

Genetic Divergence and Character Association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]

[भारतीय सरसों {ब्रैसिका जंसीआ (एल.) सजर्न एवं कॉस} में आनुवांशिक
विविधता और लक्षणों में सह-सम्बन्ध]

HARI OM MEENA

Thesis

MASTER OF SCIENCE IN AGRICULTURE

(Genetics and Plant Breeding)



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**Department of Genetics and Plant Breeding
College of Agriculture, Ummedganj, Kota
Agriculture University, Kota (Rajasthan)**

**Genetic Divergence and Character Association in
Indian Mustard [*Brassica juncea* (L.) Czern & Coss]**

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Thesis

**Submitted to the
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In Partial Fulfilment of the Requirement for
the Degree of**

**Master of Science in Agriculture
(Genetics and Plant Breeding)**



**By
Hari Om Meena
2020**

**College of Agriculture, Ummedganj, Kota
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Date:

This is to certify that this thesis entitled “**Genetic Divergence and Character Association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]**” submitted for the degree of **Master of Science in Agriculture** in the subject of **Genetics and Plant Breeding** embodies bonafide research work carried-out by **Mr. Hari Om Meena** under my guidance and supervision and that no part of this thesis has been submitted to any other degree. The assistance and help received during the course of investigation have been fully acknowledged. The draft of the thesis was also approved by the advisory committee on **14.08.2020**.

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Rapeseed-mustard group of crops is the major oilseed crop of India. This crop accounts for nearly one-third of the oil produced in India, making it the country's key edible oilseed crop. Among the oilseed crops, Rapeseed and mustard is third in production after soybean and groundnut in India. In India, rapeseed–mustard is grown in diverse agro-climatic conditions ranging from north-eastern/north-western hills to down south under irrigated/rainfed, timely/late sown and mixed cropping. Since these crops are cultivated mainly in the rain-fed and resource scarce regions of the country, their contribution to livelihood security of the small and marginal farmers in these regions is also very important. Rapeseed-mustard crops fit well in the rainfed cropping system due to its low water requirement.

Rapeseed-mustard crops in India comprise of traditionally grown indigenous species, namely toria (*Brassica rapa* L. var. toria), brown sarson (*Brassica rapa* L. var. brown sarson), yellow sarson (*Brassica rapa* L. var. yellow sarson), Indian mustard (*Brassica juncea*), black mustard (*Brassica nigra*) and taramira (*Eruca sativa*), which have been grown since about 3,500 BC along with non-traditional species like gobhi sarson (*Brassica napus*) and Ethiopian mustard or Karan rai (*Brassica carinata*).

The average contribution of rapeseed-mustard to the total oilseed production in India was 24.3%, during 2018-19 with an average productivity of 1499 kg/ha as compared to 1234 kg/ha of total oilseeds. It is grown in an area of 6.2 million hectares in the country with production of 9.3 million tonnes. In Rajasthan, rapeseed-mustard is cultivated in an area of 2.76 million hectares, which is 57% of total area under oilseeds in the state (4.81 million hectares). It has 63% share in total oil seeds production of the state (7.69 million tonnes) with 4.84 million tonnes of production and 1740 kg/ha of average yield. (Anonymous, 2018-19).

Indian-mustard [*Brassica juncea* (L.) Czern & Coss] occupies considerably large acreage among the Brassica group of oil seed crops accounting for about 85% of the total area under rapeseed-mustard in the country. It is popularly known as rai, raya or laha. *Brassica juncea* (AABB, 2n=36) is an amphidiploids species which is the inter-specific cross between *Brassica rapa* (AA, 2n=20) and *Brassica nigra* (BB,

2n=16). It is self-compatible and largely self-pollinated crop (85-90%), yet five to twenty per cent cross pollination is observed due to honeybees.

Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Gujarat and West Bengal states accounted for nearly 84.6% area and 92.3% production of rapeseed-Mustard in the country (Anonymous 2018-19). Mustard vegetable oil is the world's second leading source of protein meal. This crop is not only used as food purposes but also serve as important material for the industries. In general, it consists of 36 to 42% oil, 17 to 25% protein, 8 to 10% fiber, 6 to 10% moisture and 10 to 12% extractable substances. Erucic acid and glucosinolate are the anti-nutritional components present in the oil. Gobhi sarson (*Brassica napus*) and turnip rape (*Brassica campestris*) have low erucic acid as compared to other oilseed crops of *Brassica* family. The meal cake left after oil extraction forms important cattle feed and may also be used as organic manure. Brassicas are rich source of vitamins, minerals and contains many medicinal properties. They will be provided high amounts of vitamin C, other than soluble fiber and contain multiple nutrients with potent anti-cancer properties. Mustard oil is used in India for cooking and frying purposes and also used in preparation of hair oil and medicines. Tender leaves of young plants are used as green vegetable and are good source of sulphur and other minerals in diet. It is known to be more drought tolerant and shattering resistant than other cultivated species of *Brassica*. Therefore, has an enormous cultivation potential in semi-arid areas.

Because of shortage of oilseed in the country, India is importing oil from different parts of the world. The major objective of the present-day breeding programmes, therefore, should be higher oil productivity and greater yield stability. Since, mustard crops in general gives lower yields than cereals, it has led people to believe that Brassica crop may have a lower genetic potential. However, it has been indicated that the Brassica crop has a higher genetic potential for yield as compared to cereals. To meet out the present oil requirements, there is an urgent need to increase the yield potential of *Brassica juncea* through genetic interventions.

In any crop genetic diversity is the basic requirement for its further genetic improvement. Variation not only provides a basis for selection but also put forward some valuable information regarding selection of diverse parents to be used in hybridization programme. Breeding for high seed yield and other economic characters

is a very important objective in any crop improvement programme. Yield is a complex character dependent on several other characters. Improvement for yield thus depends on the magnitude of genetic variability of different quantitative characters. Hence, measurement, evaluation and manipulation of genetic variability for yield is needed for overall improvement.

The assessment of genetic variability parameters including phenotypic and genotypic coefficients of variation, heritability in broad sense and genetic advance as per cent of mean is a prerequisite for making effective selection (Manjunath *et al.*, 2017). An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection. The character showing high heritability along with low genetic advance can be improved by inter-mating superior genotypes of segregating population developed from combination breeding. The proper evaluation of important crop species helps in the identification and utilization of improved genotypes (Jan *et al.*, 2016).

Knowledge on genetic diversity in *Brassica juncea* could help breeders and geneticists to understand the structure of genotypes, predict which combinations would produce the best off-springs and facilitate to widen the genetic basis of breeding material for selection. Multivariate analysis using Mahalanobis D^2 statistic has been used as a powerful tool to estimate the degree of divergence in populations and to assess the relative contribution of different characters to the total divergence in many of the crop plants. It provides a measurement of relative contribution of different components on diversity both in inter and intra-cluster levels.

Correlation coefficient provides symmetrical measurement of degree of association between two characters help in understanding the nature and magnitude of association among yield and its components. Direct and indirect effect of independent component traits on yield measured by path coefficient analysis is fruitful for genetic improvement because direct selection is not effective for low heritable polygenic traits like yield.

Therefore, the present investigation was undertaken to estimate the genetic divergence in 60 Indian mustard genotypes of diverse geographic origin and explore

potential to evaluate the relationship of these genotypes based on quantitative trait data. This study thus focuses on studying genetic variation for different component traits and their associations for enhancing the plant yield. Keeping in view the above facts, the present investigation was aimed with the following objectives:

- To estimate the magnitude of genetic variability for different yield contributing traits in the experimental material.
- To assess the extent and nature of genetic divergence among the genotypes using D^2 analysis.
- To estimate nature and magnitude of association among the yield contributing traits.
- To assess the direct and indirect effect for yield by path coefficient analysis.

The relevant literatures related to the present study on “**Genetic divergence and character association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]**” were reviewed.

A thorough understanding of the genetic diversity, extent of variation, genetic architecture of plant and heritability of characters among the genotypes would help in developing sound plant improvement programs. As the available literature pertaining to the present study on Indian mustard is very meager, work done in other allied species are considered and reviewed under the following aspects.

2.1 Genetic variability parameters

2.2 Genetic divergence analysis

2.3 Character association analysis

2.4 Path coefficient analysis

2.1 Genetic variability parameters

An insight into the magnitude of variability present in a crop species is of most importance as it provides the basis for effective selection. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait.

Total variability is a metric trait which is divided into genotypic variability and phenotypic variability. The assessment of genetic variability for yield and its components is a pre-requisite for improvement of the crop to the desired level.

A summary of literature reviewed on mustard and other allied species is presented below.

Kumar *et al.* (2006) reported high heritability and genetic advance for 1000-seed weight, number of siliquae per plant and plant height in a study involving 19 genotypes of Indian mustard selected from diverse genotypes.

Ram and Verma (2010) studied 36 genotypes of Indian mustard and reported high heritability for number of siliquae per plant and 1000-seed weight. The estimate of high heritability accompanied with high expected genetic advance number for

siliquae per plant and 1000-seed weight indicating the presence of additive gene action in the expression of these traits.

Singh *et al.* (2011) reported high genotypic coefficient of variation (GCV) coupled with high heritability for length of main shoot, seed yield and days to maturity in a study involving different genotypes of Indian mustard. High magnitude of heritability and moderate genetic advance for days to 50% flowering indicated that improvement in this trait could be done through selection.

Yadava *et al.* (2011) studied 30 diverse genotypes of Indian mustard and observed high heritability coupled with high genetic advance for 1000-seed weight. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation for all the observed characters. High PCV and GCV were observed for point to first branch, seed yield per plant, point to first siliqua, number of secondary branches per plant and 1000-seed weight.

Lohia *et al.* (2013) studied genetic variability, heritability and character association among the various traits of Indian mustard. Analysis of variance revealed significant difference among the genotypes for all the characters indicating presence of wide spectrum of genetic variability. Observed high heritability revealed that these attributes exhibited more contribution of additive genetic variance and marginal role of non-additive in their inheritance.

Priyamedha *et al.* (2013) studied 110 early generation (F_3) lines of Indian mustard. Higher heritability coupled with higher genetic advance expressed as percentage of mean observed for number of secondary branches per plant and seed yield plant.

Singh *et al.* (2013) studied genetic variability among the various traits of Indian mustard in two environments. He observed high heritability for days to first flowering, siliqua length and seed yield per plant in both the environments. Genetic advance values were high for plant height, number of siliquae on main shoot and seed yield per plant under both the environments, whereas, genetic advance as per cent of mean was high for seed yield per plant, 1000-seed weight, number of secondary branches per plant and siliqua length.

Tripathi *et al.* (2013) studied 20 diverse genotypes of Indian mustard and observed significant differences for all the traits among the genotypes. PCV and GCV

were observed maximum for secondary branches per plant, biological yield per plant and seed yield per plant in both, normal and critical condition (NS and SS). High heritability coupled with high genetic advance as per cent of mean was observed for secondary branches per plant followed by plant height, length of main raceme, siliquae on main raceme, 1000-seed weight, biological yield per plant, seed yield per plant and harvest index in NS and in SS.

Devmani *et al.* (2014) studied 30 genotypes of Indian mustard and found maximum genetic variability for biological yield per plant and minimum for days to maturity as reflected by GCV. Heritability estimates in broad sense were high for 1000-seed weight, day to maturity, day to flowering, plant height and main shoot length. Genetic advance as percent over mean was high for biological yield per plant, 1000-seed weight, seed yield per plant, number of secondary branches per plant and main shoot length.

Lodhi *et al.* (2014) studied 90 diverse genotypes of Indian mustard and observed higher PCV and GCV for number of secondary branches per plant, seed yield per plant and 1000-seed weight. High heritability in conjunction with high genetic advance were observed for seed yield per plant, number of secondary branches per plant, 1000-seed weight, number of seeds per siliqua, primary branch angle, number of primary branches per plant, siliqua angle, siliquae on main shoot and siliqua length.

Shekhawat *et al.* (2014) studied 60 genotypes of Indian mustard for 13 different characters. Considerable variability was observed for all the characters. The characters like days to 50% flowering, days to maturity, number of secondary branches per plant, length of main branch, number of siliquae per plant, number of seeds per siliqua, test weight and seed yield per plant showed high estimates of GCV as well as heritability.

Synrem *et al.* (2014) studied genetic variability in intra-specific crosses of *Brassica juncea* and found highest heritability coupled with high genetic advance as per cent of mean for number of secondary branches per plant followed by seed yield per plant and number of primary branches per plant. Maximum GCV and PCV were exhibited by number of secondary branches per plant followed by seed yield per plant and number of primary branches per plant.

Tomar *et al.* (2014) studied 104 treatments (80 F₁s + 24 Parents) of Indian mustard (*Brassica juncea* L.). Higher heritability coupled with high genetic advance were found for days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, 1000-seed weight, harvest index and seed yield per plant.

Akabari and Niranjana (2015) studied 36 genotypes of Indian mustard and found high heritability values coupled with high genetic advance in case of number of siliquae per plant, plant height, length of main branch and yield per plant, indicating that selection for these traits would be effective in Indian mustard improvement.

Bibi *et al.* (2016) studied ten genotypes of Indian mustard for different characters. Considerable variability was observed for all traits. High heritability in conjunction with high genetic advance was noted in plant height, siliqua length and seed yield per plant.

Uzair *et al.* (2016) studied genetic variability and heritability in Indian mustard and observed high heritability in aggregation with high genetic development was noted in plant height, siliqua length and seed yield which gave the indication that these traits were under the control of additive gene which will be more useful in expecting the gain under collection than heritability alone, while days taken to flowering, days taken to maturity, number of branches per plant, number of seeds per siliqua and 1000-seed weight revealed capricious trends.

Meena *et al.* (2017) observed high genetic advance coupled with high heritability for seed yield, 1000-seed weight, siliqua length, plant height and number of primary branches per plant in 28 F₁ crosses and 11 parental genotypes of Indian mustard.

Tiwari *et al.* (2017) studied genetic variability parameters of Indian mustard and observed higher heritability coupled with higher genetic advance by number of primary branches, number of secondary branches, number of siliquae per plant, number of seeds per siliqua, harvest index and 1000-seed weight.

Yadav *et al.* (2017) studied genetic variability, heritability and genetic advance for 11 quantitative characters. Higher to moderate genotypic and phenotypic coefficient of variation were observed for primary branches per plant, secondary

branches per plant, number of siliquae, seeds per siliqua, test weight, seed yield per hectare. Maximum heritability was recorded in siliqua length and test weight.

Dawar *et al.* (2018) evaluated 30 genotypes in Indian mustard and recorded high to low heritability for plant high, days to first flower, germination percentage and number of primary branches per plant, number of siliquae per plant, seed yield per plant. The magnitude of GCV and PCV for seed yield per plant, number of siliquae per plant, plant height and number of primary branches per plant.

Malik *et al.* (2018) studied genetic variability in 35 genotypes of Indian mustard and found high heritability and genetic advance for days to 50% flowering, plant height and biological yield per plant. Although, number of secondary branches per plant, seed yield per plant and harvest index had moderate to high heritability with moderate genetic advance. Days to 75% maturity, length of siliqua, 1000-seed weight and oil content had low heritability indicating that these traits were under the influence of environmental factors and selection on the basis of these traits could not be effective.

Maurya *et al.* (2018) evaluated 50 germplasm of Indian mustard to estimate some genetic parameters. Higher GCV was found for 1000-seed weight, biological yield per plant, secondary branches plant and seed yield per plant. High heritability estimates were observed for biological yield, plant height, oil content, main raceme length, 1000-seed weight, siliquae on main raceme, number of secondary branches per plant, seed yield per plant and days to maturity. The expected genetic advance as per cent of mean was high for 1000-seed weight, biological yield, number of secondary branches plant and seed yield per plant.

Singh *et al.* (2018) studied 60 germplasm of Indian mustard and observed high heritability coupled with high genetic advance for 1000-seed weight followed by plant height, seed yield per plant and length of main raceme. The magnitudes of PCV and GCV were high for seed yield per plant, 1000-seed weight, secondary branches per plant and length of main raceme.

Yadav and pandey (2018) evaluated 20 germplasm of Indian mustard found that seed yield per plant, biological yield per plant, test weight, harvest index, siliqua primary branches and secondary branches as well as siliquae on primary mother axis observed high GCV and PCV. Test weight, biological yield per plant, seed yield per

plant and siliquae on primary mother axis exhibited higher heritability and higher genetic advance.

Kumari *et al.* (2019) studied 38 gnotypes of Indian mustard and observed high heritability coupled with high genetic advance for days to 50% flowering, number of siliquae per plant, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant, seed yield per plot, biological yield and seed yield per plant. Higher GCV and PCV were recorded for seeds per siliqua.

Rout *et al.* (2019) reported high heritability coupled with high genetic advance as per cent of mean for number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, biological yield per plant, harvest index, seed yield per plant and 1000-seed weight in a study involving 19 genotypes of Indian mustard.

Ray *et al.* (2019) evaluated 19 germplasm of Indian mustard to estimate some genetic parameters. Highest mean was observed for number of siliquae per plant followed by plant height and days to maturity. Highest GCV and PCV were recorded for number of secondary branches, number of siliquae per plant and seed yield per plant. High heritability coupled with high genetic advance recorded for number of secondary branches, number of siliquae per plant, seed yield per plant and biological yield.

2.2 Genetic divergence analysis

One of the potent techniques of assessing genetic divergence is the D^2 statistic proposed by Mahanalobis in 1936. He gave the idea of multivariate analysis for the assessment of genetic diversity. The grouping of genotypes into different clusters based on genetic diversity was done by Rao, 1952 using the method given by Tocher. D^2 analysis of genetic divergence by several workers on different crop plants including Indian mustard has been reviewed and noticed a close correspondence between genetic divergence and a degree of heterosis in crosses. This technique measures the forces of differentiation at two levels, namely intra-cluster and inter-cluster levels and thus helps in the selection genetically divergent parents for exploitation in hybridization programme. The utility of D^2 analysis in providing a basis for selection of parents for hybridization has been emphasized by different

workers. A brief review of available published works relating to genetic divergence has been presented in the following paragraphs.

Goswami and Behl (2006) studied genetic divergence in Indian mustard and recorded higher inter-cluster distances between IV and VI, II and V, IV and V, I and VI. In environment II (E_2), the inter-cluster distances between cluster VI and XV to between XV and X. Higher inter-cluster distances were also recorded between X and VI followed by X and IX, IV and VIII, XV and XII, X and V XIII, XIV and VIII, XIII and X, XIII and XI, VIII and VII. In environment I (E_1), cluster III exhibited less number of days to flowering, high oil content, high main shoot length and cluster II showed less number of days to maturity and plant height.

Singh *et al.* (2010) concluded that seed yield, test weight, branches per plant, seed per silique, siliques per plant, plant height, harvest index and siliques on raceme had contributed maximum towards diversity among the genotypes of Indian mustard. The genotypes from cluster V had short stature, earliest in days to 50% flowering and maturity and cluster VIII had highest silique length, number of seed per silique, 1000-seed weight and seed yield along with high value of number of primary and secondary branches per plant, main raceme length and oil content. The cluster V and VIII were among the most divergent clusters having high seed yield performance along with its contributing traits and high in oil content.

Belete *et al.* (2011) studied multivariate analysis of genetic divergence among 36 genotypes of Ethiopian mustard (*Brassica carinata*) genotypes. Cluster VII was relatively the highest in oleic and the lowest in erucic acid in its seed oil. Genotypes in cluster II and IV showed the highest erucic acid and the highest oil content in their seeds.

Roy *et al.* (2011) evaluated 54 genotypes of Indian mustard and recorded maximum inter-cluster distance between clusters VII and XX followed by the distance between clusters III and XX, clusters XX and XXI and clusters I and XX. Minimum inter-cluster distance was observed between clusters IV and XIV indicating minimum divergence between the genotypes in these two clusters. Maximum intra-cluster distance was recorded in cluster XX indicating higher genetic diversity among the genotypes in that cluster. Cluster VII exhibited the maximum fiber yield per plant and stick weight plant.

Goyal *et al.* (2012) studied genetic diversity among 200 elite germplasms by classifying into seven clusters and found cluster I and cluster VI as most diverse based on inter-cluster distance.

Shathi *et al.* (2012) reported highest inter-cluster distance between clusters I and IV, while the lowest inter-cluster distance was observed between clusters V and VI. Cluster II had the highest intra-cluster distance, while cluster II had the lowest intra-cluster distance. The contribution of genotypes for cluster II had the maximum number of genotypes, while clusters IV, V and VI had the minimum number of genotypes.

Kumar *et al.* (2013) studied 22 genotypes of Indian mustard and observed maximum inter-cluster distance between clusters I and II, indicating wide divergence among the genotypes of these clusters.

Lodhi *et al.* (2013) assessed the genetic divergence in Indian mustard using D^2 statistics for 15 characters enabled grouping of all the genotypes into nine clusters. Cluster I was the largest comprising 20 genotypes followed by cluster II consisting of 18 genotypes and cluster III with 15 genotypes. Whereas, clusters IV, V, VI, VII, VIII and IX contained 10, 8, 7, 7, 3 and 2 genotypes, respectively. The cluster V exhibited maximum intra-cluster distance, while maximum inter-cluster distance was observed between cluster VIII and IX.

Khan *et al.* (2013) classified the genotypes into six clusters and found highest inter-cluster distance between clusters I and cluster V. They showed that yield per plant, number of siliquae per plant and days to maturity were prominent towards the genetic divergence.

Kumar and Pandey (2013) studied genetic diversity in 46 genotypes of Indian mustard by grouping into seven clusters using D^2 statistics. Maximum divergence was observed between V and VI. The clusters numbers II, VI, VII, V were more divergent with high seed yield and cluster I and IV had maximum number of genotypes.

Pandey *et al.* (2013) grouped 45 genotypes of Indian mustard into eight clusters using Tocher's method and observed intra-cluster distance was maximum for cluster VI followed by cluster III. The maximum inter-cluster distance was found between cluster II and III indicating high genetic divergence among genotypes of these groups.

Chaurasia *et al.* (2014) studied 64 genotypes of Indian mustard into seven non-overlapping clusters. The maximum number of genotypes were grouped in cluster III (17) followed by cluster I (14), cluster II (13), cluster V (6), clusters-VI and VII (5 in each) and cluster IV (4). Clusters pair III and IV followed by VII and VI were found to be most divergent. Days to flowering followed by days to maturity and plant height contributed maximum towards genetic diversity.

Singh *et al.* (2014) reported in 30 genotypes of Indian mustard by grouping into four clusters for different quality characters. Genotypes of cluster IV showed maximum value for plant height (185.73), number of secondary branches per plant (32.55) and days to 50% flowering (71.23). Whereas, genotypes of cluster III showed maximum value for seed yield per plant (28.36 g), number of pods per plant (728.12) and chlorophyll content (3.60).

Verma *et al.* (2016) studied genetic divergence in Indian mustard using Mahalanobis D^2 -statistics and grouped them into five clusters. Plant height, number of siliquae on main shoot and days to maturity were found the best discriminatory characters for the selection of diverse genotypes.

Saleem *et al.* (2017) evaluated 167 germplasm for qualitative and quantitative traits of Indian mustard. Highest significant diversity was recorded for different agromorphological characters and maximum variance was recorded for pod shattering followed by plant height, days to 100% flowering and main raceme length. The contribution of first three PCs in the total PCs was 23.25, 12.87 and 11.24, respectively. Among all the investigated accessions two genotypes 26,813 and 26,817 showed great potential for seeds per silique, 1000-seed weight and seed yield per plant.

Devi *et al.* (2017) studied 45 genotypes including local cultivars, advanced lines and notified varieties. They grouped the genotypes into seven clusters in which cluster IV exhibited highest intra-cluster distance followed by cluster VI. The inter-cluster distance was found maximum between cluster V & VII.

Gupta *et al.* (2018) evaluated 35 genotypes of Indian mustard and grouped into six clusters using Tocher's method for different quality characters. Highest inter-cluster distance was observed between cluster II and IV followed by cluster II and V and cluster III and VI. The relative contribution of each character towards divergence

were maximum for oil yield per plant followed by seeds per siliqua, oil content, test weight, plant height and days to maturity. Test weight contributed maximum towards divergence followed by oil yield per plant, oil content, seeds per siliqua, number of secondary branches per plant and siliqua length.

Kumari and Kumari (2018) experimented with 31 genotypes of intra specific crosses of *Brassica juncea* and found maximum inter-cluster distance between clusters II and III. The second most divergent clusters were III and IV. Among the traits 1000-seed weight contributed maximum to genetic divergence followed by days to flower initiation and siliqua length.

Singh *et al.* (2018) studied 60 genotypes of Indian mustard using D^2 statistics. The genotypes were grouped into nine clusters by Tocher's clustering pattern. They identified the superior clusters which have maximum inter-cluster (cluster VI) and intra-cluster (VII cluster) distances and opinioned that these clusters can thus be used for hybridization programme.

Tudu *et al.* (2018) grouped 30 genotypes of Indian mustard into seven cluster using D^2 statistic and recorded maximum contributed of number of secondary branches per plant towards divergence followed by siliqua length, number of seeds per siliqua and 1000-seed weight. Cluster I was the largest group accommodating 12 genotypes followed by cluster III and cluster IV with seven genotypes in each, while clusters II, V, VI and VII accommodated only one genotype in each cluster.

Rout *et al.* (2019) studied different genotype of Indian mustard and recorded maximum intra-cluster divergence in cluster VI followed by cluster V, IV and I. Maximum inter-cluster distance was found between cluster VII and V followed by cluster VII and VI, cluster VII and IV and cluster VII and I. This indicates that efficient breeding programme can be formulated to improve yield potential by hybridization between genotypes from these clusters.

Tripathi *et al.* (2019) conducted an experiment to assess genetic diversity among 25 genotypes of Indian mustard by grouping into six clusters based on D^2 analysis. The cluster I with nine strains was the largest among all the clusters followed by cluster III, II, IV, V and VI. The inter-cluster distance was recorded highest between cluster III and cluster IV. The minimum inter-cluster distance was observed between cluster I and IV.

Gadi *et al.* (2020) assessed genetic divergence in Indian mustard. Cluster V recorded maximum intra-cluster distance, while maximum inter-cluster distance was detected between cluster XI and VI among all the 11 clusters. Cluster I was used to be the most important comprising 11 genotypes pursuing by cluster IV consisting of seven genotypes, cluster II and V (five genotypes), cluster VIII (two genotype) whereas, rest have single genotypes each.

2.3 Character association analysis

Knowledge of character associations between quantitative characters helps in making selection in the field, particularly for seed yield. If, high correlation exists between a relatively low heritable character like yield and a highly heritable character like number of siliquae per plant, selection can be based on the later for improvement in the former. Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variable.

Ramanjaneyulu and Giri (2007) studied correlation in Indian mustard and found that test weight, seeds per siliqua, number of siliquae per plant, number of branches per plant and plant height showed significantly and positive association with seed yield.

Acharya and Patil (2008) observed significant and positive correlation between seed yield and plant height followed by total number of primary branches per plant, number of secondary branches per plant, test weight, days to 50% flowering, days to maturity, length of main raceme, siliquae on main raceme and seeds per siliqua in Indian mustard.

Sirohi *et al.* (2008) studied 30 genotypes of Indian mustard for different traits and found that all the traits showed higher genotypic correlations than phenotypic correlations. Seed yield per plant showed significant positive correlation with biological yield and harvest index.

Singh *et al.* (2011) studied correlation among the various traits of Indian mustard and reported that seed yield had significant positive association with days to 50% flowering, days to maturity, plant height, length of main shoot, number of siliquae on main shoot and 1000-seed weight both at genotypic and phenotypic levels. Seed yield also exhibited positive and significant correlation with oil content only at genotypic level indicating that these are the major yield attributing traits.

Ara *et al.* (2013) evaluated different genotypes of Indian mustard for correlation coefficient analysis and reported that seed yield per plant had significant and highest positive correlation with plant height, days to 50% flowering, length of siliqua and seeds per siliqua.

Lohia *et al.* (2013) studied correlation in 100 genotypes of Indian mustard and reported that seed yield had significant positive association with number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per siliqua and 1000-seed weight, both at genotypic and phenotypic levels.

Rathod *et al.* (2013) reported significant and positive correlation of seed yield per with harvest index, biological yield per plant, number of siliquae per plant and number of secondary branches per plant at both genotypic and phenotypic levels in Indian mustard. They reported that among the component traits, biological yield per plant had significant and positive association with harvest index and oil content at genotypic level.

Priyamedha *et al.* (2013) evaluated 110 early generation line of Indian mustard for correlation coefficient analysis and observed higher positive and significant association of seed yield per plant with number of secondary branches per plant, number of siliquae on main shoot and total siliquae per plant both at genotypic and phenotypic level.

Singh *et al.* (2013) studied 50 genotypes of Indian mustard and reported positive significant correlation with seed yield per plant for main shoot length, siliqua length, number of seeds per siliqua and 1000-seed weight in E_1 , whereas in E_2 it was positively associated with plant height, main shoot length, number of siliquae on main shoot and 1000-seed weight.

Uddin *et al.* (2013) studied seven parental genotypes and their 21 F_2 progenies of *Brassica rapa* for correlation coefficient analysis observed higher significant and positive association with seed yield per plant for number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant.

Iqbal *et al.* (2014) reported higher significant and positive correlation in Indian mustard between seed yield per plant and plant height, number of seeds per siliqua, number of siliquae per plant and length of siliqua.

Lodhi *et al.* (2014) evaluated 90 diverse genotypes of Indian mustard for 15 quantitative traits and found that Seed yield per plant was positively and significantly correlated with number of primary branches per plant, number of secondary branches per plant, primary branch angle, main shoot length, siliqua length and number of seeds per siliqua.

Shekhawat *et al.* (2014) studied 60 genotypes of Indian mustard was recorded higher positive, significant and strong correlation of seed yield per plant with number of siliques per plant test weight and number of seeds per siliqua. It was negatively and significantly correlated with days to 50% flowering and days to maturity. Out of these characters, days to 50% flowering was significantly and positively correlated with days to maturity. Negative and significant correlation between days to maturity and number of seeds per siliqua was observed.

Husan *et al.* (2015) evaluated 10 diverse genotypes of Indian mustard for seed yield and its components and correlation of other traits with seed yield per plant. Significantly positive correlation of seed yield with plant height, branches per plant and seeds per plant at both the phenotypic and genotypic levels was observed.

Islam *et al.* (2016) reported that seed yield per plant had significant positive association with plant height, number of primary branches per plant, number of siliques per plant, seeds per siliqua and siliqua length at genotypic and phenotypic levels.

Kumar *et al.* (2016) studied correlation in 30 Indian mustard genotypes and recorded high significant positive correlation coefficients with seed yield for harvest index and total biological yield per plant both at genotypic and phenotypic levels. Seed yield had negatively correlated with days to 50% flowering and days to maturity.

Meena *et al.* (2017) studied diverse genotypes of Indian mustard and reported that seed yield per plant had positive significant correlation both at phenotypic and genotypic levels with days to maturity, plant height, primary branches per plant, secondary branches per plant, siliques on main shoot and biological yield per plant.

Singh *et al.* (2017) observed highly significant and positive correlation for seed yield per plant with days to flowering, days to maturity, length of main raceme and number of siliques per plant in diverse genotypes of Indian mustard.

Dawar *et al.* (2018) recorded significant and positive correlation in Indian mustard for seed yield per plant and plant height, number of primary branches per plant, number of siliquae per plant and 1000-seed weight at genotypic level.

Devi (2018) studied 12 genotypes of Indian mustard and reported that seed yield per plant was highest positive significant genotypic correlation with biological yield per plant and siliquae on main raceme.

Gupta *et al.* (2018) evaluated 30 diverse genotypes of Indian mustard to assess the correlation for yield and yield related traits under timely (TS) and late sown (LS) conditions. Highly significant and positive association with biological yield per plant followed by harvest index, siliquae on main raceme, length of main raceme, 1000-seed weight and number of secondary branches per plant both, under timely and late sown conditions was observed. On the other hand, plant height possessed highly significant and positive association with seed yield per plant only under timely sown condition.

Ompal *et al.* (2018) studied correlation coefficient with 12 yield contributing characters of 12 varieties of Indian mustard. Grain yield per plant recorded highly positive significant correlation with Biological yield and some other traits at phenotypic level.

Rout *et al.* (2018) studied 38 germplasm of Indian mustard and results revealed that number of siliquae per plant and harvest index had highly significant positive association with seed yield per plant.

Roy *et al.* (2018) reported that seed yield per plant had positively and significantly correlated with pod length, number of seeds per pod and oil content. Negative significant association of seed yield was observed with days to first flowering and total biomass.

Tantuway *et al.* (2018) studied 30 Indian mustard genotypes for traits like, plant height number of primary branches number of secondary branches length of main raceme and number of siliquae per plant and recorded positive and significant correlation with seed yield per plant. Siliqua length was found to be negatively and significantly correlated with seed yield per plant.

Khan *et al.* (2019) observed that siliquae per plant, biological yield per plant, secondary branches per plant and harvest index were positively and significantly associated with seed yield per plant in some genotypes of Indian mustard.

Kumari *et al.* (2019) studied 38 genotypes of Indian mustard and observed that seed yield was positively correlation with plant height, number of secondary branches per plant, number of siliquae per plant, siliqua length, main raceme length, number of siliquae main raceme, test weight, seed yield per plant, seed yield per plot and biological yield.

2.4 Path coefficient analysis

The path analysis is simply standardized partial regression coefficient analysis which may be useful in choosing the characters that have direct and indirect effect on yield. When more characters are included in the calculation of correlations, the matrix becomes complex and the utility of inter-relationships among the components present a confusing picture due to inter-relationship among the components themselves. So, in order to find out a clear picture of the inter-relationship between the seed yield and other yield attributes, the direct and indirect effects are worked out using path analysis. The available literature on the present study was reviewed as under.

Ramanjaneyulu and Giri (2007) studied path analysis in Indian mustard genotypes and revealed that positive direct effect on seed yield was due to plant height and number of productive branches per plant. Negative indirect effect on seed yield was due to number of siliquae per plant and seeds per siliqua.

Acharya and Patil (2008) studied path analysis in Indian mustard with seed yield and observed that higher direct effect was due to number of secondary branches, days to 50% flowering, days to maturity and seeds per siliqua.

Sirohi *et al.* (2008) conducted path analysis experiment with 30 genotypes of Indian mustard and found that positive direct effect on seed yield was due to harvest index and biological yield. Indirect contribution was revealed by harvest index on seed yield.

Ara *et al.* (2013) studied different genotypes of Indian mustard and reported that siliquae per plant had the highest positive direct effect on seed yield followed by seeds per siliqua, length of siliqua and plant height.

Rathod *et al.* (2013) observed higher positive direct effect due to harvest index, length of siliqua, days to 50% flowering, oil content, number of secondary branches per plant and number of primary branches per plant on seed yield.

Priyamedha *et al.* (2013) evaluated 110 early generation line of Indian mustard for path coefficient analysis and found that different traits viz., number of secondary branches per plant, number of siliquae on main shoot and total siliquae per plant had positive direct effect on seed yield per plant indicating that indirect selection for these traits in early generations would be effective in improving seed yield.

Uddin *et al.* (2013) studied seven parental genotypes and their twenty-one F₂ progenies of *Brassica rapa* for path analysis and observed high positive direct effect on seed yield via days to 50% flowering, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant, siliqua length, seeds per siliqua and 1000-seed weight. Days to maturity and plant height had the negative direct effect on yield per plant.

Iqbal *et al.* (2014) reported that higher positive direct effect on seed yield per plant was due to number of siliquae per plant, number of seeds per siliqua and 1000-seed weight. These characters should be included in selecting the genotypes for higher seed yield in mustard.

Lodhi *et al.* (2014) studied 90 diverse genotypes of Indian mustard for fifteen quantitative traits. Path analysis revealed that main shoot length, number of primary branches per plant, number of seeds per siliqua and primary branch angle showed positive direct effect on seed yield per plant which suggested that selection for number of primary branches per plant, primary branch angle, main shoot length, number of seeds per siliqua would be quite effective in improving seed yield in Indian mustard.

Shekhawat *et al.* (2014) observed in 60 genotypes of Indian mustard through path analysis that number of siliquae per plant, test weight and number of seeds per siliqua have positive and high direct effects with seed yield per plant, indicating importance of these characters.

Tahira *et al.* (2014) studied different genotypes of Indian mustard for path analysis and found that seed yield per plant had positive direct contribution of seed per pod and oil content. Indirect effect of pod length on seed yield was also positive.

Hence, the characters, like seed per pod and oil content would be of great use for indirect selection for improvement in seed yield.

Husan *et al.* (2015) revealed through path coefficient analysis in Indian mustard that direct effect on seed yield was high and positive via various traits, viz., seeds per siliqua, 1000-seed weight and days to maturity.

Dipti *et al.* (2016) conducted path analysis in Indian mustard and reported that number of pods on main branch had highest direct contribution to seed yield per plant followed by 1000-seed weight and siliqua density on main shoot. It suggests the selection for these traits would be quite effective in improving seed yield of Indian mustard.

Kumar *et al.* (2016) studied 30 genotypes of Indian mustard and recorded positive direct effect on seed yield through harvest index, followed by total biological yield per plant, days to maturity, siliqua length and at the time of maturity both at genotypic and phenotypic levels.

Dawar *et al.* (2018) recorded highest positive direct effect on seed yield was exhibited through total number of siliquae per plant, plant height, 1000-seed weight, number of primary branches and number of seed per siliqua in Indian mustard.

Devi (2018) studied 12 genotypes of Indian mustard for path analysis and reported that days to 50% flowering showed maximum positive direct effect on seed yield. However, the highest indirect effect of this trait was exhibited through biological yield per plant.

Gupta *et al.* (2018) evaluated 30 diverse genotypes of Indian mustard to assess path coefficient for yield and yield related traits under timely (TS) and late sown (LS) conditions. He recorded high positive direct effect on seed yield due to biological yield per plant followed by harvest index both under timely and late sown conditions. Plant height emerged as most important indirect yield component under timely sown condition. Secondary branches per plant (at genotypic level) and plant height (at phenotypic level) showed maximum indirect effect on seed yield per plant via biological yield per plant under late sown condition.

Ompal *et al.* (2018) observed high positive direct effect on seed yield through biological yield per plant followed by some other traits both at genotypic and

phenotypic path analysis. Resultant direct selection for these traits would be effective for further yield improvement in given genotype of Indian mustard.

Rout *et al.* (2018) studied 38 genotypes of Indian mustard and reported that seed yield per plant had positive and direct influence of harvest index, biological yield, number of siliquae per plant at genotypic level. At phenotypic level path coefficient analysis showed high positive and direct influence of harvest index and biological yield per plant towards seed yield in Indian mustard.

Roy *et al.* (2018) observed high positive direct effect on seed yield via oil content, leaf area index followed by number of seeds per pod and pod length in Indian mustard. They suggested that selection for oil content, leaf area index, number of seeds per pod and pod length would be quite effective in improving seed yield in late sown Indian mustard.

Khan *et al.* (2019) concluded through path coefficient analysis in Indian mustard that biological yield per plant and harvest index imposed high positive direct effect on seed yield per plant. Hence, these characters should be given more weightage in selection programme of high yielding Indian mustard genotypes.

Kumari *et al.* (2019) studied path coefficient analysis in Indian mustard and observed high positive direct effect on seed yield through plant height, number of primary branches per plant, number of secondary branches per plant, siliqua length, seeds per siliqua, main raceme length, number of siliquae on main raceme and number of siliquae per plant.

Chapter-III

MATERIALS AND METHODS

The present investigation entitled “**Genetic divergence and character association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]**” was conducted during *Rabi* 2019. The techniques followed and materials used during investigation are described under following sub heads:

3.1 Experimental site and location

The experiment was carried out at Agricultural Research Station, Ummedganj, Kota, Agriculture University, Kota, Rajasthan. It is situated at the north-western part of India and lies between 23°30' and 30°11' North latitude and 69°29' and 78°17' East longitude. It has an average elevation of 271 meter (889 ft) from sea level.

3.2 Climate and weather condition

Kota has a semi-arid climate (Koppen climate classification BSh) with high temperatures throughout the year. Summers are long, hot and dry, starting in late March and lasting till the end of June. The average temperature is above 40°C in May and June and frequently exceed 45°C with temperature as high as 48.4°C also been recorded. The monsoon season follows with comparatively lower temperatures but higher humidity and frequent, torrential downpours. The average rainfall is about 662 mm, which is most commonly received during June to September. The monsoons subside in October and temperature rises again. The brief, mild winter starts in late November and lasts until the last week of February. The temperatures during winter season range between 26.7°C (max.) to 12°C (min.). The standard weekly meteorological data for the period of this investigation recorded at the Meteorological Observatory, Agricultural Research Station, Ummedganj, Kota, Agriculture University, Kota are presented in Table. 3.1.

3.3 Experimental materials

The experimental materials for the present investigation comprised of 60 genotypes of Indian mustard received from different rapeseed mustard research centres of the country (Table 3.1). Thus, the genotypes are of diverse geographical origin representing a broad spectrum of variability.

**Table 3.1 Weekly meteorological data at Agricultural Research Station, Kota
(October 2019-April 2020)**

Standard Week	Standard week period	Temperature		Rainfall (mm)	Rainy days	RH (%)
		Max.	Min.			
40	01 Oct.- 07 Oct.	32.00	24.00	0.00	0.00	84.0
41	08 Oct. - 14 Oct.	31.71	23.00	0.00	0.00	88.14
42	15 Oct. - 21 Oct.	33.60	18.90	0.00	0.00	86.4
43	22 Oct. - 28 Oct.	32.00	18.21	0.00	0.00	82.57
44	29 Oct. - 4 Nov.	32.36	18.86	0.00	0.00	73.86
45	05 Nov.-11 Nov.	31.57	17.29	0.00	0.00	84.57
46	12 Nov.-18 Nov.	31.40	17.40	0.00	0.00	90.40
47	19 Nov.- 25 Nov.	30.10	16.50	0.00	0.00	84.40
48	26 Nov. -02 Dec.	30.00	17.40	0.00	0.00	91.40
49	03 Dec. - 9 Dec.	26.80	14.70	0.00	0.00	85.40
50	10 Dec.-16 Dec.	26.36	14.29	0.00	0.00	83.14
51	17 Dec. - 23 Dec.	24.14	9.79	0.00	0.00	83.71
52	24 Dec. - 31 Dec.	21.64	7.14	0.00	0.00	83.86
01	01 Jan. - 07 Jan.	22.71	6.71	0.00	0.00	86.29
02	08 Jan. -14 Jan.	24.20	8.50	0.00	0.00	84.71
03	15 Jan. - 21 Jan.	21.29	7.93	0.00	0.55	85.00
04	22 Jan. - 28 Jan.	22.86	9.21	0.00	0.00	84.29
05	29 Jan. - 04 Feb.	23.64	9.57	0.00	0.00	84.86
06	05 Feb. - 11 Feb.	24.07	9.86	0.00	0.00	85.33
07	12 Feb. - 18 Feb.	25.71	12.43	0.00	0.00	71.86
08	19 Feb. - 25 Feb.	26.93	15.14	0.00	0.00	73.71
09	26 Feb. - 03 Mar.	27.86	15.71	0.00	0.00	78.43
10	04 Mar. - 10 Mar.	28.29	15.14	0.00	0.00	60.86
11	11Mar. - 17 Mar.	27.90	14.93	0.00	0.00	57.71
12	18 Mar. - 24 Mar.	28.79	16.21	4.00	1.00	62.43
13	25 Mar. - 31 Apr.	29.00	15.79	15.0	1.00	59.86
14	01 Apr. - 07 Apr.	35.50	17.07	0.00	0.00	34.29
15	07 Apr. - 14 Apr.	40.69	18.63	0.00	0.00	24.88
16	15 Apr. - 21 Apr.	41.08	18.75	0.00	0.00	31.71

Table 3.2 List of 60 Indian mustard genotypes used in present investigation.

S. No.	Name of the Genotypes	Source (Material received)
1.	Pusa Jai Kisan	IARI, New Delhi
2.	RH-725	CCSHAU, Hisar
3.	Pusa Bold	IARI, New Delhi
4.	PBR-91	PAU RS Bathinda
5.	Rohini	CSAUA&T, Kanpur
6.	RH-51	CCSHAU, Hisar
7.	RH-419	CCSHAU, Hisar
8.	RH-904	CCSHAU, Hisar
9.	RM-51	JNKVV ZRS Morena
10.	RGN-303	RAU ARS, Sriganaganagar
11.	RGN-34	RAU ARS, Sriganaganagar
12.	RH 10	CCSHAU, Hisar
13.	YSRL-9	IARI, New Delhi
14.	NPJ-206	IARI, New Delhi
15.	NPJ-208	IARI, New Delhi
16.	JA-96	IARI, New Delhi
17.	Pusa Mahak	IARI, New Delhi
18.	Pusa Tarak	IARI, New Delhi
19.	PM-26	IARI, New Delhi
20.	PM-28	IARI, New Delhi
21.	PDZ-1	IARI, New Delhi
22.	Shivalik	Mahyco, Maharashtra
23.	GM-1	SDAU SK Nagar
24.	Urvashi	CSAUA&T, Kanpur
25.	JM-2	JNKVV ZRS Morena
26.	Basanti	CSAUA&T, Kanpur
27.	Kranti	GBPUA&T, Pantnagar
28.	Pusa Bahar	IARI, New Delhi
29.	Vardaan	CSAUA&T, Kanpur
30.	Vaibhav	CSAUA&T, Kanpur
31.	JM-1	JNKVV ZRS Morena
32.	Ashirwad	CSAUA&T, Kanpur
33.	PM-27	IARI, New Delhi
34.	Jagannath	IARI, New Delhi
35.	GM-3	SDAU SK Nagar
36.	RH-406	CCSHAU, Hisar
37.	Shivani	BAU Ranchi, Jharkhand
38.	Giriraj	DRMR, Bharatpur
39.	RH-30	CCSHAU, Hisar
40.	Maya	CSAUA&T, Kanpur

41.	Vasundhra	CCSHAU, Hisar
42.	CS-54	CSSRI Karnal
43.	Varuna	CSAUA&T, Kanpur
44.	Krishna	GBPUA&T, Pantnagar
45.	GM-2	SDAU SK Nagar
46.	Swarn Jyoti	CCSHAU, Hisar
47.	RVM-2	SKRAU, Bikaner
48.	RH-749	CCSHAU, Hisar
49.	RH-781	CCSHAU, Hisar
50.	NRCHB-101	DRMR, Bharatpur
51.	RGN-48	RAU ARS, Sriganganagar
52.	Kanti	CSAUA&T, Kanpur
53.	RH-819	CCSHAU, Hisar
54.	EJ-20	IARI, New Delhi
55.	RGN-229	RAU ARS, Sriganganagar
56.	RGN-73	RAU ARS, Sriganganagar
57.	DRMR-601	DRMR, Bharatpur
58.	NRCDR-2	DRMR, Bharatpur
59.	RGN-236	RAU ARS, Sriganganagar
60.	JM-3	JNKVV ZRS Morena

3.4 Method of experimentation

The field experiment was laid out in a Randomized Block Design (RBD) with 3 replications and 60 test genotypes. Each genotype was represented by 2 lines of 5.0 meters row length having 30 cm spacing between lines and 10 cm spacing between plants. Sowing of the experiment was done on the 31st October 2019. The recommended agronomic practices and plant protection measures whenever necessary were followed to raise a healthy crop.

3.4.1 Sampling procedure and observations

Observations on various characters were recorded timely on randomly selected five plants from each genotype in each of the replications. Days to 50% flowering and days to maturity were recorded on plot basis. Detailed procedure adopted for recording observations is as under.

3.4.1.1 Days to 50% flowering

It was recorded as the number of days from the date of sowing to the date when 50% of the plants per genotype in the plot showed flowering.

3.4.1.2 Days to maturity

Days to maturity was recorded as the number of days taken from the date of sowing to the date on which siliquae on more than 75% plants started turning yellow.

3.4.1.3 Plant height (cm)

The plant height was measured in centimeter from ground level to the tip of the topmost silqua of the randomly selected five plants at maturity and averaged over to obtain the plant height.

3.4.1.4 Number of Primary branches per plant

All the branches arising from the main stem of the selected plants were counted after harvesting and averaged over to get number of primary branches per plant.

3.4.1.5 Number of Secondary branches per plant

All the effective branches emerging from primary branch of plant were counted at maturity and averaged over to get number of Secondary branches per plant.

3.4.1.6 Length of main axis (cm)

The length of main axis was measured in centimeters from five selected plant and averaged over to get length of main axis.

3.4.1.7 Number of siliquae per plant

The number of seed-bearing siliquae of each individual selected plant were counted and averaged over to obtain number of siliquae per plant.

3.4.1.8 Number of siliquae on main axis

Number of siliquae present on the main axis of the selected plants was counted and averaged over to obtain number of siliquae on main axis.

3.4.1.9 Length of silqua

Five siliquae from each selected plant were taken at random and length of each silqua was measured in centimeter and averaged over.

3.4.1.10 Number of seeds per silqua

Numbers of seeds obtained from five randomly selected siliquae from each plant was counted and averaged over to record the number of seeds per silqua.

3.4.1.11 1000-seed weight (g)

One thousand air dried seeds were counted from bulk of randomly selected plants and weighed by electronic balance to record 1000-seed weight in gram.

3.4.1.12 Oil content (%)

Oil content in percent was measured from bulk of randomly selected plants by using Nuclear Magnetic Resonance (NMR) at Division of Genetics, IARI, New Delhi.

3.4.1.13 Harvest index (%)

The ratio was calculated between average seed yield obtained from the 10 randomly selected plants and the average dry weight of the same randomly selected sample of 10 plants (expressed in percentage).

$$\text{Harvest index (\%)} = \frac{\text{Seed yield per plant}}{\text{Total biological yield}} \times 100$$

3.4.1.14 Seed yield per plant (g)

The total seed yield obtained from 10 randomly selected plants were threshed, cleaned, dried and weighed by electronic balance and averaged over to obtain seed yield per plant.

3.5 Statistical analysis

The data collected for each character on individual plant basis for five randomly selected plants were averaged to get mean values. The replication wise mean values for the individual characters of different genotypes were subjected to analysis of variance (ANOVA) using RBD design. The variability parameters were measured by the formula suggested by Johnson *et al.* (1955). The analysis for divergence was done following Mahalanobis (1936) D^2 statistics. Correlation coefficient was calculated as per procedure given by Singh and Choudhary (1979) whereas, path coefficient analysis was carried by the procedure suggested by Dewey and Lu (1959)

3.5.1 Analysis of variance

The data were subjected to analysis of variance adopting standard statistical methods (Panse and Sukhatme, 1985). The analysis of variance including source of variations, their degree of freedom (D.F.) and expectations of mean squares are as given below:

Source of variation	Degrees of freedom (df)	Mean sum of squares (MSS)	Expectations of Mean sum of squares
Replication	(r-1)	MSr	$\sigma^2_e + g \sigma^2_r$
Genotypes	(g-1)	MSg	$\sigma^2_e + r \sigma^2_g$
Error	(r- (r-1))(g-1)	Mse	σ^2_e
Total	(r g - 1)		

Where,

- R = Number of replications
G = Number of genotypes
MSr = Mean sum of square due to replications
MSg = Mean sum of square due to genotypes
MSe = Mean sum of square due to error
 σ^2_g = Genotypic variance
 σ^2_r = Replication variance
 σ^2_e = Error variance

Analysis of variance components

The genotypic, phenotypic and error variance were calculated as follows.

(i) Genotypic variance (σ^2_g)

The genotypic variance is due to the differences among genotypes included in the study was calculated as under:

$$\text{Genotypic variance } (\sigma^2_g) = MS_g - MS_e / r$$

(ii) Phenotypic variance (σ^2_p)

It is the sum of variance contributed by genetic causes and environmental factors. It was calculated as under:

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

(iii) Error variance (σ^2_e)

The mean square of error represented by the variation attributed to environmental causes.

$$\text{Environmental variance } (\sigma^2_e) = MSe$$

3.5.2 Variability parameters

3.5.2.1 Range

It is the difference between the lowest and the highest value for each character.

$$\text{Range} = \text{Highest value} - \text{Lowest value}$$

3.5.2.2 Mean ($\bar{X}$)

It is computed by dividing the sum of all observations in a sample by their number.

$$(\bar{X}) = \Sigma X_i / n$$

Where,

$$\begin{aligned} (\bar{X}) &= \text{General mean} \\ N &= \text{Number of observations} \\ \Sigma X_i &= \text{Summation of all the observation} \end{aligned}$$

3.5.2.3 Standard error of mean (SE_m)

The standard error of mean (SE_m) was calculated with the help of following formula.

$$S.E.m = \sqrt{\sigma_e^2 / r}$$

3.5.2.4 Coefficient of variation (CV)

(a) Phenotypic coefficient of variation (PCV)

$$P.C.V. (\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

(b) Genotypic co-efficient of variation (GCV)

$$G.C.V. (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

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

Heritability refers to the portion of variability which is heritable in nature out of the total variability. It is due to the genetic causes. Heritability in broad sense (h^2_{bs}) was calculated according to the following formula suggested by Burton and De Vane (1953).

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

The heritability is classified into three groups as suggested by Robinson *et al.* (1966).

Low	= 0-30 percent
Moderate	= 30-60 percent
High	= 60-100 percent

3.5.2.6 Genetic Advance (GA)

Expected genetic advance represents the shift in a population mean towards superior side under selection pressure after single generation of selection. This was estimated as per the formula suggested by Johnson *et al.* (1955).

$$GA = h^2_{bs} \times k \times \sigma_p$$

Where,

GA	= Genetic Advance
h^2_{bs}	= Heritability (broad sense)
k	= Selection intensity, (k = 2.06 at 5 per cent selection intensity)
σ_p	= Phenotypic standard deviation

3.5.2.7 Genetic advance expressed as percentage of mean

The expected genetic advance (GA. expressed in percentage of mean was calculated by using the method suggested by Johnson *et al.* (1955).

$$\text{Genetic advance as per cent of mean} = \frac{G.A.}{\bar{X}} \times 100$$

Genetic advance as per cent mean was classified as follows. (Johanson *et al.*, 1955)

Low	= 0-10 percent
Moderate	= 10-20 percent
High	= > 20 percent

3.6. Genetic divergence analysis

The Genetic divergence amongst different genotypes was assessed based on the estimated *inter-se* genetic distances amongst the genotypes. One of the potent

techniques of assessing genetic divergence is the D^2 statistics proposed by **Mahalanobis in 1936**. D^2 statistics technique measures the forces of differentiation at two levels, namely, intra-cluster and inter cluster levels and thus helps in the selection of genetically divergent parents for exploitation in hybridization programmes.

3.6.1 Clustering of genotypes using the D^2 values

Tocher's method was used for clustering the genotypes into different groups (**Rao, 1952**). The basis of clustering by this method was that any two varieties belonging to the same cluster would show smaller D^2 values as compared to those belonging to two different clusters. This method started with two closely associated populations to find a third population which had the smallest average of D^2 values. In the same manner, fourth one was chosen having the smallest average of D^2 values from the first three and so on. This process was repeated until D^2 values of all the genotypes were exhausted, except those that were included in the former cluster.

3.6.2 Testing differences in the population

From the variance analyses, when the null hypothesis of no treatment differences fails with regards to individual characters, a dispersion table was prepared. Using V statistic, which intern utilize Wilk's criterion (Δ), a simultaneous test of differences between mean values of a number of correlated variables was done (Rao, 1952)

$$\text{Wilk's criterion } (\Delta) = \frac{\text{Determinants of error variance and covariance matrix (E)}}{\text{Determinants of genotypic + error variance and covariance matrix}}$$

$$V \text{ statistic} = -m \log_e \Lambda = - \left(n - \frac{p+q+1}{2} \right) \log \Lambda$$

Where,

$$m = \left(n - \frac{p+q+1}{2} \right)$$

P = Number of variables or characters

Q = Degrees of freedom for population (i.e., number of genotypes-1)

N = Degrees of freedom for error + genotypes

$\log_e \Lambda$ = 2.3026 $\log_{10} \Lambda$

‘V’ statistic is distributed as χ^2 with pq degrees of freedom. The test of significance of ‘V’ statistic showed that the differences between the means in respect of the pooled effect of p characters between different populations were significant. Hence further analyses were made to estimate D^2 values.

3.6.3 Mahalanobis D^2 statistics

In the present investigation genetic divergence was estimated based on Mahalanobis generalized distance as described by **Rao (1952)**. Original variable means were transformed to un-correlated variables by the pivotal condensation method of inversion matrix. The D^2 values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combinations, the mean deviation

i.e. $d_i = Y_i^1 - Y_i^2$, where Y_i denotes the transformed variables ($i = 1, 2, 3, 4, 5, \dots, p$) were calculated and the D^2 was then calculated as sum of the squares of those deviations, i.e.

$$D^2 = \sum (Y_i^1 - Y_i^2)^2$$

Where, p = Number of characters.

The significance of D^2 values was tested by treating them as chi-square (χ^2) at p degrees of freedom where p is the number of characters considered.

3.6.4 Grouping of genotypes by Tocher’s method

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher’s method described by **Rao (1952)**. The criterion used in this method was that any two varieties belonging to the same cluster, at least on an average, show a smaller D^2 value than those belonging to two different clusters. Then inter and intra-cluster distances were calculated and their relationships were diagrammatically represented.

3.7 Character association analysis

The correlation coefficients were calculated to determine the degree of association of the characters with yield and its attributes. Genotypic and phenotypic

correlation coefficients were worked out by a method described by Singh and Chaudhary (1979).

(a) Genotypic correlation

$$r_{xy}(g) = \frac{\text{Cov. } xy(g)}{\sqrt{Vx(g).Vy(g)}}$$

(b) Phenotypic correlation

$$r_{xy}(p) = \frac{\text{Cov. } xy(p)}{\sqrt{Vx(p).Vy(p)}}$$

Where

$r_{xy}(g)$	= Genotypic correlation between x and y traits
$r_{xy}(p)$	= Phenotypic correlation between x and y traits
Cov. xy (g)	= Genotypic covariance for x and y traits
Cov. xy (p)	= Phenotypic covariance for x and y traits
$Vx(g)$	= Genotypic variance for x trait
$Vy(g)$	= Genotypic variance for y trait
$Vx(p)$	= Phenotypic variance for y trait
$Vy(p)$	= Phenotypic variance for x trait

Test of significance

The significance of correlation coefficient was tested using the following formula:

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

3.8 Path coefficient analysis

The direct and indirect effects were estimated using path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following equations were solved for estimating the various direct and indirect effects.

$$\begin{aligned} r_{1y} &= P_{1y} + r_{12}P_{2y} + \dots\dots\dots + r_{1p}P_{py} \\ r_{2y} &= r_{21}P_{1y} + P_{2y} + \dots\dots\dots + r_{2p}P_{py} \\ &\dots\dots\dots \\ &\dots\dots\dots \\ R_{py} &= r_{p1}P_{1y} + r_{p2}P_{2y} + \dots\dots\dots + P_{py} \end{aligned}$$

Where,

$P_{1y}, P_{2y}, \dots, P_{py}$ are direct effects of character 1, 2, ..., p on y and
 $r_{1y}, r_{2y}, \dots, r_{py}$ denote correlation coefficient between independent
 characters 1, 2, ..., p and dependent character 'Y'.

Residual effect

Calculated using the following formula:

$$P_{Ry} = \frac{1 - P^2 R_y + \sum P_{iy} R_{iy}}{\sqrt{1 - (P_{1y} r_{1y}) - (P_{2y} r_{2y}) - \dots - (P_{iy} r_{iy})}}$$

Where,

P_{Ry} is the residual effect

The present study comprised of 60 genotypes of Indian mustard (*Brassica juncea* L.) collected from different sources of diverse origin. The genetic variability was estimated by analysis of variance (ANOVA) and the different parameters of variability such as range, mean, (Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability, Genetic advance (GA) and GA expressed as per cent of mean were tabulated. The analysis of genetic divergence through multivariate approach included Mahalanobis D^2 analysis. The nature and extent of association among the different yield attributing traits were studied by genotypic and phenotypic correlation analysis whereas the path coefficient analysis revealed the direct and indirect effects on yield via component traits.

A complete analysis of the experiment data reveals the result as discussed under the following heads:

- 4.1 Analysis of variance
- 4.2 Mean performance of the genotypes
- 4.3 Genetic variability parameters
- 4.4 Genetic divergence analysis
- 4.5 Character association analysis
- 4.6 Path coefficient analysis

4.1 Analysis of variance:

Analysis of variance for the Randomized Block Design with respect to 60 genotypes of Indian mustard revealed significant differences among the material used in the present investigation for all the 14 characters studied viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main axis (cm), number of siliquae per plant, number of siliquae on main axis, length of silique (cm), number of seeds per silique, 1000-seed weight (g), oil content (%), harvest index (%) and seed yield per plant (g), indicating wide spectrum of variation among the genotypes (Table 4.1).

Table 4.1 Analysis of variance (ANOVA) for 14 quantitative characters in Indian mustard genotypes

Source of variation	D.F.	Mean sum of squares													
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Length of main axis (cm)	Number of siliquae per plant	Number of siliquae on main axis	Length of siliqua (cm)	Number of seeds per siliqua	1000-seed weight (g)	Oil content (%)	Harvest index (%)	Seed yield per plant (g)
Replication	2	1.51	0.41	140.96	0.68	7.81	38.82	1748.35	0.84	0.38	1.94	0.06	0.41	0.48	0.73
Treatment	59	44.63**	80.82**	559.91**	2.41**	25.50**	161.15**	3550.15**	60.28**	1.13**	5.28**	1.40**	3.53**	27.62**	11.90**
Error	118	0.61	0.52	90.66	0.49	2.38	36.87	1098.25	17.44	0.14	1.65	0.03	0.35	1.29	0.74

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

4.2 Mean performance of the genotypes

The mean performance of 60 Indian mustard genotypes for different quantitative traits is presented in the Table 4.2. The performance of the genotypes is discussed below in terms of the different characters.

4.2.1 Days to 50% flowering

The spectrum of variability of genotypes for days to 50% flowering ranged between 43.00 days (PM-28) to 61.00 days (NRCHB-101) with overall mean of 50.10 days. The genotypes like, PM-28 (43.00 days), RVM-2 (44.00 days), JM-1 (44.00 days), NRCDR-2 (44.33 days) and Pusa Tarak (44.67 days) were found earliest with respect to 50% flowering. The genotypes NRCHB-101 (61.00 days), RH-819 (60.33 days), RH-51 (56.67 days) and Urvashi (56.67 days) were found late.

4.2.2 Days to maturity

Genotypes with lowest number of days to maturity indicate the earliness which is a desirable criterion for developing of mustard varieties suitable for early *Rabi* season. The days to maturity ranges between 122.70-141.00 days, with the overall mean of the character being 134.66 days. The genotypes PM-28 (122.67 days), CS-54 (125.67 days), RH-819 (125.67 days), PDZ-1 (125.67), Swarn Jyoti (126.00 days) and GM-2 (126.67 days) were found early maturing types. The genotype Pusa Jai Kishan (141.00 days) was found late maturing followed by RH-419 (140.67 days), PBR-91 (139.67 days) and RH-10 (139.67 days).

4.2.3 Plant height

The overall mean for plant height among 60 genotypes was found to be 223.12 cm with a spectrum of variation in range from 191.27 cm (Pusa Mahak) to 253.07 cm (RH-51). Pusa Mahak (191.27) was found to be the shortest in plant height followed by PM-26 (194.00 cm) PM-28 (194.33 cm) and RH-30 (201.93), whereas RH-51 (253.07), DRMR-601 (251.20 cm), CS-54 (247.40) and RGN-34 (236.80) were found tall among the various 60 genotypes. Twenty-eight genotypes were found shorter than the mean value for plant height.

4.2.4 Number of primary branches per plant

The magnitude of number of primary branches per plant ranged from 6.60 (Vaibhav) to 11.27 (RH-406) with an average value of 8.07. The genotypes which exhibited maximum number of primary branches per plant was RH-406 (11.27) followed by EJ-20 (9.73) Pusa Tarak (9.47) PM-26 (9.47) and GM-2 (9.40). The genotypes with minimum number of primary branches per plant were Vaibhav (6.60), Shivalik (6.73), Swarn Jyoti (6.73), Kanti (6.73) and RH-819 (6.73). In total 32 genotypes showed higher number of primary branches per plant than the overall mean for this character (8.07).

4.2.5 Number of secondary branches per plant

The number of secondary branches per plant ranges between 15.27-27.70 with the overall mean of the character being 21.50. The genotypes like PM-26 (27.70), Varuna (26.20), RGN-34 (26.07) and EJ-20 (26.07) were having maximum number of secondary branches per plant. Three genotypes viz., NRCDR-2 (16.33) NRCHB-101 (16.13) and Shivani (15.27) were found with minimum number of secondary branches per plant.

4.2.6 Length of main axis

The average length of main axis was 75.25 cm while it ranged from 53.53 cm (RGN-303) to 90.47 cm (RH-51). The genotypes RH-51 (90.47), Pusa Bold (88.67), Pusa Bahar (88.60) and Vaibhav (87.27) recorded maximum length of main axis. The genotypes viz., RGN-303 (53.53), PM-26 (60.27), Kranti (60.87), Urvashi (61.47) and RH-30 (63.27), were found to have minimum length of main axis.

4.2.7 Number of siliquae per plant

The seed yield of any variety depends upon the contribution of yield determining characters and number of siliquae is an important trait among them. The average numbers of siliquae per plant was 383.29 and it ranged from 271.93-441.07. The genotypes Varuna (441.07), Pusa Jai Kishan (436.80), RH-725 (429.53), RGN-229 (429.33), RGN-34 (424.80) and CS-54 (421.80), were found statistically higher number of siliquae per plant. Lowest number of siliquae per plant was found in Shivani (271.93), Swarn Jyoti (293.00) and PBR-91 (302.40).

4.2.8 Number of siliquae on main axis

The average number of siliquae on main axis was 44.22 with maximum 54.20 (JM-3) and minimum 32.80 (PM-26). The genotypes PM-26 (32.80), JM-1 (35.40), Maya (38.53), RGN-48 (35.93) and Basanti (37.13) exhibited minimum number of siliquae on main axis, while genotypes JM-3 (54.20), RH-419 (53.73), Vasundhara (52.0) and DRMR-601 (51.2) showed maximum number of siliquae on main axis.

4.2.9 Length of siliqua

The range of observation for length of siliqua was 3.73 cm (RGN-303) to 6.69 cm (PM-27), while the overall mean for the character was 5.47 cm. The genotypes PM-27 (6.69 cm), Rohini (6.67 cm), RH-406 (6.46 cm) and NRCDR-2 (6.43 cm) RH-749 (6.41 cm) were found with highest length of siliqua. Genotypes RGN-303 (3.73 cm), NRCHB-101 (4.27 cm), Pusa Mahak (4.57 cm) and GM-1 (4.63 cm) exhibited minimum length of siliqua.

4.2.10 Number of seeds per siliqua

Seeds per siliqua ranged from 12.80 in Vasundhara to 19.33 in JM-3 and the average number of seeds per siliqua was 15.05. Maximum number of seeds per siliqua was recorded by the genotypes JM-3 (19.33), JM-1 (17.47), Giriraj (17.33), CS-54 (17.27) and RH-406 (16.80), while minimum number of seed per siliqua was showed by Vasundhara (12.80), RGN-34 (13.00), RGN-48 (13.07) and RH-30 (13.33). In total 27 genotypes showed higher number of seeds per siliqua than the overall mean of 15.05.

4.2.11 1000-seed weight

The mean value for 1000-seed weight ranged from 3.04 g (RGN-303) to 6.23 g (RH-30) with an overall mean value of 4.43 g. The genotype RH-30 found to have boldest seed with 6.23 g of 1000-seed weight followed by PBR-91 (5.74 g), Vaibhav (5.70 g) and RVM-2 (5.57 g). Lowest value of 1000-seed weight was exhibited by the genotypes, RGN-303 (3.04 g) and Kranti (3.06 g). Twenty-eight genotypes recorded more than the average value (4.43 g) for this character.

4.2.12 Oil content

The average value for this trait was 40.34% whereas it ranged from 37.13% (RGN-303) to 42.34% (PM-27). The genotypes PM-27 (42.34%), RM-51 (42.22%), Pusa Bahar (41.98%), RH-904 (41.86%) and RH-406 (41.62%) were found statistically highest for oil content %. Lowest oil content % was found in genotypes RGN-303 (37.17%), Ashirwad (37.55%), GM-1 (38.15%), Pusa Tarak (38.33%) and NPJ-208 (38.82%).

4.2.13 Harvest index

This character recorded an overall mean value of 22.65% over the 60 genotypes. The magnitude of harvest index ranged within 14.91-28.31%. The genotypes NRCDR-2 (28.31%), Ashirwad (28.03%), RH-406 (26.89%), CS-54 (26.64%) and RH-749 (26.49%) were found statistically superior with regards to this character. The genotypes RVM-2 (14.91%) RH-10 (15.90%) and EJ-20 (16.65%) recorded lowest for the character.

4.2.14 Seed yield per plant

The variation in the values of mean seed yield per plant was observed within a range of 8.43 g (RVM-2) to 16.55 g (RH-725), while the average value for seed yield per plant was 12.16 g. The genotypes RH-725 (16.55 g), Giriraj (15.64 g), RGN-303 (15.60 g), Kranti (15.44 g) and Pusa Jai Kishan (14.92 g) had higher seed yield per plant. Lowest seed yield per plant was recorded by the genotypes RVM-2 (8.43 g), RGN-48 (8.77 g) and CS-54 (9.06 g). Twenty-eight numbers of genotypes recorded more than the average value for seed yield per plant.

Table 4.2 Mean values of 60 Indian mustard genotypes for 14 quantitative characters

Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Length of main axis (cm)	Number of siliquae per plant	Number of siliquae on main axis	Length of siliqua (cm)	Number of seeds per siliqua	1000-seed weight (g)	Oil content (%)	Harvest index (%)	Seed yield per plant (g)
Pusa Jai Kisan	55.67	141.00	235.47	8.00	24.00	68.00	436.80	46.60	5.33	15.27	4.32	39.49	24.17	14.92
RH-725	52.67	129.67	237.53	9.13	20.93	80.93	429.53	49.40	6.13	14.67	5.50	41.22	24.81	16.55
Pusa Bold	47.67	138.00	226.33	8.47	21.20	88.67	339.73	45.87	4.75	14.73	4.52	41.08	20.39	14.23
PBR-91	51.67	139.67	209.67	8.53	25.47	68.40	302.40	37.67	5.77	13.67	5.74	40.48	20.55	11.90
Rohini	49.00	134.00	232.73	8.20	23.73	79.67	395.80	44.47	6.67	15.20	4.74	40.97	23.48	14.74
RH-51	56.67	133.67	253.07	7.07	22.33	90.47	382.20	43.00	5.12	14.87	4.33	40.94	25.51	12.93
RH-419	53.00	140.67	229.13	7.73	20.07	80.07	389.27	53.73	5.44	13.67	5.24	41.22	19.70	13.58
RH-904	49.00	131.00	217.40	8.27	23.33	71.40	394.27	41.50	5.66	16.67	3.55	41.86	18.52	12.83
RM-51	52.00	133.33	233.73	8.47	24.53	77.67	392.20	43.07	4.91	16.07	3.99	42.22	19.16	13.45
RGN-303	53.00	139.67	232.93	7.33	21.00	53.53	408.47	45.93	3.73	15.80	3.04	37.13	17.63	15.60
RGN-34	48.00	138.00	236.80	7.60	26.07	65.27	424.80	49.93	5.63	13.00	4.71	40.85	22.38	14.03
RH-10	55.00	139.67	244.53	8.13	20.73	73.87	370.20	40.00	4.81	14.87	3.62	40.32	15.90	11.29
YSRL-9	54.00	139.00	229.20	8.07	22.20	77.93	395.67	42.27	5.25	16.60	4.15	40.28	22.54	10.36
NPJ-206	45.00	137.67	228.13	8.33	22.33	70.13	359.60	47.40	6.11	13.67	4.58	39.86	20.39	9.83
NPJ-208	52.67	138.33	214.40	7.27	22.47	78.40	361.33	42.87	5.82	15.00	4.23	38.82	20.90	9.89
JA-96	48.00	128.67	221.60	7.60	20.40	74.13	378.80	43.53	6.14	16.40	4.70	40.78	19.39	10.04
Pusa Mahak	45.67	136.67	191.27	8.20	17.53	78.87	353.67	44.27	4.57	15.00	4.24	40.55	22.46	13.51
Pusa Tarak	44.67	129.67	235.13	9.47	19.00	74.53	345.93	40.87	5.41	13.87	4.35	38.33	21.10	11.83
PM-26	48.33	129.00	194.00	9.47	27.70	60.27	400.33	32.80	4.93	13.73	4.06	40.43	23.75	14.27
PM-28	43.00	122.67	194.33	8.40	25.93	66.87	409.07	42.20	6.23	14.13	4.70	40.46	27.46	12.65
PDZ-1	47.67	125.67	216.13	7.73	18.53	83.47	403.60	47.27	5.03	15.87	5.73	41.05	25.21	11.88
Shivalik	45.00	134.67	226.47	6.73	19.80	82.60	368.20	43.13	4.77	14.40	3.55	39.77	22.00	11.27
GM-1	47.00	128.67	234.60	7.93	22.80	78.33	402.70	43.27	4.63	13.73	4.46	38.15	23.58	11.85
Urvashi	56.67	138.33	213.67	8.60	23.27	61.47	375.67	40.13	5.55	15.60	4.70	39.69	20.25	9.26
JM-2	51.33	139.00	225.33	8.13	21.73	75.87	420.00	42.20	5.47	15.33	4.06	39.61	21.44	12.40
Basanti	53.00	139.67	226.80	7.80	22.60	74.87	391.20	37.13	5.27	14.13	4.23	41.06	22.01	9.44
Kranti	54.00	139.00	210.33	7.53	20.93	60.87	386.67	45.07	5.33	16.53	3.06	40.53	23.74	15.44
Pusa Bahar	51.67	138.67	214.20	8.33	20.87	88.60	346.93	46.47	5.57	15.13	4.01	41.98	20.30	14.24
Vardaan	47.67	138.33	219.27	7.73	21.60	75.13	382.80	47.73	5.53	14.47	3.59	39.36	26.15	10.30
Vaibhav	49.00	137.67	233.60	6.60	16.33	87.27	366.07	38.33	5.90	14.07	5.70	39.02	21.60	12.16

JM-1	44.00	130.67	209.53	7.43	25.47	73.53	414.13	35.40	5.79	17.47	4.06	41.28	23.74	11.97
Ashirwad	53.67	127.67	215.53	7.43	21.57	69.53	383.13	48.07	5.10	14.67	4.70	37.55	28.03	13.38
PM-27	51.00	138.67	226.67	8.07	22.67	82.93	375.53	40.00	6.69	14.67	5.07	42.34	26.67	11.62
Jagannath	48.00	139.00	202.00	7.60	17.80	74.87	386.00	40.80	4.89	13.40	3.65	40.18	21.89	10.63
GM-3	49.67	138.67	224.60	9.73	23.07	69.80	369.73	43.67	5.82	13.33	4.12	40.05	22.12	10.35
RH-406	52.67	136.00	211.13	11.27	22.73	85.13	393.47	45.00	6.46	16.80	4.64	41.62	26.89	9.28
Shivani	49.00	139.33	227.53	7.13	15.27	80.00	271.93	44.00	5.23	15.87	4.02	40.69	20.63	9.21
Giriraj	47.67	138.67	214.00	7.33	19.53	79.33	412.20	42.90	5.51	17.33	4.56	40.96	24.00	15.64
RH-30	53.00	138.33	201.93	8.27	18.20	63.27	360.67	45.00	5.75	13.33	6.23	39.50	23.83	14.85
Maya	47.33	126.67	220.87	9.00	20.07	73.60	415.80	38.53	4.89	14.33	4.73	40.10	22.36	13.19
Vasundhara	48.33	126.67	228.67	7.80	20.53	78.33	416.87	52.00	4.83	12.80	4.28	39.11	19.23	9.44
CS-54	46.67	125.67	247.40	9.00	24.87	75.33	421.80	45.77	5.68	17.27	5.02	39.48	26.64	9.06
Varuna	46.67	127.33	208.67	8.87	26.20	79.47	441.07	50.80	4.63	14.80	4.24	40.22	22.70	14.15
Krishna	51.67	134.67	233.73	9.13	19.40	73.47	398.87	46.73	6.21	15.73	4.34	40.15	22.21	12.67
GM-2	47.67	126.67	202.20	9.40	25.93	71.10	352.73	40.93	5.38	13.53	4.56	40.85	25.74	12.47
Swarn Jyoti	48.00	126.00	229.20	6.73	17.33	83.20	293.00	41.67	5.96	15.33	4.12	40.23	24.84	11.57
RVM-2	44.00	137.67	213.93	8.33	24.00	73.87	355.73	50.13	5.45	15.07	5.57	40.26	14.91	8.43
RH-749	48.00	135.67	221.00	8.27	21.73	70.00	399.27	43.67	6.41	13.73	5.56	41.18	26.49	13.89
RH-781	47.67	138.67	223.93	8.20	20.63	78.80	392.13	48.53	4.93	14.67	5.11	40.50	22.94	11.97
NRCHB-101	61.00	138.33	216.27	7.20	16.13	74.20	411.00	47.73	4.27	16.27	4.05	41.55	24.76	14.33
RGN-48	52.67	137.00	238.87	8.27	24.53	71.07	353.20	35.93	5.29	13.07	4.59	41.36	19.41	8.77
Kanti	47.67	126.67	234.00	6.73	19.40	78.73	343.27	39.53	6.11	14.40	4.14	39.15	23.51	9.88
RH-819	60.33	125.67	210.53	6.73	22.20	76.27	387.67	48.53	4.93	14.27	4.24	41.35	24.17	11.07
EJ-20	49.00	130.33	223.93	9.73	26.07	66.73	405.00	45.13	4.94	16.00	3.80	40.64	16.65	9.91
RGN-229	52.33	138.33	235.40	9.07	24.33	77.93	429.33	43.47	5.25	16.73	3.39	41.08	27.17	11.32
RGN-73	49.67	138.00	240.53	7.33	18.20	71.93	420.87	42.67	5.91	16.53	4.24	41.42	25.67	11.68
DRMR-601	53.67	137.67	251.20	7.53	20.27	82.40	387.73	51.20	6.27	14.13	4.54	39.32	26.13	12.77
NRCDR-2	44.33	139.00	215.00	7.60	16.33	73.33	403.53	50.47	6.43	15.40	4.53	41.50	28.31	13.43
RGN-236	51.67	139.67	213.47	7.33	19.20	77.73	349.20	42.87	5.39	16.73	4.72	40.26	19.57	13.05
JM-3	49.67	136.67	227.67	6.87	17.13	81.67	338.80	54.20	6.14	19.33	3.84	38.93	21.54	12.72
Mean	50.07	134.67	223.12	8.07	21.50	75.25	383.29	44.22	5.47	15.05	4.43	40.34	22.65	12.16
Minimum	43.00	122.67	191.27	6.60	15.27	53.53	271.93	32.80	3.73	12.80	3.04	37.13	14.91	8.43
Maximum	61.00	141.00	253.07	11.27	27.70	90.47	441.07	54.20	6.69	19.33	6.23	42.34	28.31	16.55
CD @ 5%	1.26	1.16	15.39	1.13	2.49	9.82	53.58	6.75	0.61	2.08	0.27	0.95	1.84	1.39
CV %	1.56	0.53	4.27	8.66	7.17	8.07	8.68	9.44	6.93	8.54	3.80	1.46	5.01	7.08

4.3 Genetic variability parameters

The estimates of parameters of genetic variability such as range, mean, GCV, PCV, heritability and GA of the genotypes are presented in the Table 4.3.

4.3.1 Coefficient of variation

The analyzed values of phenotypic and genotypic coefficient of variation were shown in the Table 4.3. Values of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) in general. GCV and PCV were classified into three groups as: 0-10% = low, 10-20% = medium & high = >20% (Sivasubramanian and Madhava Menon, 1973).

4.3.1.1 Phenotypic coefficient of variation (PCV)

Moderate phenotypic coefficient of variation was observed for seed yield per plant (17.38%), 1000-test weight (15.76%), number of secondary per plant (14.77%), harvest index (14.01%), number of primary branch per plant (13.16%), number of siliquae on main axis (12.74%), length of siliqua (12.58%), length of main axis (11.76%), number of siliquae per plant (11.46%) and number of seed per siliqua (11.24%). Low estimates for phenotypic coefficient of variation was exhibited for oil content % (2.94%), days to maturity (3.88%), plant height (7.04%) and days to 50% flowering (7.81%).

4.3.1.2 Genotypic coefficient of variation (GCV)

Moderate genotypic coefficient of variation was observed for seed yield per plant (15.87%), 1000-test weight (15.30%), harvest index (13.08%), number of secondary branches per plant (12.91%) and length of siliqua (10.50%). The low values of genotypic coefficient of variation was observed for oil content % (2.55%) days to maturity (3.84%), plant height (5.61%), number of seed per siliqua (7.30%), number of siliquae per plant (7.49%), days to 50% flowering (7.65%), length of main axis (8.55%), number of siliquae on main axis (8.54%) and number of primary branches per plant (9.91%). The large difference in magnitudes of GCV and PCV for number of siliquae on main axis (8.54% and 12.74%), number of siliquae per plant (7.49% and 11.46%), number of sees per siliqua (7.30% and 11.24%), number of primary branches per plant (9.91% and 13.16%) and length of main axis (8.55% and 11.76%) indicates the influence of

environmental influence on these traits. Relatively low difference in GCV and PCV for days to 50% flowering, days to maturity, number of secondary branches per plant, length of siliqua, 1000-seed weight, oil content, harvest index and seed yield per plant indicates that these are mostly governed by genetic factors and little influence of environment.

4.3.2 Heritability (broad sense)

Heritability is a useful tool to measure the hereditary and environmental factors in the expression of the characters. Highest heritability value (> 60) was observed for days to maturity (98.10%) following by days to 50% flowering (96.01%), 1000-seed weight (94.20%), harvest index (87.18%), seed yield per plant 83.41%), number of secondary branches per plant (76.43%), oil content % (75.41%), length of siliqua (69.64%), plant height (63.31%). Similarly, moderate to low heritability was showed for number of primary branches per plant (56.73%), length of main axis (52.91%), number of siliquae on main axis (45.02%). number of siliquae per plant (42.67%) and number of seed per siliqua (42.25%).

4.3.3 Genetic advance (GA)

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The range of GA among different characters was ranging from 1.24% in number of primary branches per plant to 38.47% in number of siliquae per plant. The expected GA (as per cent of mean) was found to be in a range of 4.54% (oil content %) to 30.59% (1000-seed weight). The expected GA values were found low ($< 10\%$) for number of seeds per siliqua (9.78%), plant height (9.19%), days to maturity (7.84%) and oil content % (4.54%). Moderate values of expected GA (10-20%) was recorded for length of siliqua (18.05%) days to 50% flowering (15.44%), number of primary branches (15.38%), length of mail axis (12.82%) number of siliquae on main axis (11.81%) and number of siliquae per plant (10.08%). Relatively high values of expected GA ($> 20\%$) was recorded for 1000-seed weight (30.59%), seed yield per plant (29.86%), harvest index (25.15%) and number of secondary branches per plant (23.25%). High heritability coupled with high GA was observed for 1000-seed weight, seed yield per plant and harvest index.

Table 4.3 Estimates of different parameters of variability and genetic advance under selection for 14 characters in 60 genotypes of Indian mustard

S. No.	Characters	Range		Mean	GCV (%)	PCV (%)	h^2_{bs} (%)	GA (%)	GA (% of mean)
		Minimum	Maximum						
1.	Days to 50% flowering	43.00	61.00	50.10	7.65	7.81	96.03	7.73	15.44
2.	Days to maturity	122.70	141.00	134.70	3.84	3.88	98.10	10.56	7.84
3.	Plant height (cm)	191.27	253.07	223.12	5.61	7.04	63.31	20.50	9.19
4.	Number of primary branches per plant	6.60	11.27	8.07	9.91	13.16	56.73	1.24	15.38
5.	Number of secondary branches per plant	15.27	27.70	21.50	12.91	14.77	76.43	5.00	23.25
6.	Length of main axis (cm)	53.53	90.47	75.25	8.55	11.76	52.91	9.64	12.82
7.	Number of siliquae per plant	271.93	441.07	383.29	7.49	11.46	42.67	38.47	10.08
8.	Number of siliquae on main axis	32.80	54.20	44.22	8.54	12.74	45.02	5.22	11.81
9.	Length of siliqua (cm)	3.73	6.69	5.47	10.50	12.58	69.64	0.99	18.05
10.	Number of seeds per siliqua	12.80	19.33	15.05	7.30	11.24	42.25	1.47	9.78
11.	1000-seed weight (g)	3.04	6.23	4.43	15.30	15.76	94.20	1.35	30.59
12.	Oil content (%)	37.13	42.34	40.34	2.55	2.94	75.41	1.84	4.54
13.	Harvest index (%)	14.91	28.31	22.65	13.08	14.01	87.18	5.70	25.15
14.	Seed yield per plant (g)	8.43	16.55	12.16	15.87	17.38	83.41	3.63	29.86

4.4 Genetic divergence analysis

The estimates of genetic divergence among the 60 genotypes of Indian mustard were carried out following the method of Mahalanobis D^2 statistic and as described by Rao (1952). The group constellations were done following Tocher's method (Rao, 1952).

4.4.1 Group constellations using D^2 statistics

Sixty genotypes of Indian mustard included in the present study were grouped into eight different clusters on the basis of genetic closeness or genetic divergence by D^2 . The clustering pattern of the genotypes has been shown in Table 4.4. Cluster IV was the largest with 18 genotypes, whereas cluster I was the second largest with 16 genotypes grouped together. Cluster VI was the third largest cluster based on the number of genotypes (8 genotypes) followed by cluster II (7 genotypes) and cluster III (6 genotypes). Two clusters, V and VIII comprised of two genotypes each. The remaining cluster VII comprised only one genotype (RH 406) indicating that this genotype is much more divergent than rest of the genotypes in the study.

4.4.2 Inter and intra-cluster distances

The estimates of average intra-cluster and inter cluster D^2 values among the 60 genotypes are given in Table- 4.5. Maximum intra-cluster D^2 value (47.94) was recorded in cluster VI among the eight intra-cluster distances, which revealed maximum genetic diversity among the genotypes of this group. Second highest average intra-cluster distance was observed by cluster II (40.21) followed by cluster III (40.11), cluster I (28.65), cluster VI (22.61), cluster V (19.12) and cluster VIII (14.01). The minimum average intra-cluster D^2 value (0.00) was recorded for cluster VII.

The inter-cluster distances ranged from 12.06 (between III and IV) to 52.40 (between V and VIII). The other clusters with high inter-cluster distances were V and VII (52.01) followed by cluster VI and VIII (46.81), III and V (46.37), VI and VII (42.20), IV and V (41.26) and I and V (41.05). The minimum average inter-cluster distance (D^2 value) was observed of between III and IV (12.06) followed by cluster I and VII (15.15), cluster I and IV (15.58) and cluster II and IV (15.69).

The maximum inter-cluster D^2 value indicated that genotypes of cluster V and VIII are not so closely related whereas the genotypes of cluster III and IV are closely related. It is apparent therefore, that the genotypes of these clusters do not differ so significantly with regards to their relative genetic distance as indicated from the low variation of D^2 values.

4.4.3 Cluster means for different quantitative characters (Tocher's method).

The cluster means calculated for 14 characters under study have been presented in Table 4.6. Days to 50% flowering showed highest mean for cluster number VIII (60.65) followed by cluster V (53.50) and cluster VII (52.70), while lowest mean for this character was observed for cluster number VI (48.69) followed by cluster IV (49.08), I (49.51) and cluster II (50.01). Highest mean for days to maturity was observed for cluster number V (139.35) followed by cluster VII (136.00) and cluster IV (135.76), while it was lowest for cluster number VI (129.56) and cluster VIII (132.00). Plant height exhibited highest mean for cluster III (231.33) followed by cluster VI (229.13) and cluster IV (228.00) whereas lowest mean for this character was observed in cluster number VII (211.00) followed by cluster I (213.06) and VIII (213.50). Number of primary branches per plant revealed highest mean for cluster VII (11.30) followed by cluster II (8.59), cluster III (8.23) and cluster IV (8.20). Cluster VIII (6.95) followed by cluster V (7.40) and cluster VII (7.43) showed lowest mean for number of primary branches per plant. Number of secondary branches per plant exhibited highest mean for cluster number VII (22.70) followed by cluster III (22.53) and cluster I (22.29), while it was lowest for cluster number VIII (19.15) followed by cluster VI (19.61) and cluster II (19.91). Length of main axis showed highest mean for cluster number VII (85.10) followed by cluster III (84.60) and cluster VI (78.78). It was lowest for cluster number V (57.20) followed by cluster I (73.56) and cluster IV (73.83). Number of siliquae per plant exhibited highest mean for cluster number VIII (399.35) followed by cluster V (397.57), VII (393.50), cluster IV (388.71) and cluster I (388.06), lowest mean for cluster number cluster VI (357.28) followed by cluster II (374.19) and cluster III (387.82). Number of siliquae on main axis showed highest mean for cluster number VIII (48.10) followed by cluster III (46.82), while lowest mean was indicated for cluster number I (41.51) followed by cluster II (42.36). Length of siliqua revealed highest mean for cluster VII (6.46) followed by cluster number II (5.72). Cluster number V having the lowest

mean (4.53) for this character followed by cluster VIII (4.60). Number of seed per siliqua exhibited highest mean for cluster number VII (16.80) followed by cluster V (16.15). Lowest mean for number of seed per siliqua was indicated by cluster number II (14.24) and cluster IV (14.72). Highest mean for 1000-seed weight was showed by cluster number II (5.23) followed by cluster VII (4.64). It was lowest for cluster number V (3.05) followed by cluster VIII (4.14). Oil content observed highest mean for cluster number VII (41.62) followed by cluster VIII (41.45). Cluster number V (38.83) had lowest mean for oil content followed by cluster VI (39.40). Harvest index exhibited highest mean for cluster number VII (26.89) followed by cluster VIII (24.47) and cluster VI (24.25), whereas it was lowest for cluster number V (20.69) followed by cluster IV (21.18) and cluster II (22.35). Seed yield per plant revealed highest mean for cluster number V (15.52) followed by cluster II (13.31) and cluster III (13.27). Lowest mean for seed yield per plant exhibited by cluster number VII (9.28) followed by cluster VI (11.19), cluster IV (11.63) and cluster I (12.00).

4.4.4 Relative contribution (%) of different characters to genetic divergence.

The contribution of various characters under study towards the expression of genetic divergence is presented in Table 4.7. It is clear from the table that on the basis of average D^2 the highest contribution to divergence was from seed yield per plant (11.76%), followed by 1000-seed weight (11.09%). The relative contribution of different character to the total divergence in order was number of secondary branches per plant (9.75%), harvest index (9.61%), length of siliqua (8.07%), number of primary branches per plant (8.04%), number of siliquae on main axis (7.27%), length of main axis (6.99%), number of seeds per siliqua (6.32%) and number of siliquae per plant (6.47%). Oil content contributed least towards the total divergence (1.93%) followed by days to maturity (2.76%), plant height (4.41%) and days to 50% flowering (5.53%)

Table 4.4 Distribution of 60 Indian mustard genotypes into different clusters

Cluster	Number of Genotypes	Name of genotypes
I	16	Pusa Jai Kishan, NPJ-208, YSRL-9, Pusa Mahak, PM-26, PM-28, Shivalik, Urvashi, JM-1, Basanti, Vardaan, JM-1, Jagnnath, Giriraj, GM-1, RGN-236.
II	7	RH-725, PBR-91, Pusa Tarak, RH-30, Maya, Krishna, Vaibhav.
III	6	RGN-229, Pusa Bahar, RH-51, Pusa Bold, Varuna, DRMR-601.
IV	18	Rohini, PM-27, RGN-73, NRCDR-2, EJ-20, RGN-48, RVM-2, RH-749, RH-781, Vasundhara, JA-96, NPJ-206, RGN-34, RH-10, RH-419, RH-904, RM-51, GM-3.
V	2	RGN-303, Kranti.
VI	8	PDZ-1, GM-1, Ashirwad, Shivani, CS-54, Swarn Jyoti, Kanti, GM-3.
VII	1	RH-406.
VIII	2	NRCHB-101, RH-819.

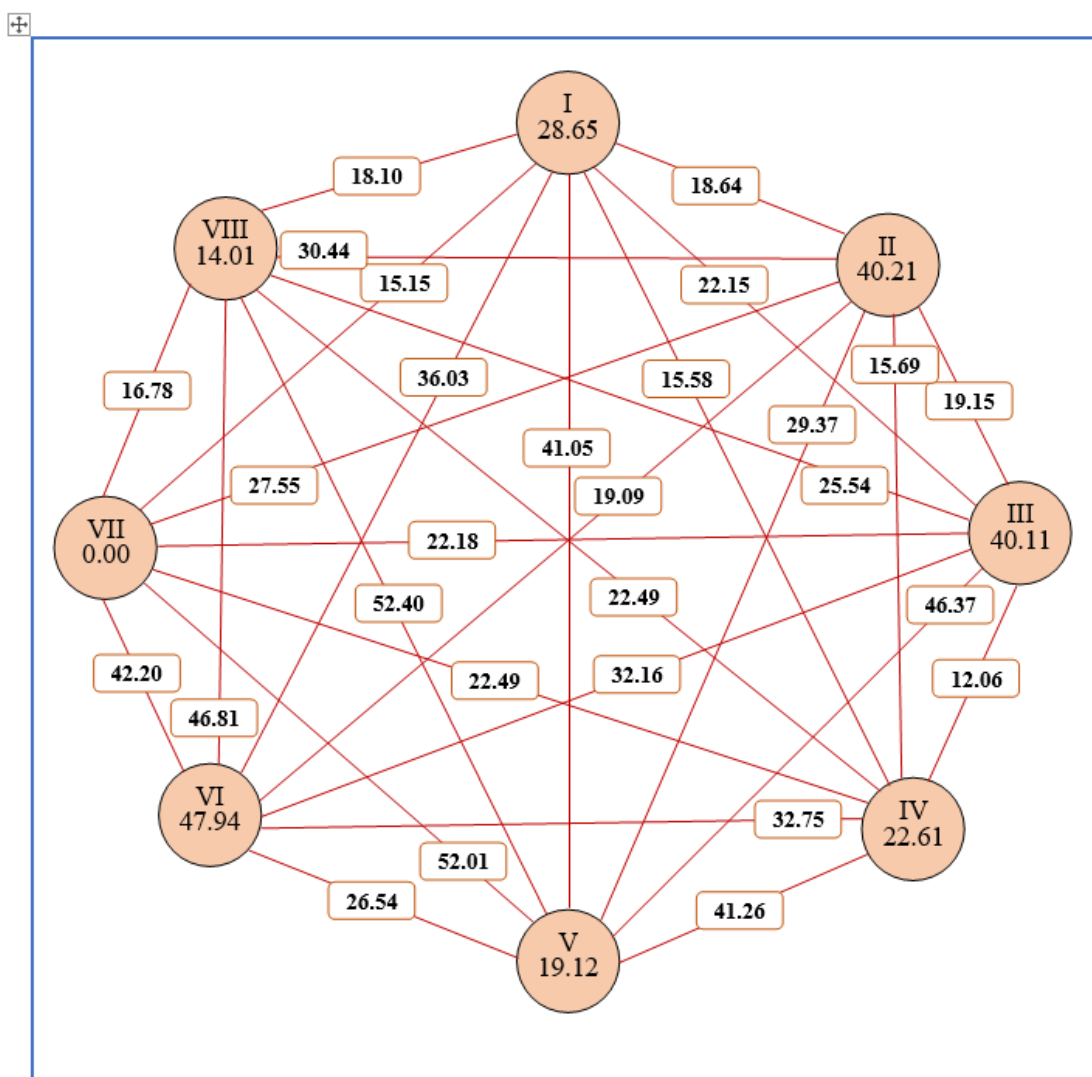


Figure 01: Cluster diagram showing average intra-cluster & inter-cluster genetic distances by Tocher's methods in Indian mustard (not to scale)

Table 4.5 Average intra-cluster (diagonal) and inter-cluster distances (D^2 values) in 60 genotypes of Indian mustard

Cluster	I	II	III	IV	V	VI	VII	VIII
I	28.65	18.64	22.15	15.58	41.05	36.03	15.15	18.10
II		40.21	19.15	15.69	29.37	19.09	27.55	30.44
III			40.11	12.06	46.37	32.16	22.18	25.54
IV				22.61	41.26	32.75	22.49	22.49
V					19.12	26.54	52.01	52.40
VI						47.94	42.20	46.81
VII							0.00	16.78
VIII								14.01

* Figures in bold letters indicate maximum and minimum (intra/inter-cluster) values

Table- 4.6 Cluster mean values of 60 genotypes for 14 characters in Indian mustard

Characters Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Length of main axis (cm)	Number of siliquae per plant	Number of siliquae on main axis	Length of siliqua (cm)	Number of seeds per siliqua	1000- seed weight (g)	Oil content (%)	Harvest index (%)	Seed yield per plant (g)
I (16)	49.51	135.72	213.06	7.96	22.29	73.56	388.06	41.51	5.36	15.13	4.21	40.19	23.00	12.00
II (7)	50.01	133.79	224.86	8.59	19.91	74.50	374.19	42.36	5.72	14.24	5.23	39.83	22.35	13.31
III (6)	51.47	135.62	231.33	8.23	22.53	84.60	387.82	46.82	5.27	15.05	4.17	40.77	23.70	13.27
IV (18)	49.08	135.76	228.00	8.20	22.16	73.83	388.71	45.32	5.67	14.72	4.56	40.91	21.18	11.63
V (2)	53.50	139.35	221.50	7.40	20.95	57.20	397.57	45.50	4.53	16.15	3.05	38.83	20.69	15.52
VI (8)	48.69	129.56	229.13	7.43	19.61	78.78	357.28	45.49	5.49	15.81	4.50	39.40	24.25	11.19
VII (1)	52.70	136.00	211.00	11.30	22.70	85.10	393.50	45.00	6.46	16.80	4.64	41.62	26.89	9.28
VIII (2)	60.65	132.00	213.50	6.95	19.15	75.25	399.35	48.10	4.60	15.30	4.14	41.45	24.47	12.70

*Figures in parentheses indicate the number of the genotypes retained in the clusters

Table 4.7 Relative contribution of different characters to genetic divergence among 60 genotypes of Indian mustard

S. No.	Characters	% contribution
1.	Days to 50% flowering	5.53
2.	Days to maturity	2.76
3.	Plant height (cm)	4.41
4.	Number of primary branches per plant	8.04
5.	Number of secondary branches per plant	9.75
6.	Length of main axis (cm)	6.99
7.	Number of siliquae per plant	6.47
8.	Number of siliquae on main axis	7.27
9.	Length of siliqua (cm)	8.07
10.	Number of seeds per siliqua	6.32
11.	1000-seed weight (g)	11.09
12.	Oil content (%)	1.93
13.	Harvest index (%)	9.61
14.	Seed yield per plant (g)	11.76

4.5 Character association analysis.

Correlation studies provide reliable information on nature, extent and the direction of selection. The association of seed yield with other component characters was studied by correlation studies. The genotypic and phenotypic values are presented in Table 4.8.

The correlation estimates at genotypic level (r_g) and phenotypic level (r_p) show close correspondence for all the characters under study. It is evident from the estimates that for most character pairs, the genotypic and phenotypic association were in same direction whereas r_g values recorded higher than r_p values. It indicates the inherent association among the traits.

4.5.1 Correlation of seed yield with other yield components

At phenotypic level, seed yield per plant was observed to be positively and significantly correlated with number of siliquae per plant (0.175*), number of siliquae on main axis (0.154*) and harvest index (0.192**). However, it was positive and non-significant with days to 50% flowering (0.129), days to maturity (0.066), number of seed per siliqua (0.029) and oil content % (0.080) were obtained. It revealed negative non-significant correlation with plant height (-0.097), number of primary branches per plant (-0.030), number of secondary branches per plant (-0.064), length of main axis (-0.066), length of siliqua (-0.081), 1000-seed weight (-0.001).

At genotypic level, seed yield per plant was observed to be positively and significantly correlated number of siliquae per plant (0.250**), number of siliquae on main axis (0.226**) and harvest index (0.232**). The characters like days to 50% flowering (0.135), days to maturity (0.072), number of seed per siliqua (0.076), 1000-seed weight (0.015) and oil content % (0.064) showed positive but non-significant correlation with seed yield. It revealed negative non-significant correlation with plant height (-0.133), number of primary branches per plant (-0.111), number of secondary branches per plant (-0.093), length of main axis (-0.132) and length of siliqua (-0.118).

4.5.2 Correlation among the yield components at genotypic and phenotypic level

4.5.2.1 Days to 50% flowering

At the phenotypic level, days to 50% flowering showed positive significant correlation with days to maturity ($r_p=0.300^{**}$) and plant height ($r_p= 0.179^*$). Positive non-significant correlation was revealed with number of siliquae per plant ($r_p= 0.031$), number of siliquae on main axis ($r_p= 0.049$), number of seed per siliqua ($r_p= 0.070$), oil content % ($r_p= 0.077$) and seed yield per plant ($r_p= 0.0129$). Negative non-significant association of this character was observed with number of primary branches per plant ($r_p= -0.091$), number of secondary branches per plant ($r_p= -0.043$), length of main axis ($r_p= -0.050$), 1000-seed weight ($r_p= -0.117$) and harvest index ($r_p= -0.003$). Significant negative correlation of days to 50% flowering was reflected with length of silique ($r_p= -0.162^*$).

At genotypic level, days to 50% flowering showed positive significant correlation with days to maturity ($r_g= 0.318^{**}$), plant height ($r_g= 0.222^{**}$), while positive non-significant correlation indicated for number of siliquae per plant ($r_g= 0.039$), number of siliquae on main axis ($r_g= 0.077$), number of seed per siliqua ($r_g= 0.108$), oil content % ($r_g= 0.086$), seed yield per plant ($r_g= 0.135$) and harvest index ($r_g= 0.001$). Negative but non-significant association was reflected by number of primary branches per plant ($r_g= -0.137$), number of secondary branches per plant ($r_g= -0.059$), length of main axis ($r_g= -0.057$) and 1000-seed weight ($r_g= -0.119$). Significant negative correlation of days to 50% flowering was observed with length of siliqua ($r_g= -0.197^{**}$).

4.5.2.2 Days to maturity

Days to maturity recorded positive non-significant correlation at phenotypic level with plant height ($r_p= 0.107$), number of siliquae on main axis ($r_p= 0.054$), length of siliqua ($r_p= 0.022$), number of seed per siliqua ($r_p= 0.050$), oil content % (0.088) and seed yield per plant ($r_p= 0.066$), whereas non-significant negative correlations were observed with number of primary branches per plant ($r_p= -0.105$), length of main axis ($r_p= -0.024$), number of siliquae per plant ($r_p= -0.145$) and 1000-seed weight ($r_p= -0.090$). Days to maturity showed significant negative correlation with number of secondary branches per plant ($r_p= -0.210^{**}$) and harvest index ($r_p= -0.219^{**}$).

Days to maturity recorded positive non-significant correlation at genotypic level with plant height ($r_g = 0.128$), number of siliquae on main axis ($r_g = 0.074$), length of siliqua ($r_g = 0.024$), number of seed per siliqua ($r_g = 0.091$), oil content % (0.103) and seed yield per plant ($r_g = 0.072$), whereas it was non-significant but negatively correlated with number of primary branches per plant ($r_g = -0.133$), length of main axis ($r_g = -0.048$) and 1000-seed weight ($r_g = -0.091$). Significant & negative correlation was reflected with number of secondary branches per plant ($r_g = -0.251^{**}$), number of siliquae per plant ($r_g = -0.230^{**}$) and harvest index ($r_g = -0.239^{**}$).

4.5.2.3 Plant height

Plant height at phenotypic level exhibited significant and positive association with length of main axis ($r_p = 0.300^{**}$), positive non-significant correlation with number of siliquae per plant ($r_p = 0.090$), number of siliquae on main axis ($r_p = 0.109$), length of siliqua ($r_p = 0.096$). Non-significant negative correlation of plant height was indicated with number of primary branches per plant ($r_p = -0.090$), number of secondary branches per plant ($r_p = -0.038$), number of seed per siliqua ($r_p = -0.009$), 1000-seed weight ($r_p = -0.045$), oil content % ($r_p = -0.144$), harvest index ($r_p = -0.067$) and seed yield per plant ($r_p = -0.097$).

Significant and positive association of plant height exhibited with length of main axis ($r_g = 0.258^{**}$) and number of siliquae on main axis ($r_g = 0.183^*$) at genotypic level. It was non-significant but positively correlated with number of siliquae per plant ($r_g = 0.070$), length of siliqua ($r_g = 0.087$), number of seed per siliqua ($r_g = 0.097$), whereas non-significant negative correlations with number of secondary branches per plant ($r_g = -0.118$), 1000-seed weight ($r_g = -0.092$), oil content % ($r_g = -0.127$), harvest index ($r_g = -0.082$) and seed yield per plant ($r_g = -0.133$) were refelected for this character. Plant height exhibited significant negative correlation with number of primary branches per plant ($r_g = -0.203^{**}$).

4.5.2.4 Number of primary branches per plant

Number of primary branches per plant showed significant and positive association with number of secondary branches per plant ($r_p = 0.438^{**}$), number of siliquae per plant ($r_p = 0.205^{**}$) and oil content % (0.160*), while non-significant positive correlation of this character was indicated with length of siliqua ($r_p = 0.054$), 1000-seed weight ($r_p = 0.111$), harvest index ($r_p = 0.009$). It showed non-significant but

negative correlation with length of main axis ($r_p = -0.138$), number of siliquae on main axis ($r_p = -0.088$), number of seed per siliqua ($r_p = -0.072$) and seed yield per plant ($r_p = -0.030$).

At genotypic level number of primary branches per plant showed significant and positive association with number of secondary branches per plant ($r_g = 0.539^{**}$), number of siliquae per plant ($r_g = 0.275^{**}$) and oil content % (0.195^{**}). However, the correlation was positive and non-significant with length of siliqua ($r_g = 0.125$), 1000-seed weight ($r_g = 0.138$) and harvest index ($r_g = 0.000$). Number of siliquae on main axis ($r_g = -0.121$), number of seed per siliqua ($r_g = -0.103$) and seed yield per plant ($r_g = -0.111$) revealed non-significant but negative correlation with this character. Significant but negative correlation with length of main axis ($r_g = -0.213^{**}$) was obtained.

4.5.2.5 Number of secondary branches per plant

Number of secondary branches per plant recorded significant positive association with number of siliquae per plant ($r_p = 0.311^{**}$), positive but non-significant correlation for oil content % ($r_p = 0.114$). This character indicated significant negative correlation with length of main axis ($r_p = -0.234^{**}$) and number of siliquae on main axis ($r_p = -0.190^*$) whereas, negative but non-significant correlations were exhibited by rest of the character at phenotypic level.

Number of secondary branches per plant recorded significant positive association with number of siliquae per plant ($r_g = 0.364^{**}$), at genotypic level. Positive non-significant correlation of this character was observed for oil content % ($r_p = 0.138$), while it was negative and non-significant with other characters like, length of siliqua, 1000-seed weight, harvest index and seed yield per plant. Significant negative correlation was found with length of main axis ($r_g = -0.420^{**}$), number of siliquae on main axis ($r_g = -0.264^{**}$) and number of seed per siliqua ($r_g = -0.180^*$).

4.5.2.6 Length of main axis

Length of main axis exhibited significant and positive association with 1000-seed weight ($r_p = 0.162^*$) and oil content % ($r_p = 0.174^*$). However, it was positive but non-significant for number of siliquae on main axis ($r_p = 0.105$), length of siliqua ($r_p = 0.120$), number of seed per siliqua ($r_p = 0.062$), harvest index ($r_p = 0.077$).

Number of siliquae per plant ($r_p = -0.050$) and seed yield per plant ($r_p = -0.066$) showed negative non-significant correlation with length of main axis at phenotypic level.

Length of main axis showed significant and positive association for most of the characters at genotypic level, like number of siliquae on main axis ($r_g = 0.249^{**}$), length of silique ($r_g = 0.173^*$), number of seed per silique ($r_g = 0.194^{**}$), 1000-seed weight ($r_g = 0.186^*$), oil content % ($r_g = 0.321^{**}$) and harvest index ($r_g = 0.172^*$).

4.5.2.7 Number of siliquae per plant

Number of siliquae per plant was positively correlated with all the character at phenotypic level. However, it was significant in case of oil content % ($r_p = 0.151^*$), harvest index ($r_p = 0.244^{**}$) seed yield per plant ($r_p = 0.175^*$). This character showed significant and positive association with number of siliquae on main axis ($r_g = 0.271^{**}$), oil content % ($r_g = 0.189^*$) harvest index ($r_g = 0.404^{**}$) and seed yield per plant ($r_g = 0.250^{**}$) at genotypic level. It was positive but non-significant for number of seed per silique ($r_g = 0.143$) and 1000-seed weight ($r_g = 0.060$). Negative and non-significant correlation with length of silique ($r_g = -0.045$) was observed.

4.5.2.8 Number of siliquae on main axis

Number of siliquae on main axis was positively correlated with length of silique ($r_p = 0.024$), number of seed per silique ($r_p = 0.067$), 1000-seed weight ($r_p = 0.054$) and harvest index ($r_p = 0.057$) at phenotypic level. However, it was significant in case of seed yield per plant ($r_p = 0.154^*$) only. This character also exhibited significant positive association with seed yield per plant ($r_g = 0.226^{**}$) at genotypic level. Number of seed per silique ($r_g = 0.135$), 1000-seed weight ($r_g = 0.091$) and harvest index ($r_g = 0.044$) were also positively correlated with number of siliquae on main axis but non-significant.

4.5.2.9 Length of silique

Length of silique showed significant and positive association with 1000-seed weight ($r_p = 0.352^{**}$), oil content % ($r_p = 0.177^*$) and harvest index ($r_p = 0.289^{**}$). It was positive but non-significant for number of seed per silique ($r_p = 0.047$). At genotypic length of silique showed significant and positive association with 1000-seed weight ($r_g = 0.442^{**}$), oil content % ($r_g = 0.261^{**}$) and harvest index

($r_g = 0.386^{**}$). It also reflected positive but non-significant correlation with number of seed per siliqua ($r_g = 0.113$).

4.5.2.10 Number of seed per siliqua

Number of seed per siliqua showed significant negative correlation with 1000-seed weight both at phenotypic ($r_p = -0.245^{**}$) and genotypic ($r_g = -0.353^{**}$). Positive but non-significant association of this character was indicated for oil content ($r_p = 0.120$), harvest index ($r_p = 0.009$) and seed yield per plant ($r_p = 0.029$). Number of seed per siliqua recorded positive association with oil content % ($r_g = 0.172^*$), harvest index ($r_g = 0.048$) and seed yield per plant ($r_g = 0.076$).

4.5.2.11 1000- Seed weight

Significant and positive association of 1000-seed weight was exhibited with harvest index at phenotypic ($r_p = 0.157^*$) as well as genotypic level ($r_g = 0.173^*$). Non-significant and positive association of this character was indicated with oil content ($r_p = 0.120$) and ($r_g = 0.142$).

4.5.2.12 Oil content

Oil content recorded non-significant and positive association with harvest index ($r_p = 0.091$, $r_g = 0.099$) and seed yield per plant ($r_p = 0.080$, $r_g = 0.064$) both at phenotypic and genotypic level.

4.5.2.13 Harvest index

Harvest index was positively and significantly correlated with seed yield at both phenotypic ($r_p = 0.192^{**}$) and genotypic ($r_g = 0.232^{**}$) levels.

Table 4.8:- Estimates of correlation coefficient for genotypic (G) and phenotypic (P) levels among 14 quantitative characters in Indian mustard

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Length of main axis (cm)	Number of siliquae per plant	Number of siliquae on main axis	Length of siliqua (cm)	Number of seeds per siliqua	1000- seed weight (g)	Oil content (%)	Harvest index (%)	Seed yield per plant (g)
Days to 50% flowering	G P	1.000 1.000													
Days to maturity	G P	0.318** 0.300**	1.000 1.000												
Plant height (cm)	G P	0.222** 0.179*	0.128 0.107	1.000 1.000											
Number of primary branches per plant	G P	-0.137 -0.091	-0.133 -0.105	-0.203** -0.090	1.000 1.000										
Number of secondary branches per plant	G P	-0.059 -0.043	-0.251** -0.210**	-0.118 -0.038	0.539** 0.438**	1.000 1.000									
Length of main axis (cm)	G P	-0.057 -0.050	-0.048 -0.024	0.258** 0.300**	-0.213** -0.138	-0.420** -0.234**	1.000 1.000								
Number of siliquae per plant	G P	0.039 0.031	-0.230** -0.145	0.070 0.090	0.275** 0.205**	0.364** 0.311**	-0.115 -0.050	1.000 1.000							
Number of siliquae on main axis	G P	0.077 0.049	0.074 0.054	0.183* 0.109	-0.121 -0.088	-0.264** -0.190*	0.249** 0.105	0.271** 0.085	1.000 1.000						
Length of siliqua (cm)	G P	-0.197** -0.162*	0.024 0.022	0.087 0.096	0.125 0.054	-0.002 -0.006	0.173* 0.120	-0.045 0.018	-0.015 0.024	1.000 1.000					
Number of seeds per siliqua	G P	0.108 0.070	0.091 0.050	0.097 -0.009	-0.103 -0.072	-0.180* -0.130	0.194** 0.062	0.143 0.010	0.135 0.067	0.113 0.047	1.000 1.000				
1000-seed weight (g)	G P	-0.119 -0.117	-0.091 -0.090	-0.092 -0.045	0.138 0.111	-0.014 -0.020	0.186* 0.162*	0.060 0.024	0.091 0.054	0.442** 0.352**	-0.353** -0.245**	1.000 1.000			
Oil content (%)	G P	0.086 0.077	0.103 0.088	-0.127 -0.144	0.195** 0.160*	0.138 0.114	0.321** 0.174*	0.189* 0.151*	-0.094 -0.119	0.261** 0.177*	0.172* 0.120	0.142 0.120	1.000 1.000		
Harvest index (%)	G P	0.001 -0.003	-0.239** -0.219**	-0.082 -0.067	0.000 0.009	-0.043 -0.036	0.172* 0.077	0.404** 0.244**	0.044 0.057	0.386** 0.289**	0.048 0.009	0.173* 0.157*	0.099 0.091	1.000 1.000	
Seed yield per plant (g)	G P	0.135 0.129	0.072 0.066	-0.133 -0.097	-0.111 -0.030	-0.093 -0.064	-0.132 -0.066	0.250** 0.175*	0.226** 0.154*	-0.118 -0.081	0.076 0.029	0.015 -0.001	0.064 0.080	0.232** 0.192**	1.000 1.000

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

4.6 Path coefficient analysis

The direct and indirect components were analyzed by using the path coefficient analysis. Better representation of relation between distinct traits is possible with the help of path analysis. For critical evaluation, the correlation coefficient needs to be split into direct and indirect effects using path coefficient analysis. Since, many characters affect a given trait, the correlation and path coefficients in combination can give a better insight into cause and effect relationship between different pairs of character. The inter-relationship of the characters as revealed by the path coefficient analysis using genotypic and phenotypic correlation are presented in Table 4.9

4.6.1 Days to 50% flowering

Days to 50% flowering had recorded positive and non-significant correlation with seed yield per plant (0.0135). It expressed negative direct effect (-0.0402) on seed yield per plant, whereas showed positive indirect effect via number of primary branches per plant (0.0055), number of secondary branches per plant (0.0024), length of main axis (0.0023), length of siliqua (0.0079) and 1000-seed weight (0.0048). Days to 50% flowering exhibited negative indirect effect through days to maturity (-0.0128), plant height (-0.0090), number of siliquae per plant (-0.0016), number of siliquae on main axis (-0.0031), number of seed per siliqua (-0.0044), oil content % (-0.0035) and harvest index (-0.0000), at genotypic level.

Days to 50% flowering had positive and non-significant correlation with seed yield per plant (0.0129) and positive direct effect (0.0735) on seed yield per plant was indicated. It showed positive indirect effect for days to maturity (0.0221), plant height (0.0131), number of siliquae per plant (0.0023), number of siliquae on main axis (0.0036), number of seed per siliqua (0.0051), oil content % (0.0057). Negative indirect effect through number of primary branches per plant (-0.0067), number of secondary branches per plant (-0.0032), length of main axis (-0.0037), length of siliqua (-0.0119), 1000-seed weight (-0.0086) and harvest index (-0.0002) was observed at phenotypic level.

4.6.2 Days to maturity

Days to maturity had showed positive non-significant correlation with seed yield per plant (0.072). It has expressed positive direct effect (0.0759) on seed yield per plant, whereas showed positive indirect effect through days to 50% flowering

(0.0242), plant height (0.0097), number of siliquae on main axis (0.0057), length of siliqua (0.0018), number of seed per siliqua (0.0069) and oil content % (0.0079). Negative indirect effect for number of primary branches per plant (-0.0101), number of secondary branches per plant (-0.0190), length of main axis (-0.0036), number of siliquae per plant (-0.0175), 1000-seed weight (-0.0069) and harvest index (-0.0181), at genotypic level.

Days to maturity had showed positive and non-significant correlation with seed yield per plant (0.066) and expressed positive direct effect (0.0890) on seed yield per plant. This trait exhibited positive effect via days to 50% flowering (0.0267), plant height (0.0095), number of siliquae on main axis (0.0048), length of siliqua (0.0019), number of seed per siliqua (0.0045) and oil content % (0.0078), negative indirect effect via number of primary branches per plant (-0.0093), number of secondary branches per plant (-0.0187), length of main axis (-0.0021), number of siliquae per plant (-0.0129), 1000-seed weight (-0.0080) and harvest index (-0.0195), at phenotypic level.

4.6.3 Plant height

At genotypic level plant height had negative and non-significant correlation with seed yield per plant (-0.133). Negative direct effect (-0.0048) of plant height was detected on seed yield per plant, whereas it showed positive indirect effect through number of primary branches per plant (0.0010), number of secondary branches per plant (0.0006), 1000-seed weight (0.0004), oil content (0.0006) and harvest index (0.0004). Plant height showed negative indirect effect via days to 50% flowering (-0.0011), days to maturity (-0.0006), length of main axis (-0.0012), number of siliquae per plant (-0.0003), number of siliquae on main axis (-0.0009), length of siliqua (-0.0004) and number of seeds per siliqua (-0.0005).

At phenotypic level plant height exhibited negative non-significant correlation with seed yield per plant (-0.097) and also expressed negative direct effect (-0.0921) on seed yield per plant. It showed positive indirect effect through number of primary branches per plant (0.0083), number of secondary branches per plant (0.0035), number of seeds per siliqua (0.0009), 1000-seed weight (0.0042), oil content % (0.0133) and harvest index (0.0062). Negative indirect effect was reflected via days to 50% flowering (-0.0165), days to maturity (-0.0099), length of main axis (-0.0277),

number of siliquae per plant (-0.0083), number of siliquae on main axis (-0.0101) and length of siliqua (-0.0088).

4.6.4 Number of primary branches per plant

Negative but non-significant correlation of number of primary branches per plant reflected with seed yield per plant (-0.111). It had negative direct effect (-0.0121) on seed yield per plant, whereas it showed positive indirect effect via days to 50% flowering (0.0166), days to maturity (0.0161), plant height (0.0247), length of main axis (0.0259), number of siliquae on main axis (0.0146) and number of seeds per siliqua (0.0126), whereas it showed negative indirect effect through number of secondary branches per plant (-0.0654), number of siliquae per plant (-0.0334), length of siliqua (-0.0152), 1000-seed weight (-0.0167), oil content % (-0.0237) and harvest index (-0.0001), at genotypic level.

At phenotypic level number of primary branches per plant showed negative but non-significant correlation with seed yield per plant (-0.030). Negative direct effect (-0.0274) of this character was indicated on seed yield per plant. Positive indirect effect via days to 50% flowering (0.0025), days to maturity (0.0029), plant height (0.0025), length of main axis (0.0038), number of siliquae on main axis (0.0024) and number of seeds per siliqua (0.0020) was observed, whereas it showed negative indirect effect for number of secondary branches per plant (-0.0120), number of siliquae per plant (-0.0056), length of siliqua (-0.0015), 1000-seed weight (-0.0030), oil content % (-0.0044) and harvest index (-0.0002).

4.6.5 Number of secondary branches per plant

Number of secondary branches per plant recorded negative and non-significant correlation with seed yield per plant (-0.093). It has expressed negative direct effect (-0.0963) on seed yield per plant, whereas positive indirect effect through days to 50% flowering (0.0056) followed by days to maturity (0.0241), plant height (0.0114), length of main axis (0.0405), number of siliquae on main axis (0.0254), length of siliqua (0.0002), number of seeds per siliqua (0.0173), 1000-seed weight (0.0014) and harvest index (0.0042) was reflected. Negative indirect effect via number of primary branches per plant (-0.0519), number of siliquae per plant (-0.0350) and oil content (-0.0137) was seen at genotypic level.

Number of secondary branches per plant had negative but non-significant correlation with seed yield per plant (-0.064). Negative direct effect (-0.0752) of this character was indicated on seed yield per plant. It showed positive indirect effect through days to 50% flowering (0.0033), days to maturity (0.0158), plant height (0.0029), length of main axis (0.0176), number of siliquae on main axis (0.0143), length of siliqua (0.0005), number of seeds per siliqua (0.0098), 1000-seed weight (0.0015), harvest index (0.0027), while negative indirect effect via number of primary branches per plant (-0.0330) and number of siliquae per plant (-0.0234) and oil content % (-0.0086) was observed at phenotypic level.

4.6.6 Length of main axis

The genotypic correlation between length of main axis was negative and non-significant with seed yield per plant (-0.132). It also had negative direct effect (-0.4213) on seed yield per plant. However, positive indirect effect through days to 50% flowering (0.0242), days to maturity (0.0201), number of primary branches per plant (0.0899), number of secondary branches per plant (0.1771), number of siliquae per plant (0.0484) was indicated. It showed negative indirect effect via plant height (-0.1089), number of siliquae on main axis (-0.1051), length of siliqua (-0.0727), number of seeds per siliqua (-0.0817), 1000-seed weight (-0.0786) oil content % (-0.1351) and harvest index (-0.0726), at genotypic level.

Negative but non-significant phenotypic correlation was observed between length of main axis and seed yield per plant (-0.066). The direct effect was also of negative magnitude (-0.0762) on seed yield per plant. It showed positive indirect effect via days to 50% flowering (0.0038), days to maturity (0.0018), number of primary branches per plant (0.0105), number of secondary branches per plant (0.0178), number of siliquae per plant (0.0038), while negative indirect effect via plant height (-0.0229), number of siliquae on main axis (-0.0080), length of siliqua (-0.0091), number of seeds per siliqua (-0.0047), 1000-seed weight (-0.0124), oil content (-0.0133) and harvest index (-0.0059) was observed at phenotypic level.

4.6.7 Number of siliquae per plant

Number of siliquae per plant exhibited positive and significant correlation with seed yield per plant (0.250**). It expressed negative direct effect (-0.0414) on seed yield per plant. This character showed positive indirect effect via days to

maturity (0.0095), length of main axis (0.0048), length of siliqua (0.0019). However, negative indirect effect via days to 50% flowering (-0.0016), plant height (-0.0029), number of primary branches per plant (-0.0114), number of secondary branches per plant (-0.0150), number of siliquae on main axis (-0.0112), number of seeds per siliqua (-0.0059), 1000-seed weight (-0.0025), oil content (-0.0078) and harvest index (-0.0167) was seen at genotypic level.

At phenotypic level also, number of siliquae per plant had positive significant correlation with seed yield per plant (0.175*). Positive direct effect (0.1514) of this character on seed yield per plant was observed. its indirect effect was positive through days to 50% flowering (0.0047), plant height (0.0136), number of primary branches per plant (0.0310), number of secondary branches per plant (0.0471), number of siliquae on main axis (0.0128), length of siliqua (0.0027), number of seeds per siliqua (0.0016), 1000-seed weight (0.0036), oil content % (0.0229), harvest index (0.0370) and negative indirect effect via days to maturity (-0.0219) and length of main axis (-0.0076) was indicated.

4.6.8 Number of siliquae on main axis

Number of siliquae on main axis recorded positive and significant correlation with seed yield per plant (0.226**) as well as positive direct effect (0.2667) on seed yield per plant. Positive indirect effect was reflected through days to 50% flowering (0.0206), days to maturity (0.0199), plant height (0.0487), length of main axis (0.0665), number of siliquae per plant (0.0724), number of seeds per siliqua (0.0360), 1000-seed weight (0.0244) and harvest index (0.0119) whereas, it was negative via number of primary branches per plant (-0.0322), number of secondary branches per plant (-0.0704), length of siliqua (-0.0040) and oil content (-0.0250), at genotypic level.

At phenotypic level number of siliquae on main axis had positive and significant correlation with seed yield per plant (0.154*) but negative direct effect (-0.1343) on seed yield per plant. This trait showed positive indirect effect via days to 50% flowering (0.0066), days to maturity (0.0073), Plant height (0.0147), length of main axis (0.0140), number of siliquae per plant (0.0114), length of siliqua (0.0033) number of seeds per siliqua (0.0089), 1000-seed weight (0.0072), harvest index (0.0076) and negative indirect effect via number of primary branches per plant

(-0.0119), number of secondary branches per plant (-0.0256) and oil content % (-0.0161).

4.6.9 Length of siliqua

Length of siliqua expressed negative but non-significant correlation with seed yield per plant (-0.118) and negative direct effect (-0.3602) on seed yield per plant. However, it showed positive indirect effect via days to 50% flowering (0.0710), number of secondary branches per plant (0.0009), number of siliquae per plant (0.0163), number of siliquae on main axis (0.0054). Negative indirect effect through days to maturity (-0.0088), plant height (-0.0313), number of primary branches per plant (-0.0451), length of main axis (-0.06215), number of seeds per siliqua (-0.0406) 1000-seed weight (-0.1593), oil content % (-0.0941) and harvest index (-0.1389) was observed at genotypic level.

Positive and non-significant correlation of length of siliqua was reflected with seed yield per plant (-0.081). It expressed negative direct effect (-0.1358) on seed yield per plant, whereas indirect effect was positive via days to 50% flowering (0.0220), number of secondary branches per plant (0.0008). Negative indirect effect through days to maturity (-0.0029), plant height (-0.0130), number of primary branches per plant (-0.0074), length of main axis (-0.0163), number of siliquae per plant (-0.0024), number of siliquae on main axis (-0.0033), number of seeds per siliqua (-0.0064), 1000-seed weight (-0.0477), oil content % (-0.0241) and harvest index (-0.0393), at phenotypic level was observed.

4.6.10 Number of seeds per siliqua

Number of seeds per siliqua reflected positive and non-significant genotypic correlation with seed yield per plant (0.076) and positive direct effect (0.1384) on seed yield per plant. This character showed positive indirect via days to 50% flowering (0.0150), days to maturity (0.0126), plant height (0.0134), length of main axis (0.0268), number of siliquae per plant (0.0198), number of siliquae on main axis (0.0187), length of siliqua (0.0156), oil content (0.0238) and harvest index (0.0067) while negative indirect effect via number of primary branches per plant (-0.0143), number of secondary branches per plant (-0.0249) and 1000-seed weight (-0.0489) at genotypic level.

At phenotypic level also, number of seeds per siliqua had positive non-significant correlation with seed yield per plant (0.029) and positive direct effect (0.00232) on seed yield per plant. Positive indirect effect through days to 50% flowering (0.0002), days to maturity (0.0001), plant height (0.0000), length of main axis (0.0001), number of siliquae per plant (0.0000), number of siliquae on main axis (0.0002), length of siliqua (0.0001), oil content % (0.0003) and harvest index (0.0000) was indicated. The indirect effect was negative through number of primary branches per plant (-0.0002), number of secondary branches per plant (-0.0003) and 1000-seed weight (-0.0006) at phenotypic level.

4.6.11 1000-seed weight

The genotypic correlation between 1000-seed weight with seed yield per plant was positive non-significant (0.015) and direct effect (0.1907) on seed yield per plant was also positive. This trait showed positive indirect effect via number of primary branches per plant (0.0262), length of main axis (0.0356), number of siliquae per plant (0.0114), number of siliquae on main axis (0.0174), length of siliqua (0.0843), oil content (0.0271), harvest index (0.0329) and negative indirect effect via days to 50% flowering (-0.0226), days to maturity (-0.0173), plant height (-0.0176), number of secondary branches per plant (-0.0027) and number of seeds per siliqua (-0.0673), at genotypic level.

The phenotypic correlation between 1000-seed weight and seed yield per plant was negative but non-significant (-0.001) while positive direct effect (0.0236) was seen on seed yield per plant. It showed positive indirect effect through number of primary branches per plant (0.0026), length of main axis (0.0038), number of siliquae per plant (0.0006), number of siliquae on main axis (0.0013), length of siliqua (0.0083), oil content % (0.0028), harvest index (0.0037) and negative indirect effect through days to 50% flowering (-0.0028), days to maturity (-0.0021), plant height (-0.0011), number of secondary branches per plant (-0.0005) and number of seeds per siliqua (-0.0058) at phenotypic level.

4.1.12 Oil content

Oil content expressed positive and non-significant genotypic correlation with seed yield per plant (0.064). Direct effect was also positive in magnitude (0.2678) on seed yield per plant. Oil content showed positive indirect effect via days 50%

flowering (0.0230), days to maturity (0.0277), number of primary branches per plant (0.0523), number of secondary branches per plant (0.0369), length of main axis (0.0859), number of siliquae per plant (0.0506), length of siliqua (0.0700), number of seeds per siliqua (0.0460), 1000-seed weight (0.0380), harvest index (0.0264) and negative indirect effect through plant height (-0.0340) and number of siliquae on main axis (-0.0251) at genotypic level.

Oil content had positive and non-significant phenotypic correlation with seed yield per plant (0.080) as well as positive direct effect (0.0758) on seed yield per plant. Indirect effect was positive due to days 50% flowering (0.0058), days to maturity (0.0067) number of primary branches per plant (0.0121), number of secondary branches per plant (0.0087), length of main axis (0.0132), number of siliquae per plant (0.0115), length of siliqua (0.0135), number of seeds per siliqua (0.0091), 1000-seed weight (0.0091) and harvest index (0.0069), while it was negative due to plant height (-0.0109) and number of siliquae on main axis (-0.0091) at phenotypic level.

4.6.13 Harvest index

Harvest index reflected positive and significant correlation with seed yield per plant (0.232**) with positive direct effect (0.3956) on seed yield per plant. Positive indirect effect via days to 50% flowering (0.0003), number of primary branches per plant (0.0002), length of main axis (0.0682) number of siliquae per plant (0.1600), number of siliquae on main axis (0.0176), length of siliqua (0.1525), number of seeds per siliqua (0.0190), 1000-seed weight (0.0683), oil content % (0.0390) and negative indirect effect due days to maturity (-0.944), plant height (-0.0323) and number of secondary branches per plant (-0.0171) was observed at genotypic level.

Similarly, harvest index also recorded positive and significant correlation with seed yield per plant (0.192**) as well as positive direct effect (0.1930) on seed yield per plant. Harvest index exhibited positive indirect effect through number of primary branches per plant (0.0017), length of main axis (0.0149), number of siliquae per plant (0.0471), number of siliquae on main axis (0.01094), length of siliqua (0.0559), number of seeds per siliqua (0.0017), 1000-seed weight (0.0304), oil content % (0.0176) and negative indirect effect through days to 50% flowering (-0.0005), days to maturity (-0.0424), plant height (-0.0129) and number of secondary branches per plant (-0.0069) at phenotypic level.

Table 4.9: Path coefficient analysis showing the direct and indirect effect of 13 characters on seed yield at genotypic and phenotypic level in Indian mustard

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Length of main axis (cm)	Number of siliquae per plant	Number of siliquae on main axis	Length of siliqua (cm)	Number of seeds per siliqua	1000-seed weight (g)	Oil content (%)	Harvest index (%)	Correlation with seed yield per plant
Days to 50% flowering	G	-0.0402	-0.0128	-0.0090	0.0055	0.0024	0.0023	-0.0016	-0.0031	0.0079	-0.0044	0.0048	-0.0035	0.0000	0.135
	P	0.0735	0.0221	0.0131	-0.0067	-0.0032	-0.0037	0.0023	0.0036	-0.0119	0.0051	-0.0086	0.0057	-0.0002	0.129
Days to maturity	G	0.0242	0.0759	0.0097	-0.0101	-0.0190	-0.0363	-0.0175	0.0057	0.0018	0.0069	-0.0069	0.0079	-0.0181	0.072
	P	0.0267	0.0890	0.0095	-0.0093	-0.0187	-0.0021	-0.0129	0.0048	0.0019	0.0045	-0.0080	0.0078	-0.0195	0.066
Plant height (cm)	G	-0.0011	-0.0006	-0.0048	0.0010	0.0006	-0.0012	-0.0003	-0.0009	-0.0004	-0.0005	0.0004	0.0006	0.0004	-0.133
	P	-0.0165	-0.0099	-0.0921	0.0083	0.0035	-0.0277	-0.0083	-0.0101	-0.0088	0.0009	0.0042	0.0133	0.0062	-0.097
Number of primary branches per plant	G	0.0166	0.0161	0.0247	-0.1213	-0.0654	0.0259	-0.0334	0.0146	-0.0152	0.0126	-0.0167	-0.0237	-0.0001	-0.111
	P	0.0025	0.0029	0.0025	-0.0274	-0.0120	0.0038	-0.0056	0.0024	-0.0015	0.0020	-0.0030	-0.0044	-0.0002	-0.030
Number of secondary branches per plant	G	0.0056	0.0241	0.0114	-0.0519	-0.0963	0.0405	-0.0350	0.0254	0.0002	0.0173	0.0014	-0.0137	0.0042	-0.093
	P	0.0033	0.0158	0.0029	-0.0330	-0.0752	0.0176	-0.0234	0.0143	0.0005	0.0098	0.0015	-0.0086	0.0027	-0.064
Length of main axis (cm)	G	0.0242	0.0201	-0.1089	0.0899	0.1771	-0.4213	0.0484	-0.1051	-0.0727	-0.0817	-0.0786	-0.1351	-0.0726	-0.132
	P	0.0038	0.0018	-0.0229	0.0105	0.0178	-0.0762	0.0038	-0.0080	-0.0091	-0.0047	-0.0124	-0.0133	-0.0059	-0.066
Number of siliquae per plant	G	-0.0016	0.0095	-0.0029	-0.0114	-0.0150	0.0048	-0.0414	-0.0112	0.0019	-0.0059	-0.0025	-0.0078	-0.0167	0.250**
	P	0.0047	-0.0219	0.0136	0.0310	0.0471	-0.0076	0.1514	0.0128	0.0027	0.0016	0.0036	0.0229	0.0370	0.175*
Number of siliquae on main axis	G	0.0206	0.0199	0.0487	-0.0322	-0.0704	0.0665	0.0724	0.2667	-0.0040	0.0360	0.0244	-0.0250	0.0119	0.226**
	P	0.0066	0.0073	0.0147	-0.0119	-0.0256	0.0140	0.0114	0.1343	0.0033	0.0089	0.0072	-0.0161	0.0076	0.154*
Length of siliqua (cm)	G	0.0710	-0.0088	-0.0313	-0.0451	0.0009	-0.0622	0.0163	0.0054	-0.3602	-0.0406	-0.1593	-0.0941	-0.1389	-0.118
	P	0.0220	-0.0029	-0.0130	-0.0074	0.0008	-0.0163	-0.0024	-0.0033	-0.1358	-0.0064	-0.0477	-0.0241	-0.0393	-0.081
Number of seeds per silique	G	0.0150	0.0126	0.0134	-0.0143	-0.0249	0.0268	0.0198	0.0187	0.0156	0.1384	-0.0489	0.0238	0.0067	0.076
	P	0.0002	0.0001	0.0000	-0.0002	-0.0003	0.0001	0.0000	0.0002	0.0001	0.0023	-0.0006	0.0003	0.0000	0.029
1000-seed weight (g)	G	-0.0226	-0.0173	-0.0176	0.0262	-0.0027	0.0356	0.0114	0.0174	0.0843	-0.0673	0.1907	0.0271	0.0329	0.015
	P	-0.0028	-0.0021	-0.0011	0.0026	-0.0005	0.0038	0.0006	0.0013	0.0083	-0.0058	0.0236	0.0028	0.0037	-0.001
Oil content (%)	G	0.0230	0.0277	-0.0340	0.0523	0.0369	0.0859	0.0506	-0.0251	0.0700	0.0460	0.0380	0.2678	0.0264	0.694**
	P	0.0058	0.0067	-0.0109	0.0121	0.0087	0.0132	0.0115	-0.0091	0.0135	0.0091	0.0091	0.0758	0.0069	0.715**
Harvest index (%)	G	0.0003	-0.0944	-0.0323	0.0002	-0.0171	0.0682	0.1600	0.0176	0.1525	0.0190	0.0683	0.0390	0.3956	0.232**
	P	-0.0005	-0.0424	-0.0129	0.0017	-0.0069	0.0149	0.0471	0.0109	0.0559	0.0017	0.0304	0.0176	0.1930	0.192**

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

Residual Effect = 0.20670 (Genotypic)

Residual Effect = 0.29358 (Phenotypic)

Knowledge of the extent and pattern of genetic variability present in a population is essential for the assessment of nature of genetic mechanism and it facilitates the selection of high yielding genotypes either for direct use as a variety or to be used in various breeding programmes. Besides this, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be used for hybridization programmes. Multivariate analysis techniques namely D^2 analysis by Mahalanobis, method was employed for the analysis of divergence and the genotypes are grouped together based on their relative genetic similarity or divergence. Information on the extent and nature of inter-relationship among characters helps in formulating efficient scheme of selection for different traits. The knowledge of phenotypic and genotypic correlations between quantitative traits is of paramount importance in the breeding programme. The characters which have high and positive correlation with yield can be used in the indirect selection for yield and as an alternate mode of selection for yield improvement. Path coefficient analysis of effective variables with the causal factor into components of direct and indirect effects is also required as it reveals the relative importance of the causal factors in producing the end product. The path coefficient analysis helps the breeders to explain direct and indirect effects and hence has extensively been used in plant breeding activities.

The present experiment was carried out with 60 genotypes of Indian mustard. The investigation entitled “**Genetic divergence and character association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]**” is an attempt to study genetic variability for the traits, diversity among the genotypes and character association. The results obtained from the experiment are being discussed under the following heads:

1. Analysis of variance
2. Mean performance of the genotypes
3. Genetic variability parameters
4. Genetic divergence analysis
5. Character association analysis
6. Path coefficient analysis

5.1 Analysis of Variance

The analysis of variance indicated highly significant differences among different genotypes of Indian mustard for all the characters under study and wide variation was observed for most of the characters as revealed by the wide range of values for all the quantitative characters studied. This suggested that adequate scope is available for selection of superior genotypes aimed at enhancing yield potential of Indian mustard. The reason for high magnitude of variability in this study may be due to the fact that genotypes selected were from different indigenous source belonging to different locations. High magnitude of variability has been earlier reported in Indian mustard genotypes by Ram and Verma (2010), Singh *et al.* (2011), Yadava *et al.* (2011), Lohia *et al.* (2013), Tripathi *et al.* (2013), Shekhawat *et al.* (2014), Akabari and Niranjana (2015), Meena *et al.* (2017), Yadav and Pandey (2018), Ray *et al.* (2019) and Rout *et al.* (2019), in which analysis of variance showed significant differences for all the characters under their study.

5.2 Mean performance of the genotypes

On the basis of mean performance of genotypes, it has been found that mustard genotypes PM-28, RVM-2, Pusa Tarak, NRCDR-2 and JM-1 were earlier with respect to days to 50% flowering. Besides this, 34 genotypes also recorded values numerically lower than the mean value for this trait. The genotypes PM-28, CS-54, RH-819, PDZ-1, Swarn Jyoti and GM-2 were found early maturing with respect to days to maturity. Twenty-four genotypes out of the total 60 evaluated, were observed to have lower days to maturity than the mean value, while 36 genotypes were found to score statistically more than the character mean indicating that these are late maturing types.

There was wide variability in plant height among the genotypes. Twenty-eight genotypes out of 60 recorded mean values less than the overall mean indicating their short stature which is a desirable character in crop improvement. The genotypes like Pusa Mahak, PM-26 and PM-28 were having shortest plant height less than 200 cm and RH-51 and DRMR-601 were found tallest, having plant height more than 250 cm.

Branching is one of the major yield attributing traits in mustard crop. In this investigation the numbers of primary branches per plant and number of secondary branches per plant were calculated and mean values for the character were tabulated

(Table 4.2). Out of the 60 genotypes, 22 genotypes recorded more than the general mean for number of primary branches per plant while 21 genotypes for number of secondary branches per plant. Genotypes RH-406 was found statistically superior than the rest with respect to number of primary branches while genotypes PM-26 and Varuna showed highest number of secondary branches per plant.

RH-51, Pusa Bold, Pusa Bahar, Vaubhav and RH-406 recorded highest and more than the mean value for length of main axis. The four genotypes viz. Varuna, Pusa Jai Kishan, RH-725, RGN-229 and RGN-34 recorded highest number of siliquae per plant, although 34 genotypes found statistically superior than the general mean for this character. Increased number of siliquae per plant in Indian mustard is an essential component for higher productivity, the genotypes with higher number of siliquae per plant should be sorted out for further breeding programmes. On the other hand, it is a well-established fact that selection for higher number of siliquae leads to compensatory decrease in seed size. It is therefore suggested that in order to maintain higher productivity, a balance must be maintained between number of siliquae and seed weight.

The genotypes namely, JM-3, RH-419, Vasundhara, DRMR-601 and RVM-2 were found with highest number of siliquae on main axis. However, 28 genotypes had higher mean values than average mean value for this character. A wide range of variation was observed for length of siliqua. Genotypes PM-27, Rohini, RH-406, RNCDR-2 and RH-749 recorded the highest mean values for this character. Number of seeds per siliqua has been reported by many workers as a key yield attributing trait. The mean value for the trait was recorded as 15.05 and the genotypes JM-3, JM-1, Giriraj and CS-54 statistically superior to rest of the genotypes for number of seed per siliqua.

The average 1000-seed weight over the genotypes was observed to be 4.43 g and 28 genotypes were found statistically superior to the mean. RH-30, PBR-91, Vaibhav and RVM-2 were considered as four best genotypes for this trait among the 60 genotypes. On the contrary these genotypes though bold seeded but are not among the top yielders and thus do not have a direct correlation with the single plant yield. This indicates that a balance should be maintained between 1000-seed weight and all other traits while selecting for the genotype.

Oil content is also an important character in oilseed crops. The average value for this trait was 40.34% and 34 genotypes showed higher oil content than the mean value for this character. PM-27, RM-51, Pusa Bahar, RH-904 and RH-406 were the top five genotypes having highest oil content among the 60 genotypes under study. The overall mean value for harvest index was recorded as 22.65% over the 60 genotypes and highest values were obtained by the genotypes NRCDR-2, Ashirwad, RH-406, CS-54 and RH-749 with regards to this character. A total of 29 genotypes were found statistically superior than the general mean value.

Improvement in the Seed yield is an artifact that results from favorable and unfavorable combinations of component traits and is the ultimate goal of plant breeding activities showing wide range of variation among the genotypes. The range of variation for the character seed yield per plant was recorded within 8.43 g to 16.55 g. RH-725, Giriraj, RGN-303, Kranti and Pusa Jai Kishan were the five top yielders genotypes that recorded highest mean seed yield per plant. The average yield per plant over 60 genotypes was recorded to be 12.16 g and 28 genotypes recorded numerically higher than the character mean. The varieties which showed higher and significant seed yield along with other yield contributing characters might be of greater use in future breeding programmes.

It is evident from the aforesaid discussion that the genotypes included in the study exhibited wide range of variability in respect of all the 14 characters. It is suggested that due to the enormous variations present, the test genotypes have the merit to be used as the base population in varietal improvement programme. The variation among the genotypes can therefore be attributed to the genetic diversity owing to the involvement of diverse parents in the development of breeding lines. Similar findings pertaining to the presence of high amount of genetic variability for the different traits including seed yield have been reported by Singh *et al.* (2011), Yadava *et al.* (2011), Lohia *et al.* (2013), Tripathi *et al.* (2013), Shekhawat *et al.* (2014), Akabari and Niranjana (2015), Meena *et al.* (2017), Yadav and Pandey (2018), Khan *et al.* (2013) and Rout *et al.* (2018).

5.3 Genetic variability parameters

Variation and selection are the two basic requirements of genetic improvement in any crop. Selection without variation is ineffective and of no use. The knowledge

on the extent of genetic variability with regards to various traits and their nature of transmission to the succeeding generations is therefore crucial for effective selection for superior genotypes.

A wide range of variability present in any crop species provides the better chances of selecting desired traits (Vavilov, 1935). It is also important for exploitation to fulfill most of the emerging needs for developing improved crop varieties. The assessment of genetic variability parameters like phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), heritability (broad sense) and genetic advance are prerequisite for making effective selection (Dipti *et al.* 2016). The estimates of PCV, GCV, heritability and genetic advance are also helpful to improve a particular plant population for a specific trait. GCV and PCV, heritability and genetic advance as per cent of mean were estimated for 14 different quantitative traits in 60 Indian mustard genotypes which are presented in Table 4.3.

5.3.1 Coefficient of variation

The estimates of phenotypic coefficient of variation (PCV) were observed to be higher than the estimates genotypic coefficient of variation (GCV) suggesting the relative influence of environment in expression of different characters. The PCV and GCV observed for seed yield per plant, 1000-seed weight, number of secondary branches per plant, harvest index, number of primary branches per plant, number of siliquae on main axis, length of siliqua, length of main axis, number of siliquae per plant and number of seeds per siliqua were found moderate which indicated that high amount of PCV and GCV played a considerable role in expression of these traits. Estimates of PCV and GCV in the present investigation were very close in characters namely days to 50% flowering, days to maturity, Plant height (cm), number of secondary branches, length of siliqua (cm), 1000-seed weight (g), oil content (%), harvest index (%) and seed yield per plant indicating negligible influence of environment and these characters may be considered stable. Hence, selection on phenotypic values of such characters is expected to be effective. Whereas, for the characters viz., Number of primary branches per plant, length of main axis, number of siliquae per plant, number of siliquae on main axis and number of seeds per siliqua, relatively large difference between PCV and GCV was observed which indicates the influence of environment is relatively high. Similar results were reported by Yadava

et al. (2011), Singh *et al.* (2013), Lodhi *et al.* (2014), Akabari and Niranjana (2015), Singh *et al.* (2018) and Ray *et al.* (2019). The character like days to 50% flowering, days to maturity, plant height and oil content % lowering the estimates indicated that improvement in these traits could be done through selection to some extent. This matched with the finding of Singh *et al.* (2011), Yadava *et al.* (2011), Lohia *et al.* (2013), Singh *et al.* (2013), Shekhawat *et al.* (2014), Akabari and Niranjana (2015), Maurya *et al.* (2018) and Yadav and Pandey (2018).

5.3.2 Heritability and genetic advance

Heritability depends upon the amount of genetic variation present in the population and environmental conditions under which the population is evaluated. The estimate of heritability (broad sense) includes both additive as well as non-additive gene effects and thus is not very much useful alone in predicting resultant effect for selecting the best genotypes. High genetic advance occurs only due to additive gene action so, heritability estimates coupled with the genetic advance would be more useful than heritability alone.

The present study revealed that estimates of broad sense heritability were high for days to maturity, days to 50% flowering, 1000-seed weight, harvest index, seed yield per plant, number of secondary branches per plant, oil content %, length of siliqua and plant height, indicating that selection would be more useful to improve these traits. Acharya and Patil (2008), Singh *et al.* (2011), Yadava *et al.* (2011), Priyamedha *et al.* (2013), Singh *et al.* (2013), Lodhi *et al.* (2014), Akabari and Niranjana (2015) and Ray *et al.* (2019) have reported similar findings. Moderate to low heritability were observed for number of primary branches per plant, length of main axis number of siliquae on main axis, number of siliquae per plant, number of seeds per siliqua indicated that improvement in this trait could be done through selection to some extent. Such heritability estimates for these characters studied have been reported earlier also by, Singh *et al.* (2011), Singh *et al.* (2013), Devmani *et al.* (2014), Tiwari *et al.* (2017) and Rout *et al.* (2019).

Genetic advance as per cent values were high for 1000-seed weight, seed yield per plant, harvest index and number of secondary branches per plant. Similar results were earlier reported by Singh *et al.* (2013), Devi (2018) and Malik *et al.* (2018). Heritability estimates coupled with genetic advance are more helpful than heritability

alone in predicting the progress from the selected better individuals. It is therefore necessary to estimate the broad sense heritability in conjunction with the genetic advance. In the present investigation 1000-seed weight, harvest index, number of secondary branches per plant and seed yield per plant recorded high estimates of heritability coupled with high genetic advance, which indicates that selection would be effective for the improvement of these traits. Genetic advance as per cent of mean for most of the characters under study are in accordance with earlier reports of Singh *et al.* (2013), Akabari and Niranjana (2015), Singh *et al.* (2018) and Rout *et al.* (2019).

5.4 Genetic divergence analysis

Classification using D^2 analysis of genetic divergence aims at grouping the genotypes precisely and objectively into various groups. In the present investigation simultaneous variations in all characters of 60 Indian mustard genotypes were tested for assessment of the nature of genetic divergence among them following Mahalanobis D^2 statistics. The results obtained have been presented and discussed in the light of similar findings by other workers in the following sections.

Genetic divergence is the diversity of the sets of genes carried by different genotypes of a species. Information on genetic resources with broad genetic diversity is a pre-requisite for genetic improvement of crops as it helps to distinguish the genotypes into genetically close and divergent types. D^2 statistic has been found quite efficient to assess genetic diversity in a set of test genotypes. Researchers can use this information on genetic dissimilarity to make decisions for selection of superior genotypes for genetic improvement or for use as parents in hybridization programme.

5.4.1 D^2 analysis

The study of genetic divergence was done following Mahalanobis D^2 statistics as described by Rao (1952). The group constellation was prepared following Tocher's method. The magnitude of D^2 values indicated considerable genetic diversity, among the selected mustard genotypes. Consequently, eight clusters were formed. It could be inferred from the pattern of clustering that sufficient divergence was present to enable the formation of individual clusters.

5.4.2 Group constellations using D²-statistics

Sixty genotypes of Indian mustard included in the present study were grouped into eight different clusters on the basis of genetic divergence or genetic closeness by D² following Tocher's method of clustering. The clustering pattern of the genotypes has been shown in Table 4.4. Cluster IV was the largest group of 18 genotypes, whereas cluster I was the second largest group consisting 16 genotypes grouped together. Cluster VI was the third largest cluster based on the genotypes (8 genotypes) followed by cluster II (7 genotypes) and cluster III (6 genotypes). Two clusters namely cluster V and cluster VIII each comprised of two genotypes. The remaining cluster VII comprised only one genotype (RH 406) indicating that this genotype is much more divergent than rest of the genotypes in the study. It was concluded that in general there was parallelism between genetic and geographic diversity. This view point has been supported by the work of Shathi *et al.* (2012), Khan *et al.* (2013), Kumar and Pandey (2013), Lodhi *et al.* (2013), Singh *et al.* (2014), Yong *et al.* (2014), Rout *et al.* (2019), Tripathi *et al.* (2019) and Gadi *et al.* (2020).

5.4.3 Intra and inter-cluster divergence

The intra-cluster distance among various clusters exhibited maximum intra-cluster distance for cluster VI and lowest intra-cluster distance was recorded for cluster VII. The maximum intra-cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregates by crossing the genotypes of the same cluster showing low value for intra-cluster distance are very low. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter-cluster distances. The little diversity and selection of parents within the cluster having higher mean for a particular character may also be useful for further developing high yielding Indian mustard varieties.

In the present study, the maximum inter-cluster distance was revealed between cluster V and VIII, followed by cluster V and VII, cluster VI and VIII and cluster III and V. This clearly indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity and could very well be used in hybridization for mustard improvement programme. The lowest inter-cluster distance was observed for cluster III and IV followed by cluster I and VII and cluster I and IV. The lowest inter-cluster distances indicate that the genotype of these clusters had close relationship and

hence, may not be emphasized upon to be used in hybridization programme. These results are somewhat in accordance with the findings of Goswami and Behl *et al.* (2006), Singh *et al.* (2010), Singh *et al.* (2011), Kumar and Pandey (2013), Pandey *et al.* (2013) Tudu *et al.* (2018) Tripathi *et al.* (2019) and Gadi *et al.* (2020).

5.4.5 Clusters means

Cluster III had highest mean values for most of the desirable characters like seed yield per plant followed by number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of siliquae on main axis, length of siliqua, number of seeds per siliqua, 1000-seed weight, oil content and harvest index. The genotypes accommodate under cluster V showed desirable traits of early days to 50% flowering and minimum plant height, maximum seed yield per plant and similarly other traits like, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of siliquae on main axis and number of seeds per siliqua.

On the basis of average D^2 the highest contribution to divergence was depicted by from seed yield per plant followed by, 1000-seed weight and number of secondary branches per plant have been also highlight by Lodhi *et al.* (2013) and Kumari A. and Kumari V. (2018). Other traits like harvest index, length of siliqua, number of primary branches per plant number of siliquae on main axis and length of main axis, such results were also supported by earlier findings of Khan *et al.* (2013) and Shekhawat *et al.* (2014). Rout *et al.* (2018) have mentioned number of siliquae per plant and number of seeds per siliqua. The lowest per cent contribution to divergence was indicated by oil content %, days to maturity, plant height and days to 50% flowering. Remaining characters contributed very little towards genetic divergence.

5.5 Character association analysis

Seed yield in Indian mustard is a complex character and is the result of correlation between yield and yield components and between yield components themselves. Therefore, it is very imperative to examine the contribution of each of the various components in order to attract the attention to which one has the greatest influence on seed yield. Estimation of phenotypic and genotypic correlations between seed yield and component characters as well as inter association provides information for choice of characters in selection programme. In the present investigation the

correlation coefficients were estimated among 14 characters at phenotypic and genotypic levels. The genotypic correlation coefficients were found to be higher than phenotypic correlation coefficients for most of the characters, indicating a strong inherent association between various characters and were masked by environmental components with regard to phenotypic expression. However, the correlation studies showed that for most of the character pairs, the genotypic and phenotypic associations were in same directions indicating an inherent association between the characters. similar results were obtained by Roy *et al.* (2018).

Correlation study revealed that number of siliquae per plant, number of siliquae on main axis and harvest index exerted high positive significant correlation with seed yield per plant both at genotypic and phenotypic levels. Thus, it can be inferred that selection based on any one of these characters either alone or in combination, will result in identifying high yielding strains. These characters were indicating their true relationship with yield and similar findings have been given by the other authors like, Ramanjaneyulu and Giri (2007), Singh *et al.* (2011), Lohia *et al.* (2013), Rathod *et al.* (2013), Priyamedha *et al.* (2013), Lodhi *et al.* (2014), Islam *et al.* (2016), Kumar *et al.* (2016), Tiwari *et al.* (2017), Devi (2018), Gupta *et al.* (2018), Ompal *et al.* (2018) Rout *et al.* (2018) and Kumari *et al.* (2019). On the other hand, plant height number of primary branches per plant, number of secondary branches per plant, length of main axis, length of siliqua and number of siliquae on main axis showed negative non-significant correlation with seed yield per plant both at genotypic and phenotypic level. These findings resemble with the results obtained by Islam *et al.* (2016), Bineeta Devi (2018), Gupta *et al.* (2018), Rout *et al.* (2018), Bhattarai (2019) and Kumari *et al.* (2019).

5.6 Path coefficient

Path analysis may be of limited utility to a plant breeder but it definitely gives an insight into a complex relationship among different characters in a biological system and provides information whether, the observed correlation is due to the direct influence through other variables. Thus, path analysis specifies the causes and also gives the relative importance of the characters. The correlation coefficient of component traits with seed yield were partitioned into their direct and indirect effects on seed yield following path coefficient analysis to ascertain further conclusive

information on choice of characters required for selection of high yielding genotypes. The path coefficient analysis not only specify the effective measure of direct and indirect causes of association, but also depicts the relative importance of each factor involved in contributing to the final product of yield.

Path coefficient analysis exhibited positive direct contribution of days to 50% flowering and number of siliquae per plant (At phenotypic level). Positive direct effect on seed yield per plant was reflected both at genotypic and phenotypic level through days to maturity, number of siliquae on main axis, number of seeds per siliqua, 1000-seed weight oil content % and harvest index. On the other hand, days to 50% flowering and number of siliquae per plant showed negative direct effect on seed yield per plant only at genotypic level. Therefore, the characters exhibited positive direct effects on seed yield should be preferred while making selection for improvement of seed yield and more emphasis should be given to these traits with greater magnitude of positive direct effect than those with smaller magnitude. The similar results were also obtained by Ara *et al.* (2013), Rathod *et al.* (2013), Priyamedha *et al.* (2013), Uddin *et al.* (2013), Iqbal *et al.* (2014), Lodhi *et al.* (2014), Shekhawat *et al.* (2014), Tahira *et al.* (2014), Husan *et al.* (2015), Dawar *et al.* (2018), Rout *et al.* (2018) and Roy *et al.* (2018). The indirect effects via any other trait were found lesser than the direct effect. However, the highest positive indirect effect on seed yield per plant was exhibited through number of siliquae per plant and length of siliqua. Positive direct effects of these traits on seed yield indicated their importance in determining this complex character and therefore, should be kept in mind while practicing selection aimed at the improvement of seed yield. The indirect effects of these characters were found lesser than the magnitudes of the direct effect on seed yield per plant which indicated that these characters were affecting the seed yield per plant directly. Similar result also reported by Ara *et al.* (2013), Priyamedha *et al.* (2013), Uddin *et al.* (2013), Iqbal *et al.* (2014), Shekhawat *et al.* (2014), Tahira *et al.* (2014), Husan *et al.* (2015) and Rout *et al.* (2018).

The present study entitled “**Genetic divergence and character association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]**” was carried out during *Rabi* 2019-20 at Agriculture Research Station, Kota, Agriculture University, Kota, Rajasthan. The materials used for the present investigation consisted of 60 indigenous Indian mustard genotypes of diverse origin. The experiment was laid out in Randomized Block Design (RBD) with three replications. Each genotype was sown in 2 rows of 5.0-meters length, with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. All the recommended agronomic practices for Indian mustard were followed to raise a healthy crop.

This investigation in Indian mustard involved assessment of genetic divergence using Mahalanobis D^2 analysis, genetic components of variation with the help of genotypic coefficients of variation, phenotypic coefficient of variation, heritability and genetic advance and also to find out relationship between the characters in addition to morphological diversity present among 60 Indian mustard genotypes. The mean data of randomly selected five plants for 14 observable traits were subjected to analysis of variance and based on that different genetic parameters were calculated. A gist of the salient findings from the investigation and the inferences drawn are presented below.

1. The analysis of variance indicated highly significant differences among the 60 genotypes of Indian mustard for 14 quantitative characters and wide variation was observed.
2. The PCV values were greater than GCV values for all the characters as the former included the variations due to environment. High to moderate estimates of PCV and GCV were observed for seed yield per plant followed in order by 1000-seed weight, number of secondary branches per plant, harvest index, number of primary branches per plant, number of siliquae on main axis, length of siliqua, length of main axis, number of siliquae per plant and number of seeds per siliqua. Which indicated that

high amount of PCV and GCV played a considerable role in expression of these traits.

3. The character viz., Number of primary branches per plant, length of main axis, number of siliquae per plant, number of siliquae on main axis and number of seeds per siliqua showed relatively large difference between PCV and GCV was observed which indicates the high influence of environment in these characters.
4. Estimates of PCV and GCV in the present investigation were very close in characters namely days to 50% flowering, days to maturity, Plant height (cm), number of secondary branches per plant, length of siliqua (cm), 1000-seed weight (g), oil content (%), harvest index (%) and seed yield per plant (%) indicated that they were less influenced by the environment.
5. The present study revealed that estimates of broad sense heritability were high for days to maturity, days to 50% flowering, 1000-seed weight (g), harvest index (%), seed yield per plant (g), oil content (%), number of secondary branches per plant, length of siliqua (cm) and plant height (cm), plays a role in an improvement of the crop yield, indicating that selection would be more useful to improve these traits.
6. Genetic advance as per cent of mean was highest for 1000-seed weight followed by Seed yield per plant, harvest index and number of secondary branches per plant.
7. Estimates of high heritability coupled with high genetic advance for seed yield per plant followed by number of secondary branches per plant, harvest index and 1000-seed weight were observed.
8. Eight clusters were obtained by Tocher's method. Cluster IV was the largest group of 18 genotypes, whereas cluster I was the second largest group consisting 16 genotypes grouped together. Cluster VI was the third largest cluster based on the genotypes (8 genotypes) followed by cluster II (7 genotypes) and cluster III (6 genotypes). Two clusters, V and VIII as in discussion comprised of two genotypes each cluster. The remaining

cluster VII comprised only one genotype (RH 406) indicating that this genotype is much more divergent than rest of the genotypes in the study.

9. The intra-cluster distance among various clusters exhibited maximum intra cluster distance for cluster VI and lowest intra-cluster distance was recorded for cluster VII.
10. In the present study, the maximum inter-cluster distance was indicated between cluster V and VIII, followed in order by cluster V and VII, cluster VI and VIII and cluster III and V.
11. The lowest inter-cluster distances were observed for cluster III and IV followed by cluster I and VII and cluster I and IV. The lowest inter-cluster distances indicate that the genotype of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme.
12. The contribution towards genetic divergence was maximum by seed yield per plant followed in order by 1000-seed weight, number of secondary branches per plant, harvest index, length of siliqua, number of primary branches per plant, number of siliquae on main axis, length of main axis and number of siliquae per plant and number of seeds per siliqua.
13. Cluster III had highest mean values for most of the desirable characters like seed yield per plant followed by number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of siliquae on main axis, length of siliqua, number of seeds per siliqua, 1000-seed weight, oil content and harvest index. The genotypes accommodate under cluster V were found desirable traits like, early days to 50% flowering and plant height, maximum for seed yield per plant and similarly other traits like, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of siliquae on main axis and number of seeds per siliqua.
14. Correlation study revealed that number of siliquae per plant, number of siliquae on main axis and harvest index exerted high positive significant

correlation with seed yield per plant both at genotypic and phenotypic levels.

15. Path coefficient analysis exhibited positive direct effect by days to 50% flowering and number of siliquae per plant (At phenotypic level). Positive direct effect was observed on seed yield per plant by days to maturity, number of siliquae on main axis, number of seeds per siliqua, 1000-seed weight oil content % and harvest index both at genotypic and phenotypic levels in present study.
16. The range of variation for the character seed yield per plant was recorded within 8.43 g to 16.55 g. The genotypes RH-725 (16.55 g), Giriraj (15.64 g), RGN-303 (15.60 g), Kranti (15.44 g) and Pusa Jai Kishan (14.92 g) were the five top yielders genotypes that recorded highest mean seed yield per plant and could be recommended for commercial cultivation or used in further breeding programme.

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Genetic divergence and character association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]

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Abstract

The present investigation entitled “**Genetic divergence and character association in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]**” was carried out during *Rabi* 2019-20 with 60 genotypes for 14 quantitative characters *viz.*, Days to 50% Flowering, days to maturity, plant height (cm), number of primary branch per plant, number of secondary branch per plant, length of main axis (cm), number of siliquae per plant, number of siliquae on main axis, length of siliqua (cm), number of seeds per siliqua, 1000-seed weight (g), oil content (%), harvest index (%) and seed yield per plant (g). The experiment was laid out in a Randomized block design with three replications at Agricultural Research Station, Ummedganj Farm, Kota (Agriculture University, Kota).

The analysis of variance indicated highly significant differences among the 60 genotypes of Indian mustard for 14 quantitative characters studied. The estimates of PCV and GCV for seed yield per plant, 1000-seed weight, number of secondary branches per plant, harvest index, number of primary branches per plant, number of siliquae on main axis, length of siliqua, length of main axis, number of siliquae per plant and number of seeds per siliqua were found moderate which indicated that high amount of PCV and GCV played a considerable role in expression of these traits. High estimates of heritability coupled with high genetic advance for 1000-seed weight, harvest index, number of secondary branches per plant and seed yield per plant indicated that selection would be effective for the improvement of these traits.

Genetic divergence assessed by Mahalanobis D^2 following Tocher's methods of clustering. Sixty genotypes studied were grouped into eight clusters. Cluster IV was the largest with 18 genotypes, whereas cluster I was the second largest with 16 genotypes grouped together. Cluster VI was the third largest cluster based on the number of genotypes (8 genotypes) followed by cluster II (7 genotypes) and cluster III (6 genotypes). Two clusters, V and VIII comprised of two genotype each. Cluster VII comprised only one genotype. Maximum intra-cluster distance was recorded for

cluster VI, whereas it was lowest for cluster VII. The maximum inter-cluster distance was revealed between cluster V and VIII followed by cluster V and VII, cluster VI and VIII and cluster III and V.

The maximum contribution towards genetic divergence was from seed yield per plant followed by 1000-seed weight, number of secondary branches per plant, harvest index, length of siliqua, number of primary branches per plant, number of siliquae on main axis, length of main axis and number of siliquae per plant and number of seeds per siliqua.

Correlation study revealed that number of siliquae per plant, number of siliquae on main axis and harvest index exerted high positive significant correlation with seed yield per plant both at genotypic and phenotypic levels.

Path coefficient analysis exhibited positive direct effect via days to 50% flowering and number of siliquae per plant (At phenotypic level). Positive direct effect on seed yield per plant observed both at genotypic and phenotypic levels through days to maturity, number of siliquae on main axis, number of seeds per siliqua, 1000-seed weight, oil content and harvest index.

The genotypes RH-725 (16.55 g), Giriraj (15.64 g), RGN-303 (15.60 g), Kranti (15.44 g) and Pusa Jai Kishan (14.92 g), were superior not only for seed yield per plant but also for related traits like harvest Index, number of siliquae per plant, number of primary and number of secondary branches per plant. These superior genotypes may be used for future breeding programme.

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भारतीय सरसों {ब्रैसिका जंसिया (एल.) सजर्न एवं कॉस} में आनुवांशिक विविधता और लक्षणों में सह-सम्बन्ध

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सारांश

वर्तमान अनुसंधान कार्य “भारतीय सरसों {ब्रैसिका जंसिया (एल.) सजर्न एवं कॉस} में आनुवांशिक विविधता और लक्षणों में सह-सम्बन्ध” शीर्षक के अन्तर्गत भारतीय सरसों के 60 जीन प्रारूपों को लेकर 14 लक्षणों के साथ रबी 2019–20 में तीन प्रतिकृति के साथ यादृच्छिक खंड अभिकल्पना में कृषि अनुसंधान केन्द्र, उम्मेदगंज, कोटा के कृषि क्षेत्र में लगाया गया।

विचरण के विश्लेषण ने अध्ययन किए गए सभी मात्रात्मक लक्षणों के लिए भारतीय सरसों के विभिन्न जीन प्रारूपों के बीच सार्थक अंतर का संकेत दिया। आनुवांशिक और प्रारूपी भिन्नता गुणांक के उच्च अनुमानों को प्रति पौधे प्राथमिक शाखाओं की संख्या, मुख्य अक्ष की लम्बाई, मुख्य अक्ष पर फलियों की संख्या, प्रति पौधे फलियों की संख्या और फली में दानों की संख्या के लिए देखा गया था। प्रति पौधे बीज की उपज के बाद प्रति पौधे में द्वितियक शाखाओं की संख्या, उपज सूचकांक और 1000-दानों के वजन ने उच्च आनुवांशिक अग्रिमता के साथ उच्च आनुवांशिकता दर्शाई। अतः इन लक्षणों में सुधार के लिए चयन प्रभावी होगा।

आनुवांशिक विविधता के अध्ययन के अनुसार 60 जीन प्रारूपों को आठ समूहों में विभाजित किया गया। समूह IV में 18 जीनप्रारूप, समूह I में 16 जीनप्रारूप, समूह VI में 8 जीनप्रारूप, समूह II में 7 जीनप्रारूप, समूह III में 6 जीनप्रारूप, समूह V और VIII में 2-2 जीनप्रारूप और समूह VII में केवल एक जीनप्रारूप देखा गया। विभिन्न समूहों के बीच की दूरी, समूह V और VIII के बीच अधिकतम पाई गई तथा सहसमूह में सबसे ज्यादा दूरी समूह VI और सबसे कम दूरी समूह VII के लिए दर्ज की गई।

आनुवांशिक विविधता में सबसे अधिक योगदान प्रति पौधे बीज की उपज के बाद 1000-दानों के वजन का ज्ञात हुआ।

सहसंबंधता अध्ययन से ज्ञात हुआ कि प्रति पौधे फलियों की संख्या, मुख्य अक्ष पर फलियों की संख्या और उपज सूचकांक के साथ लक्षण स्तर और जीन स्तर पर प्रबल धनात्मक सहसंबंध था।

पथ गुणांक विश्लेषण से ज्ञात हुआ कि फसल परिपक्वता के दिन, मुख्य अक्ष पर फलियों की संख्या, प्रति फली दानों की संख्या, 1000-दानों का वजन, तेल की प्रतिशत मात्रा और उपज सूचकांक का बीज की उपज पर प्रत्यक्ष और धनात्मक प्रभाव रहा।

जीन प्रारूप आरएच-725 (16.55 ग्राम), गिरिराज (15.64 ग्राम), आरजीएन-303 (15.60 ग्राम), क्रांति (15.44 ग्राम) और पूसा जय किसान (14.92 ग्राम) न केवल प्रति पौधे की उपज के लिए बेहतर थे, बल्कि संबंधित मात्रात्मक लक्षण, जैसे उपज सूचकांक, प्रति पौधे फलियों की संख्या, प्राथमिक शाखाओं की संख्या और द्वितियक शाखाओं की संख्या के लिए बेहतर थे। इन श्रेष्ठ जीन प्रारूपों का भविष्य के प्रजनन कार्यक्रम के लिए प्रत्यक्ष चयन किया जा सकता है।

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