



An Examination of the Use of Trait Association Analysis and Genetic Variation to Identify Quantitative Traits in Indian Mustard (*Brassica juncea* L.)

Lakki Sharma ^{a++*}, S. N. Mishra ^{b#} and Shraddha Singh ^{a++}

^a Faculty of Agriculture Science and Technology, MGU Sehore Bilkishganj, Bhopal, M.P., India.
^b SHUATS (Naini), Uttar Pradesh, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The experiment was carried out throughout the winter season rabi under irrigated and rainfed conditions to examine the durability of enhanced and high-yielding cultivars of Indian mustard. Variance analysis on 14 characters was performed individually as well as aggregated across years and places. Irrigated environments were better for expressing a larger range of characters and a higher mean for all characters. Days to maturity, plant height, point to first branch, primary branches/plant, secondary branches/plant, point to first siliqua, seed yield/plant, and days to 50% flowering all showed significant G E interaction, indicating a significant amount of predictable G E interaction. All genotypes passed the tests for the three stability parameters and were found to be stable and high yielding. Although genotype were shown to be appropriate for growth in rainfed (poor) conditions despite having greater performance for seed yield/plant. The "genotype" was

⁺⁺ Research Scholar;

[#] Assistant Professor

*Corresponding author: E-mail: lakki17394@gmail.com;

discovered to be suited for production in an irrigated (beneficial) environment and outperformed the population mean for seed yield/plant. Any breeding plan that aims to create stable, high-yielding genotypes can contain genotypes. For an increase in seed yield per plant, direct selection in the segregating generations of such parents for 1000-seed weight, point to first branch, secondary branches/plant, siliqua length, and overall number of siliquae/plant will be effective (PDF) Stability analysis in Indian mustard.

Keywords: *G E interaction; genotypes; environment; high-yielding; mustard.*

1. INTRODUCTION

“The oilseed crops *Brassica napus*, *Brassica rapa* and *Brassica juncea* are one of the most important sources of vegetable oil globally. The primary *Brassica* oilseed crops in many nations are canola quality (low erucic acid, low glucosinolates) *B. rapa* and *B. napus*. *Brassica juncea*, sometimes known as Indian mustard, is a significant oil seed crop worldwide. In India, it is frequently referred to as rai, raya, or laha. It's a member of the Cruciferae family. *Brassica juncea* is an interspecific cross between *Brassica campestris* ($2n= 20$) and *Brassica nigra* ($2n= 16$) that results in a natural amphidiploid ($2n= 36$) plant” [1]. Germany, France, China, and Canada are the top exporters of rapeseed. The world's rapeseed-mustard area, output, and productivity were 36.59 million hectares (M ha), 72.37 million tonnes (M t), and 1980 kg/ha, respectively. India is first in mustard area and second in production, after China. In terms of overall area and production worldwide, India accounts for 19.8% and 9.8%, respectively (USDA). Rapeseed mustard, groundnuts, and soybeans make up about 84% and 88% of the total area and production in India, respectively. The major rapeseed-mustard growing states in India are Rajasthan (44.97% area), Uttar Pradesh (10.60%), Madhya Pradesh (11.32%) and Haryana (12.44%). Genetic metrics including the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance (GA) are among the biometric instruments used to quantify genetic diversity [2]. The coefficient of variation is useful for revealing and comprehending the precise image of the variety that already exists within the population. Assessing the suitability of a character for selection requires consideration of both heritability and an estimate of genetic progress. The feature exhibiting high heritability and modest genetic progress can be improved by interbreeding with superior genotypes of segregating populations (produced by combination breeding) [3]. According to Kumar et al. [4], the biological technique of nanoparticle

synthesis is a comparatively easy, affordable, and sustainable technology. According to Chakraborty et al. [5], there is a large genetic variance between genotypes and phenotypes. In order to better understand the genetic makeup of yield, it may be useful to examine the contributing characteristics of the yield. The ability to breed for high yielding genotypes with desired combinations of attributes would arise [6]. The acreage, production, and productivity of the crop still vary significantly even if we have cultivars with high yield potential. The main cause of this variation is its cultivation on marginal terrain, lack of biotic and abiotic stress-resistant/tolerant cultivars for the nation's several mustard-growing regions, as well as lands that are either rainfed or have limited irrigation capacities.

The genetic diversity found in the available germplasm of a particular crop is wholly responsible for the success of any breeding strategy in general and the enhancement of a specific attribute through selection in particular.

Characters that exhibit variability must be highly heritable for the crop improvement plan to be successful since selection-based development is reliant on the heritability, level of selection, and genetic advancement of the character. Estimates of heritability and genetic progress for a variety of targeted traits assist the breeder in selecting the best breeding practises for the crop improvement strategy. Any crop enhancement program's main goal is to increase yield. Despite their continual change and environmental influence, they have a relationship with yield in terms of both nature and amplitude. Indirect selection for yield and an alternative mode of selection for yield improvement can be utilized for components with high heredity and a favourable association to yield. Path coefficient analysis is the most efficient method for determining the direct and indirect sources of relationship among the various variables when the indirect associations become complex. Path coefficient analysis helps distinguish between correlations that are

accurate (genetic influences) and exaggerated (environmental effects).

Thus, while choosing high yielding genotypes, understanding the direct and indirect effects of various components on yield is crucial. With seed yield/plant as the dependent variable and other observed features acting as the independent variables in each of the environments, path coefficient analysis was used in the current experiment.

2. ANALYSIS OF LITERATURE

The available relevant literature related to various aspects of the present study. An examination of the use of trait association analysis and genetic variation to identify quantitative traits in Indian mustard (*Brassica juncea* L.) are reviewed in order to obtain a thorough understanding of the subject and have been described under the following subheads:

Genetic Parameters of Variability, Coefficient of Variation, Heritability and Genetic advance as percentage of mean, Correlation Coefficient Analysis, Path Coefficient Analysis, Genetic Diversity Analysis.

3. GENETIC PARAMETERS OF VARIABILITY

Genetic variability is a measure of the tendency of individual genotype in a population to vary from one another. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Genetic variability for agronomic traits is the key component of breeding programmed for broadening the gene pool. The genetic variability in any breeding material is a prerequisite as it provides not only a basic for selection but also provide valuable information regarding selections of diverse parents for use in hybridization programme.

4. COEFFICIENT OF VARIATION

Shweta and Prakash [7] studied “one hundred germplasm accessions of Indian mustard and an attempt has been made to identify the genetically diverse germplasm. Results showed that variation in plant growth was prominently seen among the accessions as indicated by range of variability, mean performance and coefficient of variation”.

Patel and Vyas [8] investigated “high heritability (broad sense) associated with moderate to high genetic advance was recorded for 1000-seed weight, seed yield per plant, harvest index, palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic and erucic acid contents. The study suggested that these traits can be further improved through selection in segregating generations”.

Yadava et al. [9] evaluated “fourteen quantitative traits and carried out pooled analysis over the environments. The mean, range, phenotypic, genotypic and environmental variance, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance were calculated for number of secondary branches per plant, number of siliquae per plant and yield per plant”.

Kumar et al. (2013) analyzed “50 genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] and found that genotypic and phenotypic coefficients of variance were higher for number of secondary branches/plant and seed yield/plant under both the environments. High heritability in two environments was observed for days to 1st flowering, siliqua length and seed yield/plant”.

Zada et al. [10] observed “considerable variation in seed yield (kg/ha-1) whereas a moderate variability was observed in plant height, main raceme length, silique/main raceme, glucosinolate contents and erucic acid”.

Bind et al. [11] reported “maximum genetic variability for biological yield per plant and minimum for days to maturity as reflected by genotypic coefficient of variation. Heritability estimates in broad sense were high for 1000 seed weight, day to maturity, days to flowering, plant height and main shoot length. Genetic advance as percent over mean was high for biological yield per plant, 1000 seed weight, yield per plant, number of secondary branches and main shoot length”.

Lodhi et al. [12] reported “higher phenotypic and genotypic coefficients of variation for important traits including number of secondary branches/plant, seed yield/ plant, and 1000-seed weight. High heritability in conjunction with high genetic advance were observed for seed yield/ plant, number of secondary branches/ plant, 1000-seed weight”.

Akabari and Niranjana (2015) observed “higher value of PCV and GCV for number of secondary branches per plant, number of siliquae per plant and yield per plant indicating the existence of higher magnitude of variability among the test genotypes for effective selection in respect of the above characters”.

Dipti et al. [13] recorded “maximum value of phenotypic coefficient of variation for number of pods on main branch (36.23) followed by oil content (31.65), siliqua density on main shoot (30.72) and the highest genotypic coefficient of variation for number of pods on main branch (33.49) followed by seed yield per plant (29.18) and oil content (28.89)”.

Salam et al. (2017) noted “high GCV and PCV for only two traits viz. number of branches per plant and harvest index (%). The traits plant height (cm), siliqua length (cm), number of siliquae per plant and seed yield per plant had moderate GCV and PCV”.

Devi [14] analyzed that “coefficient of variation for GCV and PCV were found high for the traits biological yield per plant, grain yield per plant and silliqua on main raceme. Biological yield per plant, silliqua on main raceme, grain yield per plant and number of seed per silliqua exhibited higher heritability and higher genetic advance”.

Kumar et al. [15] estimated “the genetic variability, heritability and genetic advance as percentage of mean for nine quantitative characters viz. plant height, number of primary branches, number of primary branches, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, number of seeds per plant, total seed yield (g) and test weight (g). Analysis of variance showed significant differences among the accession for all characters under study”.

Raliya et al. [16] revealed that “mean sum of squares due to genotypes (treatments) were significant for all the traits studied. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters evaluated. Most of the characters including yield ha⁻¹ depicted high GCV, PCV and narrow sense heritability”.

Rout et al. [17] carried out study “with thirty eight accessions of Indian mustard and evaluated for seed yield and its yield components for twelve characters. The results revealed that number of siliqua per plant and harvest index had highly

significant positive association with seed yield per plant”.

Roy et al. [18] evaluated “forty diverse genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss] for seed yield and its yield components (fourteen characters) under late sown condition. Both phenotypic and genotypic coefficients of variation were higher for viz. plant height, number of primary branches, number of primary branches, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, number of seeds per plant, total seed yield (g)”.

Pal et al. [19] observed for “phenotypic and genotypic coefficient of variation (PCV & GCV), heritability, genetic advance (GA), correlation and path analysis for thirteen characters in seven genotypes of Indian mustard (*Brassica juncea* L.) were evaluated for seed yield and its yield contributing traits. Genetic variability indicated that the PCV was greater than GCV for all the traits studied was majorly due to the influence of environment”.

Singh [20] analyzed “variance on 11 quantitative traits was worked out which exhibited considerable amount of genetic variability in genotypes for all the traits viz., plant height, number of primary branches, number of primary branches, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, number of seeds per plant, total seed yield (g)”.

Yadav [21] “Analysis of variance indicated highly significant differences for all the characters viz. plant height, number of primary branches, number of primary branches, number of siliquae per plant, siliqua length (cm), number of seeds per siliqua, number of seeds per plant, total seed yield (g). The traits plant height (cm), siliqua length (cm), number of siliquae per plant and seed yield per plant had moderate GCV and PCV”.

5. HERITABILITY AND GENETIC ADVANCE AS PERCENTAGE OF MEAN

Singh et al. [22] recorded “low estimates of heritability for number of seeds per siliquae only in F₁ and for plant height only in F₂ generations. Moderate genetic advance was observed for number of primary branches plant and number of secondary branches per plant in both the generations”.

Tahira et al. [23] reported that “phenotypic level, seed yield per plant had significant positive correlation with oil percentage and highly significant positive correlation with plant height and siliqua length”.

Singh et al. [22] evaluated “number of days to maturity, oil content, protein content and SPAD value at the flowering stage exhibited more than 90% heritability. The genetic advance was greatest for transpiration at the flowering stage, followed by seed yield per plant, protein content, oil content and SPAD at the flowering stage. These traits also registered high heritability values”.

Priyamedha et al. (2013) studied “one hundred ten early generation (F_3) lines of Indian mustard (*Brassica juncea* L. Czern and Coss) derived from 5 crosses at Bharatpur (Rajasthan), India during rabi season 2010-11 to investigate the associations among yield components and their direct and indirect influence on seed yield in augmented block design along with 4 checks”.

Jahan et al. [24] studied “high heritability with low genetic advance in percent of mean for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50% flowering indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective”.

Salam et al. (2017) noted highest heritability estimates were observed for the traits erucic acid content followed by plant height, branches per plant, seed yield per plant, siliqua length, days to 50% flowering and harvest index (%). Genetic advance as percentage of mean was recorded higher for number of siliquae per plant, followed by seed yield per plant, days to maturity and plant height.

Roy et al. [18] studied “forty diverse genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss] for seed yield and its yield components (fourteen characters) under late sown condition. High heritability in conjunction with high genetic advance were observed for seed yield per plant, number of pods per plant, leaf area index and secondary branches per plant suggesting predominant role of additive gene action for expression of these traits”.

Singh et al. [25] reported “genetic divergence using Mahalanobis's D^2 statistics. Analysis of variance pointed towards considerable genetic variability among the 60 genotypes evaluated”.

Pal et al. [19] observed “high heritability along with high genetic advance as per cent of mean were for seed yield per plant, seeds per siliqua, siliqua length and secondary branches per plant indicating the breeding improvement through direct selection for number of siliquae per plant, followed by seed yield per plant, days to maturity and plant height”.

Singh [20] conducted “an experiment to study the correlation and path coefficient analysis of 11 quantitative traits comprised of 27 genotypes of Indian mustard including 9 parental genotypes and 18 specific F_1 crosses. High GCV and genetic advance coupled with high heritability for number of primary and secondary branches/plant, number of siliquae/plant, test weight and seed yield indicated the effectiveness of selection for these traits”.

6. CORRELATION COEFFICIENT ANALYSIS

Tahira et al. [23] reported that “genetic correlation was positive and highly significant with plant height, branches per plant, siliqua length, weight of 1000 seed and oil %age. A positive and highly significant genetic relationship was found between plant height and branches per plant, siliqua length and seeds per siliqua, oil %age and 1000 seed weight”.

Rathod et al. [26] reported that the “seed yield per plant had significant and positive correlation 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. According to them biological yield per plant had significant and positive association with harvest index and oil content at genotypic level”.

Bind et al. [11] reported that “all the characters showed positive correlation with seed yield per plant both at phenotypic and genotypic levels except days to 50 percent flowering and days to maturity”.

Lodhi et al. [12] observed that “seed yield per plant was found to be positively and significantly correlated with number of primary branches per plant, number of secondary branches per plant,

primary branch angle, main shoot length, siliqua length, and number of seed per siliqua; seed yield per plant had negative association with oil content”.

Kumar and Pandey [27] observed that “seed yield per plant was positive and significantly correlated with secondary branches per plant, siliqua length, 1000 seed weight, biological yield per plant and harvesting index at both genotypic and phenotypic level. Days to 50% flowering showed positively significant correlation with days to maturity and siliqua per plant at phenotypic level only whereas days to maturity showed negative correlation with high phenotypic value of beak length, primary branch per plant”.

Kumar et al. [28] reported that “harvest index and total biological yield per plant exerted high significant positive correlation coefficients with seed yield at both genotypic and phenotypic level. Path analysis revealed that harvest index showed maximum positive direct effect, followed by total biological yield per plant, days to maturity, siliquae length at the time of maturity and seed yield per plant at both genotypic and phenotypic levels”.

Dawar et al. [29] revealed “positive correlation and path analysis for yield and various yield components. Seed yield per plant (g.) with plant height; number of primary branch, total no. of siliqua per plant and 1000-seed weight at genotypic level was recorded. Path coefficient analysis revealed that, the highest positive direct effect on seed yield (g) was exhibited by total no. of siliqua per plant, plant height, 1000-seed weight, Number of primary branches and number of seed per siliqua had direct positive contribution towards seed yield per plant”.

Devi (2018) revealed that “biological yield per plant and siliqua on main raceme exerted had high positive significant genotypic correlation with grain yield per plant and secondary branches per plant and was found negatively correlated with grain yield per plant. Path analysis revealed that days to 50% flowering showed maximum positive direct effect however the highest indirect effect of this trait was exhibited through biological yield per plant”.

Kumar et al. [15] noted “improvement in seed yield can be achieved by selection using the correlation and path analysis data generated in this study. Total seed yield/ plant were positively correlated with siliquae length. Number of seeds/

plant and test weight had higher phenotypic direct effects on total seed yield/ plant, revealing that indirect selection for these traits would be effective in improving seed yield”.

Raliya et al. [16] revealed that “the magnitude of genotypic correlation coefficients was higher than their corresponding phenotypic coefficients. Seed yield per hectare was found to be positively correlated with 1000-seed weight, siliqua length, plant height, main shoot length and days to maturity at genotypic level”.

Rout et al. [17] carried out “with thirty eight germplasm accessions of Indian mustard evaluated for seed yield and its yield components for twelve characters. The results revealed that number of siliqua per plant and harvest index had highly significant positive association with seed yield per plant”.

Gupta et al. [30] conducted “two sets of field experiments with 30 diverse genotypes of Indian mustard including three checks (Kranti, Vardan and RGN73) to assess the correlation and path coefficients for yield and yield related traits under timely (TS) and late sown (LS) conditions”.

Roy et al. [18] observed that “the correlation study revealed that seed yield per plant was found to be positively and significantly correlated with pod length, number of seeds per pod and oil content while, negative significant association of seed yield was observed with days to first flowering and total biomass”.

Pal et al. [19] studied in “correlation analysis observed that seed yield per plant had significant and positive correlation with secondary branches per plant, siliqua per plant, biological yield per plant, harvest index, days to maturity, 1000 seed weight and oil content at both genotypic and phenotypic levels”.

Singh [20] reported that “seed yield had positively associated with plant height, days to 50% flowering, days to maturity, oil content and test weight at both genotypic and phenotypic level indicating that these traits would help in improving the seed yield. Path analysis revealed that days to 50% flowering showed maximum positive direct effect, followed by oil content, days to maturity and test weight at both genotypic and phenotypic levels”.

7. PATH COEFFICIENT ANALYSIS

Tahira et al. [23] reported that “path coefficient revealed that the plant height and siliqua length

had direct positive contribution towards seed yield per plant”.

Uke et al. [31] Observed in “seventeen genotypes of mustard showed significant variation among them for all the characters studied. The correlation studies indicated positive significant correlation of all the characters except plant height with yield. The path analysis revealed the importance of number of siliqua plant-1, number of primary branches, 1000 seed weight, leaf area at 45 DAS and dry weight at 65 DAS for improving seed yield in mustard”.

Yadava et al. [9] evaluated for “path coefficient analysis correlation coefficients to know the yield- contributing traits having true associations with seed yield. Improvement in seed yield can be achieved by selection using the correlation and path analysis data generated in this study. 1000-seed weight was positively correlated with siliqua length. 1000-seed weight and total siliquae/plant also had higher phenotypic and genotypic direct effects on seed yield/plant”.

Maurya et al. [32] studied that “the genotypic path analysis showed that maximum direct affect was contributed by days to 50% flowering (0.404) which was followed by plant height (0.226) and number of seeds per siliqua (0.114). Length of siliqua (-0.198) and 1000 seeds weight (-0.139) exhibited high negative direct effects. Whereas indirect highest positive effect was exerted by plant height followed by number of siliquae on main raceme via days to 50% flowering were the key yield contributing characters under study”.

Rathod et al. [26] in path coefficient analysis of twelve yield contributing characters clearly indicated that biological yield per plant showed the highest positive direct effect on seed yield followed by harvest index, length of siliqua, days to 50 per cent flowering, oil content, number of secondary branches per plant and number of primary branches per plant, which indicated positive direct effects in descending order and other characters contributed indirectly towards seed yield in Indian mustard.

Binda et al. [11] reported that “path coefficient analysis at genotypic level revealed that biological yield per plant had the highest direct positive effect on seed yield per plant followed by harvest index, 1000seed weight, number of seeds per siliqua and number of primary branches. Highest negative direct effect on seed

yield per plant was observed for plant height at phenotypic level”.

Lodhi et al. [12] studied that in path analysis main shoot length, number of primary branches per plant, number of seed 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 branches per plant, primary branch angle, main shoot length, number of seed per siliqua would be quite effective in improving seed yield in Indian mustard.

Dipti et al. [13] recorded Path coefficient analysis that no. of pods on main branch had the highest direct contribution towards seed yield per plant followed by 1000-seed weight and siliqua density on main shoot (1.82) which suggested that selection for these traits would be quite effective in improving seed yield in Indian mustard.

Devi, [14] studied that in path analysis days to 50% flowering showed maximum positive direct effect however the highest indirect effect of this trait was exhibited through biological yield per plant.

Gupta et al. [30] conducted two sets of field experiments with 30 diverse genotypes of Indian mustard including three checks (Kranti, Vardan and RGN73) to assess the correlation and path coefficients for yield and yield related traits under timely (TS) and late sown (LS) conditions. Path analysis identified biological yield/plant followed by harvest index, as major direct contributors towards seed yield/plant (both under timely and late sown conditions), while plant height emerged as most important indirect yield component under timely sown condition.

Kumar et al. [15] noted path coefficient analysis was carried out using correlation coefficients to know the yield contributing traits having true associations with seed yield. Improvement in seed yield can be achieved by selection using the correlation and path analysis data generated in this study.

Rout et al. [17] carried out with thirty eight germplasm accessions of Indian mustard evaluated for seed yield and its yield components for twelve characters. 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. [18] evaluated forty diverse genotypes of Indian mustard [*Brassica juncea* (L.) Czern & Coss] were evaluated for seed yield and its yield components (fourteen characters) under late sown condition. Path analysis revealed that oil content, leaf area index showed the highest positive direct effect on seed yield per plant followed by number of seeds per pod and pod length which 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.

Pal et al. [19] studied phenotypic and genotypic coefficient of variation (PCV & GCV), heritability, genetic advance (GA), correlation and path analysis for thirteen characters in seven genotypes of Indian mustard (*Brassica juncea* L.) were evaluated for seed yield and its yield contributing traits. Path coefficient analysis indicated that, among twelve yield contributing characters highest positive direct effects was noted for biological yield per plant followed by siliqua length, harvest index, 1000 seed weight, Siliqua per plant and primary branches per plant on the seed yield per plant.

Singh [20] conducted an experiment to study the correlation and path coefficient analysis of 11 quantitative traits comprised 27 genotypes of Indian mustard including 9 parental genotypes and 18 specific F1 crosses. Path analysis revealed that days to 50% flowering showed maximum positive direct effect, followed by oil content, days to maturity and test weight at both genotypic and phenotypic levels.

Yadav et al. [21] evaluated twenty five genotype of Indian mustard to determine relationship among yield and its components using direct selection parameters like variability, heritability and genetic advance for 13 yield and its contributing characters. viz., biological yield per plant followed by siliqua length, harvest index, 1000 seed weight, Siliqua per plant and primary branches per plant on the seed yield per plant

8. GENETIC DIVERSITY ANALYSIS

Singh et al. [33] recorded Cluster means for different clusters and inter cluster distances were used to judge the importance of different clusters in the improvement programme. Evaluated genotypes were grouped into thirteen clusters based on the economic traits. Cluster I was the largest, consisting of nine genotypes. Cluster X showed maximum genetic distance from cluster

VII, suggesting wide diversity between them. When the quality traits were considered for clustering the genotypes grouped into six clusters, cluster VI (largest cluster) consisted of fourteen genotypes and cluster VI had the maximum inter cluster distance from cluster III which showed presence of wider diversity among the genotypes of these two clusters.

Shathi et al. [34] grouped 25 mustard (*Brassica* sp. L) genotypes into six clusters. Cluster II had the maximum number (13) of genotypes, while Clusters IV, V, and VI had the minimum number (2) of genotypes. The highest inter-cluster distance was observed between Clusters I and IV, while the lowest inter-cluster distance was observed between Clusters V and VI. Cluster II ($D = 4.91$) had the highest intra-cluster distance, while Cluster II (5.607) had the lowest intra-cluster distance.

Pandey et al. [35] conducted D^2 analysis to measure the genetic diversity among the genotypes and revealed significant differences. The 45 genotypes were grouped in 8 clusters using Tocher's method. 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. Maximum contribution towards the divergence was accountable to 1000-grain weight (46.87%) followed by seed yield/plant (20.91%) and number of siliqua on main raceme (8.38%).

Zada et al. [10] observed "in Hierarchical cluster analysis categorized the 134 accessions into seven main clusters. First three principal components (PC_s) accounted for a total of 39.03% of variability among the accessions using agro-morphological traits. PC_1 had 17.79% of total variation in agro-morphological traits; PC_2 depicted 11.45% of total morphological variability, while PC_3 accounted for 9.80% of the total variation. Based on greater yield potential, seed yield per plant, 1000-seed weight, oil contents, protein contents and oleic acid four promising genotypes were identified for breeding and variety development programmers in Indian mustard".

Neeru et al. [36] based on the inter-cluster distances, maximum genetic diversity was observed between clusters I and IV(221.4), followed between CII and IV clusters (200.5), C IV and C IX (191.8) and C IV and C X (181.5)

indicating that genotypes from these clusters can usefully be hybridized for getting superior recombinants in segregating generations. The results of cluster and principal factor analyses confirmed each other.

Verma et al. [37] performed genetic divergence analysis on the basis of relative magnitude of D^2 values; 60 genotypes of Indian mustard were grouped into five clusters and plant height, no. of siliquae on main shoot and days to maturity were found important discriminatory characters for the selection of diverse genotypes.

Ali et al. [38] recorded cluster analysis constructed by these workers and categorized these 85 accessions into seven main groups, first five principal components (PCs) accounted for 52.02% of variations among the studied accessions using morphological traits. Out of 52.02%, PC1 had 17.29%, PC2 contributed 10.13%, PC3 (9.51%), PC4 (7.98%) and the share of variability produced by PC5 was 7.11%. During 2013, the contributions of these accessions were 27.46% (PC1), 11.33% (PC2), 8.70% (PC3), 7.27% (PC4) and 6.38% (PC5) with an overall contribution of 61.14% variability.

Devi et al. [39] showed that "analysis of variance revealed significant differences among the genotypes for all characters under study. The genotypes were grouped into 7 clusters using Tocher's method, with cluster I containing maximum genotypes (18 genotypes) followed by cluster III (9 genotypes), cluster IV (8 genotypes), cluster II (6 genotypes), cluster VI (2 genotypes) while cluster V and VII with single genotype each. Root width and length ratio, siliqua per plant, main shoot length and 1000 seed weight were the major contributors for genetic diversity among the genotypes with 23%, 21.80%, 21.32% and 20.51% respectively".

Mohan et al. [40] assessed 25 genotypes. These were grouped into 6 clusters based on D^2 analysis. The cluster-I with 9 strains had maximum genotypes among all the clusters followed by cluster-III, II, IV, V and VI. The inter cluster distance was recorded highest between cluster-III and cluster-IV (90.88). The minimum inter cluster distance was observed between cluster-I and IV (15.38).

Singh et al. [25] reported "genetic divergence using Mahalanobis's D^2 statistics. Analysis of variance pointed towards considerable genetic variability among the 60 genotypes evaluated.

On the basis of Tocher's clustering pattern, the genotypes were grouped into 9 clusters. Plant height, length of main raceme, 1000-seed weight and siliqua on main raceme were the major contributors for genetic diversity among the genotypes with 57.25%, 21.63%, 20.86% and 8.32%, respectively".

The present research entitled Exploitation of Genetic Variability and Trait Association Analysis for Quantitative Traits in Indian mustard (*Brassica juncea* L.)" was aimed to assess the genetic variability, idea of heritability, association of various quantitative and qualitative traits of germplasm accessions for improvement of Indian mustard. The research was carried out with the objectives of to determine genetic variance, heritability and genetic advance of genotypes for seed yield and other economic traits, to understand the inter-traits associations between the characters under study, to assess the direct and indirect effect of component characters on seed yield, to study the genetic divergence among selected genotypes in order to facilitate the recognition of genetically diverse genotypes for further use in breeding program [41-46].

9. CONCLUSIONS

The analysis of variance in Indian mustard revealed highly significant difference among all the genotypes for all the quantitative traits studied in all the environments which indicated the presence of sufficient variability in the material under study for selection of these traits.

The analysis of variance in Indian mustard revealed highly significant difference among all the genotypes for all the quantitative traits studied in all the environments which indicated the presence of sufficient variability in the material under study for selection of these traits.

High heritability coupled with high genetic advance as percentage of mean and estimates of genotypic coefficient of variation were higher for number of secondary branches per plant in all the environments of Indian mustard have consequent chances of improving these traits through simple selection, indicating additive gene action may be responsible for expression of these traits.

The correlation and path analysis studies showed that for developing new plant type in Indian mustard should be multiple primary and secondary branches, more number of siliquae on

main raceme, plant height, high biological yield and seed yield which improve the productivity of plant, while in addition to these traits large seed size should provide more emphasis for developing plant types in Indian mustard under different environments. A subsequent genetic diversity among the genotypes was observed most divergent are selected and be used for further hybridization/ breeding programmed. In general, higher GCV, high heritability, and high genetic progress as a percentage of mean were detected for harvest index and biological yield in the current study. Grain production per plant demonstrated that simple directional selection would be successful in enhancing these traits, suggesting that the main cause of genetic variation was the presence of additive gene effects.

Novel beneficial alleles for abiotic and biotic resistance as well as for yield contributing traits from this germplasm can be discovered thorough the use of genome-wide DNA marker systems and sequencing techniques.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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