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Enumeration of Genetic Variability Parameters and Diversity Analysis among Mutant Genotypes of Indian Mustard [*Brassica juncea* (L.) Czern & Coss.]

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ABSTRACT

The investigation was conducted during the *rabi* season (October–March) of 2019–20 and 2020–21 at the Agricultural Research Farm, Institute of Agricultural Sciences, BHU, Varanasi, Uttar Pradesh, India. The study aimed to evaluate Indian mustard mutants for variability and diversity using various quantitative traits. Twenty mutant genotypes, along with the national check Kranti, were grown in a randomized complete block design with three replications, observing 17 quantitative traits. Combined ANOVA indicated significant genotypic differences for all traits, while genotype×environment interaction was non-significant, except for seeds siliqua^{-1}. Most traits exhibited moderate genotypic and phenotypic coefficients of variation, while days to maturity, number of primary branches, siliqua length, seeds siliqua^{-1}, and chlorophyll content had low genotypic coefficients of variation. High heritability was observed for traits such as the length of the main raceme, number of secondary branches, days to 50% flowering, number of siliqua plant^{-1}, and test weight. Traits like the number of secondary branches, length of the main raceme, number of siliqua plant^{-1}, seed yield plant^{-1}, test weight, and yield ha^{-1} had high genetic advance as a percentage of the mean, while days to maturity, siliqua length, and seeds siliqua^{-1} had low values. Tocher's method grouped the genotypes into five clusters, with the highest intra-cluster distance in cluster III (9.15) and the highest inter-cluster diversity between clusters I and V. Principal component analysis identified six components explaining 82.46% of the total variability, with PC1 contributing 28.39% and PC2 accounting for 15.66%.

KEYWORDS: GCV, PCV, heritability, genetic advance, D^2 statistic, principal component

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1. INTRODUCTION

The genus *Brassica* belongs to the family Cruciferae and consists of some economically important species useful for various purposes *viz*. yielding edible roots, stems, leaves, buds, flowers and seed condiments. The genus contains over 3200 species having highly diverse morphology. Among them rapeseed-mustard is one of the most significant oilseed crop of India. Many species are used as a source of oil and some are grown as forage crop. Out of the total rapeseed-mustard production of India, Indian mustard accounts for 75–80% and contributes 24.2% of the total edible oil pool of the country (Devi et al., 2017). The species such as *B. campestris, B. napus and B. juncea* are the allotetraploids from which edible oil is extracted. Their diploid progenitors are *B. nigra, B. napus and B. carinata* (Nagaharu, 1935). India continues to be at rank 4th after Canada, China and European Union in acreage (17.19%) and after European Union, Canada and China in production (8.54%) with significant contribution in world rapeseed-mustard industry (Anonymous, 2020). The maximum utilization of any species for breeding and its adaptation to different environments depends on the level of genetic diversity it holds. The assessment of phenotypic and genotypic coefficients of variation, heritability in broad sense, and genetic advance as % of mean is a pre requisite 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 intermating superior genotypes of segregating population developed from combination breeding (Synrem et al., 2014). Knowledge on genetic diversity in *B. juncea* could help breeders and geneticists to understand the structure of germplasm, predict which combinations would produce the best offsprings (Hu et al., 2007), and facilitate to widen the genetic basis of breeding material for selection (Qi et al., 2008). Breeders aim to minimize the influence of environmental factors on the variation among genetic materials, which is quantified through heritability (Manjunath et al., 2017). Seed yield, a critical trait, is influenced not only by numerous morphological characters governed by genes but also by external environmental factors (Saroj et al., 2021). Therefore, partitioning the overall variability into heritable and non-heritable components is essential. This partitioning enables breeders to adopt suitable breeding procedures for improving genetic stocks. In addition to heritability, genetic advance-referring to the change in the mean value of a trait across successive generations-should also be considered (Shukla et al., 2006).

Genetic diversity is a fundamental driver of agriculturally significant phenomena such as heterosis and transgressive segregation (Pant et al., 2022). The presence of genetic diversity, represented by wild species, related species, breeding stocks, and mutant lines, serves as a reservoir of desirable alleles (Guerra et al., 2022). Utilization of diversity in mutant lines is crucial for breeding climate-resilient varieties, especially in the context of climate change and associated biotic and abiotic factors (Salgotra and Chauhan, 2023). Measuring genetic variability among genotypes offers more opportunities for selection and is a cornerstone of plant breeding (Mukhtar et al., 2002). Greater parental diversity increases the likelihood of obtaining high-yielding F_1 hybrids and broad-spectrum variability in segregating generations. Genetic divergence has been measured successfully by many researchers, following Mahalanobis (1936) D^2-Analysis. Genetic diversity among individuals or populations can be determined using morphological, biochemical and molecular approaches (Qi-Lun et al., 2008; Mohammadi and Prasanna, 2003). Thus, in the present investigation, a set of 20 mutant genotypes of Indian mustard along with national check Kranti were used for estimating genetic variability parameters and genetic diversity analysis using D^2 statistics and principal component analysis (PCA).

2. MATERIALS AND METHODS

2.1. Plant materials and details of experiment

The experiment was conducted at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh (221005), India during October–March *rabi* season of 2019 and 2020. The experimental materials consist of 20 mutants of Indian mustard which are derived from Bhabha atomic research centre (BARC) along with the national check Kranti (Table 1). The experiment al materials were sown in Randomized Complete Block Design (RCBD) with three replications in same field at same location in two consecutive years. Each genotype was grown in five rows in 2019–20 and 2020–21 of 5 m length in each replication, 30 cm of row-to-row distance and 10 cm of plant-to-plant distance within row was maintained. All the recommended agronomic package and practices were followed to raise a good crop. Data were recorded on 17 different traits namely plant height, days to 50% flowering, days to maturity, number of primary branches, number of secondary branches, length of main raceme, number of siliquae on main raceme, number of siliquae plant^{-1}, siliqua length, seeds siliqua^{-1}, seed yield plant^{-1}, biological yield plant^{-1}, harvest index, test weight, yield ha^{-1}, canopy temperature deficit, chlorophyll content. Five competitive plants were tagged randomly from each genotype in each replication for recording field observations for all the traits except for days to 50% flowering and days

Table 1: List of genotypes taken under investigation

Sl. No.	Name of entry/genotype	Source
1.	TPM–1	BARC, Trombay
2.	TM–52	BARC, Trombay
3.	TM–53	BARC, Trombay
4.	TM–106	BARC, Trombay
5.	TM–108	BARC, Trombay
6.	TM–108–1	BARC, Trombay
7.	TM–117	BARC, Trombay
8.	TM–130	BARC, Trombay
9.	TM–134	BARC, Trombay
10.	TM–143	BARC, Trombay
11.	TM–172–1	BARC, Trombay
12.	TM–3	BARC, Trombay
13.	TM–179	BARC, Trombay
14.	TM–204	BARC, Trombay
15.	TM–217	BARC, Trombay
16.	TM–263–3	BARC, Trombay
17.	TM–258	BARC, Trombay
18.	TM–273	BARC, Trombay
19.	TM–276	BARC, Trombay
20.	TM–277	BARC, Trombay
21.	KRANTI	I. Ag. Sc BHU, Varanasi

to maturity, which were observed on plot basis during both the years.

2.2. Statistical analysis

The data recorded for each genotype at each environment were subjected to statistical analysis like descriptive statistics and ANOVA seperately. Later the data of two seasons was analysed using combined analysis technique to infer on the influence of year as random variable on the performance of the genotypes. The combined ANOVA technique was used to assess the statistical significance of varietal variances with respect to selected 17 characters/traits. Prior to the combined ANOVA, Bartlett's test was performed to verify the homogeneity of error variances for two seasons. Homogeneity of error variance tests were conducted to determine if data from individual environments (E) could be pooled to evaluate G×E interaction using a combined ANOVA as per (Verma et al., 1987). The Homogeneity of error variances were tested with F–test or the 'variance ratio' test as described by (Gomez and Gomez, 1984). For the combined analysis, variation was partitioned into relevant sources of variation to test for differences among genotypes and for the presence of G×E interaction. The calculations for GCV and PCV followed the standard formula outlined by Searle (Searle, 1961). The methods described by Allard (Allard, 1960) were used to determine the genetic advance as a percentage of the mean (GAM) and broad-sense heritability (h^2b). The phenotypic divergence among the accessions was estimated by the multivariate techniques, as follow: Tocher's cluster analysis as described by (Rao, 1952), using Mahalanobis D^2-statistics, Mahalanobis (1936) to measure the genetic distance. To better understand the correlation between all characters studied with seed yield, principal component analysis (PCA) was performed using a matrix generated from the mean morphological data, followed by cluster analysis by K-means method and the Euclidean distance.

3. RESULTS AND DISCUSSION

The preliminary analysis of variance (ANOVA) was done separately for both the seasons and the mean sum of square values indicated high significant difference among genotypes for all the characters in both the seasons.

The Bartlett's test was found non-significant with 'F_{max}' value less than three for all the characters. Hence, it was concluded that there existed homogeneity of error variances of seasons. Under homogeneity of error variances, unweighted combined ANOVA was carried out to assess significant mean difference of genotypes across characters. The results of combined ANOVA with genotypes as a source of variation for all the characters was found statistically significant which reflected the existence of sufficient variability among the genotypes (Table 2). The influence of season indicated by year as source of variation was found statistically significant for all the characters except biological yield plant and chlorophyll content.

The interaction between genotypes and environment is hypothesized to influence phenotypic characters. This could be captured in interaction effect between genotypes and year. The interaction term was found non-significant for all the characters except seeds siliqua^{-1}. This indicated ranking of genotypes across seasons remained constant (Gomez and Gomez, 1984) for all the characters except seeds siliqua^{-1}. The similar result was reported by Iqbal et al. (2014) and Mohan Rao and Kumari (2018).

3.1. Genetic variability parameters

Genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percent of mean (GAM) have been estimated for all the characters taken under study (Table 3). According to the coefficient of variation estimation, for all of the traits, the PCV was higher than the GCV (Figure 1). Bind et al. (2014), Iqbal et al. (2015)

Table 2: Combined/pooled ANOVA of two season for 17 characters in Indian mustard (*Brassica juncea* L.)

Source of variation	df	plant height (cm)	days to 50% flowering	days to maturity	no. of primary branches	no. of secondary branches	length of main raceme (cm)	number of siliqua on main raceme	number of siliqua plant^{-1}	siliqua length (cm)
Replication within year	2	185.98	5.50	18.41	0.26	1.45	71.05*	0.49	1114.56	0.10
Year	1	1334.19**	17.43**	12.72*	4.45**	111.12**	401.28**	46.30**	10719.17**	7.68**
Year× Genotypes	2	10.83	0.22	2.88	0.26	1.25	25.58	1.72	434.86	0.15
Overall sum	5	345.56*	5.78	11.06	1.09**	23.30**	118.91**	10.15	2763.60**	1.63**
Genotypes	20	1956.89**	203.60**	254.75**	1.34**	36.32**	433.57**	153.18**	13021.09**	0.61**
Pooled error	100	137.76	11.91	45.89	0.23	1.92	15.28	14.85	752.09	0.14
CD (p=0.05)		13.44	3.95	7.76	0.55	1.59	4.48	4.41	31.41	0.42

Table 2: Continue...

Source of variation	df	seeds siliqua^{-1}	seed yield plant^{-1} (g)	biological yield plant^{-1} (g)	harvest index	test weight (g)	yield ha^{-1} (kg ha^{-1})	canopy temperature deficit	chlorophyll content
Replication within year	2	2.45	3.03	2.04	4.31	0.15	65228.61	0.43	22.60
Year	1	27.79*	15.77**	145.75	11.74**	2.51**	322388.8**	14.91*	2.51
Year× genotypes	2	5.20*	2.08	47.42	0.31	0.20	46707.70	0.12	4.77
Overall sum	5	8.62**	5.19**	48.94	4.20	0.64**	109252.28**	3.67	11.45
Genotypes	20	4.47**	14.64**	238.41**	35.40**	4.20**	309101.29**	6.28**	71.63**
Pooled error	100	1.32	1.25	40.32	5.90	0.19	27539.72	0.89	10.17
CD (p=0.05)		1.31	1.28	7.27	2.78	0.50	190.09	0.53	3.65

*, **: significant at (p=0.05) and (p=0.01) probability levels respectively

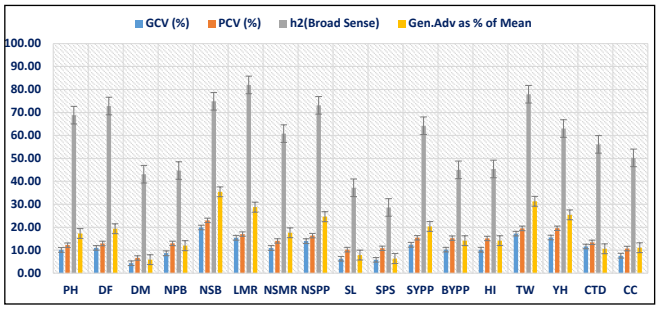

Figure 1: Graphical representation of genetic parameters of variation for 17 characters in Indian mustard

and Rameeh (2016) also reported higher values of PCV over GCV, thus it signifies the influence of environment. The PCV was low for days to maturity. And it was high for number of secondary branches. Swetha et al. (2019), (Chauhan et al., 2023), Kayaçetin (2019), and Awasthi et al. (2020) also reported low range of PCV for days to maturity. Higher range of PCV for the trait number of secondary branches can also be seen in studies by Awasthi et al. (2020); Kumar et al. (2020) and Nanjundan et al. (2022). Except these two all other traits have showed moderate range of PCV values. Moderate level of variability for traits like plant height, days to flowering, number of primary branches, length of main raceme, number of siliquae on main raceme, number of siliquae plant^{-1}, siliqua length, seeds siliqua^{-1}, seed yield plant^{-1}, biological yield plant^{-1}, harvest index, test weight and yield ha^{-1} were also reported by Anand et al. (2020) and Aragi et al. (2023).

The GCV was low for characters days to maturity, number of primary branches, siliqua length, seeds siliqua^{-1} and chlorophyll content. It was moderate for traits like plant height, days to flowering, number of secondary branches, length of main raceme, number of siliquae on main raceme, number of siliquae plant^{-1}, seed yield plant^{-1}, biological yield plant^{-1}, harvest index, test weight, yield ha^{-1} and canopy temperature deficit. Nanjundan et al. (2022) and Awasthi et al. (2020) also showed lower range of GCV values for

Table 3: Estimates of genetic parameters for 17 characters studied among 21 genotypes of Indian mustard (*Brassica juncea* L.) pooled over the years 2019–20 and 2020–21

characters	GCV (%)	PCV (%)	h^2 (%) Broad sense	GA	GA as % of Mean
PH	10.13	12.22	68.80	29.74	17.30
DF	11.02	12.91	72.80	9.94	19.38
DM	4.35	6.63	43.10	7.98	5.89
NPB	8.68	12.99	44.70	0.59	11.96
NSB	19.88	22.96	74.90	4.27	35.45
LMR	15.40	17.00	82.00	15.58	28.73
NSMR	10.95	14.04	60.80	7.72	17.60
NSPP	13.97	16.33	73.10	79.65	24.60
SL	6.25	10.24	37.20	0.36	7.85
SPS	5.78	10.82	28.60	0.80	6.37
SYPP	12.35	15.41	64.20	2.47	20.38
BYPP	10.23	15.25	45.00	7.94	14.14
HI	10.19	15.11	45.40	3.08	14.14
TW	17.21	19.50	77.90	1.49	31.27
YH	15.53	19.57	63.00	354.25	25.40
CTD	11.6	13.4	56.10	1.65	10.6
CC	7.58	10.70	50.20	4.67	11.06

PH: Plant height (cm); DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branches; NSB: Number of secondary branches; LMR: Length of main raceme (cm); NSMR: number of siliquae on main raceme; NSPP: Number of siliquae plant^{-1}; SL: Siliqua length (cm); SPS: Seeds siliqua^{-1}; SYPP: Seed yield plant^{-1} (g); BYPP: Biological yield plant^{-1} (g); HI: Harvest index; TW:Test weight (g); YH: Yield (kg ha^{-1}); CTD: Canopy temperature deficit; CC: Chlorophyll content

traits days to maturity, siliqua length and seeds siliqua^{-1} while evaluating various mustard accessions.

Heritability can be utilised to further validate the variability in a broad sense. Estimates of heritability are used to estimate the relative impact of additive genetic variance and are a key component of yield improvement criteria. Estimating heritability is essential for a good crop breeding strategy since it provides information on the index of transmissibility of quantitative traits of economic significance. The degree of heritability also aids in anticipating the behaviour of following generations by setting adequate selection criteria and analysing the level of genetic advancement.

The trait seeds siliqua^{-1} had low heritability. which indicated profound influence of the environment on the trait. Similarly, Tiwari (2019) observed low heritability for seeds siliqua^{-1} in his study based on twenty-five Indian mustard genotypes. The heritability in broad sense was moderate for days to maturity, number of primary branches, siliqua length, biological yield plant^{-1}, harvest index, canopy temperature deficit and chlorophyll content, which indicated moderate influence by environment on the traits (Anand et al., 2020; Kaur et al., 2022). Traits viz., plant height, days to 50% flowering, number of secondary branches, length of main raceme, number of siliqua on main raceme, number of siliqua plant^{-1}, seed yield plant^{-1}, yield ha^{-1} and test weight registered high heritability, thus selection for these traits would be effective. Kayacetin (2019), Shwetha et al. (2019) and Akabari and Niranjan (2015) also suggested simple mass selection could be more effective for traits like plant height, number of secondary branches, length of main raceme, number of siliqua plant^{-1}, seed yield plant^{-1}, yield ha^{-1} and test weight as these traits recorded high broad sense heritability.

The heritability estimates in broad sense alone is not a true indicator of effectiveness of selection for the trait since their scope is restricted by their interaction with the environment (Johnson et al., 1955). Hence, broad sense heritability values are considered for estimation of predicted response to selection. For probable selection, genetic advance provides a clear picture and exact vision of segregating generations. Higher heritability estimates, together with greater genetic advance confirm the scope of selection in the development of novel genotypes with desirable traits. The characters that show high heritability with high genetic advance are

controlled by additive gene action (Panse and Sukhatme, 1967), can be improved through simple or progeny selection methods. The character showing high heritability along with low genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding. Thus, genetic advance as percent mean is the reliable tool for estimating the gain for the character over the generations.

The traits days to maturity, siliqua length and seeds siliqua^{-1} showed low GAM (Synrem et al., 2014; Salam et al., 2017). While, it was moderate for plant height, days to 50% flowering, number of primary branches, number of siliqua on main raceme, biological yield plant^{-1}, harvest index, canopy temperature deficit and chlorophyll content (Kayaçetin, 2019 and Akabari and Niranjan, 2015). The characters like number of secondary branches, length of main raceme, number of siliqua plant^{-1}, seed yield plant^{-1}, test weight and yield hectare^{-1} registered high GAM thus there is opportunity for rapid advancement of these trait through selection. Shwetha et al. (2019), Tiwari (2019) and Akabari and Niranjan (2015) also suggested genetic gain can be expected employing simple selection approach for these traits as they recorded higher heritability and GAM.

3.3. Genetic divergence (D^2) analysis

Based on Mahalanobis D^2 statistics, All the 21 genotypes were grouped into 5 clusters by Tochers method (Singh and Chaudhary, 1977). The distribution of 21 genotypes into five clusters were presented in table 4. Cluster I comprised of maximum number of genotypes (13) and cluster III with 5 genotypes, whereas, the remainder of the clusters found to be solitary (Figure 2).

The average value for intra and inter-cluster distance of 5 clusters are represented in Table 5. The Intra-cluster average D^2 values ranged from 0 to 9.15. Out of 5 clusters cluster III had highest intra-cluster distance (9.15) followed by cluster I (7.87) and lowest values was zero (Figure 3). overall, 3

Table 4: Grouping of genotypes into 5 clusters (by Tocher's method)

Cluster	No. of genotypes	Name of genotypes
I	13	TM–201, TM–217, TM–263–3, TM–273, TM–258, TM–108, TM–106, TM–108–1, TM–117, TM–130, TM–179, TM–172–1, Kranti
II	1	TM–276
III	5	TM–52, TM–143, TPM–1, TM–53, TM–134
IV	1	TM–3
V	1	TM–277

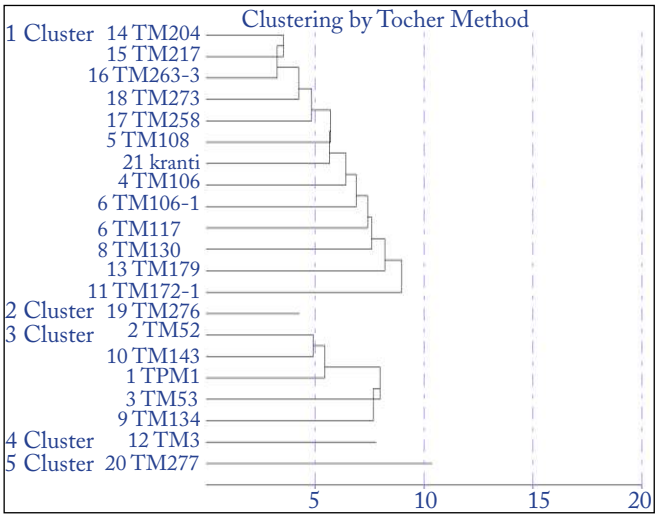

Figure 2: Dendrogram showing the relationship among the 20 mutants of Indian mustard along with check variety Kranti

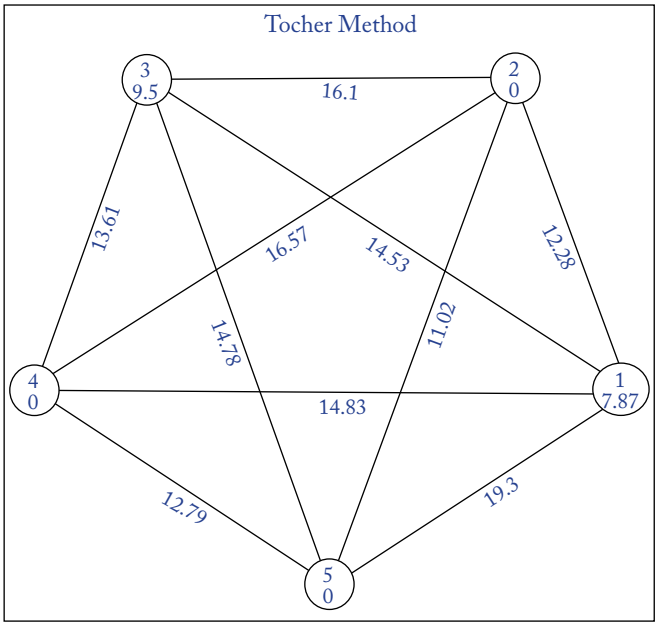

Figure 3: Cluster diagram representing 5 clusters and their intra and inter cluster distance (D^2) values

clusters had intra-cluster values zero. Inter-cluster average D^2 value ranged from 11.02 to 19.3. The least inter-cluster D^2 value was exhibited between clusters II and cluster V (11.02) while the highest D^2 value was found between cluster I and cluster V (19.3) followed by between cluster III and cluster V (17.78).

Cluster mean values for different characters are represented in Table 6. Result showed that the cluster mean of plant height ranged from 155.84 (cluster III) to 199.19 (cluster IV). Days to 50% flowering ranged from 45.5 (cluster V) to 58.83 (cluster IV). Days to maturity ranged from 131.17 (cluster V) to 142.34 (cluster IV). Number of primary branches ranged from 4.38 (cluster V) to 5.97 (cluster II).

Table 5: Average intra cluster (diagonal) – inter cluster distances for 17 characters studied among 21 genotypes of Indian mustard (*Brassica juncea* L.)

Cluster	I	II	III	IV	V
I	7.87	12.28	14.53	14.83	19.3
II	12.28	0	16.1	16.57	11.02
III	14.53	16.1	9.15	13.61	17.78
IV	14.83	16.57	13.61	0	12.79
V	19.3	11.02	17.78	12.79	0

Number of secondary branches ranged from 10.83 (cluster I) to 17.05 (cluster IV). Length of main raceme ranged from 43.04 (cluster V) to 57.34 (cluster I). Number of siliquae on main raceme ranged from 38.07 (cluster II) to 45.32 (cluster I). Number of siliquae plant^{-1} ranged from 258.68 (cluster V) to 363.02 (cluster III). Siliqua length ranged from 4.28 (cluster V) to 4.59 (cluster III). Seeds siliqua^{-1} ranged from 12.04 (cluster V) to 13.12 (cluster IV). Seed yield plant^{-1} ranged from 8.4 (cluster V) to 12.92 (cluster I). Biological yield plant^{-1} ranged from 42.54 (cluster V) to 58.74 (cluster I). Harvest index ranged from 19.87 (cluster V) to 22.57 (cluster IV). Test weight ranged from 3.02 (cluster V) to 5.08 (cluster I). Yield hectare^{-1} ranged from 883.07 (cluster V) to 1513.74 (cluster I). Canopy temperature deficit ranged from 2.75 (cluster III) to 4.78 (cluster II). Chlorophyll content ranged from 35.97 (cluster V) to 43.92 (cluster I).

The comparative role of individual trait towards diversity is presented in table 7. The more times each of the 17 characters appears in first rank, the more it will contribute to diversity. Among the 17 characters studied, seed yield plant^{-1} contributed maximum (16.2%) to diversity followed by yield hectare^{-1} (10.8%), canopy temperature deficit (10.26%), harvest index (8.51%), biological yield plant^{-1} (8.1%), seeds siliqua^{-1} (7.02%), plant height (6.48%), test weight (5.94%), chlorophyll content (5.28%), days to 50% flowering (4.86%), number of primary branches (3.78%), number of secondary branches (3.62%), number of siliqua on main raceme (3.24%), siliqua length (3.24%), number of siliqua plant^{-1} (1.62%), days to maturity (0.54%), length of main raceme (0.54%).

Table 6: Cluster means for 17 characters studied among 21 genotypes of Indian mustard (*Brassica juncea* L.)

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
PH	177.31	159.47	155.84	199.19	166.59
DF	53.51	46.67	46.1	58.83	45.5
DM	136.96	134	131.53	142.34	131.17
NPB	4.85	5.97	5.08	5.47	4.38
NSB	10.83	11.1	14.46	17.05	11.75
LMR	57.34	48.21	49.77	53.04	43.04
NSMR	45.32	38.07	41.97	43.33	40.3
NSPP	315.39	281.75	363.02	344.35	258.68
SL	4.57	4.39	4.59	4.5	4.28
SPS	12.44	12.39	12.83	13.12	12.04
SYPP	12.92	10.31	11.4	10.48	8.4
BY	58.74	50.19	55.18	47.18	42.54
HI	22.3	21.13	20.75	22.57	19.87
TW	5.08	3.07	4.74	4.08	3.02
YH	1513.74	1126.71	1289.58	1152.62	883.07
CTD	3.39	4.78	2.75	3.9	4.19
CC	43.92	38.01	40.92	37.57	35.97

3.3. Principal component analysis

Principal component analysis is a multivariate technique was used in several studies to access the interrelationship between various traits analysed with interesting traits and to clustering the genotypes. Hence, in the present study PCA was used to illustrate the correlation between the morphological traits. So, a matrix of mean values for two years was used for analysis. Contribution of the characters studied to the diversity and latent vectors, eigen values and percent variance of first five principal components is shown in Table 8 and Figure 4. The length of the vector indicates the extent of contribution of each trait to overall

Table 7: Percent contribution of different quantitative traits toward genetic diversity in pooled analysis over the environments

Sources	Time ranked 1st	Contribution %
PH	14	6.48
DF	10	4.86
DM	1	0.54
NPB	8	3.78
NSB	8	3.62
LMR	1	0.54
NSMR	7	3.24
NSPP	3	1.62
SL	7	3.24
SPS	15	7.02
SYPP	34	16.2
BYPP	17	8.1
HI	18	8.51
TW	13	5.94
YH	23	10.8
CTD	22	10.26
CC	11	5.28

PH: Plant height (cm); DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branches; NSB: Number of secondary branches; LMR: Length of main raceme (cm); NSMR: Number of siliquae on main raceme; NSPP: Number of siliquae plant^{-1}; SL: Siliqua length (cm); SPS: Seeds siliqua^{-1}; SYPP: Seed yield plant^{-1} (g); BYPP: Biological yield plant^{-1} (g); HI: Harvest index; TW: Test weight (g); YH: Yield (kg ha^{-1}); CT: Canopy temperature deficit; CC: Chlorophyll content

diversity. More the length highest is the contribution and vice-versa (Figure 4). The distribution of the genotypes based on PC1 and PC2 is represented by plotting PCA biplot in Figure 5. Saleem et al. (2017) employed PCA for assessing diversity among 167 accessions of Indian mustard based on 20 quantitative traits and showed 73.92% of the total variability was due to first seven principal components. Wang et al. (2009) also used PCoA to describe and visualise 405 individuals and 48 varieties of B. napus into four cluster. Sharma et al. (2021) assessed 150 diverse Indian mustard genotypes using an Augmented Block Design and conducted a Principal Component Analysis (PCA). The results showed that the first principal component (PC1) accounted for 70.79% of the total variation among the traits studied. Key traits such as plant height, seed yield, main shoot length, and the number of secondary branches positively correlated with PC1, indicating these traits significantly contributed to the observed variability. Principal component analysis hence conducted to estimate the relative contribution of traits towards the variation in the 21 genotypes, the first five principal components accounted for 78.58% of the entire diversity among the genotypes for all the traits investigated. All the five axes possess Eigen value of >1.0. The first principal component had eigen value 6.14 which accounted for 36.12% of total variation, indicating that this axe represents the majority of the variation for the character studied. It was mainly determined by the seed yield plant^{-1} and Seed yield ha^{-1} (0.88) followed by chlorophyll content (0.79) and length of main raceme (0.78). the second PC showed eigen value of 2.63 with 15.49% of variability. It was majorly contributed by canopy temperature deficit (0.77), days to maturity (0.64) and seeds siliqua^{-1} (-0.64). PC 3 had eigen value of 2.02 which governed 11.88% of overall variability. From the values of PC, it was found that the character number

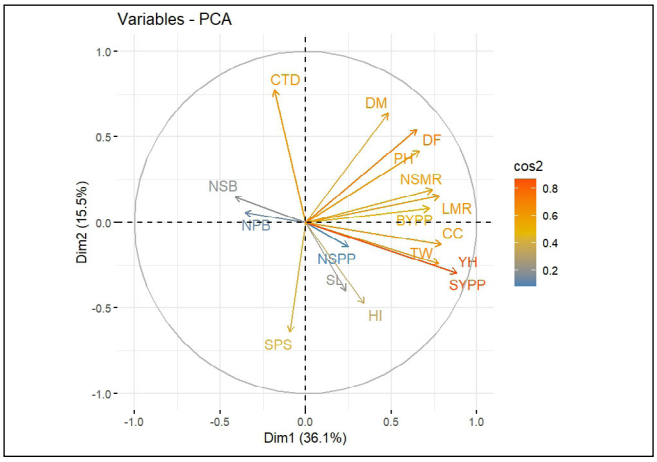

Figure 4: Contribution of different variables to total diversity as indicated by vector length

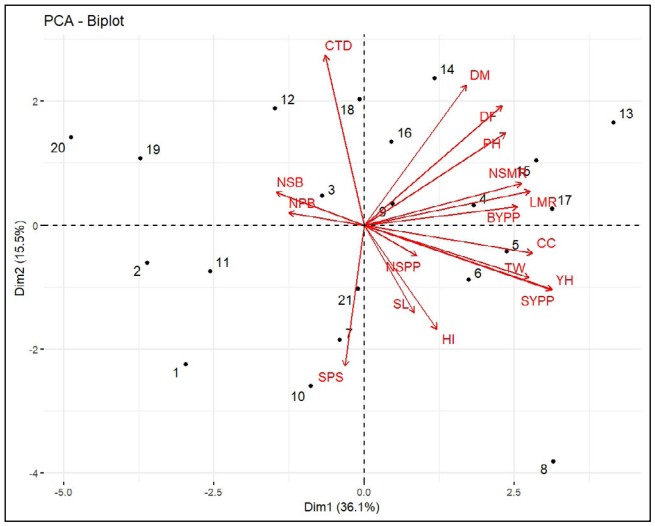

Figure 5: PCA plot showing pattern of relationships among 21 Brassica genotypes based on morphological data

Table 8: Eigenvectors and accumulated variation of the first five components (PC) from the morphological correlation matrix derived from 21 Brassica genotypes in pooled analysis over the environments

Parameters	PC1	PC2	PC3	PC4	PC5
Eigenvalue	6.14	2.63	2.02	1.48	1.08
Percent variance (%)	36.12	15.49	11.88	8.73	6.37
Cumulative variance (%)	36.12	51.60	63.49	72.21	78.58
Plant height (cm)	0.67	0.42	0.11	0.01	-0.46
Days to 50% flowering	0.65	0.55	-0.13	0.33	-0.10
Days to maturity	0.48	0.64	-0.23	0.25	-0.03
Number of primary branches	-0.35	0.06	0.63	0.34	0.33
Number of secondary branches	-0.41	0.15	0.66	0.20	0.16
Length of main raceme (cm)	0.78	0.15	0.35	-0.26	-0.13
Number of siliqua on main raceme	0.74	0.19	0.44	-0.12	-0.22
Number of siliqua plant^{-1}	0.25	-0.14	0.82	0.01	-0.13
Siliqua length (cm)	0.24	-0.40	0.19	-0.44	0.19
Seeds siliqua^{-1}	-0.09	-0.64	-0.17	0.16	-0.16
Seed yield plant^{-1} (g)	0.88	-0.30	-0.02	0.20	0.26
Biological yield plant^{-1}	0.72	0.08	-0.02	-0.46	0.38
Harvest index (%)	0.34	-0.47	0.01	0.73	-0.10
1000 seed weight (g)	0.78	-0.24	-0.16	-0.08	-0.06
Seed yield ha^{-1} (kg ha^{-1})	0.88	-0.29	-0.03	0.20	0.25
Canopy temperature deficit	-0.18	0.77	-0.09	0.13	0.43
Chlorophyll Content	0.79	-0.13	-0.13	0.12	0.32

of secondary branches (0.66) and number of siliqua plant^{-1} (0.82) contributed highest. Fourth principal component had eigen value of 1.48 and it contributed 8.73% of total variation. Harvest index (0.73) and Biological yield plant^{-1} (-0.46) accounted maximum of it. Fifth PC showed eigen value of 1.08 and contributed 6.37% of entire variation and it was majorly contributed by canopy temperature deficit (0.43), and plant height (-0.46).

4. CONCLUSION

A broad spectrum of variability among the mutants was noted for most traits, offering opportunities for selecting desirable genotypes for crop improvement. Traits like secondary branches, main raceme length, siliqua number, test weight, and seed yield showed high heritability and selection potential. Five clusters were identified, with the highest inter-cluster distance between clusters I and V, and the highest intra-cluster distance in cluster III. PCA and D2 analysis confirmed significant genetic diversity, valuable for targeted trait improvement in Indian mustard.

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