated values at $(n-2)$ degree of freedom (**Snedecor and Cochran, 1967**). If the observed value is more than the table value, the correlation coefficient is said to be significant.

3.5.7 Path analysis

Path-coefficient is a standardized partial regression coefficient, which permits the partitioning of the correlation coefficients into direct and indirect effects with the help of path coefficient analysis method as suggested by **Wright (1921)** and applied in plant breeding by **Dewey and Lu (1959)**. If grain yield per plant is consider as dependent variable (y) as factors assumed to be influenced by the other characters called independent variable ($x_1, \dots, x_i$) as causes. The path coefficient is estimated by solving following sets of simultaneous equation indicating relationship between correlation and path coefficients.

The path coefficient is estimated by solving following sets of simultaneous equation indicating relationship between correlation and path coefficients.

$$R_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \dots + r_{1i}P_{iy}$$

$$R_{2y} = P_{2y} + r_{21}P_{1y} + r_{23}P_{3y} + \dots + r_{2i}P_{iy}$$

$$R_{3y} = P_{3y} + r_{31}P_{1y} + r_{32}P_{2y} + \dots + r_{3i}P_{iy}$$

$$R_{iy} = P_{iy} + r_{i1}P_{1y} + r_{i2}P_{2y} + \dots + r_{i(i-1)}P_{iy}$$

Where,

R_{1y} to r_{1i} = coefficient of correlation between independent variable (1....i) with dependent character y

R_{12} , r_{11} to $r_{1i(i-1)}$ = coefficient of correlation among all possible combination of caused factors (independent variables) and

P_{1y} to P_{iy} = direct path effect of independent variables (1 to i) on the dependent variable y. The effect of j^{th} independent variable through j^{th} independent variable on dependent variable y was computed as $P_{1y} \times r_{ij}$. The above equation can be written in a matrix form as shown below:

$$\begin{matrix} \mathbf{A} & \mathbf{B} & \mathbf{C} \end{matrix}$$

$$\begin{Bmatrix} r_{1y} \\ r_{2y} \\ \vdots \\ \vdots \\ R_{iy} \end{Bmatrix} = \begin{Bmatrix} r_{11} & r_{12} & r_{13} & r_{14} & \dots & r_{1i} \\ r_{21} & r_{22} & r_{23} & r_{24} & \dots & r_{2i} \\ & & \ddots & & & \\ & & & \ddots & & \\ & & & & \ddots & \\ r_{i1} & r_{i2} & r_{i3} & r_{i4} & \dots & r_{ii} \end{Bmatrix} \times \begin{Bmatrix} P_{1y} \\ P_{2y} \\ \vdots \\ \vdots \\ P_{iy} \end{Bmatrix}$$

Path coefficient is estimated as follows:

$$C = B^{-1} A$$

The effect of residual factor (R) which measures the contribution of rest of the characters is not considered in caused scheme. It is calculated as follows:

$$R^2 = 1 - \sum P^2 - 2 \sum_{i,j=1} P_{iy} P_{jy} r_{ij}$$

Where, R is residual factor.

3.5.8 Estimation of genetic diversity through D^2 statistics

A measure of group distance based on multiple characters was given by **Mahalanobis, 1936 (Rao, 1952)**.

With $x_1, x_2, x_3, \dots, x_p$ as the multiple measurements available on each individual and $d_1, d_2, d_3, \dots, d_p$ as $x_1^{-1} - x_1^{-2}, x_2^{-1} - x_2^{-2}, \dots, x_p^{-1} - x_p^{-2}$, respectively, being the difference in the means of two populations, Mahalanobis D^2 statistics is defined as follows:

$$pD^2 = b_1d_1 + b_2d_2 + \dots + b_p d_p$$

Here, the b_1 values are to be estimated such that the ratio of variance between the populations to the variance within the populations is maximized. In terms of variances and covariances, the D^2 value is obtained as follows:

$$pD^2 = W^{ij} (x_i^{-1} - x_i^{-2}) (x_j^{-1} - x_j^{-2})$$

Where,

W^{ij} is the inverse of estimated variance covariance matrix.

Test of significance

Using (V) statistics which, in turn, utilizes Wilks criteria, simultaneous test of difference mean values of a number of correlated variables/characters at 'pq' d.f. (where p = number of variables/ characters and q = number of germplasm-1) done as suggested by **Rao(1952)**.

Grouping of genotypes into various clusters

Using D^2 values, different genotypes were grouped into various clusters following Ward's minimum variance method (**Ward, 1963**) using that minimizes within-cluster sums of squares across all partitions.

Average intra-cluster $D^2 = \sum D_i^2/n$ where, $\sum D_i^2$ = sum of all distances between all possible combinations (n) of the genotypes included in the cluster.

Average inter-cluster distance $D^2 = \sum D_{ij}^2/n_i \dots n_j$

Where, $\sum D_{ij}^2$ = sum of all distances between all possible combinations (n_i, n_j) of the genotypes between the clusters.

n_i = number of genotypes in i^{th} cluster

n_j = number of genotypes in j^{th} cluster

Cluster mean

Character means of lentil genotypes falling under different clusters in individuals were also calculated.

3.5.9 Heat susceptibility index (HSI) - The heat susceptibility index (HSI) which determines the adaptability of genotypes to the late sown conditions. Heat susceptibility index was calculated for grain yield and its attributes over terminal heat stress environment and non-stress environment using the formula given by Fisher and Maurer (1978):

$$HSI = 1 - (Y_t/Y_c) / 1 - (Y_{tm}/Y_{cm})$$

Where, Y_t = mean of genotype in stress environment i.e. late sown condition,

Y_c = mean of the genotype under non-stress environment i.e. the timely sown condition,

Y_{tm} = mean of all genotypes in stress environment

Y_{cm} = mean of all genotypes in non-stress environment

3.5.10 Yield Stability ratio (YS) – Yield stability ratio was calculated on the basis of seed yield under terminal heat stress and normal environment using the formula given by **Lewis (1954)**.

$$YS = \frac{\text{Seed yield under stress condition}}{\text{Seed yield under normal condition}} \times 100$$

3.5.11 Per cent mean change (PMC) – Percent mean change for character under heat stress is calculated by given formula-

$$PMC = \frac{\text{difference of mean over normal and stress condition}}{\text{mean under normal condition}} \times 100$$

Chapter 4

RESULTS AND DISCUSSION

The experimental results obtained in the present investigation entitled “**Characterization of Indian mustard (*Brassica juncea* L.) genotypes for heat tolerance at reproductive stage**” are presented in this chapter. In this experiment, a set of 200 genotypes were used, including indigenous and exotic germplasm. These 200 genotypes along with seven checks (C1- NRCHB 101, C2- NRCDR 2, C3- Krishna, C4- Pusa Agrani (SEJ-2), C5- Pusa Mustard 25 (NPJ-112), C6- Pusa Mustard 26 (NPJ-113) and C7- Radhika), were screened for terminal heat stress during *rabi*- 2021-22 by timely and late sowing under augmented complete block design at the experimental farm of RLBCAU, Jhansi. The results obtained for various aspects of current investigations have been described under the following sub-heads:

- 4.1 Analysis of variance,
- 4.2 Mean performance
- 4.3 Genetic variability parameters
- 4.4 Correlation coefficient analysis
- 4.5 Path coefficient analysis
- 4.6 Genetic Divergence analysis
- 4.7 Phenotyping for heat tolerance

4.1 Analysis of variance (ANOVA)

Existence of variability among genotypes is prime necessity in plant breeding programmes for genetic gain under any crop improvement programme. The knowledge over genetic variability present in the germplasm help plant breeders for selection of the suitable genotype. A close perusal of the analysis of variance was carried out for 15 agro-morphological and physiological parameters in augmented block design and results indicated that, highly significant genetic differences among 200 Indian mustard genotypes for most of the characters under both timely and late sown conditions and presented in **Table 4.1**. Chlorophyll fluorescence shows non-significant differences in both timely and late sown conditions whereas, chlorophyll content shows non-significant difference only in late sown conditions. The results suggested that there were sufficient amount of genetic variability existed in the mustard germplasm for most of the characters under study except chlorophyll content and chlorophyll fluorescence. **Patel et al., (2021), Rout et al., (2019),**

Srivastava and Srivastava (2019), Khan *et al.*, (2019), Singh *et al.*, (2019), Chaurasiya *et al.*, (2018), Singh *et al.*, (2018), Prasad and Patil (2018), and Akabari *et al.*, (2015) also found sufficient variability among Indian mustard genotypes and their results are in accordance with results obtained in present investigation.

4.2 Mean performance

Mean values and ranges for all the characters in both timely and late sown conditions are shown in **Table 4.2** and mean values for each genotype for all characters are given in **Appendix I**.

4.2.1 Days to 50 per cent flowering

In timely sown condition, mean for days to 50 per cent flowering was 56.65 days which ranged from 47.00 to 70.00 days. Whereas, the maximum days to 50% flowering was recorded for IC-372259 (70 days) and minimum days to 50% flowering was recorded for DRMR-610 (47.00 days).

In late sown condition, mean for days to 50% flowering was 62.3 days and it ranged from 44.00 to 73.00 days. Whereas, the maximum days to 50% flowering was recorded for IC-372259 (73 days) and minimum days to 50% flowering was recorded for RE-44 (44.00 days).

4.2.2 Days to maturity

In timely sown condition, mean for days to maturity was 125.94 days which ranged from 116.00 (EC-766136) to 140.00 (NDRE-4) days. In late sown condition, mean for days to maturity was 121.5 days and it ranged from 112.00 (EC-766136) to 136.00 (IC-372259) days.

4.2.3 Plant height (cm)

Under timely sown condition, mean values for plant height was 201.17 cm and it varied from 138.33 to 259.00 cm. The maximum plant height was recorded for IM-152 (259.00 cm) and minimum plant height was recorded for DRMR-8 (138.33 cm). In late sown condition, mean for plant height was 212.20 cm and ranged from 141.60 to 249.00 cm. The maximum and minimum plant height was recorded for EC-766204 (249.00 cm) and EC-766487 (141.60 cm), respectively.

Table 4.1 Analysis of variance (ANOVA) for yield and its contributing traits in a set of Indian mustard genotypes under timely and late sown condition.

Source	DF	Sowing	FW50	DM	PH	PB	SB	CC	LAI	FLU	MAL	TS	SAM	SSQ	SL	SSQ	SW	YP
Treatments (Adj.)	206	T	22.41 **	30.83 **	331.5 **	2.39 **	9.17 **	14.03 **	0.89 **	0.0013	181.2 *	6849.2**	43.88 **	1.26 **	0.17 **	1.26 **	0.51 **	28.03 **
		L	28.31 **	26.23 **	274.1 **	1.88 *	7.84 **	20.13	0.73 **	0.0031	146.8 **	5057.9 **	34.44 **	1.62 **	0.25 **	1.62 **	0.54 **	6.46 **
Checks	6	T	52.07 **	307.7 **	243.6	3.18 **	12.05 **	32.31 **	0.71 *	0.0005	259.0 *	1899.27	194.2 **	1.01 *	0.29 **	1.01 *	0.77 **	50.07 **
		L	46.5 **	239.2 **	309.5*	1.18	10.54 **	34.62	0.25	0.0009	155.3 *	7209.7 **	29.61 *	0.81 *	0.17	0.81 *	0.67 **	2.32
Test vs check	1	T	260.5 **	53.49 **	1449.0 **	9.29 **	29 **	21.92 **	16.51 **	0.02 **	291.07	52216**	2.39	24.6 **	3.02 **	24.62 **	3.84 **	73.99 **
		L	400.6 **	12.31	2631.2 **	40.03 **	5.79	265.8 **	5.18 **	0.0023	2294.4 **	33400 **	0.17	30.3 **	1.14 **	30.35 **	3.41 **	1.15
Test	199	T	20.32 **	22.37 **	328.6 **	2.34 **	8.99 **	13.44 **	0.82 **	0.0012	178.3 *	6770.5 **	39.55 **	1.15 **	0.15 **	1.15 **	0.48 **	27.13 **
		L	25.89 **	19.88 **	261.2 **	1.71 *	7.77 **	18.45	0.72 **	0.0031	135.76 *	4850.6 **	34.75 **	1.5 **	0.25 **	1.5 **	0.52 **	6.61 **
Blocks (Adj)	3	T	0.0006	30.46 **	0.27	13.5ns	68.34 *	3	2.61	1.27	1.35 **	0.13	44.89	0.2 *	0.52	0.2 *	0.43	5981.5 *
		L	5.85 *	0.86	139.2	0.68	0.81	82.28 *	1.22 **	0.0012	146.8	842.96	1.49	0.14	0.19	0.14	0.13	1.22
Residuals	18	T	3.13	4.36	112.6	0.54	2.97	1.84	0.26	0.0014	76.92	1286.7	14.44	0.32	0.05	0.32	0.14	5.53
		L	1.62	5.08	81.8	0.83	1.67	17.82	0.22	0.0036	55.98	1209.8	10.18	0.28	0.07	0.28	0.12	1.93

*, ** significance at 5% and 1% levels, respectively.

(T= Timely sown, L= late sown, FW50= days to 50 % flowering, DM= days to maturity, PH= plant height, PB= number of primary branches per plant, SB= number of secondary branches per plant, CC= Chlorophyll content, LAI= leaf area index, FLU= Chlorophyll fluorescence, MAL= main shoot length, TS= total siliqua per plant, SAM= siliqua on main shoot, SSQ= seeds per siliqua, SW= 1000- seed weight and YP= yield per plant)

4.2.4 Number of primary branches per plant

Across the genotypes, number of primary branches per plant ranged from 3.33 (EC-766292) to 12.33 (DRMR- 693) under timely sown condition whereas, in late sown condition it varied from 3.30 (CN-101845) to 10.3 (IC-385786). The mean values for number of primary branches were 6.06 and 5.60 under timely and late sown condition, respectively.

4.2.5 Number of secondary branches

The mean value for number of secondary branches in timely sown condition was 12.34 and it ranged from 4.33 to 23.00. The maximum values for number of secondary branches were recorded for DRMR-46 (23.00), whereas the minimum value was recorded for EC-766391 (4.33).

In late sown condition, mean value for the trait was 6.40 with a range of 2.02 to 17.90. The maximum number of secondary branches was recorded for DRMR-357(17.9) and whereas, the minimum number of secondary branches was recorded for EC-766141(2.02).

4.2.6 Chlorophyll content

In timely sown condition, average chlorophyll content was 23.71 and it ranged from 16.88 to 42.61. Maximum value for chlorophyll content was 42.61 (EC-766207) and minimum value was 16.88 (EC-766431). In late sown condition, mean value for chlorophyll content was 19.70 and it ranged from 10.00 to 34.70. Whereas the maximum chlorophyll content was recorded for EC-766423 (34.70) and minimum value was recorded for EC-766200 (10.00).

4.2.7 Leaf area index (LAI)

In timely sown condition, leaf area index varied from 1.20 (DRMR- 909) to 5.70 (PTJ-3-89) with a mean value of 3.5. Under heat stress, leaf area index varied from 0.26 (EC-766560) to 4.50 (EC-766423) with a mean value of 1.80.

4.2.8 Chlorophyll fluorescence

In timely sown condition, mean for chlorophyll fluorescence was 0.76 which ranged from 0.65 to 0.90 and the maximum chlorophyll fluorescence value was recorded for EC-766431 (0.90) while minimum chlorophyll fluorescence was recorded for IC-491455 (0.65). Under heat stress condition, mean for chlorophyll fluorescence was 0.72

and it varied from 0.45 to 0.82. Whereas, the maximum chlorophyll fluorescence was recorded for EC-766423 (0.82) and minimum was recorded for IC-491485 (0.45).

4.2.9 Main shoot length (cm)

Across the genotypes, the average for main shoot length was 71.24 cm and it ranged from 39.30 to 110.60 cm under normal sown condition. The maximum main shoot length was recorded for EC-766571(110.60 cm) whereas, minimum main shoot length was recorded for RC-132.00 (39.30 cm).

In late sown condition, the mean value for main shoot length was 74.30 cm and it ranged from 35.00 cm to 100.00 cm. The maximum main shoot length was recorded for EC-766292(100.00 cm) and minimum was recorded for RC-132 (35.00 cm).

4.2.10 Total silique per plant

Under timely sown condition, across the genotypes average total silique per plant was varied from 166.00 (EC-766060) to 611.00 (IC-399318) with the mean value of 354.70. Whereas, under late sown condition, the mean value for total silique per plant was 231.05 and it ranged from 93.30 to 473.30. The maximum total silique per plant was recorded for EC-766136 (473.30), whereas the minimum value was recorded for EC-564649-1 (93.30).

4.2.11 Number of siliquae on main shoot

In timely sown condition, the average for number of silique on main shoot was 46.00 and it varied from 29.60 to 63.30. The maximum number of silique on main shoot was recorded for DRMR-574 (63.30) and minimum was recorded for I-79 (29.60). In late sown condition, the average value of number of siliquae on main shoot was 43.10 and it ranged from 22.60 to 59.30. The maximum number of silique on main shoot was recorded for DRMR-909 (59.30), in opposite, the minimum was recorded for RC-132 (22.60).

4.2.12 Number of seeds per silique

In case of number of seeds per silique, the mean value was 14.8 and it varied from 12.06 (DRMR-13) to 18.33 (EC-766141) under timely sown condition. Under heat stress situation number of seeds per silique sown condition the average value was 13.10 and ranged from 7.00 (RC-132) to 16.60 (IM-108).

4.2.13 Silique length (cm)

In timely sown condition, the mean for silique length was 3.76 cm which ranged from 2.90 to 4.90 cm. The maximum silique length was recorded for DRMR-669 (4.90 cm), whereas the minimum was recorded for EC-564649-1 (2.90 cm). In late sown

condition, the mean value was 3.90 cm which ranged from 2.74 to 6.81 cm. The maximum siliqua length was recorded for PTJ-3-89 (6.81 cm), whereas the minimum value was recorded for CN-105364 (2.74 cm).

4.2.14 1000 seed weight (g)

In case of 1000 seed weight, the mean was 3.54 g which ranged from 2.11 to 5.31 g under normal sown condition. The maximum 1000 seed weight was recorded for DRMR-577 (5.31 g), whereas the minimum value was recorded for RC-132 (2.11 g).

In late sown condition, the mean value for this trait was 3.20 g which ranged from 1.18 to 5.40 g. The maximum 1000 seed weight was recorded for DRMR-6 (5.40 g), whereas the minimum was recorded for EC-766110 (1.18 g).

4.2.15 Yield per plant (g)

The average, yield per plant was 14.40 g under timely sown situation and it varied from 4.86 to 32.56 g. The maximum value for yield per plant was recorded for IC-73225 (32.56 g), whereas the minimum was recorded for EC-766564 (4.86 g).

Under late sown condition, the average for seed yield per plant was 6.30 g and it ranged from 2.02 to 16.95 g. The maximum yield per plant was recorded for DRMR-731(16.95 g) whereas, the minimum was recorded for EC-766141(2.02 g).

4.3 Genetic variability parameters

Existence of sufficient variability in plant genetic resources (PGR) provides opportunity for plant breeders to develop improved cultivars with desired characters and improvement through selection depends on level of genetic variability exist. The 200 Indian mustard genotypes were analysed for 15 traits to estimate variability parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance as per cent of mean and heritability (broad sense). Descriptive estimates for these parameters are presented in **Table: 4.3**.

4.3.1 Days to 50 per cent flowering

The estimates for PCV and GCV were low with values 7.97 % and 7.33 %, respectively under timely sown condition. In non-stress condition high broad sense heritability (84.57%) was associated with medium genetic advance (13.91%). Similarly, under heat stress low values for PCV and GCV were estimated *i.e.* 8.18 % and 7.92 %, respectively.

respectively and high broad sense heritability (93.73%) was coupled with moderate genetic advance (15.81%).

Table 4.2: Range, mean and S.Em. for yield and its attributing traits in Indian mustard genotypes under timely and late sown condition

Traits	Sowing time	Range	Mean
FW50	Timely	47 (DRMR-610) – 70.0 (IC – 372259)	56.65 ± 0.314
	Late	44(RE – 44) - 73(IC – 372259)	62.30 ± 0.354
DM	Timely	116(EC - 766136) - 140(NDRE – 4)	125.94 ± 0.34
	Late	112(EC – 766136) - 136 (IC – 372259)	121.5 ± 0.318
PH	Timely	138.33(DRMR-8) - 259 (IM – 152)	201.70 ± 1.246
	Late	141.6 (EC – 766487) - 249 (EC -766204)	212.20 ± 1.117
PB	Timely	3.33 (EC – 766292) - 12.33 (DRMR – 693)	6.06 ± 0.105
	Late	3.3(CN – 101845) - 10.3 (IC – 385786)	5.60 ± 0.091
SB	Timely	4.33 (EC – 766391) -23 (DRMR – 46)	12.34 ± 0.206
	Late	2.02 (EC – 766141) -17.9 (DRMR – 357)	6.40 ± 0.191
CC	Timely	16.88 (EC – 766431) - 42.61(EC – 766207)	23.71 ± 0.253
	Late	10 (EC – 766200) - 34.7(EC – 766423)	19.70 ± 0.298
LAI	Timely	1.2 (DRMR - 909) - 5.7 (PTJ - 3-89)	3.50 ± 0.063
	Late	0.26 (EC – 766560) - 4.5 (EC – 766423)	1.80 ± 0.059
FLU	Timely	0.65(IC – 491455) - 0.90 (EC – 766431)	0.76 ± 0.002
	Late	0.45 (IC - 491485) - 0.82 (EC – 766423)	0.72 ± 0.004
MAL	Timely	39.3 (RC – 132) -110.6 (EC – 766571)	71.24 ± 0.918
	Late	35 (RC - 132) - 100 (EC – 766292)	74.3 ± 0.809
TS	Timely	166.6 (EC – 766060) - 611 (IC – 399318)	354.7 ± 5.657
	Late	93.3(EC - 564649-1) - 473.3 (EC – 766136)	231.05 ± 4.807
SAM	Timely	29.6 (I – 79) - 63.3 (DRMR – 574)	46.00 ± 0.438
	Late	22.6 (RC - 132) - 59.3 (DRMR – 909)	43.10 ± 0.404
SSQ	Timely	12.06(DRMR – 13) - 18.33 (EC – 766141)	14.80 ± 0.075
	Late	7 (RC – 132) - 16.6(IM – 108)	13.10 ± 0.085
SL	Timely	2.9(EC - 564649-1) - 4.9(DRMR -669)	3.76 ± 0.027
	Late	2.74 (CN – 105364) - 6.81(PTJ - 3-89)	3.90 ± 0.034
SW	Timely	2.115 (RC – 132) - 5.315 (DRMR – 577)	3.54 ± 0.048
	Late	1.18 (EC – 766110) - 5.4 (DRMR – 6)	3.20 ± 0.05
YP	Timely	4.86 (EC – 766564) - 32.56 (IC – 73225)	14.40 ± 0.359
	Late	2.02 (EC – 766141) - 16.95 (DRMR – 731)	6.30 ± 0.176

4.3.2 Days to maturity

In timely sown, days to maturity exhibited lower PCV (3.76 %) and GCV (3.37 %). High broad sense heritability (80.52 %) was coupled with low genetic advance (6.24 %). Similar trend of variability parameters was also observed for days to maturity under late sown condition and the values for PCV and GCV were 3.67 % and 3.16 %. For days to maturity under late sown condition, high heritability (74.44%) was associated with low genetic advance as per cent of mean (5.63%)

4.3.3 Plant height

The estimates for PCV and GCV were low with values of 9.02 % and 7.31 % under stress free environment. High broad sense heritability (65.71%) was coupled with medium genetic advance as per cent of mean (12.23%). The low estimates for PCV (7.63 %) and GCV (6.32 %) were also observed under late sown condition and high values for heritability (68.68 %) with moderate genetic advance (10.81) was exhibited for the trait plant height.

4.3.4 Number of primary branches per plant

For the number of primary branches per plant, PCV estimates were high under both the sowing conditions but GCV were high in timely sown but moderate in late sown. The estimates for PCV and GCV were 25.29 % and 22.10 % in timely sown condition whereas, the values for PCV and GCV were 23.20 % and 16.67 %. For the said trait, high heritability (77.00 %) was associated with genetic advance (40.18 %) under timely sown but moderate heritability (51.56 %) was coupled with high genetic advance (24.69 %) under heat stress environment.

4.3.5 Number of secondary branches per plant

Under timely sown environment, number of secondary branches per plant exhibited high PCV estimate *i.e.* 24.35% and medium GCV *i.e.* 19.92 %. High broad sense heritability (66.90%) was also linked with high genetic advance (33.6%) for the trait. Under late sown condition, high PCV and GCV were recorded with values of 42.90 % and 37.99 %, respectively. The trait had high heritability *i.e.* 78.44 % and it is also coupled with high genetic advance 69.42 %.

4.3.6 Chlorophyll content

The estimates for PCV and GCV were moderate with values 15.44 % and 14.34 %, respectively under timely sown condition. A high value of heritability (86.31%) was

Table 4.3: Parameters of genetic variability for yield and its component traits under under timely and late sown condition

Trait	Sowing time	GCV (%)	GCV category	PCV (%)	PCV category	h^2 bs (%)	h^2 bs category	GAM (%)	GAM category
FW50	Timely	7.33	Low	7.97	Low	84.57	High	13.91	Medium
	Late	7.92	Low	8.18	Low	93.73	High	15.81	Medium
DM	Timely	3.37	Low	3.76	Low	80.52	High	6.24	Low
	Late	3.16	Low	3.67	Low	74.44	High	5.63	Low
PH	Timely	7.31	Low	9.02	Low	65.71	High	12.23	Medium
	Late	6.32	Low	7.63	Low	68.68	High	10.81	Medium
PB	Timely	22.19	High	25.29	High	77	High	40.18	High
	Late	16.67	Medium	23.21	High	51.56	Medium	24.69	High
SB	Timely	19.92	Medium	24.35	High	66.9	High	33.6	High
	Late	37.99	High	42.9	High	78.44	High	69.42	High
CC	Timely	14.34	Medium	15.44	Medium	86.31	High	27.49	High
	Late	4.03	Low	21.67	High	3.46	Low	1.55	Low
LAI	Timely	21.09	High	25.5	High	68.37	High	35.97	High
	Late	39.72	High	47.51	High	69.9	High	68.51	High
FLU	Timely	-	-	4.6	Low	-	-	-	-
	Late	-	-	7.73	Low	-	-	-	-
MAL	Timely	14.16	Medium	18.77	Medium	56.86	Medium	22.02	High
	Late	11.96	Medium	15.6	Medium	58.77	Medium	18.92	Medium
TS	Timely	20.97	High	23.3	High	81	High	38.93	High
	Late	26.26	High	30.31	High	75.06	High	46.93	High
SAM	Timely	10.86	Medium	13.63	Medium	63.48	High	17.85	Medium
	Late	11.5	Medium	13.68	Medium	70.72	High	19.96	Medium
SSQ	Timely	6.13	Low	7.2	Low	72.5	High	10.77	Medium
	Late	8.36	Low	9.28	Low	81.02	High	15.52	Medium
SL	Timely	8.3	Low	10.35	Medium	64.31	High	13.73	Medium
	Late	10.91	Medium	12.71	Medium	73.75	High	19.33	Medium
SW	Timely	16.34	Medium	19.51	Medium	70.14	High	28.23	High
	Late	19.73	Medium	22.34	High	77.99	High	35.94	High
YP	Timely	32.4	High	36.32	High	79.6	High	59.64	High
	Late	33.84	High	40.23	High	70.77	High	58.73	High

Associated with high genetic advance (27.49%). In case of heat stress environment, PCV and GCV estimates were 21.67 % and 4.03 % which fall in the category of high and low, respectively. The estimates for heritability and genetic advance were low with the values of 3.46 % and 1.55 %, respectively in late sown condition.

4.3.7 Leaf area index

The variability parameters like PCV, GCV, heritability and genetic advance were high in both the sowing condition. For the comparison under both sowing conditions, the estimates for PCV were 22.50 % and 47.51 %, respectively whereas, the estimates for GCV were 21.09 % and 39.72 %, respectively. High heritability was associated with high genetic advance under both sowing conditions. The estimates for heritability and genetic advance 68.37% and 35.97 % under normal sown condition and values for these parameters were 69.90 % and 68.51 %, respectively in late sown condition.

4.3.8 Chlorophyll fluorescence

In case of chlorophyll fluorescence, the estimates for PCV were found very low i.e. 4.60 % and 7.73 % in both sown condition. As per ANOVA results, no significant differences were observed across the genotypes for GCV, heritability and genetic advance.

4.3.9 Main shoot length (cm)

Main shoot length (cm) under both sowing conditions exhibited moderate PCV and GCV and estimates are 18.77 % and 14.16 %, respectively in timely sown and 15.60 % and 11.96 % in late sown condition, respectively. Heritability and genetic advance were in moderate range under normal and late sown condition. The estimates of heritability were 56.86 % and 58.77 %, respectively which also shown 11.96 % and 18.92 % of genetic advance.

4.3.10 Total siliqua per plant

In case of total siliqua per plant, under present study the estimated variability parameters recorded high range under both date of sowing. In timely sown condition, the estimates for PCV, GCV, heritability and genetic advance were 23.30 %, 20.97 %, 81.00 % and 38.93 %, respectively while, these parameters observed the values of 30.31 %, 26.26 %, 75.06 % and 46.93 %, respectively in late sown condition.

4.3.11 Number of siliquae on main shoot

Number of siliquae on main shoot exhibited moderate PCV (13.63%) and GCV (10.86%) in timely sown condition and in same condition higher values for heritability

63.48 % was coupled with high genetic advance as per cent of mean 17.85 %. Similarly in stress condition, PCV and GCV were in moderate range and estimates were 13.68 % and 11.50 %. Higher heritability was linked with moderate genetic advance and estimates were 70.72 % and 19.96 %, respectively.

4.2.12 Number of seeds per siliqua

The estimates for PCV and GCV were low with values 7.20 % and 6.13 %, respectively under timely sown condition. High heritability (72.50 %, 81.02%) coupled with moderate genetic advance (10.77 %, 15.52%) were reported under timely and late sown conditions, respectively. Similarly, under heat stress low values for PCV and GCV were estimated *i.e.* 9.28 % and 8.36 %, respectively.

4.3.13 Siliqua length (cm)

Under timely sown environment, siliqua length exhibited moderate PCV (10.35 %) and GCV (8.30 %). High broad sense heritability (64.31 %) was also linked with high genetic advance (13.73 %) for the trait.

Under late sown condition, moderate PCV and GCV were recorded with values of 12.71 % and 10.91 %, respectively. The trait had high heritability *i.e.* 73.75 % and it is also coupled with moderate genetic advance 19.33 %.

4.3.14 1000 seed weight (g)

For the 1000 seed weight (g), GCV(16.34%, 19.73%) estimates were moderate under both the sowing conditions but PCV estimate was moderate in timely sown (19.51%) and high in late sown condition (22.34%). For the said trait, high heritability (70.14 %) was associated with high genetic advance (28.23 %) under timely sown. Similar trend for heritability and genetic advance was observed under stress condition and values were 77.99 % and 35.94 %, respectively.

4.3.15 Yield per plant

In the case of yield per plant, the variability parameters like PCV, GCV, heritability and genetic advance were high in both the sowing condition. In relation to both the sowing condition, the estimates for PCV were 36.32 % and 40.23 %, respectively whereas, the estimates for GCV were 32.40 % and 33.84 %, respectively. High heritability was also associated with high genetic advance under both the sowing conditions. The estimates for heritability and genetic advance were 79.60 % and 59.64 % under normal sown condition and values for these parameters were 70.77 % and 58.73 %, respectively in late sown condition.

The variability at the phenotypic level is sum of genotypic effect and environmental influence which contributes towards the expression of a phenotype. The magnitudes of variability parameters like range, variance and coefficient of variation, standard error, heritability and genetic advance determine the genetic properties or potential of the germplasm/population.

Yield is a complex trait controlled by polygenes or minor genes and it is highly influenced by the environment hence, it is not a reliable character for selection. The efficacy of selection depends on genetic variability in the breeding material. This could only be accessed through standardizing the phenotypic and genotypic variances and by obtaining coefficient of variability. PCV and GCV are the suitable parameters for the estimation of available variability. Estimation of variability parameters under present study revealed that there is sufficient variability for all the 15 traits studied under 200 Indian mustard germplasm. In the present study it was found that magnitude of PCV was higher than GCV for all the characters, indicating the considerable influence of the environment on the performance of genotypes for different agro-morphological traits. Similar kind of results in Indian mustard were also reported by **Patel *et al.*, (2021), Prasad and Patil (2018), Tiwari (2019), Srivastava and Srivastava (2019), Rout *et al.*, (2019), Singh *et al.*, (2019), Singh *et al.*, (2016), Shekhawat *et al.*, (2014) and Yadava *et al.*, (2011).**

In both the sowing condition, high PCV and GCV estimates were recorded for the traits like leaf area index, total siliquae per plant and yield per plant. High PCV and GCV for these traits clearly indicate ample scope for yield improvement in mustard under normal and reproductive heat stress also. In case of number of primary branches per plant, number of secondary branches per plant, main shoot length, number of siliquae on main shoot and 1000- seed weight were observed moderate to high estimates for PCV and GCV under both normal and late sown condition. **Patel *et al.*, (2021), Tripathi *et al.*, (2019), Prasad and Patil (2018), Akabari *et al.*, (2015) and Singh *et al.*, (2013)** also reported moderate to high estimates of PCV and GCV in mustard genotypes. Low estimates of PCV and GCV were recorded for the traits like days to 50 per cent flowering, days to maturity, plant height, chlorophyll fluorescence and seeds per siliquae in both the sowing condition. The effect of environment was higher in case of number of secondary branches per plant, leaf area index and yield per plant as the difference between PCV and GCV. Number of primary branches per plant, chlorophyll content and leaf area index were comparatively

influenced under the different sowing dates as these traits shown higher change in difference of PCV and GCV and similarly they also have higher difference in PCV and GCV within the same of sowing. Hence, these traits are highly influenced by the environment. These results were in accordance with the results of **Prasad and Patil (2018), Singh et al., (2013) and Singh et al., (2011).**

For determining the response of selection, heritability is an important character and genetic improvement in yield traits requires reliable estimates of heritability. Broad sense heritability is the ratio of genotypic to phenotypic variance for all the traits and it gives an idea of the total variation accounted for genotypic effect (**Allard, 1960**) and which is a good index of transmission of trait from parents to their offspring (**Falconer, 1981**).

In present investigation broad sense heritability ranged from 3.46 % (chlorophyll content in late sown) to the 93.73 % (days to 50 per cent flowering) across the sowing dates. High heritability estimates were observed for most of the traits like days to 50 per cent flowering, days to maturity, plant height, number of secondary branches per plant, leaf area index, total siliquae per plant, number of siliquae on main shoot, number of seeds per silique, siliqua length, 1000 seed weight and yield per plant under both the sowing conditions. In the estimation of heritability, the total genetic variance was included but it is sum of the fixable (additive and additive x additive type of epistasis) and non-fixable (dominance, additive x dominance and dominance x dominance type of epistasis) variance hence, direct selection may not be always rewarding. Similar results for heritability estimates for different agro-morphological traits were also reported by **Patel et al., (2021), Rout et al., (2019), Srivastava and Srivastava (2019), Khan et al., (2019), Tripathi et al., (2019), Singh et al., (2018), Akabari et al., (2015) and Shekhawat et al., (2014).**

In present study, low heritability was observed only for chlorophyll content in late sown condition which indicates that the traits under study are more influenced by the environment. Moderate level of heritability was reported for main shoot length under both the sowing condition and for number primary branches per plant in late sown condition and these traits are comparatively more effected by the environment and genetic improvement through selection in these traits are difficult due to the masking effect of the environment on the genotypic effect. Our results were in accordance with the results observed by **Patel et al., (2021), Tiwari et al., (2019), Srivastava and Srivastava (2019), Rout et al., (2019), Khan et al., (2019), Singh et al., (2016) and Yadava et al., (2011).**

High estimates of genetic advance as per centage of mean was recorded for the traits like number of primary branches per plant, number of secondary branches per plant, leaf area index, total siliquae per plant, 1000 seed weight and yield per plant under both the sowing condition whereas, it was high in only timely sown condition for chlorophyll content and main shoot length. High genetic advance for these traits suggests that preponderance of additive gene effects in expression of these characters. Selection based on phenotypic performance for these characters in segregating generations will be effective. Similar kind of results were observed by **Patel *et al.*, (2021)**, **Rout *et al.*, (2019)**, **Chaurasiya *et al.*, (2018)**, **Tripathi *et al.*, (2019)**, **Singh *et al.*, (2018)** and **Akabari *et al.*, (2015)**.

Low estimates of genetic advance as per cent of mean were observed for days to maturity under normal and late sown condition whereas for chlorophyll content in late sown condition only. While, moderate value of genetic advance was found for days to 50 per cent flowering, plant height, number of siliquae on main shoot, seeds per siliquae and siliquae length under stress free and stressed environment. Low value for this genetic parameters suggested that non-additive gene action were involved in controlling these traits. Low value of genetic advance for 50 per cent flowering, days to maturity and plant height were also reported by **Pandey *et al.*, (2020)**, **Rout *et al.*, (2019)**, **Shekhawat *et al.*, (2014)** and **Prasad and Patil (2018)**.

High heritability always not corresponds with high value of genetic advance as per centage of mean. For genetic gain in yield, selection of traits with high heritability and genetic advance as percentage of mean is an essential prerequisite. Joint picture of heritability and genetic advance will be helpful in prediction of progress from selection and to identify selection method for improvement of a character. The GCV along with heritability will give more reliable estimate for the genetic advance through phenotypic selection. **(Burton and DeVane, 1953)**. Based on combined picture of heritability and genetic advance as percentage of mean, traits under study can be grouped in to four different categories:

a). High heritability with high genetic advance: number of secondary branches per plant, leaf area index, total siliquae per plant and 1000 seed weight and yield per plant under both timely and late sown condition whereas, number of primary branches per plant under timely sown condition. Hence, this indicates that these traits are controlled by the additive

gene effects and phenotypic selection will be rewarding. For different traits, similar results were also observed by various researchers likewise, **Patel *et al.*, (2021), Tiwari *et al.*, (2019), Srivastava and Srivastava (2019), Rout *et al.*, (2019), Singh *et al.*, (2019), Tiwari *et al.*, (2019), Prasad and Patil (2018), Singh *et al.*, (2016), Akabari *et al.*, (2015) and Yadava *et al.*, (2011).**

b). High heritability with low to moderate genetic advance: days to 50 per cent flowering, days to maturity, plant height, number of siliquae on main shoot, seeds per siliquae and siliquae length in both normal and timely sown conditions. These traits are under control of non-additive gene action. High heritability was observed due to favourable influence of the environment rather than genotype. Hence, direct selection for these traits may not be rewarding therefore, progeny testing or heterosis breeding will be suggested for the improvement of these traits in mustard. **Rout *et al.*, (2019), Pandey *et al.*, (2020), Meena *et al.*, (2017), Singh *et al.*, (2016), Lodhi *et al.*, (2016)** also found similar results.

c). Low to moderate heritability with high genetic advance: number of primary branches in late sown and siliquae on main shoot in timely sown condition. These traits are governed with additive gene action but low heritability was exhibited due to high environmental effects and direct selection will be effective for these traits. Meena *et al.*, (2017) also reported similar kind of results for traits like days to 50 per cent flowering and number of primary branches per plant.

d.) Low heritability with low genetic advance: under this category only a single trait *i.e.* chlorophyll content in late sown condition was there. Chlorophyll content is highly influenced by the environment and difference between PCV and GCV is very high and direct selection is not at all a worthy practice. Similar kinds of results were also reported by **Rout *et al.*, (2019), Shekhawat *et al.*, (2014), Singh *et al.*, (2011).**

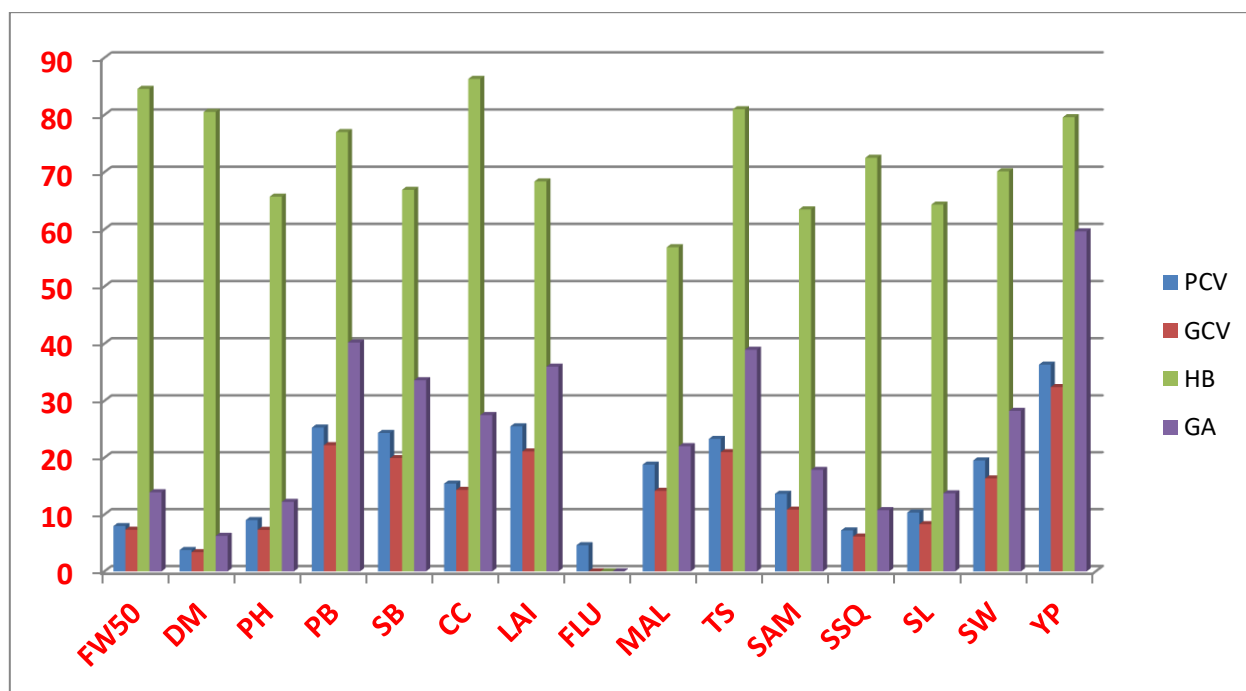


Fig. 4.3.1 Genetic variability parameters for different characters in Indian mustard genotypes under timely sown condition

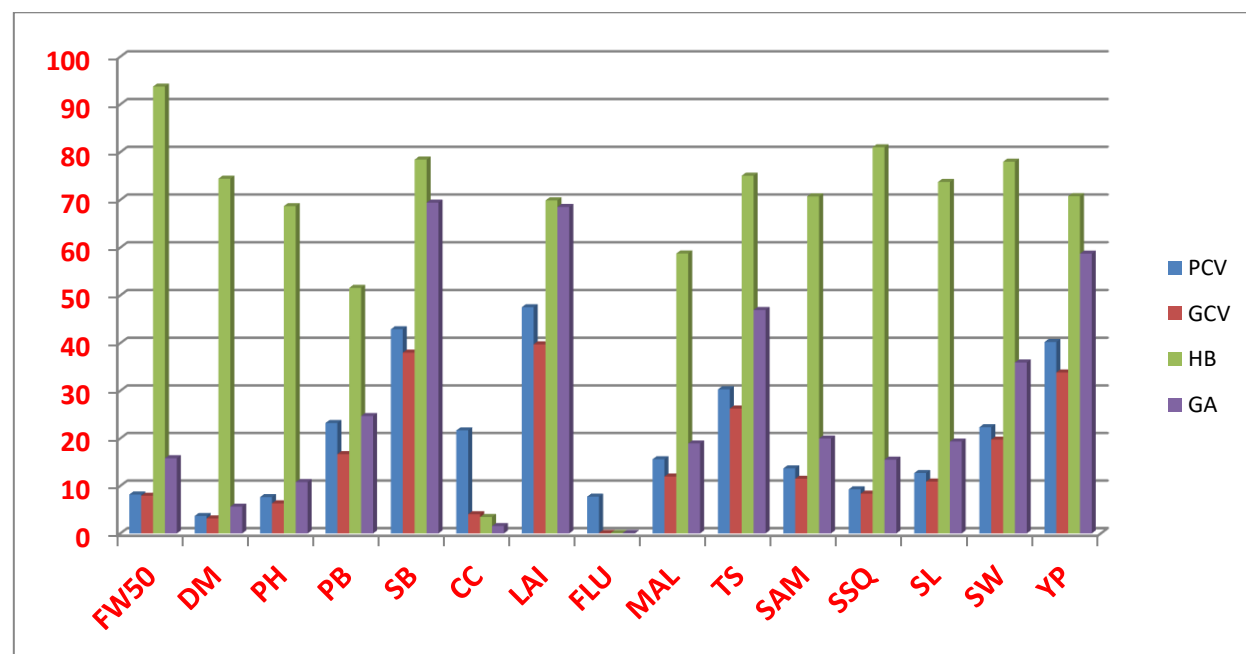


Fig. 4.3.2 Genetic variability parameters for different characters in Indian mustard genotypes under late sown condition

4.4 Correlation coefficient analysis

Seed yield is a complex polygenic character and its expression is the resultant of interaction between several component traits. Therefore, it is known as dependent trait and direct selection of such traits may not be rewarding and it is dependent on several less complex and simply inherited traits so, bringing small change in simply inherited traits will change yield trait also. Hence, inter-character association studies facilitate not only the concerned trait but also improvement in yield trait. Correlation coefficients are used to measure degree and direction of relationship between two and more variables. By virtue of the complexity of yield trait it becomes essential to measure association between yield and yield attributing (agro-morphological) traits. Positive correlation is a relationship between two variables in which both the variables are increase and decrease in same direction. In negative correlation both the variables move in opposite direction if one increasing the other is decreasing. The correlation coefficient (r) is measurement of correlation between two variables which varies between -1 to +1. Under present study, the correlation coefficients for mustard seed yield and 14 other component traits were estimated in timely and late sown condition at both genotypic and phenotypic level which is presented in **Table 4.4.1 and 4.4.2.**

The analysis showed that, in general genotypic correlation coefficients were higher in values than phenotypic correlation coefficients but nature or trend is same. This indicated that there was strong inherent association among the characters but the significant interaction of environment minimized the phenotypic relationship. Most of characters had significant correlation coefficients at both phenotypic and genotypic level in timely and late sown but some characters showed non-significant correlation. In rapeseed and mustard, the high magnitude of genotypic correlation coefficient than the corresponding phenotypic correlation coefficient is also observed by the various researchers likewise, **Pandey *et al.*, (2020), Pal *et al.*, (2019), Meena *et al.*, (2017), Lodhi *et al.*, (2016), Singh *et al.*, (2016), Akbari *et al.*, (2015) and Singh *et al.*, (2011).**

4.4.1 Genotypic correlation coefficient analysis

Genotypic correlation is also known as genetic correlation and defined as heritable or inherent correlation between two variables. It is represented as " $r_{g1.2}$ ". It has more importance for selection and genetic improvement of any trait in the crops in relation to the phenotypic correlation as genotypic correlation is more stable than phenotypic correlation.

Genetic cause of strong genetic correlation is either linkage or pleiotropy. Trait wise genetic association are discussed below.

4.4.1.1 Days to 50 per cent flowering

In timely sown condition, days to 50 per cent flowering exhibited highly significant positive correlation with days to maturity (0.862) followed by plant height (0.350) and leaf area index (0.167), whereas main axis length (0.209), siliqua on main axis (0.190), 1000 seed weight (0.186), siliqua length (0.165) and chlorophyll content (0.139) had significant and negative correlation. Number of primary branches (0.134) showed positive correlation with days to 50% flowering but values were non-significant. Remaining characters showed non-significant and negative correlation with days to 50 per cent flowering.

In late sown condition, days to 50 per cent flowering showed significant positive association with days to maturity (0.583), while significant and negative association was recorded with main axis length (0.366), seed on per siliqua (0.212), siliqua length (0.197), siliqua on main axis (0.167) and total siliqua (0.144). Rest of the traits showed non-significant positive and negative correlation with days to 50% flowering.

4.4.1.2 Days to maturity

Days to maturity showed significant positive association with days to 50% flowering (0.862), plant height (0.486) and leaf area index (0.182) while significant negative association with chlorophyll content (0.312), 1000 seed weight (0.257) and siliqua length (0.205) under timely sown condition while rest of the traits showed non-significant correlation with days to maturity in both the direction.

Under late sown condition, days to maturity showed significant positive association with only days to 50 per cent flowering (0.583), while significant negative association with main axis length (0.177) and siliqua length (0.177). Genetic correlations of days to maturity with remaining traits were non-significant but either in positive or negative direction.

4.4.1.3 Plant height (cm)

The perusal of data stated that, plant height showed significant positive association with days to maturity (0.486), days to 50 per cent flowering (0.350), leaf area index (0.329), yield per plant (0.319), total siliqua (0.244), siliqua on main axis (0.210) and primary branches per plant (0.179) while significant negative correlation was associated with chlorophyll content (0.382). All remaining traits showed non-significant and either positive or negative association with plant height.

In late sown condition, plant height showed significant and positive association with yield per plant (0.347), number of secondary branches per plant (0.323), siliqua on main axis (0.216), 1000 seed weight (0.152) and total siliqua (0.144). Genetic association of plant height with rest of traits showed non-significant association with plant height in both the direction.

4.4.1.4 Number of primary branches per plant

Number of primary branches per plant showed significant and positive association with number of secondary branches per plant (0.589), total siliqua (0.453), yield per plant (0.288) and plant height (0.179) while significant and negative association with main axis length (0.335) and 1000 seed weight (0.149) was observed, in timely sown condition. Number of primary branches per plant showed either positive or negative association with remaining characters.

Number of primary branches per plant showed significant positive association with total siliqua (0.663), yield per plant (0.278), number of secondary branches per plant (0.240) and leaf area index (0.192) while significant and negative association with main axis length (0.216), 1000- seed weight (0.186) and siliqua on main axis (0.140) in late sown situation. The rest of the traits had either positive or negative association with number of primary branches per plant but estimates were non-significant.

4.4.1.5 Number of secondary branches per plant

In timely sown condition, genetic association of number of secondary branches per plant positive and significant with traits like total siliqua (0.672), number of primary branches per plant (0.589), yield per plant (0.395), siliqua on main axis length (0.331), chlorophyll content (0.208) and siliqua length (0.143). The rest of the traits showed non-significant association with number of secondary branches per plant and direction of association is either positive or negative.

In late sown condition, number of secondary branches per plant showed significant positive correlation with yield per plant (0.950), chlorophyll content (0.419), total siliqua (0.413), leaf area index (0.342), plant height (0.323), siliqua on main axis (0.265), number of primary branches per plant (0.240) and 1000 seed weight (0.182). Number of secondary branches per plant had either positive or negative association with rest of the traits and values were non-significant.

4.4.1.6 Chlorophyll content

Chlorophyll content showed significant and positive association with only number of secondary branches per plant (0.208) while significant and negative association was found with plant height (0.382), days to maturity (0.312), leaf area index (0.165) and days to 50 per cent flowering (0.139) in normal sown condition. Chlorophyll content showed non-significant association with other than these characters.

Chlorophyll content had significant and positive association with number of secondary branches per plant (0.419), yield per plant (0.391), leaf area index (0.389), siliqua on main axis (0.175), chlorophyll fluorescence (0.168) and total siliqua (0.160) in late sown environment. Therefore, the chlorophyll content can be used for the trait for selection to improve yield in mustard. The remaining characters were associated either in positive or negative direction but values were non-significant.

4.4.1.7 Leaf area index

In timely sown environment, leaf area index showed significant and positive association with plant height (0.329), days to maturity (0.182), days to 50 per cent flowering (0.167) and yield per plant (0.150) whereas, significant and negative genetic correlation was observed with chlorophyll content (0.165). The rest of the traits showed non-significant association with leaf area index and it was either in positive or negative direction.

Under stressed environment, leaf area index showed significant and positive association with chlorophyll content (0.389), number of secondary branches per plant (0.342), yield per plant (0.297), total siliqua per plant (0.267), number of primary branches per plant (0.192) and chlorophyll fluorescence (0.141) indicating a close genetic association with these traits and can be utilized for yield improvement. Significant and negative association of leaf area index was also found with main axis length (0.139). Non-

significant association of leaf area index was also observed with rest of the traits and but direction of association was either positive or negative.

4.4.1.8 Chlorophyll fluorescence

Chlorophyll fluorescence showed significant and positive association with only two traits viz., siliqua on main axis (0.168) and yield per plant (0.142). Rest of the traits were associated non-significantly with the chlorophyll fluorescence and values were either in positive or negative direction. In late sown condition, chlorophyll fluorescence showed significant and positive association with only two traits viz., 1000 seed weight (0.170) and chlorophyll content (0.168) and other traits are just associated non-significantly.

4.4.1.9 Main axis length (cm)

The perusal of the data in **Table 4.4.1** stated that main axis length had positive and significant association with siliqua on main axis (0.488), 1000 seed weight (0.234), seeds per siliqua (0.233), yield per plant (0.197), total siliqua per plant (0.150) and in opposite direction main axis length was associated with number of primary branches per plant (0.335) and days to 50 per cent flowering (0.209). Main axis length is associated non-significantly with rest of the traits under timely sown condition.

Main axis length showed significant and positive association with siliqua on main axis (0.590), seeds per siliqua (0.310), 1000 seed weight (0.263), siliqua length (0.173) and total siliqua per plant (0.158) while main axis length was associated significantly with days to 50 per cent flowering (0.366), number of primary branches per plant (0.216), days to maturity (0.177) and leaf area index (0.139) but values in opposite direction. Rest of the characters showed non-significant association with main axis length and values were in positive and negative association.

4.4.1.10 Total siliqua per plant

For the total siliqua in normal sown condition, most of the traits like, number of secondary branches per plant (0.672), yield per plant (0.550), number of primary branches per plant (0.453), siliqua on main axis (0.433), plant height (0.244) and main axis length (0.150) had significant and positive association and rest of the traits had only non-significant association.

In late sown situation, total siliqua showed significant and positive association with number of primary branches per plant (0.663), yield per plant (0.433), number of secondary branches per plant (0.413), siliqua on main axis (0.276), leaf area index (0.267), seed per siliqua (0.196), plant height (0.144), main axis length (0.158) and chlorophyll

content (0.160) while significant and negative correlation with days to 50 per cent flowering (0.144). The remaining characters showed non-significant association but values were either in positive or negative direction.

4.4.1.11 Siliqua on main axis

In timely sown condition, siliqua on main axis showed significant and positive association with most of the traits like main axis length (0.488), total siliqua (0.433), yield per plant (0.404), number of secondary branches per plant (0.331), siliqua length (0.221), plant height (0.210), 1000 seed weight (0.195), chlorophyll fluorescence (0.168), while, significant and negative correlation was found only with days to 50 per cent flowering (0.190). The rest of the characters showed either positive or negative association with siliqua on main axis but values were non-significant.

Similarly like normal sown condition, siliqua on main axis showed significant and positive association with most of the traits like main axis length (0.590), seeds per siliqua (0.336), total siliqua (0.276), yield per plant (0.266), number of secondary branches per plant (0.265), 1000- seed weight (0.230), plant height (0.216), chlorophyll content (0.175) siliqua length (0.169) and significant and negative association with only days to 50 per cent flowering (0.167) and number of primary branches (0.140). Other than these traits are associated non-significantly with siliqua on main axis either in positive or negative direction.

4.4.1.12 Number of seeds per siliqua

In timely sown condition, seeds per siliqua showed significant and positive association with only two traits that are siliqua length (0.285) and main axis length (0.234). Non-significant association was observed with other traits.

In late sown condition, seeds per siliqua showed significant and positive association with siliqua on main axis (0.336), main axis length (0.310), total siliqua (0.196), 1000 seed weight (0.183) and siliqua length (0.172) whereas, significant but negative correlation was observed with days to 50 per cent flowering (0.212). The rest of the characters showed non-significant positive and negative association with seeds per siliqua.

4.4.1.13 Siliqua length (cm)

Siliqua length showed significant and positive association with number of seeds per siliqua (0.285), yield per plant (0.228), siliqua on main axis (0.221) and number of

secondary branches per plant (0.143) under normal sown condition. In opposite direction, significant and negative correlation was observed with days to maturity (0.205) and days to 50 per cent flowering (0.165). Non-significant association of silique length was recorded with rest of the traits in either positive or negative direction.

In late sown condition, silique length showed significant and positive association with 1000 seed weight (0.320), main axis length (0.173), number of seeds per silique (0.172) and silique on main axis (0.169) whereas significant and negative correlation was found with days to 50 per cent flowering (0.197) and days to maturity (0.177). The rest of the characters showed non-significant association with silique length.

4.4.1.14 1000 seed weight (g)

Under stress free condition, 1000 seed weight showed significant and positive association with yield per plant (0.272), main axis length (0.234) and silique on main axis (0.195) and significant and negative correlation was found with days to maturity (0.257), days to 50 per cent flowering (0.186) and number of primary branches per plant (0.149). With other characters, main axis length was connected with rest of the traits but non-significantly but either in positive or negative direction.

Under late sown condition, 1000 seed weight had significant and positive association with most of the traits like silique length (0.320), main axis length (0.263), silique on main axis (0.230), number of seeds per silique (0.183), number of secondary branches (0.182), chlorophyll fluorescence (0.170), yield per plant (0.152) and plant height (0.152) whereas, significant and negative correlation was associated with only number of primary branches per plant (0.149). The remaining all characters showed either positive or negative association with main axis length but estimates were non-significant.

4.4.1.15 Yield per plant (g)

Under timely sown condition, yield per plant showed significant and positive association with most of the traits like total silique per plant (0.550), silique on main axis (0.404), number of secondary branches per plant (0.395), plant height (0.319), number of primary branches per plant (0.288), 1000 seed weight (0.272), silique length (0.228), main axis length (0.197), leaf area index (0.150) and chlorophyll fluorescence (0.142). Rest four traits had either positive or negative association with yield per plant but values were non-significant.

Under late sown condition, yield per plant showed significant positive association with many characters like number of secondary branches per plant (0.950),

total silique per plant (0.433), chlorophyll content (0.391), plant height (0.347), leaf area index (0.297), number of primary branches per plant (0.278), silique on main axis (0.266) and 1000 seed weight (0.152) and rest of the traits are associated yield per plant with non-significant estimates.

4.4.2 Phenotypic correlation coefficient analysis

Phenotypic correlation is observable association between two variables which is not entirely heritable. It includes genotypic and environmental effects so its value differs according to different environmental situations so it is less reliable and stable than the genotypic correlation. It is represented as “ $r_{p1.2}$ ”.

4.4.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed significant positive association with days to maturity (0.830) followed by plant height (0.36), leaf area index (0.187) and number of primary branches per plant (0.150) whereas main axis length (0.203), 1000 seed weight (0.199), silique length (0.187) and silique on main axis (0.183) had significant and negative correlation under timely sown condition. Rest of the traits had non-significant correlation with days to 50 per cent flowering either in positive or negative direction.

Under late sown condition, days to 50 per cent flowering showed significant positive association with days to maturity (0.570) and plant height (0.140), while significant and negative association with main axis length (0.383), seeds per silique (0.228), silique length (0.210) and silique on main axis (0.161). Genetic correlations of days to maturity with remaining traits were non-significant but either in positive or negative direction.

4.4.2.2 Days to maturity

In timely sown condition, days to maturity exhibited highly significant days to 50% flowering (0.830), plant height (0.471) and leaf area index (0.181) while significant and negative association with chlorophyll content (0.294), 1000 seed weight (0.255) and silique length (0.224). Remaining characters showed non-significant and negative correlation with days to maturity. In late sown condition, days to maturity showed significant and positive association with only days to 50 % flowering (0.583),

Table: 4.4.1 Genotypic correlation coefficients (rg) among various yield and yield component traits in Indian mustard genotypes under timely and late sown condition

[illegible]

while significant and negative association was observed with main axis length (0.180) and siliqua length (0.180). Rest of the traits showed non-significant positive and negative correlation with days to 50% flowering.

4.4.2.3 Plant height (cm)

The perusal of data stated that, plant height showed significant and positive association with days to maturity (0.471), days to 50% flowering (0.360), leaf area index (0.340), yield per plant (0.321), total siliqua (0.251), siliqua on main axis (0.210) and primary branches per plant (0.190) while significant and negative correlation was observed with only chlorophyll content (0.374). All remaining traits showed non-significant and either positive or negative association with plant height.

In late sown condition, plant height showed significant and positive association with yield per plant (0.338), number of secondary branches per plant (0.322), siliqua on main axis (0.213), total siliqua per plant (0.153), 1000 seed weight (0.140) and plant height (0.140). Genetic association of plant height with rest of traits showed non-significant association with plant height in both the direction.

4.4.2.4 Number of primary branches per plant

Number of primary branches per plant showed significant and positive association with number of secondary branches per plant (0.590), total siliqua (0.455), yield per plant (0.293), plant height (0.190) and days to 50 per cent flowering (0.150) while significant and negative association with main axis length (0.333) and 1000 seed weight (0.160) was observed, in timely sown condition. Number of primary branches per plant showed either positive or negative association with remaining characters.

Number of primary branches per plant showed significant positive association with total siliqua per plant (0.667), yield per plant (0.267), number of secondary branches per plant (0.235) and leaf area index (0.203) while significant and negative association with main axis length (0.236), 1000 seed weight (0.198) and siliqua on main axis (0.140) in late sown situation. The rest of the traits had either positive or negative association with number of primary branches per plant but estimates were non-significant.

4.4.2.5 Number of secondary branches per plant

In timely sown condition, genetic association of number of secondary branches per plant positive and significant with traits like total siliqua (0.674), number of primary

branches per plant (0.590), yield per plant (0.389), siliqua on main axis length (0.310) and chlorophyll content (0.194). The rest of the traits showed non-significant association with number of secondary branches per plant and direction of association is either positive or negative.

In late sown condition, number of secondary branches per plant showed significant positive correlation with yield per plant (0.941), chlorophyll content (0.418), total siliqua (0.408), leaf area index (0.334), plant height (0.322), siliqua on main axis (0.263), number of primary branches per plant (0.235) and 1000 seed weight (0.184). Number of secondary branches per plant had either positive or negative association with rest of the traits and values were non-significant.

4.4.2.6 Chlorophyll content

Chlorophyll content showed significant and positive association with only number of secondary branches per plant (0.194) while significant and negative association was found with plant height (0.374), days to maturity (0.294) and leaf area index (0.173) in normal sown condition. Chlorophyll content showed non-significant association with other than these characters.

Chlorophyll content had significant and positive association with number of secondary branches per plant (0.418), yield per plant (0.386), leaf area index (0.368), siliqua on main axis (0.176), chlorophyll fluorescence (0.165) and total siliqua (0.143) in late sown environment. Therefore, the chlorophyll content can be used for the trait for selection to improve yield in mustard under heat stress. The remaining characters were associated either in positive or negative direction but values were non-significant.

4.4.2.7 Leaf area index

In timely sown condition, leaf area index showed significant and positive association with plant height (0.340), days to maturity (0.181), days to 50 per cent flowering (0.187) and yield per plant (0.154) whereas, significant and negative genetic correlation was observed with chlorophyll content (0.172). The rest of the traits showed non-significant association with leaf area index and it was either in positive or negative direction.

Under stressed environment, leaf area index showed significant and positive association with chlorophyll content (0.368), number of secondary branches per plant (0.334), yield per plant (0.294), total siliqua per plant (0.269), number of primary branches per plant (0.203) and chlorophyll fluorescence (0.143) indicating a close genetic

association with these traits and can be utilized for yield improvement. Significant and negative association of leaf area index was also found with main axis length (0.148). Non-significant association of leaf area index was also observed with rest of the traits and but direction of association was either positive or negative.

4.4.2.8 Chlorophyll fluorescence

Chlorophyll fluorescence showed significant and positive association with only traits viz. yield per plant (0.143). Rest of the traits were associated non-significantly with the chlorophyll fluorescence and values were either in positive or negative direction. In late sown condition, chlorophyll fluorescence showed significant and positive association with only two traits viz. 1000 seed weight (0.168) and chlorophyll content (0.165) and other traits are just associated non-significantly.

4.4.2.9 Main axis length (cm)

The perusal of the data in **Table: 4.4.2** stated that main axis length had positive and significant association with silique on main axis (0.494), 1000 seed weight (0.230), seeds per silique (0.225), yield per plant (0.200) and total silique per plant (0.150) and in opposite direction main axis length was associated with number of primary branches per plant (0.333) and days to 50 per cent flowering (0.203). Main axis length is associated non-significantly with rest of the traits under timely sown condition.

Main axis length showed significant and positive association with silique on main axis (0.582), seeds per silique (0.326), 1000 seed weight (0.280) and silique length (0.185) while main axis length was associated significantly with days to 50 per cent flowering (0.383), number of primary branches per plant (0.236), days to maturity (0.180) and leaf area index (0.148) but values in opposite direction. Rest of the characters showed non-significant association with main axis length and values were in positive and negative association.

4.4.2.10 Total silique per plant

For the total silique per plant in normal sown condition, most of the traits like, number of secondary branches per plant (0.674), yield per plant (0.550), number of primary branches per plant (0.455), silique on main axis (0.433), plant height (0.251) and main axis length (0.150) had significant and positive association and rest of the traits had only non-significant association.

In late sown situation, total siliqua showed significant and positive association with number of primary branches per plant (0.667), yield per plant (0.426), number of secondary branches per plant (0.408), siliqua on main axis (0.275), leaf area index (0.269), seed per siliqua (0.171), plant height (0.153), chlorophyll content (0.143) and main axis length (0.140). The remaining characters showed non-significant association but values were either in positive or negative direction.

4.4.2.11 Siliqua on main axis

In timely sown condition, siliqua on main axis showed significant and positive association with most of the traits like main axis length (0.494), total silique per plant (0.420), yield per plant (0.400), number of secondary branches per plant (0.310), siliqua length (0.230), plant height (0.210) and 1000 seed weight (0.200) while, significant and negative correlation was found only with days to 50 per cent flowering (0.183). The rest of the characters showed either positive or negative association with siliqua on main axis but values were non-significant.

Similarly like normal sown condition, siliqua on main axis showed significant and positive association with most of the traits like main axis length (0.582), seeds per siliqua (0.330), total siliqua (0.275), yield per plant (0.270), number of secondary branches per plant (0.263), 1000 seed weight (0.231), plant height (0.213), chlorophyll content (0.176), siliqua length (0.170) and significant and negative association with only days to 50 per cent flowering (0.161) and number of primary branches (0.136). Other than these traits are associated non-significantly with siliqua on main axis either in positive or negative direction.

4.4.2.12 Number of seeds per siliqua

In timely sown condition, seeds per siliqua showed significant and positive association with only two traits that are siliqua length (0.310) and main axis length (0.225). Non-significant association was observed with other traits.

In late sown condition, seeds per siliqua showed significant and positive association with siliqua on main axis (0.330), main axis length (0.326), 1000 seed weight (0.200), siliqua length (0.183) and total siliqua per plant (0.171) whereas, significant but negative correlation was observed with days to 50 per cent flowering (0.228). The rest of the characters showed non-significant positive and negative association with seeds per siliqua.

4.4.2.13 Siliqua length (cm)

Silique length showed significant and positive association with number of seeds per siliqua (0.310), siliqua on main axis (0.230) and yield per plant (0.214) under normal sown condition. In opposite direction, significant and negative correlation was observed with days to 50 per cent flowering (0.210) and days to maturity (0.180). Non-significant association of silique length was recorded with rest of the traits in either positive or negative direction.

In late sown condition, siliqua length showed significant and positive association with 1000 seed weight (0.330), main axis length (0.185), number of seeds per siliqua (0.183) and siliqua on main axis (0.170) whereas significant and negative correlation was found with days to 50 per cent flowering (0.210) and days to maturity (0.180). The rest of the characters showed non-significant association with siliqua length.

4.4.2.14 1000 seed weight (g)

Under stress free condition, 1000 seed weight showed significant and positive association with yield per plant (0.263), main axis length (0.230) and siliqua on main axis (0.200) and significant and negative correlation was found with days to maturity (0.255), days to 50 per cent flowering (0.199) and number of primary branches per plant (0.160). With other characters, main axis length was connected with rest of the traits but non-significantly but either in positive or negative direction.

Under late sown condition, 1000 seed weight had significant and positive association with most of the traits like siliqua length (0.330), main axis length (0.280), siliqua on main axis (0.231), number of seeds per siliqua (0.200), number of secondary branches (0.184), chlorophyll fluorescence (0.168), yield per plant (0.154) and plant height (0.140) whereas, significant and negative correlation was associated with only number of primary branches per plant (0.198). The remaining all characters showed either positive or negative association with main axis length but estimates were non-significant.

4.4.2.15 Yield per plant (g)

Under timely sown condition, yield per plant showed significant and positive association with most of the traits like total siliqua per plant (0.550), siliqua on main axis (0.400), number of secondary branches per plant (0.389), plant height (0.319), number of primary branches per plant (0.288), 1000 seed weight (0.263), siliqua length (0.214), main axis length (0.200), leaf area index (0.154) and chlorophyll fluorescence (0.143). Rest four

traits had either positive or negative association with yield per plant but values were non-significant.

Under late sown condition, yield per plant showed significant positive association with many characters like number of secondary branches per plant (0.941), total siliqua per plant (0.426), chlorophyll content (0.386), plant height (0.338), leaf area index (0.294), siliqua on main axis (0.270), number of primary branches per plant (0.267) and 1000 seed weight (0.154) and rest of the traits are associated yield per plant with non-significant estimates.

Genetic improvement in dependent trait like seed yield can be achieved by strong selection to any independent trait which is positively and strongly correlated with dependent trait. Significant correlation of yield per plant with various characters indicated the ample scope for simultaneous improvement of these traits with yield per plant. A close perusal of the phenotypic and genotypic correlation coefficients suggested that seed yield per plant was positively and significantly correlated with plant height, number of primary branches per plant, number of secondary branches per plant, leaf area index, total number of siliquae per plant, siliquae on main shoot and 1000 seed weight under both normal and late sown conditions indicating that these traits are less influenced by the environment and an increase in any of these component traits will result in the increase of seed yield per plant. Positive and significant association with these yield component traits in Indian mustard were also reported by the **Pandey *et al.*, (2021), Chaturvedi *et al.*, (2021), Ray *et al.*, (2019), Srivastava and Srivastava (2019), Kumar *et al.*, (2019), Kumar *et al.*, (2018), Singh *et al.*, (2016), Roy *et al.*, (2018), Bind *et al.*, (2014) and Singh and Singh (2010).** Based on current study findings Indian mustard yield potential can be increased by applying the strong selection to plant height, number of primary branches per plant, number of secondary branches per plant, leaf area index, total number of siliquae per plant, siliquae on main shoot and 1000 seed weight irrespective of sowing time and under climate change scenario, these traits will be helpful in developing terminal heat tolerant genotype. Similarly, number of secondary branches per plant is significantly correlated with total number of siliqua, siliqua on main shoot and yield per plant irrespective of sowing dates and association is at both genotypic and phenotypic level. Therefore, study suggested that increase in number of secondary branches will ultimately the major yield contributor in mustard. Total siliqua per plant and siliqua density on main shoot *i.e.* siliquae on main shoot along with 1000 seed weight are the major yield governing traits in Indian mustard

irrespective of the environment. Similar trend of results were also reported by the various researchers like **Lavanya *et al.*, (2022), Pandey *et al.*, (2021), Chaturvedi *et al.*, (2021), Dinesh *et al.*, (2020), Srivastava and Srivastava (2019), Khan *et al.*, (2019), Pal *et al.*, (2019), Pandey and Yadav (2018), Gupta *et al.*, (2018), Solanki *et al.*, (2017), Singh *et al.*, (2016), Yadav *et al.*, (2011), Singh and Singh (2010) and Singh *et al.*, (2013).**

Table: 4.4.2 Phenotypic correlation coefficients (rp) among various yield and its component traits in Indian mustard genotypes under timely and late sown condition

[illegible]

4.5 Path analysis

Path coefficient analysis is simply a standardized partial regression coefficient which divided the correlation coefficient into direct and indirect effect of independent traits with dependent variable and value assigned to a path is known as path coefficient. Seed yield is a multiplex trait which is result of direct and indirect contribution of different yield attributing traits. It is a tool which quantifies the direct effect of independent variable and its indirect effects through various traits on dependent variable *i.e.* yield. It will help to selection of superior genotypes based on traits which contribute more towards seed yield than others yield contributing traits. Therefore, in present study path coefficient analysis was carried out by taking yield per plant as dependent trait and other traits as independent variables under both the sowing conditions and results are presented in **Table 4.5**.

4.5.1 Days to 50 per cent flowering

Days to 50 per cent flowering exerted direct negative effect (-0.075) on yield per plant in timely sown condition. It also exhibited indirect effect on yield per plant *via* plant height (0.071) and days to maturity (0.038) in positive direction whereas indirect negative effect *via* 1000 seed weight (-0.039), siliqua length (-0.030) on yield per plant.

Days to 50 per cent flowering showed direct negative effect (-0.017) on yield per plant in late sown environment. On yield per plant, it also showed indirect positive effect *via* number of primary branches per plant (0.008), plant height (0.006) and indirect negative effect *via* number of secondary branches per plant (-0.057) and main axis length (-0.016).

4.5.2 Days to maturity

Days to maturity showed direct positive effect (0.046) on yield per plant in timely sown while it has negative direct effect (-0.018) in late sown condition. On yield per plant, it also showed indirect positive effect *via* plant height (0.093) and number of primary branches per plant (0.014) whereas indirect negative effect *via* days to 50 per cent flowering (-0.062) and 1000 seed weight (-0.050) in normal sown condition. While in late sown condition, positive indirect effect on yield per plant was also exerted by the days to maturity *via* number of secondary branches per plant (0.050) and number of primary

branches per plant (0.003) and indirect effect in negative direction was also reported *via* days to 50 per cent flowering (-0.009) and main axis length (-0.007).

4.5.3 Plant height (cm)

Plant height exerted direct positive effect on yield per plant irrespective of sowing time and estimates of direct effects are 0.198 in timely sown and 0.045 in late sown. Under timely sown environment, plant height exhibited indirect positive effect *via* total siliqua per plant (0.086) and number of primary branches per plant (0.026) and indirect negative effect *via* chlorophyll content (-0.038), days to 50 per cent flowering (-0.027). Under late sown condition, indirect positive effect *via* number of secondary branches per plant (0.296), number of primary branches per plant (0.006) whereas, indirect negative effect *via* 1000 seed weight (-0.004), days to 50 per cent flowering (-0.002) was exhibited by plant height on yield per plant.

4.5.4 Number of primary branches per plant

Number of primary branches per plant had direct positive effect (0.143) on yield per plant under both the environment and estimates for direct effects were 0.143 and 0.063, respectively. In the normal sown condition, indirect positive effect of number of primary branches per plant was also recorded through other independent variables like total siliqua per plant (0.156), plant height(0.036) whereas, negative indirect negative effect *via* 1000 seed weight (-0.031) and main axis length (-0.026) was exerted on yield.

In the late sown condition, indirect positive effect on dependent variable was exhibited through *via* number of secondary branches per plant (0.216) and 1000 seed weight (0.006) whereas, indirect effect in negative direction was observed *via* main axis length (-0.009) and leaf area index (-0.007).

4.5.5 Number of secondary branches per plant

On yield per plant, number of secondary branches per plant had direct positive effect irrespective of sowing condition and values for direct effects were 0.023 in normal and 0.922 in late sown condition. Number of secondary branches per plant exerted indirect effect in desirable direction through total siliqua per plant (0.231), number of primary branches per plant (0.084) in timely sown environment but in late sown condition, indirect positive effect was exerted through number of primary branches per plant (0.014) and plant height (0.014). Negative indirect effect was exhibited *via* seeds per siliqua (-0.005) and days to maturity (-0.002) in timely sown whereas, in late sown condition indirect negative

effect was exhibited through leaf area index (-0.011) and 1000 seed weight (-0.006) on yield per plant.

4.5.6. Chlorophyll content

Chlorophyll content showed direct positive effect on dependent variable i.e yield per plant in both the environment and values are 0.102 and 0.016, respectively. In normal sown condition, it showed indirect positive effect *via* total silique per plant (0.036) and 1000 seed weight (0.019) whereas, indirect negative effect was showed through plant height (-0.074) and days to maturity (-0.013) on yield per plant. Chlorophyll content also exerted indirect positive effect *via* number of secondary branches per plant (0.385) and plant height (0.004) whereas, indirect negative effect was observed *via* leaf area index (-0.012) and main axis length (-0.003) on yield per plant in late sown condition.

4.5.7. Leaf area index

On yield per plant, leaf area index had direct positive effect (0.071) in normal sown condition whereas it had negative direct effect (-0.034) on dependent variable i.e. yield per plant. Leaf area index exerted indirect effect in desirable direction through plant height (0.066) and total silique per plant (0.022) in timely sown environment but in late sown condition, indirect positive effect was exerted through number of secondary branches per plant (0.307) and number of primary branches per plant (0.012). Negative indirect effect was exhibited *via* chlorophyll content (-0.017) and days to 50 per cent flowering (-0.014) in timely sown whereas, in late sown condition indirect negative effect was exhibited through main axis length (-0.006) on yield per plant.

4.5.8. Chlorophyll fluorescence

Chlorophyll fluorescence showed direct positive effect on dependent variable i.e. yield per plant in both the environment and values are 0.072 and 0.009, respectively. In normal sown condition, it showed indirect positive effect *via* total silique per plant (0.021) and seeds per silique (0.016) whereas, indirect negative effect was showed through 1000 seed weight (-0.006) and days to maturity (-0.005) on yield per plant. Chlorophyll fluorescence also exerted indirect positive effect *via* number of secondary branches per plant (0.105) and chlorophyll content (0.002) whereas, indirect negative effect was observed *via* 1000 seed weight (-0.005) on yield per plant in late sown condition.

4.5.9 Main axis length (cm)

Main shoot length exerted direct positive effect on yield per plant irrespective of sowing time and estimates of direct effects are 0.078 in timely sown and 0.041 in late sown. Under timely sown environment, main shoot length exhibited indirect positive effect *via* total silique per plant (0.051) and silique on main shoot (0.045) and indirect negative effect *via* chlorophyll number of primary branches per plant (-0.047) and seeds per silique (-0.030). Under late sown condition, indirect positive effect *via* days to 50 per cent flowering (0.006) and leaf area index (0.005) whereas, indirect negative effect *via* number of secondary branches per plant (-0.030) and number of primary branches per plant (-0.014) was exhibited by main axis length on yield per plant.

4.5.10 Total silique per plant

Total silique per plant had direct positive effect (0.344) on yield per plant in normal sown condition and it was in undesirable direction under late sown condition i.e. (-0.003). In the normal sown condition, indirect positive effect of total silique per plant was also recorded through other independent variables like number of primary branches per plant (0.065) and plant height (0.049) whereas, negative indirect negative effect *via* number of secondary branches per plant (-0.015) and seed on per silique (-0.012) was exerted on yield.

In the late sown condition, indirect positive effect on dependent variable was exhibited through number of secondary branches per plant (0.376) and number of primary branches per plant (0.042) whereas, indirect effect in negative direction was observed *via* leaf area index (-0.009).

4.5.11 Silique on main axis

Silique on main axis exerted direct positive effect (0.075) on yield per plant in timely sown condition. It also exhibited indirect effect on yield per plant *via* total silique per plant (0.144) and plant height (0.041) in positive direction whereas indirect negative effect *via* seeds per silique (-0.011) and number of secondary branches per plant (-0.007) on yield per plant.

Silique on main axis showed direct negative effect (-0.002) on yield per plant in late sown environment. On yield per plant, it also showed indirect positive effect *via* number of secondary branches per plant (0.242) and main axis length (0.024) and indirect negative effect *via* number of primary branches per plant (-0.008) and 1000 seed weight (-0.007).

4.5.12 Number of seeds per siliqua

Number of seeds per siliqua showed direct negative effect (-0.134) on yield per plant in timely sown while it has slight positive direct effect (0.0009) in late sown condition. On yield per plant, it also showed indirect positive effect *via* total silique per plant (0.032) and siliqua length (0.049) whereas indirect negative effect *via* plant height (-0.011) and number of primary branches per plant (-0.010) in normal sown condition. While in late sown condition, positive indirect effect on yield per plant was also exerted by the number of secondary branches per plant (0.116) and main axis length (0.013) and indirect effect in negative direction was also reported *via* 1000 seed weight (-0.006) and number of primary branches per plant (-0.005).

4.5.13 Siliqua length (cm)

Siliqua length exerted direct positive effect on yield per plant irrespective of sowing time and estimates of direct effects are 0.160 in timely sown and 0.021 in late sown. Under timely sown environment, siliqua length exhibited indirect positive effect *via* 1000 seed weight (0.024) and total silique per plant (0.037) and indirect negative effect *via* number of seeds per siliqua (-0.041) and days to maturity (-0.010). Under late sown condition, indirect positive effect *via* number of secondary branches per plant (0.076) and main axis length (0.007) whereas, indirect negative effect *via* 1000 seed weight (-0.011) and number of primary branches per plant (-0.007) was exhibited by siliqua length on yield per plant.

4.5.14 1000 seed weight (g)

1000 seed weight had direct positive effect (0.198) on yield per plant in normal sown condition and it was in undesirable direction under late sown condition i.e. (-0.034). In the normal sown condition, indirect positive effect of 1000 seed weight was also recorded through other independent variables like total silique per plant (0.037) and siliqua length (0.020) whereas, negative indirect effect *via* number of primary branches per plant (0.022) and number of seeds per siliqua (0.014) was exerted on yield.

In the late sown condition, indirect positive effect on dependent variable was exhibited through number of secondary branches per plant (0.169) and siliqua length (0.006) whereas, indirect effect in negative direction was observed *via* number of primary branches per plant (0.012).

A low residual effect at phenotypic level was observed on seed yield per plant in both the environment and estimates for residuals are 0.54 in normal sown and 0.10 in late sown. Low values of the residuals are indicating that characters those were not studied in the present investigation had very less effect on seed yield per plant. So, the traits under study were adequate to study the effect on seed yield in Indian mustard. Similar kind of results were also reported by the several researchers like, **Srivastava and Srivastava (2019), Ompal *et al.*, (2018), Kumar *et al.*, (2016) and Gupta *et al.*, (2018).**

A critical perusal of path coefficient analysis revealed that high direct effects on seed yield were exerted by plant height, chlorophyll content, main shoot length and silique length without the influence of the sowing period. It is evident from correlation results that plant height had a positive significant correlation with seed yield per plant and rest other traits also had positive correlation with yield. That clearly explains the true genetic relationship between these traits and direct selection through these traits will be rewarding to improve seed yield. Similar findings were also reported by the **Lavanya *et al.*, (2022), Ray *et al.*, (2019), Srivastava and Srivastava (2019), Kumar *et al.*, (2019), Tantuway *et al.*, (2018), Gupta *et al.*, (2018), Singh *et al.*, (2016) and Singh and Singh (2010).**

Table: 4.5.1 Phenotypic path coefficients showing direct and indirect effects of yield and its component traits in Indian mustard genotypes under timely and late sown conditions.

Trait	Sowing time	FW50	DM	PH	PB	SB	CC	LAI	FLU	MAL	TS	SAM	SSQ	SL	SW
FW50	Timely	-0.07553	0.03899	0.07147	0.02105	0.00193	-0.01380	0.01341	-0.00808	-0.01599	-0.02021	-0.01680	0.01577	-0.03014	-0.03931
	Late	-0.01711	-0.00617	0.00640	0.00802	-0.05790	0.00087	0.00324	0.00008	-0.01603	0.00039	0.00040	-0.00022	-0.00438	0.00277
DM	Timely	-0.06270	0.04697	0.09335	0.01403	0.00110	-0.03023	0.01300	-0.00793	-0.00875	0.00594	-0.01014	0.01261	-0.03604	-0.05042
	Late	-0.00974	-0.01084	0.00341	0.00358	0.05014	0.00208	0.00060	-0.00046	-0.00744	0.00019	0.00028	-0.00006	-0.00374	0.00284
PH	Timely	-0.02722	0.02211	0.19832	0.02653	-0.00162	-0.03846	0.02407	0.00012	0.00909	0.08626	0.01916	0.00751	-0.00511	0.00059
	Late	-0.00239	-0.00081	0.04574	0.00661	0.29659	0.00147	-0.00183	-0.00001	-0.00119	-0.00048	-0.00053	-0.00005	-0.00048	-0.00478
PB	Timely	-0.01112	0.00461	0.03679	0.14304	-0.01372	0.00421	0.00620	0.00162	-0.02624	0.15669	-0.00125	0.01002	0.01326	-0.03125
	Late	-0.00218	-0.00061	0.00480	0.06307	0.21690	0.00007	-0.00701	-0.00049	-0.00987	-0.00207	0.00034	-0.00009	-0.00237	0.00674
SB	Timely	0.00626	-0.00222	0.01383	0.08438	-0.02325	0.02001	0.00366	0.00382	0.00169	0.23175	0.02843	-0.00551	0.01890	0.00756
	Late	0.00107	-0.00059	0.01471	0.01483	0.92216	0.00672	-0.01149	0.00106	-0.00137	-0.00127	-0.00066	0.00012	0.00177	-0.00628
CC	Timely	0.01013	-0.01380	-0.07412	0.00586	-0.00452	0.10292	-0.01241	-0.00118	-0.00210	0.03663	-0.00285	0.00400	-0.01309	0.01936
	Late	-0.00092	-0.00140	0.00418	0.00029	0.38523	0.01608	-0.01266	0.00151	-0.00360	-0.00044	-0.00044	0.00005	-0.00086	-0.00142
LAI	Timely	-0.01409	0.00850	0.06644	0.01234	-0.00118	-0.01778	0.07185	0.00264	-0.00276	0.02284	0.00970	0.01034	-0.00802	-0.00675
	Late	0.00161	0.00019	0.00244	0.01284	0.30746	0.00591	-0.03446	0.00139	-0.00621	-0.00084	-0.00017	0.00003	0.00209	0.00171
FLU	Timely	0.00844	-0.00516	0.00032	0.00322	-0.00123	-0.00168	0.00263	0.07223	0.00995	0.02161	0.01526	0.01637	0.01516	-0.00601
	Late	-0.00016	0.00054	-0.00004	-0.00333	0.10506	0.00262	-0.00518	0.00927	0.00024	-0.00013	-0.00030	0.00005	0.00087	-0.00586
MAL	Timely	0.01533	-0.00522	0.02288	-0.04766	-0.00050	-0.00274	-0.00252	0.00913	0.07875	0.05154	0.04535	-0.03019	0.01815	0.04556
	Late	0.00655	0.00193	-0.00130	-0.01487	-0.03017	-0.00138	0.00511	0.00005	0.04186	-0.00044	-0.00145	0.00031	0.00391	-0.00947
TS	Timely	0.00444	0.00081	0.04972	0.06513	-0.01566	0.01096	0.00477	0.00454	0.01180	0.34411	0.03856	-0.01250	0.01754	0.02136
	Late	0.00215	0.00065	0.00701	0.04204	0.37626	0.00230	-0.00929	0.00038	0.00588	-0.00311	-0.00069	0.00016	-0.00095	0.00291
SAM	Timely	0.01381	-0.00518	0.04136	-0.00194	-0.00719	-0.00319	0.00758	0.01200	0.03887	0.14442	0.09188	-0.01128	0.03665	0.03934
	Late	0.00276	0.00122	0.00976	-0.00860	0.24252	0.00282	-0.00234	0.00111	0.02434	-0.00086	-0.00250	0.00031	0.00358	-0.00789
SSQ	Timely	0.00886	-0.00441	-0.01109	-0.01067	-0.00095	-0.00306	-0.00553	-0.00880	0.01770	0.03201	0.00771	-0.13436	0.04952	0.02204
	Late	0.00390	0.00064	-0.00245	-0.00574	0.11687	0.00089	-0.00126	0.00050	0.01362	-0.00053	-0.00082	0.00094	0.00386	-0.00672
SL	Timely	0.01417	-0.01054	-0.00631	0.01181	-0.00274	-0.00838	-0.00359	0.00681	0.00890	0.03757	0.02096	-0.04142	0.16064	0.02480
	Late	0.00354	0.00191	-0.00103	-0.00705	0.07683	-0.00065	-0.00341	0.00038	0.00773	0.00014	-0.00042	0.00017	0.02119	-0.01111
SW	Timely	0.01499	-0.01195	0.00059	-0.02256	-0.00089	0.01005	-0.00245	-0.00219	0.01811	0.03710	0.01824	-0.01495	0.02011	0.19812
	Late	0.00139	0.00090	0.00641	-0.01245	0.16966	0.00067	0.00173	0.00159	0.01161	0.00027	-0.00058	0.00019	0.00690	-0.03412

Residual effects, In timely sown condition: 0.54

late sown condition = 0.10

4.6 Genetic divergence

The ultimate target of any crop improvement programme is development of superior genotypes with desirable combination of traits and that can be used as a cultivar. Under climate change scenario, development of the terminal heat tolerant genotypes, crop germplasm attracted the attention of plant breeders as these are the natural reservoir for genetic variability. The potential of genetic diversity is successfully exploited in the several crops and suitable donors were identified achieve breeding objectives. Mahalanobis D^2 statistics is most widely used and potent biometrical tool in quantifying the degree of diversity. Therefore, looking the above facts, in present investigation Mahalanobis D^2 statistics is used to assess the genetic diversity exist in the Indian mustard germplasm under late and timely sown condition. Due to large set of germplasm in evaluation, application of D^2 statistics gets crippled. Under these conditions, Heirarchical cluster analysis (HCA) based on Mahalanobis distances was employed for estimating the genetic divergence among 200 genotypes in each environment and the results obtained from present study were discussed below:

4.6.1 Cluster formation based on Hierarchical Cluster Analysis (HCA)

The mean values of 200 Indian mustard genotypes along with checks were used for hierarchical cluster analysis (HCA) based on Mahalanobis distances and all the genotypes were grouped in six clusters in each environment. The grouping of each genotype into different clusters is presented in **Table: 4.6.1**. Under timely sown condition, it can be seen from results that Cluster I had the largest (73) number of genotypes followed by the cluster VI (40 genotypes), cluster V (31 genotypes), cluster III (28 genotypes), cluster II (22 genotypes) and cluster IV (13 genotypes) which was smallest. Similarly in late sown condition, all genotypes were grouped in six clusters only and maximum numbers of genotypes were in cluster III (80 genotypes), followed by cluster I (57 genotypes), cluster IV (45 genotypes), cluster II (18 genotypes), cluster IV (6 genotypes) and cluster V (1 genotype), which is minimum. All genotypes in different clusters were denoted by their entry number in dendrogram and entry number directly corresponds to the name of genotypes given in **Table: 3.2** and dendrogram of mustard genotypes derived through HCA separately in both timely and late sown conditions are depicted in **Figure 4.6.1 and Figure 4.6.2**.

Table: 4.6.1 Distribution of 200 Indian mustard genotypes into different clusters using Hierarchical cluster analysis

Cluster No.	Number of genotypes		Name of genotypes	
	Timely	Late	Timely	Late
I	73	57	DRMR – 137, EC - 399300, IM – 76, DRMR – 138, EC - 766560, IM – 170, DRMR – 579, EC -766391, PBR – 97, DRMR - 582, EC - 766381, RE – 44, DRMR – 683, IC – 766334, EC - 766611, DRMR – 686, EC -7 66322, EC - 766576, DRMR – 689, EC - 766311, EC - 766571, DRMR – 691, EC – 766207, EC – 766278, DRMR - 692, EC – 766060, EC – 766234, RC – 571, EC – 764501, EC – 766211, RC - 891-1, EC – 766325, EC – 76657, RC – 1271, EC – 766498, EC – 399293, CN – 34005, EC – 766564, EC – 766616, CN – 113780, EC – 766393, EC – 766594, CN – 34008, EC – 766322, EC – 766094, CN – 105233, IC - 766029, EC - 766095, CN – 105379, DRMR – 6, NDRE – 4, KDM - 49-1, DRMR – 266, I – 79, RB – 60, DRMR – 611, IC – 491455, EM – 1, DRMR – 680, IC – 491175, NPJ - 113, PUSA BAHAR, NC – 37362, RCQR - 9901, RC – 1270, CN – 105309, RNN – 505, RLC – 3, AJ – 3, RJ – 10, NRCHB – 101, SEJ – 2, PM - 25	DRMR - 46, DRMR - 48, DRMR – 576, DRMR – 577, DRMR – 578, DRMR - 683, DRMR – 686, DRMR - 691, DRMR – 5, DRMR – 359, DRMR – 361, DRMR – 610, DRMR – 611, DRMR – 624, DRMR - 625, DRMR - 680, DRMR – 900, DRMR – 909, CN – 34008, CN – 105233, RC – 1270, RC – 1271, NC – 37362, NPJ- 113, IC – 122137, IC – 341108, IC – 375924, IC – 422156, IC - 422172, IC – 481011, IC – 73225, EC - 766576, EC – 766211, EC – 399318, EC – 399293, IC - 70302, IC – 766129, IC – 321424, EC - 766110, EC - 766127, IC – 491175, IC – 531377, IC – 589683, IC – 497904, PCR – 9403, PBR – 97, RGN – 34, EC - 564649-1, RJ - 10, RE - 44, PM - 30, I – 79, NRCHB - 101, NRCDR - 2, SEJ - 2, PM - 25, PM - 26
II	22	18	EC – 766557, IC - 766214, EC -766401, EC – 766069, EC – 766124, DRMR – 906, EC – 766296, EC – 399308 EC – 766487, EC -766141, EC – 766292, EC – 766470, EC – 766344, EC - 66431 , EC – 766276, EC – 766312, EC - 564649-1, EC - 766402, EC – 766270, NRCDR -2, PM - 26, Radhika	KDM - 49-1, RCQR - 9901, RNN – 505, NDRE – 4, EC - 399300, EC - 766423, IC - 320378, IC -766377, DRMR – 6, DRMR – 7, DRMR – 9, DRMR – 357, IC -2 06741, IC – 372259, EC – 399302, Krishna, IM – 76, Radhika
III	28	80	DRMR – 362, RC – 132, EC – 766310, DRMR – 726, DTM – 50, DRMR – 364, PR - 2001-42, EC -766204, DRMR – 731, IM – 152, DRMR – 693, IC – 531377, IC - 320378, DRMR – 900, IC – 11721, DRMR – 711, IC - 589676, IC – 766614, DRMR – 909, IC - 206741, RC -3 71-1, EC -766423, DRMR – 359, SITARA SAGAR, IC – 491348, DRMR – 358, IC – 481011, Krishna	DRMR – 2, EC – 766344, EC -766611, EC -766234, DRMR – 12, EC – 766200, EC – 766276, EC – 766207, DRMR – 33, EC – 764501, EC – 766278, EC – 766557, DRMR – 136, EC - 766622, EC – 766270, EC – 766060, DRMR – 137, EC – 766325, EC – 766234, EC -766204, DRMR – 362, EC – 766115, EC - 766069, CN - 105257, DRMR – 574, EC – 766498, EC - 766576, CN - 105312, DRMR -582, EC – 766564, EC – 571648, CN – 105309, DRMR – 689, EC - 766489, EC – 399308, IC – 491485, DRMR - 692, EC – 766393, EC – 766470, IC - 589676, DRMR – 693, EC – 766207, EC – 766616, IC – 11721, DRMR -710, EC – 766322, EC – 766555, DRMR – 11, RC - 891-1, IC - 766214,

				EC - 766094, DRMR – 360, CN – 34005, IC – 766098, EC – 766312, DRMR - 626, CN – 105364, IC - 766029, EC -766095, DRMR - 669, CN – 101813, CN – 105379, IC – 766299, DRMR – 726, DRMR – 4, NC – 660, DRMR - 358, DRMR - 731, AJ – 11, DJ – 5, AJ – 3, GR – 325, RB – 60, DJ – 12, RLC – 3, IM – 108, EM – 1, IM – 3, RH – 30, PM - 67
IV	13	45	DRMR – 2, DRMR – 8, DRMR – 7, DRMR – 33, DRMR – 12, DRMR – 4, DRMR – 9, DRMR – 46, DRMR – 13, DRMR – 5, DRMR – 11, DRMR – 48, EC - 766207	EC – 766296, EC - 766292, EC - 766594, IC -399318, EC – 766431, EC -766402, EC -766401, EC -766571, IC – 491455, EC - 766134, EC -766136, EC - 766560, EC - 766391, EC - 766381, EC - 766335, IC – 766334, EC - 766322, EC - 766311, EC – 766310, EC – 766124, EC – 766487, IC – 766614, IC – 491348, IC – 766313, DRMR – 8, DRMR – 264, DRMR – 266, DRMR – 906, DRMR – 138, DRMR – 364, DRMR – 579, DRMR - 711, CN -101845, CN – 113780, EC - 766141, RC - 371-1, IM – 152, IM – 170, DJ – 65, DTM - 50, PTJ - 3-64, NPJ – 161, PR - 2001-42, PUSA BAHAR, PTJ - 3-89
V	31	1	DRMR – 136, DRMR – 264, IC – 122137, EC -766134, DRMR – 574, DRMR – 357, IC – 341108, EC - 766136, DRMR – 576, DRMR – 360, IC – 375924, EC - 766200, DRMR – 577, IM – 3, IC – 422156, EC – 766115, DRMR – 578, RGN – 34, IC - 422172, IC - 70302, CN-105364, CN - 101845, IC – 73225, IC - 766377, GR – 325, RH - 30, IC – 766313, IC – 589683, IM – 108, PCR – 9403, IC - 497904	DRMR - 13
VI	40	6	DRMR - 710, EC – 571648, EC - 766110, DRMR – 361, CN – 105257, EC – 399302, EC - 766234, DRMR – 610, CN – 105312, RHUR - 2 -1, EC – 766555, EC - 766127, DRMR – 624, CN – 101813, IC – 76612, EC - 766335, DRMR – 625, DJ – 12, DJ – 5, AJ – 11, BASANTI, PM - 30, IC – 766299, EC – 766622, DRMR - 626, DJ – 65, PTJ - 3-64, IC – 399318, EC - 766489, DRMR - 669, NPJ – 161, IC – 321424, IC – 766098, NC – 660, PM – 67, IC – 372259, RC -371, IC – 491485, PTJ - 3-89, EC - 399318	BASANTI, RHUR - 2 -1, RC - 371, RC – 132, RC – 571, SITARA SAGAR

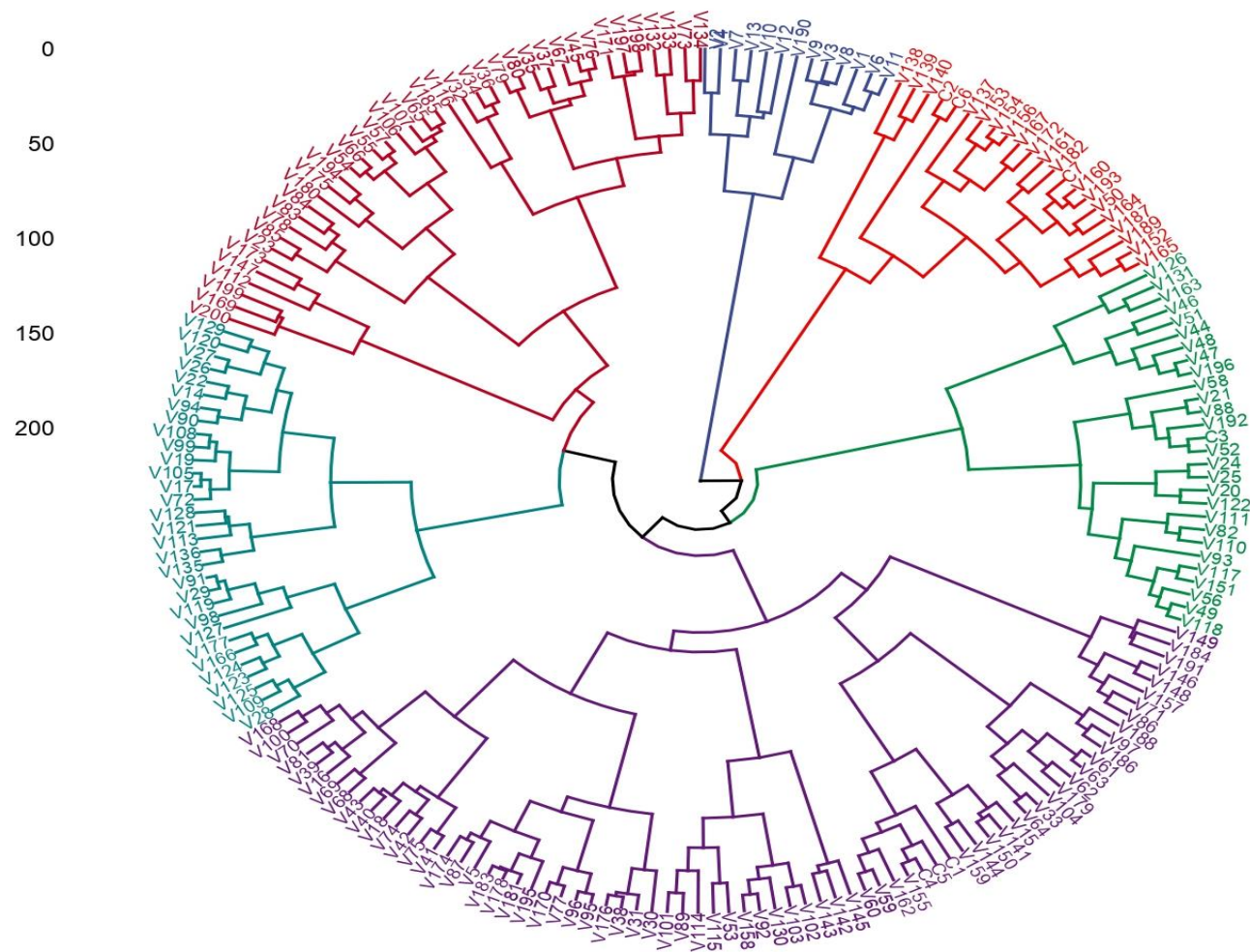


Figure: 4.6.1 Spherical dendrogram for 200 Indian mustard genotypes based on HCA under timely sown condition.

Similar kind of studies in Indian mustard were also carried out by the different scientists namely **Gadi *et al.*, (2020)**, **Tripathi *et al.*, (2019)**, **Nagda *et al.*, (2018)**, **Rathod *et al.*, (2017)**, **Mohan *et al.*, (2017)**, **Lodhi *et al.*, (2016)** and **Gupta *et al.*, (2015)**.

4.6.2 Inter and Intra-cluster distance

The genotypes which were grouped in same cluster are less distinct with each other than those placed into different clusters. Inter-cluster distance i.e. the distance between two clusters is measure of degree of divergence between the genotypes fall in those clusters. Hence, greater is the distance between two clusters, more will be the divergence between them and vice-versa. Average intra and inter-cluster distances in both the environment are represented in **Table: 4.6.2** and diagonal values are presented and described below.

Under timely sown condition, intra-cluster distance was highest for the cluster I (9.89) followed by cluster III (9.05), cluster V (8.73), cluster IV (8.72), cluster VI (8.59) and cluster II (7.10) whereas, in late sown condition the highest intra-cluster distance was observed in cluster II (11.07) followed by cluster III (10.82), cluster I (9.82), cluster IV (9.43), cluster VI (7.23) and lowest values was recorded for cluster V (0.0) due to single genotype in this cluster.

Wide genetic diversity is depicted by the cluster which had maximum inter-cluster distance and genotypes from these clusters can be used in hybridization either exploit heterosis or to take advantage of transgressive segregation. In opposite, it is not advisable to take crossing between genotypes with least inter-cluster distance. Therefore, measures of inter-cluster distance provide the suitable donors for various traits from diverse clusters which could be expected to manifest high heterosis. Several researchers advised earlier that, hybridization between genotypes obtained from divergent clusters with high inter-cluster distance would yield superior transgressive segregants for selection in Indian mustard. Similar results were also observed by **Lien *et al.*, (2021)**, **Malviya *et al.*, (2021)**, **Nagda *et al.*, (2018)**, **Tudu *et al.*, (2018)**, **Lodhi *et al.*, (2016)**, **Singh *et al.*, (2014)** and **Kumar and Pandey (2013)** also find same results.

In timely sown condition, the maximum inter-cluster distance was exhibited by the cluster III and IV (11.53) followed by cluster I and V (11.48), cluster V and VI (10.78) and cluster I and II (10.77). Meanwhile, the least inter-cluster distance was observed by the

cluster III and VI (9.18) followed by cluster I and IV (9.73) and cluster I and III (9.80). If the genotypes, from cluster III and IV will be hybridized with each other than there will be higher chance of obtaining genetic variability in F₂ and succeeding generations to obtain transgressive segregants.

Table 4.6.2: Intra (diagonal) and Inter-cluster (off-diagonal) distances between clusters based on hierarchical cluster analysis in Indian mustard genotypes under timely and late sown conditions.

Cluster	Sowing	I	II	III	IV	V	VI
I	Timely	9.89	10.77	9.80	9.73	11.48	10.31
	Late	9.82	10.62	11.44	10.04	8.24	11.95
II	Timely	10.77	7.10	10.21	10.59	9.87	10.27
	Late	10.62	11.07	11.31	10.59	8.15	13.01
III	Timely	9.80	10.21	9.05	10.56	11.53	9.18
	Late	11.44	11.31	10.82	10.27	8.70	12.55
IV	Timely	9.73	10.59	10.56	8.72	9.90	9.89
	Late	10.04	10.59	10.27	9.43	8.63	11.31
V	Timely	11.48	9.87	11.53	9.90	8.73	10.78
	Late	8.24	8.15	8.70	8.63	0.00	9.96
VI	Timely	10.31	10.27	9.18	9.89	10.78	8.59
	Late	11.95	13.01	12.55	11.31	9.96	7.23

Under late sown condition, the maximum inter cluster distance was found between cluster II and VI (13.01) followed by cluster III and VI (12.55), cluster I and VI (11.95) and cluster I and III (11.44). Meanwhile, the lowest inter-cluster distance was observed between cluster II and cluster IV followed by cluster I and V (8.24) and cluster IV and V (8.63). If the genotypes, from cluster II and VI will be hybridized with each other than there will be more chance of obtaining genetic variability in F₂ and succeeding generations to obtain transgressive segregants for heat tolerance and other agro-morphological traits. Similar kind of results were also reported by **Malviya et al., (2021), Gadi et al., (2020), Tripathi et al., (2019), Nagda et al., (2018), Devi et al., (2017), Rathod et al., (2017), Mohan et al., (2017), Lodhi et al., (2016), Gupta et al., (2015), Singh et al., (2014) and Kumar and Pandey (2013).**

4.6.3 Cluster mean values for different clusters

The cluster mean values for 15 agro-morphological and physiological traits under normal and late sown conditions were estimated and summarized in **Table: 4.6.3**. A critical analysis into results revealed that all the clusters exhibited varying differences for all the characters under study and variable mean is observed in both the condition. Cluster mean analysis helps in identification of suitable donors for hybridization to obtain superior segregants separately under normal and timely sown conditions to enhance the seed yield. The details description of the cluster mean is discussed below:

- a) In case of days to 50 per cent flowering, lowest cluster mean was observed in cluster V (53.58 days) in normal sown condition whereas, in late sown condition lowest cluster mean for days to 50 per cent flowering was exhibited by cluster I (57.82 days) which is desirable to develop early maturing genotypes.
- b) The cluster mean values for days to maturity was found to be lowest in cluster IV (122.77 days) in timely sown situation and in cluster I (119.72 days) under in late sown condition.
- c) Among six clusters in each environment, for plant height, highest cluster mean value was recorded for cluster III and estimates under timely sown and late sown were 210.58 and 218.78, respectively.
- d) The highest cluster mean value for number of primary branches per plant was recorded 8.29 (cluster III) in timely sown and 6.89 (cluster VI) in late sown situation.
- e) Cluster III observed highest mean value of 14.67 for number of secondary branches per plant in normal sown condition. Whereas, in late sown condition highest mean value for secondary branches per plant was observed for cluster V (17.94) and this cluster also recorded second high value under timely sown condition i.e. 14.35.
- f) Chlorophyll content was recorded highest by the cluster IV (32.12) in timely sown condition and it was highest in cluster V (26.68) in late sown condition.
- g) Leaf area index was recorded highest in cluster V (4.14) and it also recorded second high value for leaf area index i.e. 2.93 in late sown condition but high value in late sown condition was observed in cluster II.

- h) The highest chlorophyll fluorescence values were recorded by cluster VI (0.78) and cluster II and cluster V (0.75), in normal and timely sown condition, respectively.
- i) Main shoot length had highest cluster mean values of 79.11 cm for the cluster II in normal sown condition and in late sown condition the highest cluster mean values was observed for cluster IV (78.98 cm)
- j) Cluster V showed highest cluster mean values for total silique per plant in both normal and timely sown condition and estimates were 394.24 and 286.67, respectively.
- k) For the number of silique on main shoot, cluster V recorded highest value irrespective of sowing date. The cluster mean values were 51.13 and 48.00 in normal and late sown condition.
- l) In case of number of seeds per silique, cluster II was recorded for highest cluster mean values under both normal and late sown condition and the estimates were 16.04 and 13.98 in normal and late sown condition.
- m) Cluster VI recorded highest cluster mean value for siliquae length i.e. 3.86 cm in normal sown condition and in late sown condition maximum cluster value was observed by the cluster IV (4.12 cm)
- n) For 1000 seed weight, cluster V recorded highest cluster mean values in both normal and late sown condition and the mean values were 3.84 g and 3.92 g in timely and late sown condition. Even in heat stress this cluster recorded higher 1000 seed weight than normal condition.
- o) In case of seed yield per plant, cluster III was promising under normal sown condition and it recorded cluster mean value of 16.45 g while, under heat stress cluster VI was the promising for seed yield per plant and it recorded mean value of 8.66 g and this cluster also had second high value for seed yield per plant in timely sown condition i.e. 16.38 g.

In general, an overview of the above results showed that cluster V included most of the genotypes which were promising under both the environment for most of the yield attributing traits like total silique per plant, number of silique on main shoot and seed weight and these genotypes can be used as donors in breeding high yielding varieties. Genotypes under cluster V are also having high values for number of secondary branches per plant in both the situation. To develop early maturing genotypes in Indian mustard, genotypes from cluster V in timely sown condition and

Table: 4.6.3 Cluster mean values for yield and yield component traits among 200 Indian mustard genotypes under timely and late sown condition

Traits	Sowing	I	II	III	IV	V	VI
FW50	Timely	56.64	54.80	59.45	58.38	53.58	56.98
	Late	57.82	65.63	63.84	63.00	63.00	66.33
DM	Timely	125.49	127.17	129.46	122.77	122.81	126.83
	Late	119.72	126.00	121.08	122.56	123.00	123.83
PH	Timely	205.84	196.80	210.58	174.77	197.69	198.45
	Late	206.23	213.44	218.78	207.29	213.00	202.28
PB	Timely	5.74	4.58	8.29	6.38	5.87	5.86
	Late	5.26	5.36	5.55	6.21	6.00	6.89
SB	Timely	10.77	10.77	14.67	12.77	14.35	12.59
	Late	6.81	8.90	5.89	5.68	17.94	8.66
CC	Timely	22.44	23.00	22.94	32.12	24.69	23.67
	Late	21.10	24.88	17.97	19.13	26.68	21.37
LAI	Timely	3.56	2.75	3.45	2.79	4.14	3.82
	Late	1.75	2.96	1.53	1.73	2.93	2.43
FLU	Timely	0.75	0.77	0.77	0.74	0.76	0.78
	Late	0.74	0.75	0.70	0.74	0.75	0.71
MAL	Timely	72.65	79.11	65.33	62.51	73.67	68.82
	Late	78.97	69.56	71.83	78.98	63.00	56.83
TS	Timely	329.50	292.34	394.01	330.49	394.24	377.02
	Late	220.75	215.51	214.42	279.27	286.67	183.50
SAM	Timely	45.29	45.02	46.86	42.46	51.13	45.17
	Late	44.28	42.07	42.04	45.01	48.00	33.83
SSQ	Timely	14.76	16.04	14.83	14.63	15.44	14.28
	Late	13.38	13.98	13.13	13.24	13.20	9.10
SL	Timely	3.75	3.83	3.75	3.68	3.79	3.86
	Late	3.95	3.88	3.83	4.12	3.63	3.82
SW	Timely	3.70	3.68	3.22	3.78	3.84	3.20
	Late	3.41	3.28	3.28	3.02	3.92	2.60
YP	Timely	13.57	11.14	16.45	10.50	15.50	16.38
	Late	6.87	7.84	5.94	5.68	7.94	8.66

genotypes from cluster I in terminal heat stress can be used in hybridization. It can be concluded from all the above findings that the cluster V recorded the highest cluster means for most of yield attributing traits and these genotypes can be used as potential donor for the hybridization programme. The results of current study were in accordance to the findings of earlier researchers like **Malviya *et al.*, (2021)**, **Tripathi *et al.*, (2019)**, **Tudu *et***

al., (2018), *Devi et al.*, (2017), *Lodhi et al.*, (2016), *Singh et al.*, (2016) and **Kumar and Pandey (2013)**.

4.7 Phenotyping for heat tolerance

The current study intended to investigate the effect of heat stress during reproductive stage in Indian mustard through several agro morphological and physiological traits in addition to yield parameters. Two sowing date were used during study, normal sowing is 14 November for normal crop growth and to avoid terminal heat stress and second is 8 December to expose different mustard genotypes to heat stress at reproductive stage and comparative picture provides the tolerance level in the mustard genotypes. The mean temperature during reproductive stage is depicted in **Table 3.1** and **Fig. 3.1**. The increased temperature at reproductive stage during the late sown condition decreases the yield attributing traits except in tolerant genotypes. Thus, the primary objective of evaluating 200 mustard genotypes along with seven checks is to identify sources of terminal heat tolerance in Indian mustard germplasm for utilization in the breeding scheme. The results of current investigation with respect to heat tolerance are presented below:

4.7.1. Per cent yield change (%)

It is an important indicator to determine response of genotypes under heat stress condition and results are presented in **Table: 4.7.1**. Under the heat stress, in general yield reduction was noticed and the average yield reduction was 50.36 per cent whereas maximum yield reduction of 87.88 % was observed in (EC-766311) and the yield increment was observed under heat tolerant genotypes and maximum increment was observed for NDRE-4 (50.91%). The genotypes namely NDRE-4, EC-399300, DRMR-13, DRMR-9, DRMR-7, DRMR-357, DRMR-6, EC-66423 and IM-76 showed either increment or less reduction in yield under terminal stress and are designated as heat tolerant genotypes. In checks, PM-26 showed low reduction in yield (-4.39%).

4.7.2 Heat susceptibility index (HSI)

HSI and YSI were estimated using standardized formula proposed by Fisher and Maurer (1978) and results are presented in **Table: 4.7.1**. The lowest value of HSI was reported by NDRE-4 (-0.92) followed by the EC-399300 (-0.83), DRMR-13 (-0.51), DRMR-9 (-0.42), DRMR-7 (-0.38), DRMR-357 (-0.27), DRMR-6 (-0.11), EC-766423 (-

0.07) and IM-76 (-0.01) and these genotypes are categorized as the promising genotypes for heat tolerance. Whereas, highest HSI was observed for the genotypes EC-766311 (1.58) followed by EC-399302 (1.57), DRMR-266 (1.57) and IC-321424 (1.52) and these genotypes are categorized as susceptible genotypes. It was estimated for all test genotypes under heat stress condition. The HSI ranged from -0.92 to 1.58 and average value of HSI was 0.90. Under the checks, PM-26 showed minimum heat susceptibility value (-0.09) among the check varieties.

4.7.3. Yield stability index (YSI) or heat tolerance index (HTI)

Yield stability ratio is also a good criterion for selecting the tolerant genotype under stressed condition. Under present study YSI is ranged from 0.12 to 1.51 and average value for YSI was 0.50 and values for each genotype are given in **Table: 4.7.1**. The high value of YSI is considered promising with respect to heat tolerance and vice versa. The highest value for YSI was recorded by the genotype NDRE-4 (1.51) followed by EC-399300 (1.46), DRMR-13 (1.28), DRMR-9 (1.23), DRMR-7 (1.21), DRMR-357 (1.15), DRMR-6 (1.06), PM-26 (1.04), EC-766423 (1.04) and IM-76 (1.01) and these values were generally in the same direction as observed under HSI. Low values for YSI were recorded for the genotypes such as EC-766311 (0.12), EC-399302 (0.12), DRMR-266 (0.13) and IC - 321424 (0.16) *etc.* In case of checks, maximum value for YSI was recorded for PM-26 (1.04) followed by Pusa Agrani (0.67) and NRCDR-2 (0.64) *etc.*

Based on all three indicators, nine tolerant genotypes were identified for heat stress conditions which showed low reduction in yield, low HSI and high YSI than other genotypes under heat stress condition. Best tolerant genotypes were NDRE-4, EC-399300, DRMR-13, DRMR-9, DRMR-7, DRMR-357, DRMR-6, EC-766423 and IM-76. The above results suggested that adequate differences were observed among the mustard germplasm in terms of heat tolerance based on HSI and YSI/HTI. The germplasms with lower values (<1) of HSI are more stable in both the sowing conditions and can be used in developing heat tolerant Indian mustard genotype to maintain yield stability under climate change scenario. These results are in close agreement with the findings of earlier researchers **Sharma *et al.*, (2022), Sandhu *et al.*, (2019), Ram *et al.*, (2017), Sharma and Sardana (2014), Sharma (2014) and Chauhan *et al.*, (2009).**

Table: 4.7.1 Per cent yield change, Heat susceptibility Index (HSI) and Yield stability Index (YSI) of each genotype of Indian mustard

S.No.	Genotypes	% yield change	HSI	YSI	S.No.	Genotypes	% yield change	HSI	% yield change	S.No.	Genotypes	% yield change	HSI	YSI
1	DRMR - 2	54.73	0.98	0.45	31	DRMR -582	44.86	0.81	0.55	61	RC - 1271	80.04	1.44	0.20
2	DRMR - 8	28.79	0.52	0.71	32	DRMR - 610	47.28	0.85	0.53	62	RC - 1270	27.67	0.50	0.72
3	DRMR - 4	57.10	1.03	0.43	33	DRMR - 611	39.75	0.71	0.60	63	RLC - 3	47.42	0.85	0.53
4	DRMR - 5	46.62	0.84	0.53	34	DRMR - 624	50.09	0.90	0.50	64	NC - 37362	39.22	0.71	0.61
5	DRMR - 6	-5.89	-0.11	1.06	35	DRMR - 625	65.41	1.18	0.35	65	NC - 660	52.12	0.94	0.48
6	DRMR - 7	-21.41	-0.38	1.21	36	DRMR - 626	78.49	1.41	0.22	66	CN - 105257	36.85	0.66	0.63
7	DRMR - 9	-23.38	-0.42	1.23	37	DRMR -669	75.52	1.36	0.24	67	CN - 105312	56.47	1.02	0.44
8	DRMR - 11	12.42	0.22	0.88	38	DRMR - 680	33.30	0.60	0.67	68	CN - 105309	52.41	0.94	0.48
9	DRMR - 12	45.32	0.81	0.55	39	DRMR - 683	72.47	1.30	0.28	69	CN - 34005	78.27	1.41	0.22
10	DRMR - 13	-28.27	-0.51	1.28	40	DRMR - 686	48.32	0.87	0.52	70	CN - 113780	10.23	0.18	0.90
11	DRMR - 33	40.13	0.72	0.60	41	DRMR - 689	70.95	1.28	0.29	71	CN - 34008	19.62	0.35	0.80
12	DRMR - 46	61.87	1.11	0.38	42	DRMR - 691	53.31	0.96	0.47	72	CN - 105364	59.97	1.08	0.40
13	DRMR - 48	72.75	1.31	0.27	43	DRMR -692	54.78	0.98	0.45	73	CN - 101813	77.98	1.40	0.22
14	DRMR - 136	62.14	1.12	0.38	44	DRMR - 693	69.89	1.26	0.30	74	CN - 105233	32.66	0.59	0.67
15	DRMR - 137	33.43	0.60	0.67	45	DRMR -710	58.47	1.05	0.42	75	CN - 105379	65.35	1.17	0.35
16	DRMR - 138	76.81	1.38	0.23	46	DRMR - 711	19.59	0.35	0.80	76	AJ - 11	72.62	1.31	0.27
17	DRMR - 264	76.36	1.37	0.24	47	DRMR - 726	43.05	0.77	0.57	77	AJ - 3	34.20	0.61	0.66
18	DRMR - 266	87.16	1.57	0.13	48	DRMR - 731	18.15	0.33	0.82	78	DJ - 5	0.51	0.01	0.99
19	DRMR - 357	-14.80	-0.27	1.15	49	DRMR - 900	79.27	1.43	0.21	79	DJ - 12	50.93	0.92	0.49
20	DRMR - 358	72.81	1.31	0.27	50	DRMR - 906	43.11	0.77	0.57	80	DJ - 65	32.47	0.58	0.68
21	DRMR - 359	73.51	1.32	0.26	51	DRMR - 909	36.66	0.66	0.63	81	RJ - 10	63.09	1.13	0.37
22	DRMR - 360	70.36	1.26	0.30	52	Sitara Sagar	31.67	0.57	0.68	82	DTM - 50	35.32	0.64	0.65
23	DRMR - 361	10.12	0.18	0.90	53	Pusa Bahar	71.29	1.28	0.29	83	PTJ - 3-89	36.80	0.66	0.63
24	DRMR - 362	39.42	0.71	0.61	54	BASANTI	21.01	0.38	0.79	84	PTJ - 3-64	64.90	1.17	0.35
25	DRMR - 364	78.40	1.41	0.22	55	RHUR - 2 -1	28.54	0.51	0.71	85	NPJ - 161	52.41	0.94	0.48
26	DRMR - 574	69.71	1.25	0.30	56	RC -371-1	73.91	1.33	0.26	86	KDM - 49-1	79.92	1.44	0.20
27	DRMR - 576	66.93	1.20	0.33	57	RC -371	52.98	0.95	0.47	87	RB - 60	64.44	1.16	0.36
28	DRMR - 577	56.63	1.02	0.43	58	RC - 132	68.90	1.24	0.31	88	PR - 2001-42	68.40	1.23	0.32
29	DRMR - 578	49.82	0.90	0.50	59	RC - 571	45.97	0.83	0.54	89	EM - 1	80.29	1.44	0.20
30	DRMR - 579	61.22	1.10	0.39	60	RC - 891-1	65.67	1.18	0.34	90	GR-325	78.09	1.40	0.22

S.No.	Genotypes	% yield change	HSI	YSI	S.No.	Genotypes	% yield change	HSI	% yield change	S.No.	Genotypes	% yield change	HSI	YSI
91	IM - 108	55.18	0.99	0.45	130	EC -399300	-46.38	-0.83	1.46	169	EC - 399318	75.53	1.36	0.24
92	IM - 76	-0.50	-0.01	1.01	131	EC -766423	-3.64	-0.07	1.04	170	EC - 399293	74.99	1.35	0.25
93	IM - 152	67.97	1.22	0.32	132	EC -766110	29.25	0.53	0.71	171	EC - 571648	81.61	1.47	0.18
94	IM - 3	45.71	0.82	0.54	133	EC -766234	37.41	0.67	0.63	172	EC - 399308	73.83	1.33	0.26
95	IM - 170	47.40	0.85	0.53	134	EC -766127	72.43	1.30	0.28	173	EC - 399302	87.56	1.57	0.12
96	PBR - 97	16.36	0.29	0.84	135	EC -766134	6.70	0.12	0.93	174	EC - 764501	66.03	1.19	0.34
97	RE - 44	42.73	0.77	0.57	136	EC -766136	78.77	1.42	0.21	175	EC - 766622	53.65	0.96	0.46
98	RGN - 34	66.75	1.20	0.33	137	EC -766141	81.32	1.46	0.19	176	EC - 766325	58.56	1.05	0.41
99	RH - 30	54.41	0.98	0.46	138	EC - 66431	38.42	0.69	0.62	177	EC - 766115	56.39	1.01	0.44
100	NPJ- 113	51.21	0.92	0.49	139	EC -766402	45.73	0.82	0.54	178	EC - 766498	60.14	1.08	0.40
101	RCQR-9901	40.93	0.74	0.59	140	EC -766401	73.26	1.32	0.27	179	EC - 766564	26.78	0.48	0.73
102	RNN - 505	40.32	0.72	0.60	141	EC -766611	42.48	0.76	0.58	180	EC -766489	59.72	1.07	0.40
103	NDRE - 4	-50.92	-0.92	1.51	142	EC -766576	43.55	0.78	0.56	181	EC - 766393	61.72	1.11	0.38
104	I - 79	49.18	0.88	0.51	143	EC -766571	49.15	0.88	0.51	182	EC - 766470	69.60	1.25	0.30
105	PCR - 9403	57.53	1.03	0.42	144	EC -766560	62.11	1.12	0.38	183	EC - 766616	28.69	0.52	0.71
106	PM - 67	77.99	1.40	0.22	145	EC -766391	42.69	0.77	0.57	184	EC - 766594	42.34	0.76	0.58
107	PM -30	68.20	1.23	0.32	146	EC -766381	28.13	0.51	0.72	185	EC - 766555	71.82	1.29	0.28
108	CN -101845	25.26	0.45	0.75	147	EC -766335	79.65	1.43	0.20	186	EC - 766094	75.78	1.36	0.24
109	IC - 122137	68.08	1.22	0.32	148	IC - 766334	49.40	0.89	0.51	187	EC - 766312	69.58	1.25	0.30
110	IC - 11721	53.79	0.97	0.46	149	EC -766322	12.87	0.23	0.87	188	EC -766095	72.31	1.30	0.28
111	IC -206741	27.84	0.50	0.72	150	EC -766311	87.89	1.58	0.12	189	EC - 564649-1	81.76	1.47	0.18
112	IC - 372259	73.96	1.33	0.26	151	EC - 766310	41.51	0.75	0.58	190	EC - 766207	43.96	0.79	0.56
113	IC - 341108	49.46	0.89	0.51	152	EC - 766296	65.03	1.17	0.35	191	EC - 766322	15.88	0.29	0.84
114	IC - 491455	37.93	0.68	0.62	153	EC - 766292	32.06	0.58	0.68	192	IC - 320378	66.46	1.19	0.34
115	IC - 491175	72.81	1.31	0.27	154	EC - 766276	68.07	1.22	0.32	193	IC - 766214	53.05	0.95	0.47
116	IC - 491485	76.39	1.37	0.24	155	EC - 766278	74.94	1.35	0.25	194	IC - 766098	59.52	1.07	0.40
117	IC - 531377	52.74	0.95	0.47	156	EC - 766270	80.88	1.45	0.19	195	IC -766029	64.54	1.16	0.35
118	IC -589676	61.19	1.10	0.39	157	EC - 766234	41.23	0.74	0.59	196	IC - 766614	71.17	1.28	0.29
119	IC - 589683	69.82	1.26	0.30	158	EC - 766211	12.78	0.23	0.87	197	IC - 766129	72.34	1.30	0.28
120	IC - 497904	54.85	0.99	0.45	159	EC - 766207	19.47	0.35	0.81	198	IC - 766299	50.80	0.91	0.49
121	IC - 70302	13.88	0.25	0.86	160	EC - 766557	53.97	0.97	0.46	199	IC - 399318	83.96	1.51	0.16
122	IC - 491348	69.79	1.25	0.30	161	EC - 766124	11.05	0.20	0.89	200	IC - 321424	84.46	1.52	0.16
123	IC - 375924	38.50	0.69	0.62	162	EC - 766060	20.71	0.37	0.79	C 1	NRCHB-01	49.17	1.03	0.51
124	IC - 422156	60.32	1.08	0.40	163	EC -766204	64.25	1.16	0.36	C 2	NRCDR-2	36.48	0.76	0.64
125	IC -422172	37.58	0.68	0.62	164	EC - 766487	34.62	0.62	0.65	C 3	Krishna	69.58	1.45	0.30
126	IC - 481011	39.02	0.70	0.61	165	EC - 766344	39.05	0.70	0.61	C 4	SEJ-2	32.89	0.69	0.67
127	IC - 73225	73.84	1.33	0.26	166	EC - 766200	75.75	1.36	0.24	C 5	PM-25	59.92	1.25	0.40
128	IC - 766313	25.05	0.45	0.75	167	EC - 766069	58.89	1.06	0.41	C 6	PM-26	-4.39	-0.09	1.04
129	IC -766377	73.90	1.33	0.26	168	EC - 766576	42.13	0.76	0.58	C 7	Radhika	51.59	1.08	0.48

4.7.4 Effect of terminal heat stress on agro-morphological and physiological traits

Under present study effect of the terminal heat was observed on various agro-morphological and physiological traits and compared with best checks for various traits. The results of per cent mean change with comparison to checks and mean values of promising genotypes against heat tolerance are presented in **Table: 4.7.2** and **Table: 4.7.3** and the results are discussed below:

4.7.4.1 Days to 50 per cent flowering

Days to 50 per cent flowering was increased by 10.21 % in heat stress condition in comparison to timely sown condition. Thermo-susceptible genotypes took less number of days to attain 50 per cent flowering as compared to thermo-tolerant genotypes. In checks, Radhika took minimum days (56 days) to 50 per cent flowering and increment was 4.63% as compare to timely sown. Among promising genotypes for heat tolerance, the genotype EC-399300 attained 50 per cent flowering in 63.00 days under stress condition and mean per cent change for 50 per cent flowering was 1.61 % due to delayed sowing. This increase in days to 50 per cent flowering is observed by favourable weather condition for vegetative growth (**Table 3.1 and Fig. 3.1**)

4.7.4.2 Days to maturity

The per cent mean reduction in days to maturity due to delayed sowing was 3.46 %. Due to heat stress at reproductive stage, all genotypes were attained maturity earlier than normal sown condition. Best check for days to maturity was Pusa agrani (SEJ-2), it took 112.00 days and reduction per cent was 1.75 %. EC-766423 showed maximum reduction (5.6 %) among promising genotypes for heat tolerance and it attained maturity only in 118.0 days.

4.7.4.3 Plant height (cm)

Plant height was increased under stress by 6.21% under late sowing with respect to timely sowing. Among checks, maximum increment (7.13%) for plant height was found in NRCDR-2 (199.33 cm) due to delayed sowing. Best promising heat tolerant genotype was DRMR-9 (230 cm) and it showed 45.87 % increment in plant height under stress. In general, under heat stress increase in plant height is also associated with less number of secondary branches per plant.

4.7.4.4 Number of primary branches per plant

Number of primary branches per plant was decreased by 1.70 % in late sown as compare to timely sown. In late sown, SEJ-2 found best in among all checks for number of

primary branches per plant (4.5) and reduction per cent was just 1.74 % under stress. Promising genotypes for heat tolerance showed minimum reduction in number of primary branches per plant and it was recorded by the genotype DRMR-357 with only 4.50% reduction due to stress.

4.7.4.5 Number of secondary branches per plant

The per cent mean reduction in late sown condition with respect to timely sown condition for number of secondary branches was 45.53 %. Radhika was found as best check for number of secondary branches per plant (9.33) with only reduction of 11.81 %. DRMR-7 found as best line for number of secondary branches per plant (11.85) among promising genotypes with 18.5% increment in late sown compare to timely sown. The reduction in number of secondary branches leads to reduction in yield per plant as these branches are silique bearing branches.

4.7.4.6 Chlorophyll content

The per cent mean reduction for chlorophyll content in late sown condition was 15.70 % as compare to the timely sown condition. Among all checks, NRCDR-2 showed maximum increment (11.68 %) in chlorophyll content under stress condition. The genotype, EC-766423 found as best genotypes for chlorophyll content (34.72) among all promising genotypes and chlorophyll content increase in late sown was 32.87 %.

4.7.4.7 Leaf area index

Leaf area index decreased under heat stress by 45.58% with respect to normal condition. NRCHB-101 showed less reduction (28.87%) in among all checks with LAI of 1.7 in stress condition. In promising genotypes, maximum increment in leaf area index value was 67.39 % for the genotype EC-766423 with 4.57 leaf area index value in late sown condition.

4.7.4.8 Chlorophyll fluorescence

Delayed sowing decreases the chlorophyll fluorescence by 4.58%. For chlorophyll fluorescence, NRCHB-101, NRCDR-2, Krishna found best check with zero per cent reduction in late sown. Among promising genotypes for heat tolerance, best genotypes was IM-76 (0.75 fv/fm) and increment in chlorophyll fluorescence was 8.69% in late sown condition.

4.7.4.9 Main shoot length (cm)

The per cent mean increment in late sown condition with respect to timely sown condition for main shoot length was 3.10%. In late sown environment, genotype Radhika was found as best check for main shoot length (91.50 cm) with 51.43% increment among all checks. Best genotype in late sown for main shoot length was found DRMR-7 (83.33 cm) with 70.06% increment over best check.

4.7.4.10 Total siliqua per plant

The per cent mean reduction for total siliqua was 31.90% due to heat stress. The genotype, SEJ-2 was found as best check in stress condition for total siliqua per plant (260.00) with minimum reduction of 14.44%. The genotype, EC-399300 with minimum reduction in total siliqua per plant (6.00%) was found promising under late sown and it recorded 328.0 siliqua per plant under stress.

4.7.4.11 Number of siliquae on main shoot

For number of siliquae on main shoot, the per cent mean reduction was 5.24 % under late sown condition. Among all checks, NRCDR-2 was identified as best check for siliqua on main axis (44.83) with 6.30 % increment under late sown condition. Best stress tolerant genotype for number of siliquae on main shoot (43.33) was found NDRE-4 and it recorded 44.00 per cent increment for this trait.

4.7.4.12 Number of seeds per siliqua

Number of seeds per siliqua was reduced to 11.30 % under delayed sowing condition. Best check among all, was PM- 26 (14.55) with minimum reduction of 6.00 % under heat stress condition. The promising genotype, DRMR-13 was found as best tolerant genotypes for seeds per siliqua (13.20) under late sown condition with maximum increment of 9.36 %.

4.7.4.13 Siliqua length (cm)

Reduction in siliqua length was 5.06% under late sown in comparison to the timely sown. Maximum siliqua length was found in NRCDR-2 (4.38 cm) among all checks and increase of 5.79 % was observed in heat stress condition over normal condition. Best tolerant genotype was DRMR-357 (5.07 cm) which shows 36.65 % increment in siliqua under heat stress environment but in general number of seeds per siliqua was not increased with this trait under stress and cause behind may be due to less pollen viability under high temperature at reproductive phase.

4.7.4.14 1000 seed weight (g)

1000 seed weight decreased under late sown by 7.51 %. Among all checks, best check for 1000 seed weight was Krishna (3.47 g) which shows increment of 2.66 % under stress. Maximum increment of 24.44 % for 1000 seed weight was observed under heat stress environment and it was recorded by DRMR-13 (3.92 g) which is identified as potential source to increase 1000 seed weight. **(Table 4.7.2)**

4.7.4.15 Yield per plant (g)

Yield per plant shown the mean reduction of 50.36 % under delayed sowing. Among the checks, PM-26 recorded maximum 6.66 g yield per plant in heat stress condition which is 4.38% higher than the timely sown. Best tolerant genotype in stress condition for yield per plant is NDRE-4 which shows yield increment of 50.79 % and attained the yield of 10.42 g. **(Table 4.7.2)**

Due to heat stress maximum reduction was found for yield per plant 50.36% followed by leaf area index (45.58%), number of secondary branches per plant (45.53%), total siliqua per plant (31.90%), seed per siliqua (11.30%). Based on per cent change in yield per plant, HSI, YSI, per cent change in all characters; nine genotypes were identified as promising one for the heat tolerance. Among Most tolerant genotype was NDRE-4 and best check was PM-26 whereas, most susceptible genotype was EC-766311 among all test genotypes. The heat stress at all crop growth stages obstructs the mustard productivity but it is causing considerable yield losses at reproductive stage. Heat stress during the reproductive stage or grain filling stage affects photosynthate and its translocation and deposition in developing grain, thereby lowering the 1000 seed weight and altering the seed quality, and ultimately affecting the yield. These results are in line with the findings of **Sharma *et al.*, (2022), Mohan *et al.*, (2020), Sandhu *et al.*, (2019), Singh *et al.*, (2014), Sharma and Sardana (2014), Sharma (2014) and Chauhan *et al.*, (2009).**

Table: 4.7.2 Character wise per cent mean change under heat stress at reproductive stage and comparison of promising genotype with check varieties.

S. No.	Trait	Per cent mean change for genotype	Best check	Per cent change for check	Promising genotype	Per cent change for promising genotype	Superiority for promising genotype over best check
1	FW50	-10.21%	Radhika	-4.63%	EC-399300	-1.61%	3.02%
2	DM	3.46%	SEJ-2	1.75%	EC-766423	5.6%	3.85%
3	PH	-6.21%	NRCDR-2	-7.13%	DRMR-9	-45.87%	38.74%
4	PB	1.70%	SEJ-2	1.74%	DRMR-357	4.50%	2.76%
5	SB	45.53%	Radhika	11.81%	DRMR-7	-18.5%	30.31%
6	CC	15.70%	NRCDR-2	-11.68%	EC-766423	-32.87%	21.19%
7	LAI	45.58%	NRCHB-101	28.87%	EC-766423	-67.39%	96.26%
8	FLU	4.58%	NRCHB-101	0%	IM-76	-8.69%	8.69%
9	MAL	-3.10%	Radhika	-51.43%	DRMR-7	-70.06	30.59%
10	TS	31.90%	SEJ-2	14.44%	EC-399300	6%	8.44%
11	SAM	5.24%	NRCDR-2	-6.30%	NDRE-4	-44%	37.7%
12	SSQ	11.30%	PM-26	6.00%	DRMR-13	-9.36%	15.36%
13	SL	-5.06%	NRCDR-2	-5.79%	DRMR-357	-36.65%	30.86%
14	SW	7.51%	Krishna	-2.66%	DRMR-13	-24.44%	21.78%
15	YP	50.36%	PM-26	-4.38%	NDRE-4	-50.79%	46.41%

Table: 4.7.3 Performance of promising Indian mustard genotypes against heat tolerance at reproductive phase.

Traits	Sowing	DRMR-6	DRMR-7	DRMR-9	DRMR-13	DRMR-357	IM-76	NDRE-4	EC-399300	EC-766423
FW50	Timely	58.00	58.00	58.00	61.00	57.00	62.00	68.00	62.00	56.00
	Late	59.00	60.00	59.00	63.00	63.00	68.00	72.00	63.00	64.00
DM	Timely	122.00	122.00	123.00	127.00	125.00	133.00	140.00	133.00	125.00
	Late	119.00	117.00	121.00	123.00	121.00	128.00	135.00	130.00	118.00
PH	Timely	186.33	168.33	157.67	191.00	210.00	217.33	225.67	186.67	185.67
	Late	216.67	235.00	230.00	213.00	217.67	218.33	227.67	218.33	205.00
PB	Timely	5.67	6.33	6.00	8.00	7.33	6.33	7.00	7.67	8.67
	Late	5.00	5.67	5.00	6.00	7.00	5.33	6.33	5.33	7.00
SB	Timely	12.67	10.00	12.00	16.67	17.67	10.00	13.00	13.00	13.67
	Late	13.52	11.85	12.52	17.94	17.99	10.00	13.42	13.52	13.37
CC	Timely	30.40	30.78	30.74	32.60	24.09	24.01	24.45	28.50	26.13
	Late	26.93	28.64	27.67	26.68	22.63	25.35	22.53	28.67	34.72
LAI	Timely	3.63	3.00	2.67	2.10	4.03	3.97	3.90	3.87	2.73
	Late	3.93	3.20	3.20	2.93	3.87	4.27	4.00	4.07	4.57
FLU	Timely	0.75	0.75	0.73	0.75	0.74	0.69	0.69	0.72	0.78
	Late	0.78	0.76	0.76	0.75	0.78	0.75	0.75	0.75	0.82

Table: 4.7.3 Performance of promising Indian mustard genotypes against heat tolerance at reproductive phase.

MAL	Timely	79.00	49.00	61.33	53.33	89.67	74.33	43.00	57.33	56.00
	Late	83.67	83.33	67.67	63.00	85.00	76.67	53.33	68.33	59.67
TS	Timely	269.00	264.00	341.00	345.33	394.00	291.00	262.67	349.67	440.00
	Late	223.33	243.33	319.67	286.67	346.67	250.67	214.33	328.67	376.67
SAM	Timely	41.00	41.67	45.67	39.00	53.67	45.67	30.00	41.00	56.67
	Late	44.67	49.67	45.33	48.00	51.00	48.33	43.33	42.33	55.67
SSQ	Timely	14.67	15.40	13.53	12.07	15.27	15.00	14.53	15.20	15.20
	Late	14.73	15.53	13.57	13.20	14.87	15.80	14.47	15.40	15.00
SL	Timely	3.99	3.59	4.34	3.73	3.71	3.77	3.41	3.45	3.37
	Late	4.86	4.19	4.22	3.63	5.07	3.98	3.59	3.81	3.99
SW	Timely	4.92	4.02	4.46	3.15	4.27	3.17	2.51	2.51	3.58
	Late	5.40	4.29	4.85	3.92	4.22	3.09	2.93	3.05	3.55
YP	Timely	11.82	9.76	7.71	6.19	13.06	9.95	6.91	7.19	12.9
	Late	12.52	11.85	9.52	7.94	14.99	10	10.42	10.52	13.37
HSI		-0.11	-0.38	-0.42	-0.51	-0.27	-0.01	-0.92	-0.83	-0.07
YSI		1.06	1.21	1.23	1.28	1.15	1.01	1.51	1.46	1.04

Chapter 5

SUMMARY AND CONCLUSIONS

The present experiment entitled, “**Characterization of Indian mustard (*Brassica juncea* L.) genotypes for heat tolerance at reproductive stage**” was carried out at Seed and Research Farm, Rani Lakshmi Bai Central Agricultural University (RLBCAU), Jhansi Block D-3, during *rabi*, 2021-2022.

The present study was undertaken with the following objective:

1. To find out genetic variability and diversity in mustard germplasm based on agro-morphological traits,
2. To estimate the nature of association between yield and its attributing traits and direct and indirect effect of various characters on seed yield and,
3. Phenotyping of Indian mustard genotypes to identify heat tolerance under normal and terminal heat stress environments.

The experimental materials consisted of 200 Indian mustard genotypes procured from ICAR-DRMR, Bharatpur and ICAR-NBPGR, New Delhi were used to find out genetic variability, genetic diversity, correlation analysis and path analysis and phenotyping against heat tolerance at reproductive phase. To expose crop against terminal heat stress the sowing delayed (10 December, 2022) and for comparative study for the performance of various genotypes under heat stress normal sowing is also carried out (14 November, 2022). For the identification of promising genotypes against heat tolerance heat susceptibility index and yield stability index is estimated. Under present investigation various quantitative traits like days to 50 percent flowering, days to maturity, plant height, number of primary and secondary branches per plant, chlorophyll content, leaf area index, chlorophyll fluorescence, main shoot length (cm), total silique per plant, number of silique per plant, number of seeds per silique, silique length, 1000 seed weight (g) and yield per plant (g) were recorded and subjected to statistical analysis to derive information on above mentioned objectives.

- ❖ The analysis of variance revealed significant genetic differences were present among Indian mustard genotypes for most of the characters under study. Except, chlorophyll fluorescence and chlorophyll content which shows non-significant differences in both timely and late sown conditions and only in late sown

conditions, respectively. The results suggested existence of adequate amount of variability among the experimental material and hence, a greater scope for improvement of desired characters through selection.

- ❖ A wide range of mean values among the genotypes for different traits under study were observed. The magnitudes of PCV estimates were higher than the corresponding GCV estimates for all the characters, indicating that considerable effect of environment on the performance of genotypes. In both the sowing condition, high PCV and GCV estimates were recorded for the traits like leaf area index, total siliquae per plant and yield per plant. High PCV and GCV for these traits clearly indicate ample scope for yield improvement in mustard under normal and reproductive heat stress also.
- ❖ High heritability with high genetic advance was observed for number of secondary branches per plant, leaf area index, total silique per plant and 1000 seed weight and yield per plant under both timely and late sown condition. Hence, this indicates that these traits are having predominant role of additive gene action and phenotypic selection will be rewarding.
- ❖ In general, genotypic correlation coefficients were greater in values than phenotypic correlation coefficients but nature or trend is same. Results suggested that there was strong genetic association among the characters but the significant influence of environment minimized the phenotypic relationship.
- ❖ The inter-character association at phenotypic and genotypic correlation coefficients suggested that seed yield per plant was positively and significantly correlated with plant height, number of primary branches per plant, number of secondary branches per plant, leaf area index, total number of siliquae per plant, siliquae on main shoot and 1000- seed weight under both normal and late sown conditions indicating that these traits are less influenced by the environment and an increase in any of these component traits will result in the increase of seed yield per plant.
- ❖ Path coefficient study suggested that high direct effects on seed yield were exerted by plant height, chlorophyll content, main shoot length and silique length without the influence of the sowing period. That clearly explains the true genetic relationship between these traits and direct selection through these traits will be rewarding to improve seed yield.

- ❖ Genetic divergence study based on Mahalanobis D^2 statistic revealed that the entire 200 genotypes used under study are grouped into six different clusters in each environment. Under timely sown condition, Cluster I was found largest cluster which included 73 genotypes followed by Cluster III and cluster VI (40 genotypes), cluster V (31 genotypes), cluster III (28 genotypes), cluster II (22 genotypes) and cluster IV (13 genotypes). Whereas, in late sown condition maximum numbers of genotypes were in cluster III (80 genotypes), followed by cluster I (57 genotypes), cluster IV (45 genotypes), cluster II (18 genotypes), cluster IV (6 genotypes) and cluster V (1 genotype), which is minimum.
- ❖ In timely sown condition, the maximum inter-cluster distance was exhibited by the cluster III and IV (11.53) whereas, minimum distance was observed between cluster III and VI (9.18). Under late sown condition, the maximum inter cluster distance was found between cluster II and VI (13.01) followed by cluster III and VI (12.55), cluster I and VI (11.95) and cluster I and III (11.44). If the genotypes from these clusters are crossed the sufficient genetic variability for various traits can be generated including heat tolerance.
- ❖ An overview of cluster mean results revealed that cluster V included most of the genotypes which were promising under both the environment for most of the yield component traits like total silique per plant, number of siliqua on main shoot and seed weight and these genotypes can be used as donors in breeding high yielding varieties. Genotypes under cluster V are also having high values for number of secondary branches per plant in both the situation that also had positive correlation with seed yield per plant.
- ❖ For the objective of phenotyping for heat tolerance, based on the results of heat susceptibility index, yield stability index and percent yield change parameters genotypes, NDRE-4, EC-399300, DRMR-13, DRMR-9, DRMR-7, DRMR-357, DRMR-6, EC-766423 and IM-76 were found promising for heat tolerance at reproductive stage in Indian mustard.

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Appendix:I- Mean values of 200 Indian mustard genotypes along with seven checks under timely and late sown conditions

S. No.	Accessions No.	FW50		DM		PH		PB		SB		CC		LAI	
		T	L	T	L	T	L	T	L	T	L	T	L	T	L
1.	DRMR - 2	57.00	64.00	118.00	113.00	165.33	200.33	5.67	4.33	11.33	5.17	31.67	18.74	1.93	1.93
2.	DRMR - 8	59.00	65.00	121.00	115.00	138.33	201.00	9.00	8.33	16.00	6.29	31.75	20.34	2.50	2.23
3.	DRMR - 4	60.00	66.00	125.00	120.00	185.67	215.00	5.33	7.00	8.67	4.53	30.88	20.57	2.47	2.50
4.	DRMR - 5	56.00	60.00	119.00	118.00	168.33	204.00	6.00	5.00	13.67	4.92	28.25	20.41	2.83	2.67
5.	DRMR - 6	58.00	59.00	122.00	119.00	186.33	216.67	5.67	5.00	12.67	13.52	30.40	26.93	3.63	3.93
6.	DRMR - 7	58.00	60.00	122.00	117.00	168.33	235.00	6.33	5.67	10.00	11.85	30.78	28.64	3.00	3.20
7.	DRMR - 9	58.00	59.00	123.00	121.00	157.67	230.00	6.00	5.00	12.00	12.52	30.74	27.67	2.67	3.20
8.	DRMR - 11	61.00	65.00	126.00	122.00	201.33	232.00	4.67	6.33	9.33	7.92	32.64	23.35	3.47	2.40
9.	DRMR - 12	58.00	65.00	124.00	118.00	189.33	231.33	7.00	6.00	12.67	8.61	31.96	20.69	2.57	1.97
10.	DRMR - 13	61.00	63.00	127.00	123.00	191.00	213.00	8.00	6.00	16.67	17.94	32.60	26.68	2.10	2.93
11.	DRMR - 33	58.00	60.00	123.00	120.00	165.33	224.67	4.00	5.67	8.67	5.93	31.40	16.74	3.57	2.10
12.	DRMR - 46	57.00	59.00	121.00	119.00	188.67	194.00	10.0	5.67	23.00	5.23	30.38	23.23	2.90	1.93
13.	DRMR - 48	59.00	63.00	124.00	118.00	160.67	195.00	7.33	4.67	14.00	4.39	31.93	20.84	3.27	1.80
14.	DRMR - 136	53.00	62.00	118.00	117.00	199.00	217.33	6.67	4.00	15.33	7.05	27.42	18.77	4.90	2.10
15.	DRMR - 137	59.00	65.00	126.00	118.00	209.67	211.67	7.67	6.33	16.33	10.99	19.32	17.84	4.23	2.60
16.	DRMR - 138	59.00	63.00	125.00	122.00	203.67	212.00	5.00	6.33	7.33	3.72	19.01	17.72	3.73	2.93
17.	DRMR - 264	56.00	64.00	123.00	117.00	211.33	221.33	6.00	8.33	15.00	3.84	23.58	19.89	4.30	2.23
18.	DRMR - 266	52.00	60.00	118.00	116.00	207.33	209.67	6.67	7.67	14.33	3.32	28.92	22.64	3.87	1.87
19.	DRMR - 357	57.00	63.00	125.00	121.00	210.00	217.67	7.33	7.00	17.67	17.99	24.09	22.63	4.03	3.87
20.	DRMR - 358	57.00	61.00	126.00	122.00	220.67	219.00	8.67	6.33	20.00	4.92	23.84	20.60	2.97	2.07
21.	DRMR - 359	58.00	64.00	128.00	124.00	205.67	215.67	7.67	6.00	16.33	5.40	23.69	22.39	4.53	1.77
22.	DRMR - 360	56.00	62.00	125.00	120.00	233.33	248.33	7.00	6.67	15.00	5.90	24.64	20.50	5.17	1.40
23.	DRMR - 361	56.00	63.00	124.00	121.00	185.33	225.33	5.00	7.00	10.67	9.41	25.69	22.60	4.13	2.17
24.	DRMR - 362	61.00	66.00	131.00	123.00	185.00	237.67	7.00	5.67	16.33	7.28	25.29	23.94	3.87	2.07
25.	DRMR - 364	58.00	64.00	127.00	124.00	195.00	216.00	8.00	6.00	19.33	5.23	27.46	20.02	3.90	1.70
26.	DRMR - 574	55.00	59.00	125.00	122.00	221.33	225.33	6.33	5.67	16.67	7.57	26.34	16.93	4.33	2.07
27.	DRMR - 576	56.00	59.00	125.00	122.00	206.33	232.67	5.67	6.33	14.33	7.57	26.96	22.57	4.93	2.10
28.	DRMR - 577	53.00	56.00	121.00	117.00	190.00	205.67	7.00	4.67	14.67	8.06	24.91	18.61	5.17	1.87
29.	DRMR - 578	51.00	57.00	119.00	115.00	178.67	200.00	5.67	4.67	12.00	7.32	26.00	19.50	3.50	2.50
30.	DRMR - 579	54.00	58.00	121.00	120.00	209.00	230.67	7.67	4.33	9.67	8.14	23.68	20.09	3.77	1.53
31.	DRMR -582	56.00	64.00	124.00	120.00	213.00	237.00	6.67	6.00	12.67	9.00	21.43	20.98	2.30	1.10
32.	DRMR - 610	47.00	54.00	116.00	114.00	164.67	210.00	8.00	5.33	13.67	7.89	24.52	20.30	2.27	1.70
33.	DRMR - 611	48.00	55.00	118.00	115.00	189.67	209.00	5.67	5.67	9.33	8.91	26.16	20.09	3.13	2.07
34.	DRMR - 624	48.00	54.00	117.00	114.00	186.00	217.00	7.33	6.00	16.33	10.53	22.19	17.48	3.80	2.27
35.	DRMR - 625	48.00	53.00	119.00	115.00	188.00	195.33	6.67	4.67	14.67	4.98	24.85	19.29	2.73	1.37
36.	DRMR - 626	56.00	57.00	126.00	122.00	193.33	193.33	8.67	4.67	17.67	4.64	22.29	17.59	3.47	2.43
37.	DRMR -669	56.00	64.00	125.00	119.00	201.67	229.67	7.67	4.67	15.00	5.59	22.42	21.09	3.43	1.47
38.	DRMR - 680	56.00	62.00	124.00	120.00	204.00	209.67	6.00	5.33	12.67	10.32	20.26	18.95	3.33	1.83
39.	DRMR - 683	60.00	58.00	131.00	124.00	214.33	214.00	6.67	5.33	11.33	6.49	20.60	17.69	4.13	1.17

40.	DRMR - 686	53.00	62.00	122.00	121.00	217.33	208.67	7.67	6.33	13.33	10.80	23.75	22.86	5.13	2.00
41.	DRMR - 689	55.00	64.00	126.00	122.00	210.33	216.00	7.33	5.33	12.33	6.54	23.66	22.31	3.17	1.40
42.	DRMR - 691	54.00	58.00	125.00	120.00	217.67	214.67	6.33	5.00	9.00	8.45	26.99	23.62	3.13	1.77
43.	DRMR -692	55.00	68.00	125.00	123.00	232.33	239.00	7.33	6.00	12.67	8.32	22.37	20.68	3.83	1.57
44.	DRMR - 693	56.00	64.00	127.00	122.00	222.00	216.00	12.33	4.67	18.00	6.18	20.84	15.41	2.60	1.53
45.	DRMR -710	56.00	65.00	126.00	120.00	209.67	214.67	7.00	7.33	12.00	6.79	25.64	24.09	3.67	1.23
46.	DRMR - 711	62.00	65.00	132.00	128.00	214.67	236.67	8.00	7.00	16.00	8.81	21.19	21.52	3.07	3.03
47.	DRMR - 726	64.00	68.00	133.00	128.00	225.33	239.00	8.67	9.00	11.33	10.07	20.18	19.42	2.53	3.33
48.	DRMR - 731	62.00	64.00	133.00	126.00	225.00	241.67	8.33	10.0	13.00	12.96	18.31	21.06	2.20	3.03
49.	DRMR - 900	56.00	58.00	129.00	125.00	209.33	227.67	8.33	5.00	16.67	4.62	23.90	25.19	2.80	1.77
50.	DRMR - 906	53.00	55.00	126.00	123.00	192.33	206.67	5.67	5.67	10.67	8.52	20.02	20.97	2.03	1.97
51.	DRMR - 909	53.00	53.00	127.00	124.00	216.33	234.67	8.33	6.33	19.00	11.39	24.38	26.49	1.20	1.93
52.	Sitara Sagar	63.00	65.00	131.00	127.00	203.33	206.67	8.33	6.67	14.00	13.40	22.91	20.33	4.30	1.33
53.	PUSA BAHAR	61.00	67.00	130.00	126.00	185.67	188.67	6.00	3.33	8.33	4.51	24.59	22.91	4.67	2.20
54.	BASANTI	66.00	68.00	134.00	129.00	192.00	205.00	6.00	6.33	11.00	10.68	22.47	24.50	4.60	1.67
55.	RHUR - 2 -1	62.00	66.00	131.00	127.00	191.67	213.33	5.67	8.33	11.00	10.49	23.92	22.31	4.63	2.83
56.	RC -371-1	63.00	69.00	133.00	127.00	210.33	198.67	10.00	4.33	14.00	4.50	24.97	20.48	3.97	3.10
57.	RC -371	57.00	67.00	125.00	120.00	192.33	192.00	6.33	6.00	10.33	5.96	23.85	21.06	4.10	2.63
58.	RC - 132	60.00	67.00	128.00	122.00	223.67	191.67	8.33	8.00	11.33	4.56	24.42	18.50	3.87	2.53
59.	RC - 571	57.00	65.00	124.00	118.00	211.33	205.00	5.67	6.00	10.33	6.88	23.55	21.52	4.07	3.57
60.	RC - 891-1	59.00	67.00	128.00	119.00	225.00	224.67	6.00	5.00	9.33	6.81	22.22	17.26	4.13	2.00
61.	RC - 1271	51.00	57.00	120.00	116.00	184.67	210.00	6.33	4.33	11.00	3.81	23.94	22.01	2.80	1.50
62.	RC - 1270	51.00	56.00	121.00	117.00	163.33	190.67	5.00	4.00	8.33	4.57	26.55	23.13	2.93	1.60
63.	RLC - 3	51.00	57.00	119.00	116.00	182.00	216.00	6.33	5.33	11.33	7.17	22.50	17.32	3.13	1.07
64.	NC - 37362	50.00	61.00	119.00	115.00	205.33	224.33	6.00	8.00	12.00	10.84	29.86	21.01	3.20	1.03
65.	NC - 660	58.00	62.00	127.00	124.00	198.67	224.33	5.33	6.00	9.00	7.74	20.76	18.84	3.97	1.43
66.	CN - 105257	64.00	71.00	133.00	125.00	197.00	232.00	6.00	6.67	10.67	5.25	19.94	20.12	4.17	0.63
67.	CN - 105312	59.00	66.00	126.00	120.00	211.67	221.67	6.67	5.00	9.00	5.02	18.77	21.10	4.40	1.03
68.	CN - 105309	56.00	60.00	122.00	117.00	216.67	219.33	5.33	4.00	9.00	6.80	18.49	21.19	4.73	0.77
69.	CN - 34005	57.00	66.00	124.00	116.00	220.67	218.67	5.67	4.67	6.67	2.89	19.05	19.86	4.90	1.33
70.	CN - 113780	56.00	60.00	123.00	120.00	223.33	225.00	4.67	4.00	7.33	4.74	18.13	17.14	4.83	0.87
71.	CN - 34008	56.00	55.00	123.00	119.00	219.00	236.33	4.33	6.33	10.00	9.06	19.66	20.75	3.63	0.70
72.	CN - 105364	59.00	67.00	126.00	120.00	203.33	200.67	6.00	5.33	15.67	6.38	22.25	16.38	4.47	1.07
73.	CN - 101813	53.00	59.00	122.00	118.00	203.33	208.33	5.67	4.33	12.33	5.78	24.23	13.52	4.17	0.83
74.	CN - 105233	56.00	60.00	126.00	123.00	216.67	200.33	5.00	4.67	10.67	7.69	23.91	19.80	4.23	1.53
75.	CN - 105379	57.00	65.00	128.00	123.00	210.67	221.00	6.67	6.67	13.67	9.91	23.42	22.19	4.33	1.27
76.	AJ - 11	57.00	67.00	127.00	122.00	205.67	228.67	6.67	7.67	13.67	4.77	22.71	16.00	4.60	1.10
77.	AJ - 3	56.00	67.00	125.00	120.00	216.67	233.67	5.00	7.00	11.67	11.28	19.39	21.47	3.77	0.97
78.	DJ - 5	62.00	63.00	133.00	129.00	213.67	237.67	5.00	8.67	10.00	8.45	20.46	22.18	4.73	0.73
79.	DJ - 12	54.00	65.00	123.00	118.00	206.33	230.33	6.00	5.00	11.67	8.11	22.95	20.53	4.93	0.47
80.	DJ - 65	54.00	58.00	124.00	121.00	192.00	220.67	5.33	4.33	10.00	9.93	20.47	17.25	5.03	1.33
81.	RJ - 10	56.00	62.00	125.00	120.00	209.67	230.33	7.00	6.00	12.67	7.15	20.47	21.42	5.07	2.73
82.	DTM - 50	64.00	71.00	136.00	129.00	216.33	215.00	8.33	6.33	13.00	6.07	20.61	23.38	4.60	1.83

83.	PTJ - 3-89	54.00	62.00	127.00	121.00	212.67	228.67	5.67	6.00	15.00	8.17	21.98	15.31	5.73	1.77
84.	PTJ - 3-64	64.00	68.00	135.00	130.00	213.67	205.00	5.00	4.00	13.33	4.57	21.18	22.31	5.60	1.63
85.	NPJ - 161	54.00	65.00	126.00	124.00	208.00	211.00	5.00	5.00	10.00	5.36	26.55	22.55	5.27	1.40
86.	KDM - 49-1	63.00	69.00	134.00	129.00	218.33	209.67	5.00	4.00	9.00	2.12	21.46	22.62	4.40	1.50
87.	RB - 60	57.00	65.00	127.00	122.00	213.33	214.00	5.33	4.67	16.33	6.25	23.76	17.53	4.47	1.57
88.	PR - 2001-42	57.00	66.00	126.00	123.00	213.00	201.33	9.00	5.67	15.33	5.42	20.02	17.41	4.27	1.37
89.	EM - 1	59.00	66.00	129.00	123.00	231.00	200.00	4.33	4.33	6.67	2.97	21.53	19.21	4.83	1.53
90.	GR - 325	56.00	69.00	124.00	118.00	234.00	221.33	6.00	4.67	12.33	3.40	20.78	21.28	4.20	1.53
91.	IM - 108	52.00	56.00	122.00	117.00	186.67	193.00	5.67	3.33	13.33	6.30	21.92	14.83	3.73	2.03
92.	IM - 76	62.00	68.00	133.00	128.00	217.33	218.33	6.33	5.33	10.00	10.00	24.01	25.35	3.97	4.27
93.	IM - 152	63.00	69.00	135.00	129.00	259.00	220.33	8.00	6.00	13.67	7.50	19.88	19.79	4.10	2.30
94.	IM - 3	53.00	63.00	124.00	118.00	230.00	225.33	4.67	4.67	13.33	8.78	24.42	19.27	4.23	1.83
95.	IM - 170	57.00	67.00	129.00	123.00	224.33	217.33	5.33	5.00	14.00	8.13	20.15	23.94	3.67	1.37
96.	PBR - 97	58.00	68.00	131.00	125.00	241.67	227.00	5.33	6.00	12.00	9.35	19.16	24.91	3.93	1.97
97.	RE - 44	49.00	44.00	118.00	115.00	191.33	198.67	4.67	3.67	9.00	5.63	20.92	21.59	3.57	1.50
98.	RGN - 34	49.00	45.00	119.00	116.00	219.33	213.33	7.00	4.67	15.00	6.31	23.99	18.81	4.17	1.73
99.	RH - 30	56.00	63.00	127.00	122.00	207.67	207.67	5.67	5.00	14.00	6.30	20.25	27.09	4.97	1.33
100.	NPJ- 113	57.00	59.00	128.00	124.00	204.67	204.33	5.00	4.33	6.00	5.09	21.86	21.53	5.07	2.37
101.	RCQR-9901	62.00	70.00	135.00	130.00	221.00	222.67	4.67	4.33	10.00	8.26	20.27	22.34	4.80	2.57
102.	RNN - 505	63.00	68.00	136.00	131.00	218.33	212.00	5.67	4.67	13.33	6.30	19.06	24.45	4.40	3.30
103.	NDRE - 4	68.00	72.00	140.00	135.00	225.67	227.67	7.00	6.33	13.00	13.42	24.45	22.53	3.90	4.00
104.	I - 79	49.00	56.00	119.00	114.00	205.67	180.00	6.67	5.33	12.00	6.27	23.54	21.37	4.60	1.87
105.	PCR - 9403	56.00	62.00	126.00	123.00	210.33	183.00	5.67	6.00	13.67	6.17	21.10	23.79	4.20	1.93
106.	PM - 67	63.00	68.00	134.00	130.00	204.33	212.33	5.67	4.33	15.00	3.96	18.63	18.13	3.90	1.53
107.	PM -30	57.00	62.00	126.00	123.00	187.33	205.67	4.67	3.33	12.00	3.79	21.18	21.52	4.50	1.37
108.	CN -101845	53.00	59.00	123.00	119.00	190.00	211.67	5.67	4.67	14.67	5.69	22.68	21.00	4.47	1.67
109.	IC - 122137	52.00	58.00	121.00	117.00	182.00	211.00	6.00	5.00	17.00	5.98	25.30	29.27	4.50	1.70
110.	IC - 11721	63.00	69.00	133.00	129.00	216.33	230.00	9.33	6.67	16.67	6.34	21.09	29.23	4.80	1.53
111.	IC -206741	68.00	71.00	137.00	132.00	241.67	208.00	8.33	5.33	11.67	4.72	23.11	25.82	4.67	2.80
112.	IC - 372259	70.00	73.00	139.00	136.00	184.00	182.67	4.67	6.33	8.67	4.48	25.32	23.82	4.50	2.03
113.	IC - 341108	52.00	55.00	122.00	119.00	193.33	177.00	7.00	6.67	15.00	3.91	26.38	19.57	4.30	1.27
114.	IC - 491455	62.00	69.00	134.00	129.00	238.00	241.33	8.33	5.00	14.33	8.53	20.55	26.60	5.10	1.77
115.	IC - 491175	62.00	61.00	134.00	126.00	201.33	212.00	5.00	4.00	8.67	4.99	21.16	17.68	5.03	1.23
116.	IC - 491485	63.00	63.00	136.00	133.00	201.33	203.00	9.33	4.33	14.00	4.81	19.69	21.25	4.73	1.13
117.	IC - 531377	54.00	58.00	125.00	120.00	203.33	171.67	9.33	5.67	15.33	7.60	24.14	20.12	4.20	1.83
118.	IC -589676	58.00	67.00	128.00	123.00	208.00	219.33	7.67	6.33	15.67	8.19	25.17	23.09	3.87	1.13
119.	IC - 589683	53.00	57.00	124.00	121.00	199.00	195.67	6.67	5.33	14.00	5.82	25.23	17.06	4.30	1.00
120.	IC - 497904	57.00	56.00	126.00	123.00	191.00	191.67	5.33	5.33	12.67	7.16	22.86	11.13	4.60	1.53
121.	IC - 70302	47.00	53.00	117.00	114.00	166.33	201.67	4.67	6.33	11.67	7.26	25.02	20.41	3.83	1.93
122.	IC - 491348	59.00	63.00	129.00	126.00	224.67	224.33	8.67	4.67	17.67	4.85	21.87	22.56	4.50	1.03
123.	IC - 375924	56.00	59.00	126.00	122.00	189.00	203.33	5.00	4.67	12.33	6.97	24.62	21.29	3.90	1.83
124.	IC - 422156	55.00	58.00	124.00	121.00	192.67	203.67	5.33	4.67	12.67	6.21	27.23	24.48	4.00	2.83
125.	IC -422172	56.00	58.00	125.00	122.00	175.33	204.33	6.33	5.67	15.67	9.41	28.15	28.85	3.83	2.67

126.	IC - 481011	57.00	61.00	125.00	120.00	194.33	219.33	10.33	8.00	16.33	9.70	24.82	25.67	3.83	2.67
127.	IC - 73225	48.00	53.00	117.00	120.00	199.33	212.67	6.67	5.00	17.00	8.52	28.04	23.12	3.37	1.97
128.	IC - 766313	48.00	53.00	118.00	120.00	177.00	198.33	6.00	8.33	17.33	3.72	24.42	15.89	4.00	4.43
129.	IC -766377	57.00	63.00	124.00	122.00	192.00	182.33	6.00	5.00	14.67	4.41	30.68	26.91	4.00	4.37
130.	EC -399300	62.00	63.00	133.00	130.00	186.67	218.33	7.67	5.33	13.00	13.52	28.50	28.67	3.87	4.07
131.	EC -766423	56.00	64.00	125.00	118.00	185.67	205.00	8.67	7.00	13.67	13.37	26.13	34.72	2.73	4.57
132.	EC -766110	49.00	55.00	119.00	114.00	187.00	211.00	8.67	7.33	15.00	10.02	26.20	22.04	3.43	3.10
133.	EC -766234	56.00	67.00	124.00	119.00	192.67	231.67	6.33	4.67	12.33	4.13	24.90	21.26	3.47	2.33
134.	EC -766127	48.00	52.00	117.00	113.00	176.67	226.33	5.00	6.33	12.33	5.01	22.63	18.51	4.03	2.07
135.	EC -766134	47.00	53.00	117.00	113.00	172.33	212.67	4.67	8.00	14.33	6.83	25.99	25.52	3.77	4.03
136.	EC -766136	47.00	52.00	116.00	112.00	185.00	207.33	5.00	8.33	14.33	2.86	26.29	14.81	3.33	4.07
137.	EC -766141	51.00	52.00	120.00	118.00	167.00	206.33	4.67	7.00	12.67	2.03	26.09	19.89	2.13	4.23
138.	EC - 66431	57.00	54.00	125.00	123.00	179.33	214.33	4.00	6.67	8.00	7.27	16.88	19.28	1.70	2.50
139.	EC -766402	56.00	64.00	125.00	119.00	169.33	173.33	4.33	5.00	10.67	4.11	28.72	20.02	2.73	0.83
140.	EC -766401	56.00	63.00	126.00	123.00	201.00	192.33	3.67	6.33	11.33	3.87	24.09	20.45	2.57	0.73
141.	EC -766611	57.00	64.00	126.00	122.00	205.00	222.33	5.67	6.67	12.33	8.70	18.88	18.48	3.03	1.60
142.	EC -766576	58.00	61.00	127.00	125.00	212.33	197.67	4.33	5.67	5.33	4.44	21.23	19.59	3.27	1.97
143.	EC -766571	57.00	62.00	126.00	122.00	213.67	212.00	7.00	6.33	10.33	7.75	26.91	17.28	2.13	0.53
144.	EC -766560	58.00	63.00	125.00	121.00	194.67	187.00	4.67	5.33	13.00	4.13	19.95	16.07	3.07	0.27
145.	EC -766391	56.00	68.00	125.00	119.00	189.67	184.67	5.33	7.33	4.33	3.98	25.68	26.94	3.17	0.67
146.	EC -766381	57.00	62.00	125.00	121.00	197.00	189.67	7.33	8.00	12.00	6.15	23.45	21.37	3.00	1.20
147.	EC -766335	66.00	70.00	132.00	129.00	206.00	183.00	4.67	6.33	10.00	4.35	20.28	16.75	3.27	0.47
148.	IC - 766334	65.00	69.00	130.00	127.00	215.00	194.33	8.67	10.3	13.33	3.07	23.64	14.50	2.90	1.33
149.	EC -766322	60.00	65.00	128.00	124.00	205.00	201.00	5.00	5.67	11.00	9.03	19.68	17.32	3.53	1.00
150.	EC -766311	56.00	71.00	124.00	121.00	217.00	180.33	7.00	6.33	11.67	2.14	20.47	11.48	2.97	1.20
151.	EC - 766310	56.00	64.00	126.00	122.00	209.00	209.00	6.67	8.33	9.00	8.58	22.47	22.36	3.57	0.30
152.	EC - 766296	56.00	65.00	128.00	123.00	218.00	211.00	3.67	4.33	11.67	4.81	23.16	16.74	3.57	0.90
153.	EC - 766292	56.00	64.00	126.00	123.00	173.33	214.67	3.33	4.67	7.00	5.44	19.94	15.34	3.33	0.83
154.	EC - 766276	58.00	65.00	129.00	124.00	192.67	205.67	3.67	4.67	9.33	4.51	24.78	11.21	3.50	0.60
155.	EC - 766278	58.00	66.00	123.00	118.00	207.67	224.33	4.33	3.67	9.67	2.81	20.46	17.68	2.67	1.57
156.	EC - 766270	56.00	69.00	127.00	121.00	202.00	188.67	4.00	8.33	8.33	2.34	20.90	16.56	3.47	0.83
157.	EC - 766234	65.00	68.00	131.00	127.00	221.33	246.67	5.33	6.33	12.67	4.89	18.87	12.43	4.03	0.87
158.	EC - 766211	64.00	65.00	133.00	129.00	211.00	240.00	4.00	5.33	8.33	6.71	22.87	12.59	3.27	0.47
159.	EC - 766207	56.00	63.00	124.00	121.00	191.33	233.67	5.00	5.00	11.33	7.73	19.87	13.00	2.20	1.77
160.	EC - 766557	56.00	63.00	128.00	123.00	202.67	218.67	5.33	4.67	10.67	4.64	21.16	11.01	2.47	1.63
161.	EC - 766124	47.00	54.00	122.00	117.00	191.33	223.00	4.33	7.67	14.33	9.07	18.56	10.14	2.23	1.83
162.	EC - 766060	58.00	68.00	125.00	119.00	198.33	211.00	5.33	5.33	5.00	4.67	20.02	13.71	2.00	1.63
163.	EC -766204	56.00	58.00	127.00	117.00	182.33	249.00	5.67	5.33	10.67	5.34	20.36	11.95	1.73	1.37
164.	EC - 766487	62.00	68.00	135.00	128.00	210.33	141.67	5.00	9.00	10.00	5.92	22.06	12.94	1.97	1.30
165.	EC - 766344	58.00	64.00	130.00	126.00	208.33	224.67	3.67	7.33	10.00	5.87	19.04	16.81	3.03	1.13
166.	EC - 766200	58.00	63.00	129.00	126.00	199.00	218.00	4.33	6.00	12.00	3.93	21.71	10.00	3.07	1.50
167.	EC - 766069	62.00	66.00	132.00	127.00	207.67	219.00	4.67	5.33	8.67	3.27	23.07	10.93	3.63	1.27
168.	EC - 766576	57.00	60.00	124.00	120.00	199.00	218.33	4.00	4.33	7.33	4.78	22.62	17.29	4.30	1.20

169.	EC - 399318	57.00	65.00	126.00	120.00	221.33	201.33	4.33	3.33	12.67	6.37	26.71	24.15	3.77	1.30
170.	EC - 399293	55.00	59.00	125.00	121.00	210.00	209.67	5.33	4.67	13.67	5.11	20.02	25.50	2.87	1.60
171.	EC - 571648	55.00	66.00	125.00	117.00	213.67	200.33	6.33	3.67	14.00	3.30	26.87	17.66	3.73	1.60
172.	EC - 399308	56.00	65.00	126.00	123.00	209.00	196.67	4.67	5.33	9.33	3.81	27.98	19.02	3.97	1.50
173.	EC - 399302	63.00	69.00	134.00	128.00	223.33	202.33	4.67	5.33	11.67	2.53	22.71	16.03	3.03	1.40
174.	EC - 764501	58.00	65.00	128.00	122.00	214.33	226.33	4.33	5.00	11.33	4.78	21.92	25.07	3.17	1.20
175.	EC - 766622	56.00	66.00	125.00	120.00	182.67	223.00	3.67	6.33	11.00	6.13	25.70	15.57	2.90	1.17
176.	EC - 766325	61.00	68.00	128.00	123.00	194.67	213.67	6.00	7.00	12.00	4.91	21.91	13.62	2.43	1.63
177.	EC - 766115	57.00	64.00	129.00	124.00	183.67	205.67	5.00	5.00	11.67	5.00	22.07	16.39	2.77	1.80
178.	EC - 766498	56.00	65.00	124.00	120.00	188.00	194.00	5.00	4.33	13.00	4.51	24.37	13.53	2.47	1.70
179.	EC - 766564	48.00	55.00	121.00	118.00	179.33	206.33	5.00	5.67	8.33	3.56	23.69	14.46	2.60	1.53
180.	EC - 766489	51.00	63.00	123.00	117.00	172.33	221.67	4.67	5.33	14.00	3.61	23.03	15.21	2.47	1.90
181.	EC - 766393	57.00	64.00	124.00	119.00	193.00	215.00	5.00	4.33	12.67	4.55	22.02	17.77	2.27	1.67
182.	EC - 766470	54.00	66.00	126.00	122.00	216.33	228.67	5.00	6.67	14.33	2.77	21.92	17.09	2.13	1.57
183.	EC - 766616	56.00	64.00	124.00	119.00	200.33	232.00	5.67	7.00	11.67	8.68	23.89	20.23	2.87	2.00
184.	EC - 766594	56.00	61.00	125.00	123.00	200.33	221.00	5.67	8.00	11.33	5.81	22.55	12.98	2.80	1.90
185.	EC - 766555	58.00	68.00	128.00	121.00	179.00	226.00	4.33	5.33	10.67	4.06	22.09	17.00	2.80	1.57
186.	EC - 766094	48.00	59.00	120.00	115.00	187.33	201.33	6.00	6.33	8.33	3.98	22.31	10.80	2.43	1.33
187.	EC - 766312	47.00	56.00	126.00	120.00	188.33	194.67	5.33	4.67	12.33	3.31	23.16	11.66	2.67	1.43
188.	EC - 766095	49.00	54.00	124.00	119.00	191.33	203.67	4.33	4.67	7.33	3.97	21.28	12.79	2.80	1.43
189.	EC - 564649-1	50.00	58.00	124.00	119.00	215.00	183.67	4.67	4.33	13.33	2.73	26.33	17.01	2.80	1.37
190.	EC - 766207	57.00	59.00	123.00	119.00	192.00	208.67	3.67	5.33	10.00	4.62	42.61	17.49	3.03	1.33
191.	EC - 766322	58.00	64.00	124.00	118.00	181.67	223.00	5.67	4.33	10.33	4.94	17.90	17.07	3.00	1.33
192.	IC - 320378	61.00	68.00	129.00	123.00	174.67	225.00	6.67	5.00	12.00	3.28	23.12	18.09	1.80	1.73
193.	IC - 766214	56.00	65.00	124.00	118.00	202.67	217.33	5.00	4.00	9.00	4.41	22.64	12.65	2.73	1.73
194.	IC - 766098	50.00	58.00	125.00	120.00	175.33	203.67	4.33	4.67	9.67	3.91	24.11	12.62	2.47	1.50
195.	IC - 766029	57.00	61.00	126.00	121.00	193.33	203.33	4.67	5.33	15.00	6.23	26.08	17.85	3.13	1.07
196.	IC - 766614	59.00	64.00	128.00	122.00	210.33	214.33	6.67	5.33	11.33	4.40	23.61	14.75	2.97	0.93
197.	IC - 766129	56.00	54.00	127.00	123.00	214.33	178.67	6.33	5.33	16.00	6.19	27.97	11.65	2.93	0.83
198.	IC - 766299	58.00	64.00	128.00	122.00	211.67	213.33	5.67	5.00	16.67	8.84	30.71	19.87	2.60	0.70
199.	IC - 399318	61.00	67.00	134.00	133.00	234.67	213.67	6.33	4.67	16.67	4.25	26.18	22.14	2.10	1.33
200.	IC - 321424	57.00	59.00	125.00	121.00	203.00	201.33	4.00	4.33	14.33	4.82	33.90	19.08	2.70	1.27
	Min.	47.00	44.00	116.00	112.00	138.33	141.60	3.33	3.30	4.33	2.02	16.88	10.00	1.20	0.26
	Max.	70.00	73.00	140.00	136.00	259.00	249.00	12.33	10.3	23.00	17.9	42.61	34.70	5.70	4.50
	Mean	56.65	62.30	125.94	121.50	201.17	212.20	6.06	5.60	12.34	6.40	23.71	19.70	3.50	1.80
201.	NRCHB-101	54.50	57.75	118.75	115.5	199.08	194.42	4.42	3.5	8.5	4.75	28.47	22.21	2.39	1.7
202.	NRCDR-2	51.25	58.00	134.5	129.25	184.67	199.33	4.72	4.17	11.42	6.42	24.21	27.04	2.3	1.63
203.	Krishna	60.50	65.75	131.00	127.25	201.25	214.17	6.67	4.83	13.42	8.58	24.62	25.57	3.27	1.16
204.	Sej-2	50.00	57.25	114.00	112.00	184.25	194.75	4.58	4.50	11.33	6.42	22.72	20.87	3.17	1.13
205.	PM-25	50.25	55.25	114.75	112.25	187.00	195.25	6.33	4.83	10.25	7.59	21.40	18.82	2.53	1.38
206.	PM-26	53.25	57.75	133.50	129.00	197.48	200.72	5.88	4.00	13.33	5.67	22.72	21.50	3.17	1.06
207.	Radhika	54.00	56.50	124.75	120.75	200.75	214.33	5.83	5.00	10.58	9.33	28.57	25.04	2.47	1.39
	C.V.	3.15	2.06	1.66	1.86	5.30	4.29	12.24	16.4	14.12	19.79	5.69	20.98	14.6	26.6

No.	Accessions No.	FLU		MAL		TS		SAM		SSQ		SL		SW		YP	
		T	L	T	L	T	L	T	L	T	L	T	L	T	L	T	L
1.	DRMR - 2	0.78	0.77	73.67	64.00	338.33	208.33	38.33	46.00	14.80	14.00	3.67	3.27	3.61	2.41	11.43	5.17
2.	DRMR - 8	0.75	0.76	59.67	62.33	348.00	240.00	42.00	36.67	14.60	14.20	3.25	4.37	2.65	2.26	8.83	6.29
3.	DRMR - 4	0.75	0.77	49.33	55.67	295.67	253.33	38.33	37.33	13.07	13.00	3.11	3.71	2.98	2.13	10.56	4.53
4.	DRMR - 5	0.72	0.79	65.00	75.67	246.00	206.67	56.33	50.33	14.13	11.13	3.51	4.67	3.98	3.06	9.21	4.92
5.	DRMR - 6	0.75	0.78	79.00	83.67	269.00	223.33	41.00	44.67	14.67	14.73	3.99	4.86	4.92	5.40	11.82	12.52
6.	DRMR - 7	0.75	0.76	49.00	83.33	264.00	243.33	41.67	49.67	15.40	15.53	3.59	4.19	4.02	4.29	9.76	11.85
7.	DRMR - 9	0.73	0.76	61.33	67.67	341.00	319.67	45.67	45.33	13.53	13.57	4.34	4.22	4.46	4.85	7.71	9.52
8.	DRMR - 11	0.76	0.75	53.00	47.67	251.00	193.00	36.33	46.67	13.87	12.80	3.33	3.89	4.03	4.71	9.04	7.92
9.	DRMR - 12	0.72	0.76	55.33	52.67	346.67	242.00	38.00	45.67	13.60	11.93	3.47	3.43	4.67	3.12	15.74	8.61
10.	DRMR - 13	0.75	0.75	53.33	63.00	345.33	286.67	39.00	48.00	12.07	13.20	3.73	3.63	3.15	3.92	6.19	7.94
11.	DRMR - 33	0.75	0.75	64.33	94.33	207.33	264.00	40.67	50.00	15.80	12.80	3.92	3.80	3.32	3.25	9.91	5.93
12.	DRMR - 46	0.71	0.73	71.00	80.00	556.00	201.67	49.67	41.67	16.80	12.00	4.36	4.34	3.99	3.96	13.71	5.23
13.	DRMR - 48	0.70	0.75	65.67	85.67	371.67	222.00	43.67	43.33	16.40	14.33	4.45	4.26	4.38	3.55	16.12	4.39
14.	DRMR - 136	0.72	0.72	76.33	77.67	412.00	203.67	52.33	46.67	15.20	15.00	3.53	4.04	3.78	3.89	18.62	7.05
15.	DRMR - 137	0.71	0.74	66.67	68.33	349.00	205.00	44.67	41.33	14.67	13.47	3.68	4.15	3.75	3.52	16.51	10.99
16.	DRMR - 138	0.81	0.76	83.00	78.67	252.67	221.67	48.00	43.33	15.60	15.40	4.13	4.75	4.51	3.65	16.04	3.72
17.	DRMR - 264	0.76	0.74	78.33	76.67	416.67	336.67	50.33	47.00	15.40	13.60	3.81	4.26	3.59	3.50	16.24	3.84
18.	DRMR - 266	0.77	0.63	95.00	75.33	470.67	257.33	52.67	46.00	14.67	14.87	4.19	4.93	3.99	2.67	25.84	3.32
19.	DRMR - 357	0.74	0.78	89.67	85.00	394.00	346.67	53.67	51.00	15.27	14.87	3.71	5.07	4.27	4.22	13.06	14.99
20.	DRMR - 358	0.81	0.64	92.00	66.67	465.33	221.67	61.00	39.67	15.40	13.07	3.67	4.57	3.49	3.99	18.11	4.92
21.	DRMR - 359	0.79	0.74	81.67	67.00	353.33	171.00	46.00	41.00	15.87	13.80	4.19	4.83	3.60	3.19	20.39	5.40
22.	DRMR - 360	0.73	0.74	63.33	53.33	383.00	145.00	45.00	28.00	15.27	11.67	3.52	3.88	3.41	2.86	19.91	5.90
23.	DRMR - 361	0.78	0.76	66.00	66.00	183.33	220.67	37.67	44.00	13.80	12.80	3.19	4.59	3.38	3.66	10.47	9.41
24.	DRMR - 362	0.77	0.74	65.33	52.67	303.00	247.67	50.33	35.33	13.93	10.60	3.21	3.63	2.64	2.87	12.02	7.28
25.	DRMR - 364	0.80	0.76	69.00	63.33	428.00	244.67	55.67	40.00	13.87	11.87	3.83	4.45	3.30	3.18	24.23	5.23
26.	DRMR - 574	0.78	0.77	86.33	85.33	469.33	277.67	63.33	44.67	15.00	12.73	3.57	3.61	4.07	4.02	24.99	7.57
27.	DRMR - 576	0.78	0.77	85.67	94.33	466.00	229.33	60.00	57.00	14.07	13.73	3.51	3.93	4.69	4.58	22.88	7.57
28.	DRMR - 577	0.78	0.77	61.67	79.67	410.33	236.67	37.67	42.67	15.60	13.87	4.15	3.85	5.32	4.26	18.58	8.06
29.	DRMR - 578	0.77	0.79	69.00	85.00	300.33	223.33	48.33	50.33	16.53	14.13	4.36	4.34	4.13	3.07	14.58	7.32
30.	DRMR - 579	0.77	0.78	60.00	66.67	341.67	239.00	37.67	48.70	12.33	12.07	3.61	4.75	4.82	3.73	20.98	8.14
31.	DRMR - 582	0.78	0.73	74.67	86.00	318.00	239.67	42.00	48.00	12.27	13.07	3.26	3.17	4.09	2.93	16.33	9.00
32.	DRMR - 610	0.79	0.76	69.67	72.33	369.33	229.00	39.67	39.00	14.40	13.93	3.65	3.73	3.37	3.30	14.97	7.89
33.	DRMR - 611	0.76	0.73	76.33	79.33	285.33	221.33	41.00	52.00	14.73	13.73	3.83	4.18	3.17	2.50	14.79	8.91
34.	DRMR - 624	0.78	0.70	85.33	84.00	487.67	284.33	49.00	42.33	14.53	13.33	4.07	3.99	3.75	3.27	21.11	10.53
35.	DRMR - 625	0.79	0.74	87.00	82.67	436.00	183.67	47.33	49.67	14.73	14.60	4.66	4.61	3.37	3.43	14.39	4.98
36.	DRMR - 626	0.80	0.55	72.33	67.33	562.67	139.00	45.00	37.00	14.40	14.33	3.89	4.01	2.66	3.99	21.56	4.64
37.	DRMR - 669	0.78	0.72	85.00	61.00	441.00	174.33	48.67	42.33	15.33	14.67	4.93	4.08	3.85	2.82	22.82	5.59
38.	DRMR - 680	0.78	0.73	65.00	80.67	319.67	251.67	45.00	43.00	13.53	12.33	3.42	3.11	4.00	3.49	15.48	10.32
39.	DRMR - 683	0.78	0.74	73.67	90.33	450.00	179.00	55.67	50.00	14.67	13.47	3.89	3.56	4.21	4.72	23.59	6.49
40.	DRMR - 686	0.77	0.71	87.00	88.00	409.00	336.67	56.00	50.67	14.07	14.33	3.95	3.33	4.20	3.64	20.90	10.80
41.	DRMR - 689	0.77	0.74	81.33	77.33	339.00	208.67	55.00	42.00	13.73	14.27	3.94	3.95	3.44	3.22	22.51	6.54

42.	DRMR - 691	0.79	0.70	75.33	84.67	323.00	261.67	53.67	49.33	13.93	14.40	3.75	4.29	3.90	3.33	18.10	8.45
43.	DRMR -692	0.78	0.73	81.00	65.67	430.67	256.67	50.33	38.33	15.13	12.53	4.09	3.56	3.55	3.42	18.39	8.32
44.	DRMR - 693	0.76	0.71	44.67	63.33	490.33	163.33	44.33	36.67	14.40	12.80	4.03	4.43	2.71	2.77	20.54	6.18
45.	DRMR -710	0.80	0.66	71.67	57.67	334.33	351.67	45.00	44.00	14.87	12.07	4.33	3.58	3.12	2.75	16.35	6.79
46.	DRMR - 711	0.77	0.72	70.67	87.00	473.00	401.33	52.33	50.00	15.00	12.53	4.48	3.70	3.32	2.29	10.96	8.81
47.	DRMR - 726	0.80	0.77	52.33	54.00	372.67	377.00	47.33	40.33	14.20	12.53	4.04	3.57	3.06	3.28	17.69	10.07
48.	DRMR - 731	0.78	0.74	77.00	86.33	466.33	457.00	48.33	47.33	14.80	15.20	4.11	3.90	3.94	2.97	20.72	16.96
49.	DRMR - 900	0.76	0.77	67.33	79.67	451.33	250.33	47.33	48.00	13.27	13.67	3.53	3.25	3.42	2.92	22.29	4.62
50.	DRMR - 906	0.74	0.74	70.33	83.33	264.67	361.33	48.67	47.00	15.53	15.00	4.28	4.16	3.69	2.98	14.97	8.52
51.	DRMR - 909	0.75	0.72	71.67	98.00	584.67	370.33	61.67	59.33	14.93	12.80	4.27	3.56	3.45	3.40	17.98	11.39
52.	SITARASAG AR	0.77	0.72	53.67	54.33	343.67	190.00	36.67	42.33	15.07	9.53	4.03	4.19	3.07	2.32	19.61	13.40
53.	PUSA BAHAR	0.71	0.72	64.33	86.33	252.67	168.33	46.67	50.67	14.33	11.20	3.81	4.47	4.34	3.06	15.71	4.51
54.	BASANTI	0.76	0.73	51.67	69.67	267.33	208.33	41.67	39.33	14.60	11.00	3.96	4.03	3.01	2.69	13.52	10.68
55.	RHUR - 2 -1	0.74	0.64	70.33	62.67	315.00	263.33	48.00	39.33	14.00	10.33	3.99	3.45	3.31	2.60	14.68	10.49
56.	RC -371-1	0.75	0.70	51.00	61.67	371.33	239.33	41.67	42.67	12.80	9.80	3.32	3.91	2.37	2.31	17.24	4.50
57.	RC -371	0.73	0.76	60.33	61.00	294.00	195.00	41.33	31.00	14.13	9.67	4.14	4.16	2.79	3.36	12.68	5.96
58.	RC - 132	0.80	0.69	39.33	35.00	248.00	126.33	35.33	22.67	15.13	7.00	4.49	3.15	2.12	2.00	14.67	4.56
59.	RC - 571	0.73	0.71	60.67	58.33	238.00	118.00	47.33	28.33	14.00	7.07	3.94	3.91	3.13	2.60	12.73	6.88
60.	RC - 891-1	0.74	0.72	79.00	61.33	256.33	208.33	48.33	57.00	15.33	13.93	3.91	4.30	3.16	3.77	19.83	6.81
61.	RC - 1271	0.72	0.76	54.33	76.33	276.67	189.00	40.33	45.67	13.20	12.40	3.67	3.57	3.87	4.50	19.10	3.81
62.	RC - 1270	0.70	0.77	48.33	80.67	224.00	182.33	31.67	32.67	12.93	12.20	3.43	3.55	3.65	3.97	6.31	4.57
63.	RLC - 3	0.70	0.53	54.33	79.00	258.00	228.33	37.33	37.00	14.80	13.73	3.72	3.67	3.34	3.63	13.63	7.17
64.	NC - 37362	0.76	0.76	76.33	63.67	261.00	316.33	42.33	33.00	14.87	12.33	3.66	3.62	3.06	4.27	17.84	10.84
65.	NC - 660	0.76	0.76	72.67	68.33	281.33	267.00	40.67	32.33	14.13	12.93	3.61	3.67	2.91	4.07	16.16	7.74
66.	CN - 105257	0.77	0.73	50.33	76.33	291.33	255.33	43.33	48.00	13.47	11.87	3.73	3.13	2.47	2.34	8.31	5.25
67.	CN - 105312	0.78	0.76	73.00	62.33	275.00	192.67	45.33	38.33	15.00	13.40	4.54	4.37	3.03	4.17	11.52	5.02
68.	CN - 105309	0.80	0.76	59.67	72.33	277.00	178.00	52.33	47.67	14.33	13.73	4.25	4.03	2.85	2.97	14.30	6.80
69.	CN - 34005	0.79	0.77	61.67	64.00	300.67	142.33	57.67	44.67	14.13	12.00	3.67	3.56	3.68	2.23	13.29	2.89
70.	CN - 113780	0.81	0.74	66.00	86.00	235.00	207.33	44.00	42.67	14.67	13.27	4.32	3.69	4.03	3.03	5.28	4.74
71.	CN - 34008	0.79	0.75	60.33	73.33	286.33	277.33	40.00	43.00	14.13	12.47	3.70	3.53	3.44	3.02	11.27	9.06
72.	CN - 105364	0.78	0.73	78.33	60.67	388.00	236.00	51.67	39.33	15.73	12.80	4.30	2.74	3.15	1.80	15.95	6.38
73.	CN - 101813	0.77	0.66	47.33	69.33	402.67	136.67	44.67	39.00	14.47	15.13	4.21	3.49	3.48	1.72	26.27	5.78
74.	CN - 105233	0.78	0.70	85.00	69.67	320.00	241.00	57.00	40.00	14.20	13.47	3.78	3.17	3.40	1.84	11.42	7.69
75.	CN - 105379	0.79	0.67	82.00	66.00	354.67	270.00	54.33	45.33	14.67	14.80	4.09	3.72	3.96	3.66	28.60	9.91
76.	AJ - 11	0.80	0.65	64.00	54.67	371.00	271.67	48.00	41.00	14.40	12.53	4.47	3.01	3.12	2.44	17.41	4.77
77.	AJ - 3	0.79	0.76	75.67	61.67	369.33	225.33	53.00	40.33	13.20	12.07	3.93	3.35	3.98	2.77	17.15	11.28
78.	DJ - 5	0.81	0.55	79.67	67.33	287.33	321.67	48.00	40.00	12.33	13.27	3.80	3.07	2.22	2.05	8.49	8.45
79.	DJ - 12	0.79	0.73	77.00	74.33	395.67	172.00	44.33	46.67	13.67	12.40	4.23	4.21	3.74	3.64	16.53	8.11
80.	DJ - 65	0.81	0.78	59.33	75.00	356.33	270.67	42.67	48.00	13.67	11.80	4.43	4.17	3.82	3.33	14.71	9.93
81.	RJ - 10	0.81	0.75	69.67	88.67	401.33	231.00	48.00	51.00	14.87	11.53	4.06	4.27	4.16	4.13	19.38	7.15
82.	DTM - 50	0.80	0.75	70.67	78.33	387.33	261.67	42.00	47.67	14.53	13.87	3.17	3.77	2.93	2.64	9.38	6.07
83.	PTJ - 3-89	0.81	0.63	79.33	68.33	345.00	285.33	49.33	43.33	14.73	13.40	3.74	6.81	4.02	3.50	12.93	8.17

84.	PTJ - 3-64	0.81	0.67	79.67	82.00	323.67	217.67	50.33	43.67	15.33	13.40	3.78	3.75	2.42	2.82	13.03	4.57
85.	NPJ - 161	0.80	0.73	76.33	74.67	231.33	169.00	41.00	43.33	12.40	11.87	3.11	6.50	3.02	3.51	11.27	5.36
86.	KDM - 49-1	0.76	0.75	50.33	66.00	312.67	105.33	36.33	37.67	13.67	12.53	3.20	3.29	2.87	2.27	10.56	2.12
87.	RB - 60	0.72	0.78	92.33	76.67	426.33	147.67	52.33	39.00	16.33	13.80	4.34	4.30	4.94	2.92	17.58	6.25
88.	PR - 2001-42	0.78	0.78	76.67	67.67	328.67	166.00	41.33	41.67	16.40	12.60	4.07	3.68	3.46	2.68	17.14	5.42
89.	EM - 1	0.75	0.73	77.33	75.00	367.00	192.00	46.00	46.67	14.67	13.67	3.63	3.39	3.60	2.25	15.07	2.97
90.	GR - 325	0.74	0.78	66.33	64.00	476.33	179.33	52.00	41.00	15.07	12.07	3.71	3.68	3.65	2.54	15.54	3.40
91.	IM - 108	0.75	0.78	77.67	79.33	332.00	121.00	50.33	43.67	16.13	16.60	4.11	5.13	4.36	4.12	14.05	6.30
92.	IM - 76	0.69	0.75	74.33	76.67	291.00	250.67	45.67	48.33	15.00	15.80	3.77	3.98	3.17	3.09	9.95	10.00
93.	IM - 152	0.75	0.74	79.00	62.00	345.67	275.67	43.33	43.67	14.00	13.13	2.97	3.84	3.97	2.99	23.42	7.50
94.	IM - 3	0.76	0.69	83.67	80.67	423.33	264.00	55.33	53.33	14.87	13.20	3.36	4.29	3.80	3.62	16.17	8.78
95.	IM - 170	0.75	0.77	88.33	74.00	414.33	289.00	54.67	48.33	14.27	13.13	3.57	4.41	4.12	3.19	15.46	8.13
96.	PBR - 97	0.74	0.72	88.67	73.33	429.00	196.00	54.67	49.67	14.20	12.47	3.57	3.95	3.80	3.54	11.18	9.35
97.	RE - 44	0.76	0.73	82.33	99.33	318.33	188.00	47.67	45.67	14.60	12.60	3.27	4.19	3.77	3.18	9.84	5.63
98.	RGN - 34	0.79	0.76	60.33	79.67	401.00	196.67	55.67	47.67	16.33	13.27	3.88	4.01	4.71	3.43	18.98	6.31
99.	RH - 30	0.74	0.63	84.00	67.33	326.67	188.67	54.33	40.67	15.80	11.67	3.88	4.39	3.81	3.06	13.81	6.30
100.	NPJ- 113	0.78	0.77	65.67	62.00	277.67	163.00	42.00	43.33	13.53	14.00	3.53	3.94	4.28	3.26	10.43	5.09
101.	RCQR-9901	0.71	0.74	84.33	69.00	406.67	145.33	54.00	39.33	14.47	12.60	3.69	3.99	3.20	2.94	13.98	8.26
102.	RNN - 505	0.70	0.72	66.33	73.33	327.00	173.67	38.33	39.33	14.93	12.60	3.53	3.63	2.90	2.43	10.55	6.30
103.	NDRE - 4	0.69	0.75	43.00	53.33	262.67	214.33	30.00	43.33	14.53	14.47	3.41	3.59	2.51	2.93	6.91	10.42
104.	I - 79	0.73	0.76	49.67	76.00	346.33	246.00	29.67	42.67	15.20	12.80	3.53	3.83	3.04	2.54	12.33	6.27
105.	PCR - 9403	0.75	0.74	85.00	61.33	398.33	193.33	52.33	39.00	15.73	13.93	3.71	3.77	3.74	3.57	14.53	6.17
106.	PM - 67	0.75	0.74	64.67	68.00	390.00	129.67	44.67	43.00	13.13	11.47	3.08	3.59	3.00	3.32	17.99	3.96
107.	PM -30	0.70	0.73	71.33	83.33	295.67	147.00	42.67	44.00	13.73	13.07	3.37	3.36	3.10	3.73	11.92	3.79
108.	CN -101845	0.70	0.73	76.00	97.00	330.33	253.00	46.00	52.33	15.53	13.67	3.61	3.77	3.56	2.21	7.61	5.69
109.	IC - 122137	0.77	0.74	65.00	95.33	377.33	252.00	49.67	50.00	14.60	13.07	3.75	4.16	4.91	4.24	18.75	5.98
110.	IC - 11721	0.77	0.76	57.33	56.00	429.33	294.00	35.33	34.00	15.33	12.40	3.29	3.39	2.35	2.82	13.73	6.34
111.	IC -206741	0.78	0.76	54.33	63.00	287.00	150.33	40.00	34.67	14.13	13.53	3.17	3.26	2.26	2.08	6.54	4.72
112.	IC - 372259	0.75	0.68	74.00	49.33	368.67	203.00	45.33	30.33	16.33	12.87	3.75	3.24	2.44	1.88	17.19	4.48
113.	IC - 341108	0.73	0.78	62.33	69.67	405.67	286.00	52.33	38.00	15.53	12.87	3.34	3.38	2.45	1.88	7.74	3.91
114.	IC - 491455	0.65	0.74	62.00	88.67	497.00	202.67	48.67	48.67	16.33	12.40	4.06	3.78	3.31	3.88	13.74	8.53
115.	IC - 491175	0.70	0.72	92.67	66.00	428.67	127.67	51.33	39.33	15.27	12.80	3.47	3.97	4.67	4.63	18.35	4.99
116.	IC - 491485	0.74	0.46	45.33	66.67	537.33	142.00	32.67	41.33	15.33	13.73	3.50	3.56	2.73	2.38	20.39	4.81
117.	IC - 531377	0.76	0.76	68.33	71.33	441.33	226.00	47.67	39.33	15.27	13.60	3.42	3.51	2.78	2.72	16.07	7.60
118.	IC -589676	0.77	0.66	75.67	63.00	445.33	225.00	51.00	39.67	14.47	13.13	3.37	3.84	3.79	2.40	21.11	8.19
119.	IC - 589683	0.75	0.76	72.00	71.67	380.33	182.67	54.33	45.00	16.60	14.53	4.20	4.60	3.42	3.88	19.30	5.82
120.	IC - 497904	0.77	0.78	83.33	73.67	426.33	186.33	57.33	39.67	15.73	14.07	3.63	3.69	2.52	1.92	15.86	7.16
121.	IC - 70302	0.80	0.77	82.33	79.33	288.33	225.00	54.00	38.33	14.33	13.00	3.51	4.21	2.67	2.50	8.43	7.26
122.	IC - 491348	0.80	0.77	65.00	88.67	415.33	211.33	53.00	49.33	15.60	14.07	4.12	4.22	3.28	2.76	16.07	4.85
123.	IC - 375924	0.78	0.75	55.33	71.33	382.00	227.67	48.67	43.67	14.20	13.13	3.14	3.75	3.61	2.57	11.33	6.97
124.	IC - 422156	0.78	0.77	64.00	86.33	351.33	178.67	55.00	50.67	15.27	13.20	3.54	4.13	4.97	4.66	15.65	6.21
125.	IC -422172	0.80	0.73	68.00	81.00	403.00	267.67	43.67	45.67	14.93	14.40	3.71	3.71	4.07	3.33	15.07	9.41
126.	IC - 481011	0.77	0.72	65.00	71.67	445.00	304.33	48.67	48.67	15.27	13.47	3.71	3.80	4.84	2.77	15.91	9.70

127.	IC - 73225	0.75	0.74	66.33	70.33	458.67	229.33	50.67	36.00	17.73	16.00	4.92	4.41	5.12	3.71	32.56	8.52
128.	IC - 766313	0.79	0.75	82.33	73.00	401.33	365.00	48.67	39.33	15.60	12.40	3.87	3.84	2.81	2.37	4.96	3.72
129.	IC - 766377	0.76	0.72	79.00	76.00	542.33	160.67	52.33	43.33	15.33	14.07	3.70	3.55	3.56	3.55	16.88	4.41
130.	EC - 399300	0.72	0.75	57.33	68.33	349.67	328.67	41.00	42.33	15.20	15.40	3.45	3.81	2.51	3.05	7.19	10.52
131.	EC - 766423	0.78	0.82	56.00	59.67	440.00	376.67	56.67	55.67	15.20	15.00	3.37	3.99	3.58	3.55	12.90	13.37
132.	EC - 766110	0.82	0.58	50.67	69.33	484.00	354.67	45.00	42.00	13.53	13.73	4.07	3.75	3.14	1.18	14.16	10.02
133.	EC - 766234	0.84	0.69	54.33	75.67	362.00	191.33	43.67	46.00	15.20	12.47	3.79	3.58	3.25	3.33	6.59	4.13
134.	EC - 766127	0.86	0.60	60.00	95.67	387.67	234.33	48.33	46.00	15.13	12.47	3.90	3.97	2.98	2.59	18.17	5.01
135.	EC - 766134	0.74	0.77	63.00	77.33	394.00	397.67	50.00	41.00	16.27	13.13	3.97	3.93	2.96	2.36	7.32	6.83
136.	EC - 766136	0.73	0.76	77.00	66.67	443.00	473.33	46.33	38.67	16.53	13.00	4.47	4.00	3.20	2.06	13.47	2.86
137.	EC - 766141	0.83	0.75	90.67	83.67	387.00	344.00	43.67	48.67	18.33	13.80	4.58	3.32	2.56	2.47	10.85	2.03
138.	EC - 66431	0.91	0.72	97.33	92.33	221.67	342.00	50.00	51.67	15.87	14.60	3.89	4.03	3.93	2.81	11.81	7.27
139.	EC - 766402	0.86	0.75	98.33	91.33	227.33	208.67	42.00	50.67	15.07	12.07	3.48	3.38	3.54	3.12	7.58	4.11
140.	EC - 766401	0.84	0.76	86.00	89.33	287.67	306.00	37.67	42.67	15.47	13.87	3.82	3.96	4.33	2.07	14.47	3.87
141.	EC - 766611	0.67	0.74	83.67	75.67	351.00	264.33	40.00	47.00	15.87	13.53	3.77	4.14	4.20	3.92	15.13	8.70
142.	EC - 766576	0.74	0.73	97.00	86.00	336.33	182.00	44.00	43.00	16.07	13.00	4.33	4.09	3.05	3.48	7.86	4.44
143.	EC - 766571	0.77	0.75	110.6	94.00	396.33	290.33	47.67	53.00	15.67	13.87	3.99	3.97	3.29	4.29	15.24	7.75
144.	EC - 766560	0.71	0.74	100.3	90.67	389.33	254.67	49.33	46.33	15.27	13.47	3.89	3.92	2.56	3.34	10.90	4.13
145.	EC - 766391	0.72	0.73	82.00	79.00	208.33	327.33	35.33	43.33	14.67	13.53	3.25	3.73	2.71	3.54	6.95	3.98
146.	EC - 766381	0.76	0.78	45.67	73.00	378.33	327.67	39.00	41.00	15.27	13.93	3.38	3.39	3.26	2.91	8.56	6.15
147.	EC - 766335	0.72	0.79	71.67	70.67	356.33	209.67	46.33	40.33	15.60	12.40	4.00	3.37	3.06	3.12	21.37	4.35
148.	IC - 766334	0.76	0.70	47.33	56.67	395.00	309.67	33.67	38.33	15.40	13.67	3.41	3.45	2.99	2.08	6.07	3.07
149.	EC - 766322	0.73	0.69	40.00	83.67	368.33	425.00	40.33	49.67	16.07	14.00	3.50	3.87	4.05	3.33	10.36	9.03
150.	EC - 766311	0.70	0.80	78.33	67.00	378.33	289.00	47.00	43.67	15.67	14.67	3.89	4.29	3.25	3.78	17.64	2.14
151.	EC - 766310	0.76	0.80	69.67	76.33	328.00	323.33	41.67	44.00	15.33	12.80	3.43	3.60	3.10	3.61	14.67	8.58
152.	EC - 766296	0.73	0.78	87.33	97.00	254.67	221.33	47.67	52.67	15.20	13.73	3.51	3.71	3.34	3.31	13.75	4.81
153.	EC - 766292	0.74	0.77	76.67	100.6	256.00	164.67	45.00	47.33	16.20	13.67	4.15	4.51	3.83	3.58	8.01	5.44
154.	EC - 766276	0.77	0.76	79.33	96.00	237.33	218.67	43.00	30.00	15.47	13.40	3.86	3.76	3.65	3.48	14.11	4.51
155.	EC - 766278	0.74	0.81	71.33	79.00	275.33	160.00	47.00	45.33	15.20	13.47	4.37	3.98	3.12	3.01	11.21	2.81
156.	EC - 766270	0.76	0.58	89.33	88.00	244.67	233.00	43.33	38.33	16.33	13.67	4.37	3.74	3.69	3.40	12.25	2.34
157.	EC - 766234	0.78	0.73	70.33	84.00	345.33	237.33	40.00	43.00	15.40	13.53	3.47	3.61	4.15	4.03	8.32	4.89
158.	EC - 766211	0.71	0.79	72.33	97.67	255.67	205.00	43.33	58.00	14.13	13.60	3.41	3.98	3.92	4.80	7.69	6.71
159.	EC - 766207	0.75	0.58	70.33	76.67	344.33	270.67	42.67	44.33	15.73	12.60	3.43	3.77	2.28	3.40	9.60	7.73
160.	EC - 766557	0.75	0.70	67.00	80.67	365.67	202.33	43.67	39.00	16.87	12.53	3.84	3.74	3.15	3.42	10.08	4.64
161.	EC - 766124	0.77	0.72	93.00	81.67	344.33	333.00	51.67	41.67	17.00	13.20	4.05	4.37	4.04	2.95	10.19	9.07
162.	EC - 766060	0.74	0.55	55.67	96.00	166.67	269.00	43.33	50.67	15.00	13.07	3.91	3.95	2.52	3.21	5.89	4.67
163.	EC - 766204	0.78	0.73	71.00	73.33	448.67	237.00	53.67	40.67	15.40	12.67	3.74	3.65	4.29	3.56	14.94	5.34
164.	EC - 766487	0.76	0.74	73.33	72.00	284.33	354.67	47.67	36.67	16.00	13.87	3.77	4.18	3.80	4.23	9.06	5.92
165.	EC - 766344	0.75	0.70	75.00	79.33	264.67	323.33	45.00	38.67	15.20	13.80	3.61	4.22	3.42	4.16	9.64	5.87
166.	EC - 766200	0.77	0.64	67.00	65.00	363.33	219.33	46.00	36.67	14.60	13.07	3.91	3.90	4.64	3.30	16.20	3.93
167.	EC - 766069	0.76	0.71	68.33	73.67	282.67	145.67	42.67	41.33	17.67	12.53	3.50	3.82	2.68	3.25	7.96	3.27
168.	EC - 766576	0.77	0.67	80.33	71.00	292.33	130.33	46.00	44.33	15.47	14.53	3.43	4.24	4.74	3.76	8.26	4.78
169.	EC - 399318	0.76	0.70	91.67	68.00	586.00	186.33	51.33	42.00	15.00	13.33	3.43	4.05	5.03	3.82	26.05	6.37

170.	EC - 399293	0.78	0.69	88.33	83.67	446.33	222.33	57.00	44.00	13.40	13.20	3.76	3.83	4.91	2.97	20.44	5.11
171.	EC - 571648	0.76	0.72	66.67	76.33	419.00	138.33	40.00	37.33	14.60	12.40	4.02	3.91	3.88	3.56	17.92	3.30
172.	EC - 399308	0.78	0.73	85.00	70.33	333.33	189.00	45.33	40.33	16.40	13.33	3.28	4.27	4.12	4.32	14.55	3.81
173.	EC - 399302	0.78	0.76	57.67	60.67	338.00	112.67	48.67	31.33	14.87	13.13	3.27	3.60	2.53	2.63	20.34	2.53
174.	EC - 764501	0.72	0.75	91.67	71.33	342.00	193.67	42.67	39.33	14.33	13.20	3.95	3.59	5.21	3.33	14.08	4.78
175.	EC - 766622	0.76	0.74	58.67	64.67	270.33	202.67	45.00	42.00	12.20	12.87	3.87	3.57	3.19	3.51	13.23	6.13
176.	EC - 766325	0.76	0.70	60.67	56.00	288.67	210.33	35.33	31.67	13.53	12.40	3.38	3.47	4.15	3.82	11.84	4.91
177.	EC - 766115	0.79	0.66	75.00	73.00	276.67	149.67	47.67	43.67	13.73	13.07	3.25	4.25	4.07	2.97	11.47	5.00
178.	EC - 766498	0.73	0.67	78.67	77.67	296.33	137.67	44.67	38.33	14.53	13.00	3.76	3.83	3.69	3.40	11.31	4.51
179.	EC - 766564	0.74	0.65	55.33	77.33	308.33	219.67	40.33	44.00	14.47	12.93	3.50	3.67	3.14	3.17	4.87	3.56
180.	EC -766489	0.72	0.72	64.33	72.00	416.67	207.00	45.67	46.00	12.13	13.00	3.06	3.97	2.70	2.64	8.95	3.61
181.	EC - 766393	0.74	0.70	75.00	75.67	313.00	132.67	46.33	39.00	15.07	12.33	4.32	3.83	4.37	4.14	11.89	4.55
182.	EC - 766470	0.73	0.68	72.67	61.33	333.33	253.67	52.00	33.67	15.20	12.33	4.13	3.52	4.66	3.82	9.11	2.77
183.	EC - 766616	0.76	0.76	76.00	80.33	295.00	300.33	47.67	43.67	15.20	12.93	4.02	4.05	3.68	4.36	12.18	8.68
184.	EC - 766594	0.76	0.72	63.33	88.67	387.67	361.33	33.33	41.67	16.53	12.80	3.23	5.03	5.19	3.16	10.08	5.81
185.	EC - 766555	0.74	0.73	67.00	82.67	288.00	156.33	42.00	42.67	14.67	13.07	3.63	3.91	3.36	3.92	14.39	4.06
186.	EC - 766094	0.77	0.55	88.67	93.33	366.00	212.33	48.00	48.33	14.40	12.87	3.39	3.85	3.42	2.53	16.43	3.98
187.	EC - 766312	0.70	0.72	85.67	71.00	265.67	119.33	47.33	37.00	16.13	13.33	3.56	4.44	3.01	3.00	10.87	3.31
188.	EC -766095	0.75	0.73	74.67	90.67	344.33	184.33	43.00	43.33	16.40	13.20	3.10	4.97	3.17	3.57	14.35	3.97
189.	EC - 564649-1	0.79	0.75	91.33	65.00	315.33	93.33	45.67	30.33	15.13	12.67	2.95	4.03	3.21	3.74	14.97	2.73
190.	EC - 766207	0.77	0.64	92.00	64.67	385.33	183.33	42.33	35.00	16.07	13.33	3.09	3.95	3.98	2.50	8.25	4.62
191.	EC - 766322	0.72	0.71	54.33	76.33	222.00	162.67	32.67	42.33	16.73	13.20	3.13	3.65	4.23	5.07	5.88	4.94
192.	IC - 320378	0.79	0.75	64.00	51.33	272.00	115.67	39.33	33.33	15.73	12.93	3.99	3.50	2.67	2.27	9.77	3.28
193.	IC - 766214	0.75	0.78	65.67	82.33	302.00	182.33	40.33	49.33	16.40	13.20	3.82	3.99	4.36	3.97	9.39	4.41
194.	IC - 766098	0.77	0.76	68.67	82.67	259.00	196.00	41.67	49.00	13.33	13.20	4.07	3.58	2.44	2.84	9.66	3.91
195.	IC -766029	0.80	0.56	95.33	82.67	366.33	253.00	49.67	48.00	13.73	13.07	3.74	4.16	3.59	3.58	17.58	6.23
196.	IC - 766614	0.79	0.69	61.00	83.33	339.67	234.33	49.00	43.67	14.33	12.87	4.02	3.78	2.93	2.45	15.27	4.40
197.	IC - 766129	0.79	0.72	61.33	67.67	455.67	172.67	49.67	35.33	14.13	12.87	4.57	4.07	3.79	3.36	22.37	6.19
198.	IC - 766299	0.77	0.70	70.33	78.67	527.67	249.33	48.33	47.67	13.80	14.20	3.83	3.73	3.11	3.53	17.96	8.84
199.	IC - 399318	0.76	0.71	92.00	82.33	611.00	185.33	52.67	44.67	15.40	13.33	3.67	3.69	3.14	2.75	26.50	4.25
200.	IC - 321424	0.77	0.71	84.33	77.67	476.33	242.33	52.00	44.67	14.67	13.27	3.21	3.79	4.23	3.49	31.03	4.82
	Min.	0.65	0.45	39.30	35.00	166.60	93.30	29.60	22.60	12.06	7.00	2.90	2.74	2.11	1.18	4.86	2.02
	Max.	0.90	0.82	110.6	100.0	611.00	473.30	63.30	59.30	18.33	16.60	4.90	6.81	5.31	5.40	32.56	16.95
	Mean	0.76	0.72	71.24	74.30	354.70	231.05	46.00	43.10	14.80	13.10	3.76	3.90	3.54	3.20	14.40	6.30
201.	NRCHB-101	0.71	0.71	82.00	85.42	288.5	122.42	61.25	44.42	16.80	14.80	4.56	4.31	4.51	3.81	14.42	7.33
202.	NRCDR-2	0.74	0.74	64.83	90.42	298.00	207.23	42.17	44.83	16.12	14.77	4.14	4.38	4.11	4.16	11.35	7.21
203.	Krishna	0.71	0.71	60.00	74.25	328.00	205.08	41.50	43.92	15.70	14.08	3.83	3.94	3.38	3.47	17.16	5.22
204.	Sej-2	0.74	0.73	72.08	84.75	303.92	260.01	46.42	45.75	15.27	13.93	4.27	4.03	3.45	3.27	10.61	7.12
205.	PM-25	0.73	0.69	72.33	83.92	281.17	196.75	43.67	40.33	16.02	13.65	4.28	4.35	4.22	3.31	14.92	5.98
206.	PM-26	0.74	0.71	62.92	77.83	341.00	163.58	42.92	38.20	15.48	14.55	3.86	3.91	3.67	3.13	6.38	6.66
207.	Radhika	0.74	0.72	60.42	91.50	320.08	204.17	43.00	43.67	15.72	14.00	3.90	4.04	4.26	4.07	13.82	6.69
	C.V.	5	8.30	12.38	9.91	10.27	15.35	8.24	7.40	3.75	4.01	6.13	6.48	10.5	10.3	16.58	21.69

Name: Ms. Amita Singh

ID. No.: RLBCAU/AG/PG/034

Semester and year of admission: IV and 2021-22

Degree: M.Sc. Agriculture

Department: Genetics and Plant Breeding

Major Subject: Genetics and Plant Breeding

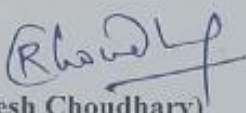
Thesis Title: "Characterization of Indian mustard (*Brassica juncea* L.) genotypes for heat tolerance at reproductive stage"

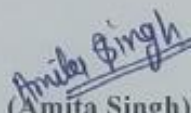
Advisor: Dr. Rakesh Choudhary

ABSTRACT

The present experiment entitled "Characterization of Indian mustard (*Brassica juncea* L.) genotypes for heat tolerance at reproductive stage" was carried out during rabi 2021-22 at Block D-3, Seed and Research Farm, Rani Lakshmi Bai Central Agricultural University (RLBCAU), Jhansi. In current investigation, a total of two hundred genotypes with seven checks of Indian mustard were sown in augmented block design to estimate genetic variability, genetic divergence, association analysis and for comparative phenotyping against terminal heat, sowing is done at different dates (normal and late sown). The analysis of variance was carried out for fifteen agro-morphological and physiological characters and results indicated highly significant genetic differences for most of the characters under both timely and late sowing condition except chlorophyll content in only late sown whereas, chlorophyll fluorescence showed non-significant difference in both the environment. The magnitudes of PCV estimates were higher than the corresponding GCV estimates for all the characters, indicating that considerable effect of environment on the performance of genotypes. High estimates of GCV and PCV were found for the characters viz., leaf area index, total siliqua per plant and yield per plant under both the environment. High heritability was coupled with high genetic advance as per cent of mean for number of secondary branches per plant, leaf area index, total siliqua per plant, 1000-seed weight and yield per plant under both timely and late sown conditions which indicated the predominant role of additive gene action in inheritance of these traits. In correlation studies revealed that seed yield per plant had significant positive association with plant height, number of primary branches per plant, number of secondary branches per plant, leaf area index, total number of siliqua per plant, siliqua on main shoot and 1000- seed weight under both normal and late sown conditions. The

positive direct effects on seed yield per plant were exerted by plant height, chlorophyll content, main shoot length and siliqua length without the influence of the sowing period which depicted true genetic relationship between these traits. Based on Mahalanobis D^2 statistic, the entire 200 genotypes used under study are grouped into six different clusters in each environment. Under both the environment, Cluster V recorded the highest cluster means for most of yield attributing traits like total siliqua per plant, number of siliqua on main shoot and seed weight and these genotypes can be used as potential donor for the hybridization programme. Based on results of heat screening parameters like heat susceptibility index, yield stability index and percent yield change, genotypes viz. NDRE-4, EC-399300, DRMR-13, DRMR-9, DRMR-7, DRMR-357, DRMR-6, EC-766423 and IM-76 were found promising for heat tolerance at reproductive stage in Indian mustard.


(Rakesh Choudhary)
(Chairperson)


(Amita Singh)
(Student)

नाम: अमिता सिंह

परिचयांक : RLBCAU/AG/PG/034

सत्र एवं प्रवेश वर्ष: IV and 2020-21

उपाधि: परास्नातक (कृषि)

विभाग: आनुवंशिकी एवं पादप प्रजनन

मुख्य विषय: आनुवंशिकी एवं पादप प्रजनन विभाग

शोध ग्रंथ शीर्षक: "प्रजनन स्तर पर उच्च ताप सहनशीलता के लिए भारतीय सरसों (*त्रैसिका जुन्सिया* एल.) जीनोटाइप का निरूपण"

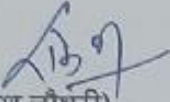
सलाहकार: डॉ. राकेश चौधरी

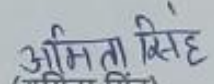
सारांश

प्रस्तुत शोध अध्ययन रबी 2021-22 में रानी लक्ष्मी बाई केंद्रीय कृषि विश्वविद्यालय, झांसी के बीज और अनुसंधान प्रक्षेत्र के डी-3 ब्लॉक में शीर्षक "प्रजनन स्तर पर उच्च ताप सहनशीलता के लिए भारतीय सरसों (*त्रैसिका जुन्सिया* एल.) जीनोटाइप का निरूपण" पर आधारित है। वर्तमान शोध भारतीय सरसों में आनुवंशिक विविधता, अंतर लक्षण संबंध का प्रत्यक्ष एवं अप्रत्यक्ष प्रभाव, आनुवंशिक भिन्नता एवं प्रजनन स्तर पर उच्च ताप सहनशीलता के आंकलन के उद्देश्य से किया गया। इसके लिए भारतीय सरसों के सात चेक किस्मों के साथ कुल दो सौ जीनोटाइप को ऑगमेंटेड ब्लॉक डिजाइन में बोया गया तथा प्रजनन स्तर पर उच्च ताप सहनशीलता के अध्ययन के लिए बुवाई दो समयांतराल (समय से बुवाई एवं देरी से बुवाई) पर की गयी।

विविधता विश्लेषण से यह ज्ञात हुआ कि अध्ययन में सम्मिलित दो सौ जीनोटाइप में अधिकांश आकारिकी लक्षणों के लिए दोनों बुवाई समय में पर्याप्त आनुवंशिक विविधता पायी गयी। केवल पर्णहरित मात्रा के लिए देर से बुवाई में तथा क्लोरोफिल फ्लोरेसेंस के लिए दोनों बुवाई के दौरान आनुवंशिक विविधता नहीं पायी गयी। सामान्यतः अभिलक्षित विविधता गुणांक (PCV) का आनुवंशिक विविधता गुणांक (GCV) से अधिकता परिवेश प्रभाव को दर्शाता है। दोनों बुवाई के समय, GCV और PCV के अनुमान, पत्ती क्षेत्र सूचकांक (LAI), प्रति पौध कुल फलियाँ और प्रति पौध उपज के लिए उच्च पाए गए। समय पर और देर से बोई जाने वाली दोनों स्थितियों के तहत उच्च आनुवंशिकता एवं उच्च आनुवंशिक प्रगति विभिन्न लक्षणों जैसे प्रति पौध माध्यमिक शाखाओं की संख्या, पत्ती क्षेत्र सूचकांक, प्रति पौध कुल फलियाँ, 1000-बीज वजन और प्रति पौध उपज के लिए प्रदर्शित हुई, जो इन लक्षणों के लिए एडिटिव जीन क्रिया की प्रमुख भूमिका को दर्शाता है। सहसंबंध विश्लेषण से पता चला है कि पौधे की ऊंचाई, प्रति पौध प्राथमिक शाखाओं की संख्या, प्रति पौध माध्यमिक शाखाओं की संख्या, पत्ती क्षेत्र सूचकांक, प्रति पौध फलियों की कुल संख्या, मुख्य शाखा पर फलियाँ और 1000- बीज वजन के साथ महत्वपूर्ण सकारात्मक संबंध दोनों बुवाई परिस्थितियों प्रति पौध बीज उपज के साथ पाया गया। पथ गुणांक विश्लेषण से ज्ञात हुआ की सामान्य और देर से बुवाई की स्थितियों में पौधे की ऊंचाई, पर्णहरित मात्रा, मुख्य शाखा की लम्बाई, फली की लम्बाई का सकारात्मक प्रत्यक्ष प्रभाव प्रति पौध उपज पर देखा गया। अतः भारतीय सरसों में बीज उपज के लिए इन लक्षणों के आधार पर प्रत्यक्ष चयन सार्थक

होगा। D2- विक्षेपण के आधार पर, अध्ययन में सम्मिलित 200 जीनोटाइप को प्रत्येक वातावरण में छह अलग-अलग समूहों में वर्गीकृत किया गया और समूह V ने अधिकांश उपज घटकों जैसे प्रति पौध फलियों की कुल संख्या, मुख्य शाखा पर कुल फलियों की संख्या, 1000-बीज वजन के लिए उच्चतम औसत, प्रदर्शित किया जिससे इस समूह के जीनोटाइपों को संकरण कार्यक्रम के लिए संभावित दाता के रूप में इस्तेमाल किया जा सकता है। गर्मी संवेदनशीलता सूचकांक (HSI), उपज स्थिरता सूचकांक (YSI) और प्रतिशत उपज परिवर्तन मानकों के आधार पर जीनोटाइप, NDRE-4, EC-399300, DRMR-13, DRMR-9, DRMR-7, DRMR-357, DRMR-6, EC-766423 और IM-76 को भारतीय सरसों में प्रजनन स्तर पर गर्मी सहनशीलता के लिए आशाजनक पाया गया।


(राकेश चौधरी)
सलाहकार


(अमिता सिंह)
लेखक

CURRICULUM VITAE

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Father's name : Ume Singh
Mother's name : Pushpa Devi
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Permanent Address : Vill- Khevaliyon Ki Dhani, Post- Kakoda, Th.-
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333029

Academic Qualifications

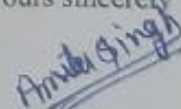
Degree	Board/University	Institution/School	Year of passing	Percent/OGPA
High School	Rajasthan Board of Secondary Education, Ajmer	Tagore Children Academy Sr.SS, Surajgarh(jhunjhunu)	2010	90.33
Intermediate	Rajasthan Board of Secondary Education, Ajmer	Tagore Children Academy Sr.SS, Surajgarh, (Jhunjhunu)	2012	83.60
B.Sc. (Agriculture)	Indira Gandhi Krishi Vishwavidyalaya, Raipur (C. G.)	SG College of Agriculture & Res. Station, Jagdalpur (Bastar)	2020	8.23
M.Sc. (Agriculture) Genetics and Plant Breeding	Rani Lakshmi Bai Central Agricultural University	College of Agriculture	2022	86.40

DECLARATION:

I do hereby declare that all information given above is true to the best of my knowledge and belief.

Place: Jhansi

Yours sincerely


(Amita Singh)