PLANT SCIENCE TODAY
Vol 12(sp1): 1-10
https://doi.org/10.14719/pst.9222

eISSN 2348-1900

RESEARCH ARTICLE

Trait profiling for yield improvement in Indian mustard using multivariate and radar plot analyses

Raj Kumar[1*], Mukesh Kumar[1], Lokesh Kumar Gangwar[1], Vivek Kumar[1], Anjali[1], Supriya Singh[1], Nirdesh Kumar Chaudhary[2], Soyal Kumar[1] & Ajar Nath Yadav[3]

[1]Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut 250 110, Uttar Pradesh, India
[2]Department of Genetics and Plant Breeding, Raja Balwant Singh College, Bichpuri, Agra 283 105, Uttar Pradesh, India
[3]Department of Genetics and Plant Breeding and Biotechnology, Eternal University, Sirmaur 173 101, Himachal Pradesh, India

*Correspondence email - : rajkumarmtg@gmail.com

Received: 30 April 2025; Accepted: 30 June 2025; Available online: Version 1.0: 14 August 2025; Version 2.0: 28 August 2025

Cite this article: Raj K, Mukesh K, Lokesh KG, Vivek K, Anjali, Supriya S, Nirdesh KC, Soyal K, Ajar NY. Trait profiling for yield improvement in Indian mustard using multivariate and radar plot analyses. Plant Science Today. 2025; 12(sp1): 1-10. https://doi.org/10.14719/pst.9222

Abstract

The study was performed to estimate genetic variability, selection parameters, principal component analysis (PCA) and radar plot (spider) analysis using 55 genotypes which were evaluated during *Rabi* season 2023-2024 at the Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, for 13 traits with three replications. The analysis of variance (ANOVA) revealed highly significant differences for all traits. A higher phenotypic coefficient of variation (PCV) was observed compared to the genotypic coefficient of variation (GCV) for the respective traits. High PCV and GCV values were recorded for seed yield and harvest index. High genetic advance coupled with high heritability was observed for seed yield, number of branches on the main raceme, test weight and siliqua length. Radar plot analysis revealed significant multi-trait variability among the traits. At both genotypic and phenotypic levels, seed yield revealed a positive significant association with number of siliquae on the main raceme, length of main raceme, siliqua length, seeds per siliqua and test weight. A high direct effect on seed yield was observed through harvest index and biological yield in path coefficient analysis. The cumulative percentage of explained variance by the three principal components with Eigenvalues greater than one was 80.15 %. Radar plot analysis revealed that the genotype RH-725 × Pusa Agrani and Pusa Agrani × CS-60 were identified as promising high-yielding and high oil content, respectively. The study revealed that traits such as seed yield, test weight, harvest index, siliqua length and genotypes RH -725 × Pusa Agrani, RH-725 × Kranti, Pusa Agrani × CS-60 and Pusa Bold × CS-60 can be further used for breeding programs.

Keywords: correlation; genetic variability; path analysis; PCA; radar plot

Introduction

Indian mustard (*Brassica juncea* L. Czern & Coss) is widely cultivated in Australia, Canada, India, Pakistan, China and a few European countries as an important oilseed crop belonging to the Brassicaceae (Cruciferae) family, having a genome size of around 922 Mb (1, 2). *B. juncea* is an amphidiploid crop (2n = 36, AABB), originated through natural hybridization between *B. campestris* (2n = 20, AA) and *B. nigra* (2n = 16, BB), followed by spontaneous chromosome duplication. This amphidiploid nature, along with its large and complex genome, contributes significantly to its broad genetic diversity and enhances its breeding potential by enabling the incorporation of alleles from both ancestral genomes (3-5). The oil has been used in cosmetics (e.g. hair care), pickles, traditional medicines and culinary flavoring (6). It contains protein (26 g/100 g), carbohydrates (28 g/100 g), fibre (12g/100 g) and fat (36 %) with oil content (OC) ranging from 37 % to 49 %. Along with major components, it also has significant levels of vitamins (C and K), minerals (Cu, Fe, Ca, Zn, Mn, Se and Mg) (7-9). A major breeding objective is the development of high-yielding genotypes with superior oil quality (e.g., oil composition and fatty acid profile). The effective utilization of diverse germplasm through hybridization plays a crucial role in the genetic improvement (10, 11).

Genetic variability includes the phenotypic coefficient of variation (PCV), the genotypic coefficient of variation (GCV) and heritability, which allows understanding the ability of traits to transfer into the next generation, whereas genetic advance helps to know the portion of genetic traits gained from their respective parents. Character association analyses (correlation and path coefficient) help in understanding traits relationships and categorizing into direct and indirect effects, respectively, whereas PCA allows easy understanding the variation by compressing the total variation into a principal component. Multivariate graphical techniques, like radar plots (spider plots), provide an intuitive visualization for comparing multiple traits in plant breeding such as days to maturity, plant height, number of primary and secondary branches, siliqua per plant, test weight, seed yield, biological yield and harvest index, simultaneously across genotypes, aiding in genotype selection for breeding programs (12, 13). Such tools aid in identifying superior genotypes based on yield and associated agronomic traits. The aim of the present study is to understand genetic variability, selection parameters, principal component analysis and radar plot analysis.

Materials and Methods

Ten diverse genotypes, namely, RH-725, Pusa Jai Kisan, PM-28, Pusa Bold, Pusa Agrani, PM-29, CS-60, Kranti, Giriraj and RH-749 were used for hybridization. Genotype used in hybridization aimed to address the different aspects of crop improvement, like Pusa Agrani and RH-725 used for short-duration and early sowing, respectively. PM-29 was used in crossing as it has lower erucic acid, which plays a crucial role in oil quality. Kranti has resistance to *Alternaria* blight and aphids, whereas CS-60 has tolerance to salinity and alkalinity. Pusa Bold, PM-28, Pusa Jai Kisan have bold seed size, high oil content whereas Giriraj have high yield as yield improvement is the main research objective for breeders and it can be improved by improving yield and its related components like bold seed size, high oil content and high yield (14, 15). The details of genotypes including their pedigree and features are presented in supplementary material (Table S1).

Experimental details

The ten genotypes of Indian mustard were hybridized using a half-diallel design to produce 45 hybrids at the Crop Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, during *Rabi* 2022-23. The complete set of experimental materials comprised 55 genotypes, such as 10 parents and 45 hybrids that were evaluated in a randomized complete block design (RCBD) with three replications.

Observations recorded

Thirteen quantitative characters were recorded during the experiment: i) days to 50 % blooming (DFB), ii) days to maturity (DM), iii) plant height (PH), iv) branches on a main raceme (BMR), v) siliquae on a main raceme (SMR), vi) length of a main raceme (LMR), vii) siliqua length (SL), viii) seeds per siliqua (SPS), ix) biological yield per plant (BY), x) harvest index (HI), xi) oil content (OC), xii) test weight (TW) and xiii) seed yield per plant (SY). Five plants from each genotype in each replication were randomly selected and tagged before maturity except for DFB and DM, which were assessed on a population basis.

Statistical analysis

Analysis of variance (ANOVA) was based on the model: $Pijk = \mu + vij + bk + eijk$. (i, j = 1...t; k = 1...b). PCV and GCV were calculated (16).

$$GCV\ (\%) = \left[\frac{\sqrt{\sigma^2 g}}{\bar{X}}\right] \times 100 \quad \text{.....(Eqn. 1)}$$

$$GCV\ (\%) = \left[\frac{\sqrt{\sigma^2 p}}{\bar{X}}\right] \times 100 \quad \text{.....(Eqn. 2)}$$

Where, PCV is the phenotypic coefficient of variation. GCV is the genotypic coefficient of variation and is the $\bar{X}$ population means of the characters.

$$H^2 = \left(\frac{\sigma^2 g}{\sigma^2 p}\right) \times 100 \quad \text{.....(Eqn. 3)}$$

Heritability broad sense (bs) was calculated as per the following formula (17).

Where, H^2 is the heritability in broad sense, σ^2 g is the genotypic coefficient of variance and σ^2 p is the phenotypic coefficient of variance.

Classifications were done as: >80 % high, 60-80 % medium and <60 % low (18). Genetic advance and genetic advance over percent mean were estimated as per the following formula (19, 20).

$$GA = K \times \sigma p \times H^2 \quad \text{.....(Eqn. 4)}$$

$$GAM = \left(\frac{GA}{\bar{X}}\right) \times 100 \quad \text{.....(Eqn. 5)}$$

The correlation and path coefficients were calculated as per the following formula (21, 22).

$$r_{xy} = \frac{MSPt}{(MSt_x \cdot MSt_y)^{1/2}} \quad \text{.....(Eqn. 6)}$$

Where, r_{xy} is the correlation between attributes x and y, MSPt is mean sum of products of genotypes, MSt_x is mean square of treatments for variable x and MSt_y is mean square of treatments for variable y.

$$R^2 = b'_1 r_{1y} + b'_2 r_{2y} + b'_3 r_{3y} + \ldots \quad \text{.....(Eqn. 7)}$$

$$Residual\ effect = 1 - R^2 \quad \text{.....(Eqn. 8)}$$

Where, b'_1, b'_2, b'_3...= standardized partial regression of x_1, x_2, x_3.. and r_{1y}, r_{2y}, r_{3y},...= correlation coefficient between x_1, x_2, x_3,.. and y.

PCA was performed using FactoMineR in R and Agrianalyze online software (https://www.agrianalyze.com/PrincipalComponentAnalysisGPB) whereas PCA visualization in R was performed through the ggbiplot library. The normalized dataset (0–100 %) was then used to generate a radar chart using R Studio (R version 4.4.3, performed on a cloud-based R Studio environment) employing the FMSB package. To ensure comparability across traits measured in different units and scales, trait values were normalized using Min-Max normalization according to the following formula (23).

$$Normalized\ value = \frac{X - Min\ (X)}{Max(X) - Min\ (X)} \times 100 \quad \text{.....(Eqn. 9)}$$

Where X represents the original value for each trait.

Results and Discussions

ANOVA for thirteen traits revealed highly significant variation across all traits for all sources of variation, including treatments, parents, hybrids and parents versus hybrids, while replication effects were non-significant, suggesting uniform environmental conditions across replications. The ANOVA

results for 13 quantitative traits are presented in Table 1. These results indicate that sufficient variation was present in the germplasm, which is a key requirement for the success of any plant breeding program. The presence of heritable variation in germplasm paves the way for developing high-yielding varieties. Similar observations of significant analysis of variance of all traits were also reported in previous studies (24-26).

Genetic variability analysis

The mean and range performance of all 13 traits is presented in Table 2. The SY in parents ranged from 14.92 (Kranti) to 23.04 (CS-60) with a mean of 17.79, whereas in hybrids it ranged from 15.14 (Pusa Jai Kisan × PM-29) to 31.48 (PM-29 × Kranti) with a mean of 22.50. Similarly, the overall mean performance, including parents and hybrids, SY, ranged from 14.92 (Kranti) to 31.48 (PM-29 × Kranti), with an overall mean of 21.60. Similar observations of SY for mean performance were also reported in previous studies (27-30).

Genetic variability parameters for all traits are presented in Table 2.The GCV and PCV of SY (22.75 and 23.96), HI (20.27 and 20.79), BMR (14.91 and 16.23), BY (13.92 and 15.41), TW (11.22 and 12.02), LMR (11.14 and 12.82), SL (10.77 and 11.67), SMR (9.67 and 10.53), SPS (9.02 and 10.28), DFB (8.26 and 8.66), PH (5.10 and 8.00), DM (3.08 and 3.20) and OC (2.99 and 3.18) were observed respectively. The high GCV and PCV (more than 20 %) were observed only for SY and HI. Similar high observations for GCV and PCV for SY were also reported in earlier research (24, 27, 31). For moderate GCV and PCV for the traits BMR and TW, similar observations were also reported, whereas similar low GCV and PCV for DFB and PH were also studied in earlier research (31-33).The high PCV compared to their respective GCV was observed in all traits studied revealing the effect of the environment on trait expression and the selection of traits solely based on the coefficient of variation may produce misleading results. Similar observations of high PCV compared to their respective GCV were also studied (25, 31, 34).

Heritability (bs) estimate is the ratio of genotypic to phenotypic variance expressed as a percentage. It is an indicator of character transmission from parents to offspring. High heritability (> 80 %) was observed for traits HI (95.07), DM (92.76), DFB (90.88), SY (90.18), OC (88.54), TW (87.19), SL (85.15), BMR (84.43), SMR (84.36) and BY (81.58).The moderate heritability (60-80 %) was observed for traits SPS (76.97) and LMR (75.46), whereas low heritability (less than 60 %) was observed for trait PH (40.71). A high heritability estimate indicates phenotypic performance-based selection, but it does not always imply a significant genetic gain. It aids plant breeders in selecting superior genotypes from a genetically diverse population. Similar observations for high heritability

Table 1. Combined ANOVA for parents and hybrids for 13 traits.

SV	df	DFB	DM	PH	BMR	SMR	LMR	SL	SPS	BY	HI	OC	TW	SY
Replication	2	5.26	5.28	9.18	0.19	13.61	3.75	0.13	0.018	0.144	5.13	0.308	0.063	4.75
Genotypes	54	50.55**	61.67**	383.17**	2.68**	67.25**	201.42**	0.84**	4.246**	428.22**	86.34**	4.54**	1.20**	75.38**
Parents	9	68.00**	68.02**	270.91**	3.83**	26.04**	159.84**	0.46**	4.53**	13.34**	37.47**	4.70**	1.14**	22.73**
Hybrids	44	41.68**	56.00**	338.33**	1.90**	69.13**	179.17**	0.83**	3.84**	456.66**	94.39**	4.06**	1.08**	75.49**
P vs Hybrids	1	283.75**	253.67**	3365.74**	26.33**	355.31**	1554.57**	4.44**	19.51**	2910.78**	172.07**	24.58**	7.13**	544.15**
Error	108	1.64	1.56	125.24	0.16	3.91	19.70	0.046	0.385	29.97	1.47	0.188	0.056	2.64

*, ** significant at 5 % and 1 % level, respectively. **SV**: source of variation, **df**: degree of freedom, **DFB**: days to 50 % blooming, **DM**: days to maturity, **PH**: plant height, **BMR**: branches on a main raceme, **SMR**: siliquae on a main raceme, **LMR**: length of a main raceme, **SL**: siliqua length, **SPS**: seeds per siliqua, **BY**: biological yield per plant, **HI**: harvest index, **OC**: oil content, **TW**: test weight and **SY**: seed yield per plant.

Table 2. Genetic variability analysis for 13 traits.

Parameters	Mean	Min	Max	GCV (%)	PCV (%)	Heritability (%)	GA	GA % mean
DFB	48.89	41.67	59.33	8.26	8.66	90.88	7.93	16.22
DM	145.17	132.00	158.00	3.08	3.20	92.76	8.88	6.12
PH	181.75	162.73	206.73	5.10	8.00	40.71	12.19	6.71
BMR	6.15	3.70	7.80	14.91	16.23	84.43	1.74	28.23
SMR	47.51	40.40	58.13	9.67	10.53	84.36	8.69	18.30
LMR	69.89	51.80	88.80	11.14	12.82	75.46	13.93	19.93
SL	4.77	4.00	5.85	10.77	11.67	85.15	0.98	20.47
SPS	12.58	9.87	15.93	9.02	10.28	76.97	2.05	16.30
BY	82.76	71.40	116.00	13.92	15.41	81.58	21.44	25.90
HI	26.24	17.27	42.64	20.27	20.79	95.07	10.68	40.72
OC	40.24	37.38	43.15	2.99	3.18	88.54	2.34	5.80
TW	5.50	4.12	6.87	11.22	12.02	87.19	1.19	21.59
SY	21.64	14.92	31.48	22.75	23.96	90.18	9.63	44.51

GCV: genotypic coefficient of variation, **PCV**: phenotypic coefficient of variation, **GA**: genetic advance, **DFB**: days to 50 % blooming, **DM**: days to maturity, **PH**: plant height, **BMR**: branches on a main raceme, **SMR**: siliquae on a main raceme, **LMR**: length of a main raceme, **SL**: siliqua length, **SPS**: seeds per siliqua, **BY**: biological yield per plant, **HI**: harvest index, **OC**: oil content, **TW**: test weight and **SY**: seed yield per plant.

for DM, OC and DFB were reported earlier studies (25, 27, 31, 35).

Genetic advance is an important selection parameter to select desired variables. Thus, it adds an advantage over heritability as a guide factor to the breeding program. The high (> 20 %) genetic advances were observed for traits SY (44.51), HI (40.72), BMR (28.23), biological yield (25.90), TW (21.59) and SL (20.47). Similar high genetic advances for SY and TW were reported in previous studies (25, 27, 31, 35). The moderate genetic advances (10 % to 20 %) were observed for traits LMR (19.93), SMR (18.30), SPS (16.30) and DFB (16.22), whereas low genetic advances (< 10 %) were observed for traits PH (6.71), DM (6.12) and OC (5.80). A similar moderate genetic advance for LMR, SPS and DFB, whereas low for DM was also observed (36). The high genetic advance having high heritability was observed for traits SY, followed by HI, BMR, BY, TW and SL, indicating the presence of additive action allows these traits are promising for selection in early generations. Similar high genetic advances with high heritability for SY were also reported (24, 25, 35). For other yield-contributing traits like HI and BMR, similar observations were reported earlier (31, 37). The moderate and low genetic advances with high heritability were observed for DFB, DM, SMR and OC, indicating the influence of non-additive gene action. The moderate and low genetic advances with heritability were observed for PH, LMR and SPS, indicating the environment's effect on these traits. A similar moderate genetic advance with high heritability for DFB was also observed (36).

The radar chart provides an integrated visual summary of genotype performance across multiple traits. Fig. 1 revealed that PH and DM showed relatively higher normalized values, indicating superior performance in these attributes for the genotype analyzed. Moderate scores were observed for LMR and BY, suggesting acceptable yield attributes. Traits such as SL, BMR and TW exhibited relatively lower normalized values, suggesting areas where improvement may be needed. The compactness and spread of the radar chart pattern indicate trait stability and potential trade-offs. Higher values across most traits point toward desirable genotypes suitable for advancement in breeding pipelines (38).

Correlation coefficient analysis

Correlation studies provide symmetrical measurement of the degree and direction of the relationship between yield and its related traits. Therefore, selection of key yield components and their correlation with yield is crucial in designing an efficient breeding strategy for producing superior genotypes (18, 20). The correlation estimates for 13 traits are presented in Table 3. Genotypic and phenotypic associations of SY showed a positive significant correlation (p< 0.01) with BMR, SMR, LMR, SL, SPS, BY, HI, OC and TW, whereas a positive non-significant correlation with PH along with negative significant associations with DFB and DM. Generally, genotypic associations were slightly higher for respective traits than their respective phenotypic associations, revealing strong inherent among traits. Similar observations of higher genotypic correlations compared to their respective phenotypic correlations have also been reported (36, 39). A similar correlation between BMR with SY has been studied (40-42). Likewise, correlations involving SMR have also been reported, whereas for SPS, similar associations were reported (40, 43, 44). For trait BY and HI, similar correlations with SY were also reported in studies (41, 44). A similar negative correlation of DFB and DM with SY was also observed (36).

A significant correlation between two traits may arise from shared biosynthetic pathways, the pleiotropic action of a single gene influencing multiple traits or genetic linkage, where genes controlling different traits are located close together on the same chromosome and are inherited together. Pleiotropy

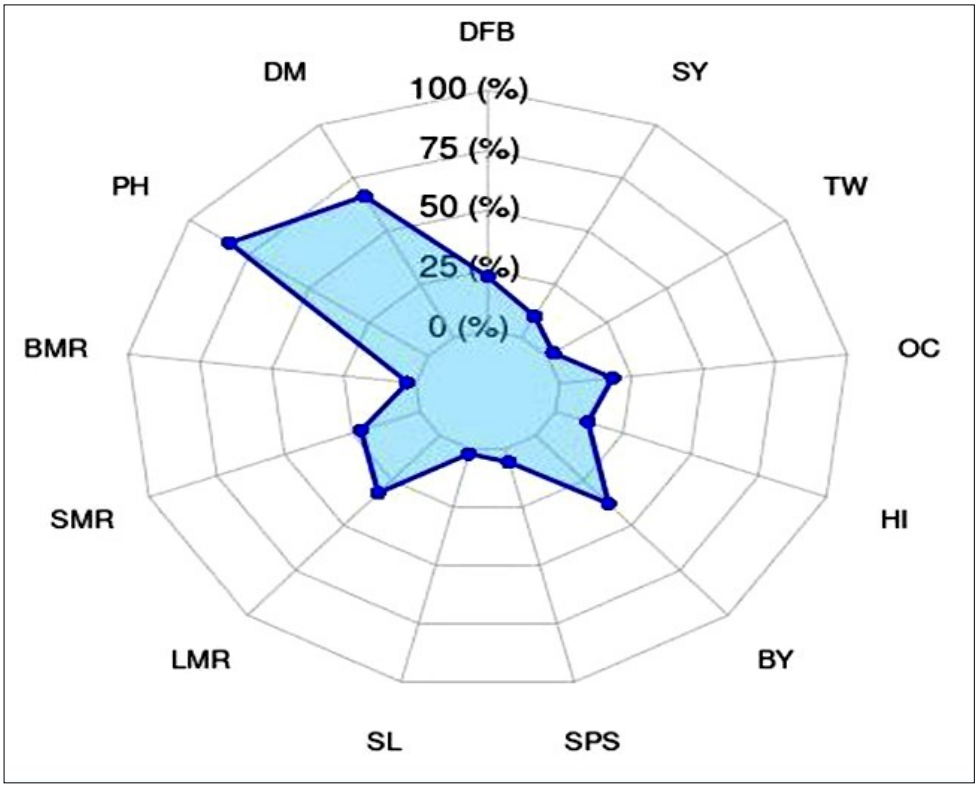

Fig. 1. Radar (spider) plot for 13 quantitative traits.

Table 3. Genotypic (G) and phenotypic (P) correlation analysis for 13 traits.

Traits		DFB	DM	PH	BMR	SMR	LMR	SL	SPS	BY	HI	OC	TW	SY
DFB	G		0.682**	-0.313**	-0.412**	-0.274**	-0.452**	-0.320**	-0.309**	-0.235**	-0.255**	-0.244**	-0.259**	-0.350**
	P		0.637**	-0.161*	-0.359**	-0.231**	-0.382**	-0.277**	-0.264**	-0.202**	-0.237**	-0.218**	-0.227**	-0.315**
DM	G			-0.135	-0.183*	-0.225**	-0.493**	-0.394**	-0.480**	-0.288**	-0.299**	-0.285**	-0.199*	-0.453**
	P			-0.069	-0.166*	-0.194*	-0.402**	-0.351**	-0.421**	-0.250**	-0.274**	-0.266**	-0.185*	-0.407**
PH	G				0.407**	0.256**	0.334**	0.031	0.122	0.162*	-0.062	-0.034	0.203**	0.011
	P				0.264**	0.181*	0.369**	0.028	0.120	0.237**	-0.020	0.004	0.187*	0.116
BMR	G					0.369**	0.454**	0.252**	0.222**	0.246**	0.226**	0.181*	0.460**	0.314**
	P					0.316**	0.388**	0.203**	0.151	0.239**	0.202**	0.154*	0.406**	0.294**
SMR	G						0.577**	0.620**	0.529**	0.420**	0.343**	0.509**	0.524**	0.574**
	P						0.461**	0.532**	0.443**	0.354**	0.319**	0.454**	0.456**	0.517**
LMR	G							0.619**	0.600**	0.500**	0.419**	0.615**	0.666**	0.659**
	P							0.470**	0.485**	0.504**	0.365**	0.505**	0.577**	0.622**
SL	G								0.675**	0.489**	0.501**	0.511**	0.559**	0.763**
	P								0.512**	0.403**	0.458**	0.453**	0.479**	0.672**
SPS	G									0.546**	0.361**	0.614**	0.619**	0.667**
	P									0.437**	0.297**	0.498**	0.523**	0.551**
BY	G										-0.110	0.441**	0.470**	0.485**
	P										-0.106	0.398**	0.429**	0.518**
HI	G											0.430**	0.525**	0.809**
	P											0.396**	0.461**	0.787**
OC	G												0.525**	0.654**
	P												0.449**	0.605**
TW	G													0.744**
	P													0.666**
SY	G													
	P													

*, ** significant at 5 % and 1 % level, respectively. **DFB**: days to 50 % blooming, **DM**: days to maturity, **PH**: plant height, **BMR**: branches on a main raceme, **SMR**: siliquae on a main raceme, **LMR**: length of a main raceme, **SL**: siliqua length, **SPS**: seeds per siliqua, **BY**: biological yield per plant, **HI**: harvest index, **OC**: oil content, **TW**: test weight and **SY**: seed yield per plant.

can result in coordinated expression of traits due to common genetic control, while linkage reflects physical proximity of genes that may not functionally interact but are co-inherited, leading to apparent associations between traits. The positive significant correlation allows us to select the principal traits indirectly by selecting these traits, whereas negative significant revealed traits are negatively correlated and the selection of these traits reduces the correlated traits.

Direct and indirect effect analysis

The correlation coefficient estimated for various pairs of traits was subjected to path coefficient estimation for partitioning correlation values into the indirect and direct effects, which helps to formulate an effective selection strategy. The effects of various traits on SY are presented in Table 4.

Direct effect

The direct effect of genotypic and phenotypic path coefficients on SY was observed by HI (0.768 and 0.798), BY (0.487 and 0.557), SL (0.079 and 0.042), TW (0.073 and 0.025), days to 50% blooming (0.037 and 0.033), SMR (0.037 and 0.028), OC (0.033 and 0.023), SPS (-0.005 and 0.009), PH (-0.019 and 0.0009), BMR (-0.020 and -0.025), LMR (-0.048 and -0.010) and DM (-0.076 and -0.044), respectively. High direct and positive effects indicate that these traits can be directly targeted in selection programs. Similar observations of a high positive direct effect on SY by HI were observed, whereas BY similar estimates were studied previously (41, 44, 45).

Principal component analysis

Principal component analysis (PCA) was conducted on 13 traits across 55 genotypes. As per Kaiser's rule, PCA with Eigenvalues more than 1 are considered for further interpretation. It was observed that a total of three principal components having Eigenvalues more than 1. The Eigenvalues and percentage of contribution in total variance of PC1, PC2 and PC3 are 8.27 with 63.66 %, 1.12 with 8.64 % and 1.02 with 7.86 %, respectively. The cumulative percentage of these three components to total variance is 80.15%. The pictorial representation of Eigenvalues and percentages of explained variances are represented in Fig. 2. The pictorial representation of all PC correlations with 13 traits is represented in Fig. 3. PC1 shows a high and positive correlation with DFB (0.28) and DM (0.25), whereas the other 11 traits are showing a negative correlation. Similar PC1 correlation observations of DFB were reported, whereas for DM, similar estimates were studied (46-48). PC2 is showing a positive association with HI (0.68) following SY (0.35), DM (0.25),

Table 4. Genotypic (G) and phenotypic (P) path analysis for SY.

Traits		DFB	DM	PH	BMR	SMR	LMR	SL	SPS	BY	HI	OC	TW	SY
DFB	**G**	**0.0375**	-0.0523	0.0060	0.0085	-0.0103	0.0218	-0.0255	0.0016	-0.1146	-0.1960	-0.0081	-0.0190	-0.350**
	P	**0.0338**	-0.0281	-0.0001	0.0092	-0.0065	0.0038	-0.0117	-0.0024	-0.1128	-0.1889	-0.0051	-0.0058	-0.315**
DM	G	0.0256	**-0.0767**	0.0026	0.0038	-0.0084	0.0238	-0.0314	0.0024	-0.1401	-0.2300	-0.0095	-0.0146	-0.453**
	P	0.0215	**-0.0441**	-0.0001	0.0043	-0.0054	0.0040	-0.0148	-0.0039	-0.1397	-0.2184	-0.0062	-0.0048	-0.407**
PH	G	-0.0117	0.0103	**-0.0193**	-0.0084	0.0096	-0.0161	0.0025	-0.0006	0.0789	-0.0478	-0.0011	0.0149	0.0110
	P	-0.0055	0.0031	**0.0009**	-0.0068	0.0051	-0.0037	0.0012	0.0011	0.1319	-0.0157	0.0001	0.0048	0.1160
BMR	G	-0.0154	0.0140	-0.0078	**-0.0206**	0.0138	-0.0219	0.0201	-0.0011	0.1198	0.1735	0.0060	0.0338	0.314**
	P	-0.0121	0.0073	0.0002	**-0.0258**	0.0089	-0.0039	0.0086	0.0014	0.1335	0.1615	0.0036	0.0105	0.294**
SMR	G	-0.0103	0.0173	-0.0049	-0.0076	**0.0374**	-0.0279	0.0493	-0.0027	0.2044	0.2635	0.0169	0.0385	0.574**
	P	-0.0078	0.0085	0.0002	-0.0081	**0.0280**	-0.0046	0.0224	0.0041	0.1972	0.2551	0.0106	0.0118	0.517**
LMR	G	-0.0169	0.0378	-0.0064	-0.0094	0.0216	**-0.0483**	0.0492	-0.0030	0.2437	0.3219	0.0204	0.0489	0.659**
	P	-0.0129	0.0177	0.0003	-0.0100	0.0129	**-0.0100**	0.0198	0.0045	0.2811	0.2918	0.0118	0.0149	0.622**
SL	G	-0.0120	0.0302	-0.0006	-0.0052	0.0232	-0.0299	**0.0795**	-0.0034	0.2382	0.3852	0.0170	0.0411	0.763**
	P	-0.0094	0.0155	0.0000	-0.0052	0.0149	-0.0047	**0.0421**	0.0047	0.2251	0.3657	0.0105	0.0123	0.672**
SPS	G	-0.0116	0.0368	-0.0024	-0.0046	0.0198	-0.0290	0.0537	**-0.0050**	0.2660	0.2773	0.0204	0.0455	0.667**
	P	-0.0089	0.0185	0.0001	-0.0039	0.0124	-0.0048	0.0216	**0.0092**	0.2440	0.2375	0.0116	0.0135	0.551**
BY	G	-0.0088	0.0221	-0.0031	-0.0051	0.0157	-0.0242	0.0389	-0.0028	**0.4870**	-0.0843	0.0147	0.0346	0.485**
	P	-0.0068	0.0110	0.0002	-0.0062	0.0099	-0.0050	0.0170	0.0040	**0.5578**	-0.0843	0.0093	0.0111	0.518**
HI	G	-0.0096	0.0229	0.0012	-0.0047	0.0128	-0.0202	0.0398	-0.0018	-0.0534	**0.7688**	0.0143	0.0386	0.809**
	P	-0.0080	0.0121	0.0000	-0.0052	0.0089	-0.0037	0.0193	0.0027	-0.0589	**0.7984**	0.0092	0.0119	0.787**
OC	G	-0.0092	0.0219	0.0007	-0.0037	0.0190	-0.0297	0.0407	-0.0031	0.2150	0.3310	**0.0332**	0.0386	0.654**
	P	-0.0074	0.0117	0.0000	-0.0040	0.0127	-0.0050	0.0191	0.0046	0.2219	0.3162	**0.0233**	0.0115	0.605**
TW	G	-0.0097	0.0153	-0.0039	-0.0095	0.0196	-0.0322	0.0445	-0.0031	0.2291	0.4036	0.0174	**0.0735**	0.744**
	P	-0.0077	0.0081	0.0002	-0.0105	0.0128	-0.0058	0.0202	0.0048	0.2394	0.3684	0.0104	**0.0257**	0.666**

Resi- 0.00387(G) and Resi- 0.01028 (P). *****, ****** significant at 5 % and 1 % level, respectively. **DFB**: days to 50 % blooming, **DM**: days to maturity, **PH**: plant height, **BMR**: branches on a main raceme, **SMR**: siliquae on a main raceme, **LMR**: length of a main raceme, **SL**: siliqua length, **SPS**: seeds per siliqua, **BY**: biological yield per plant, **HI**: harvest index, **OC**: oil content, **TW**: test weight and **SY**: seed yield per plant.

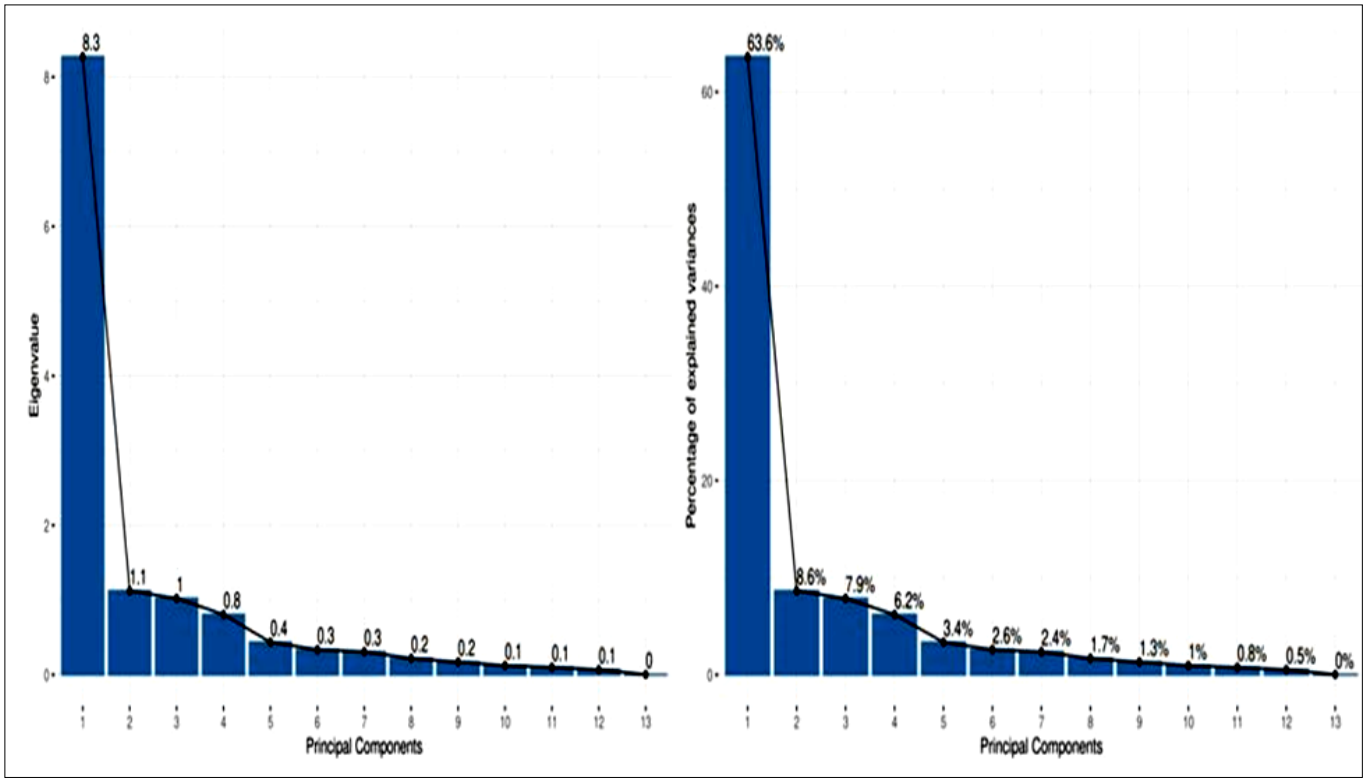

Fig. 2. Scree plot of 13 PCs with Eigenvalues and percent of explained variance PC of Indian mustard.

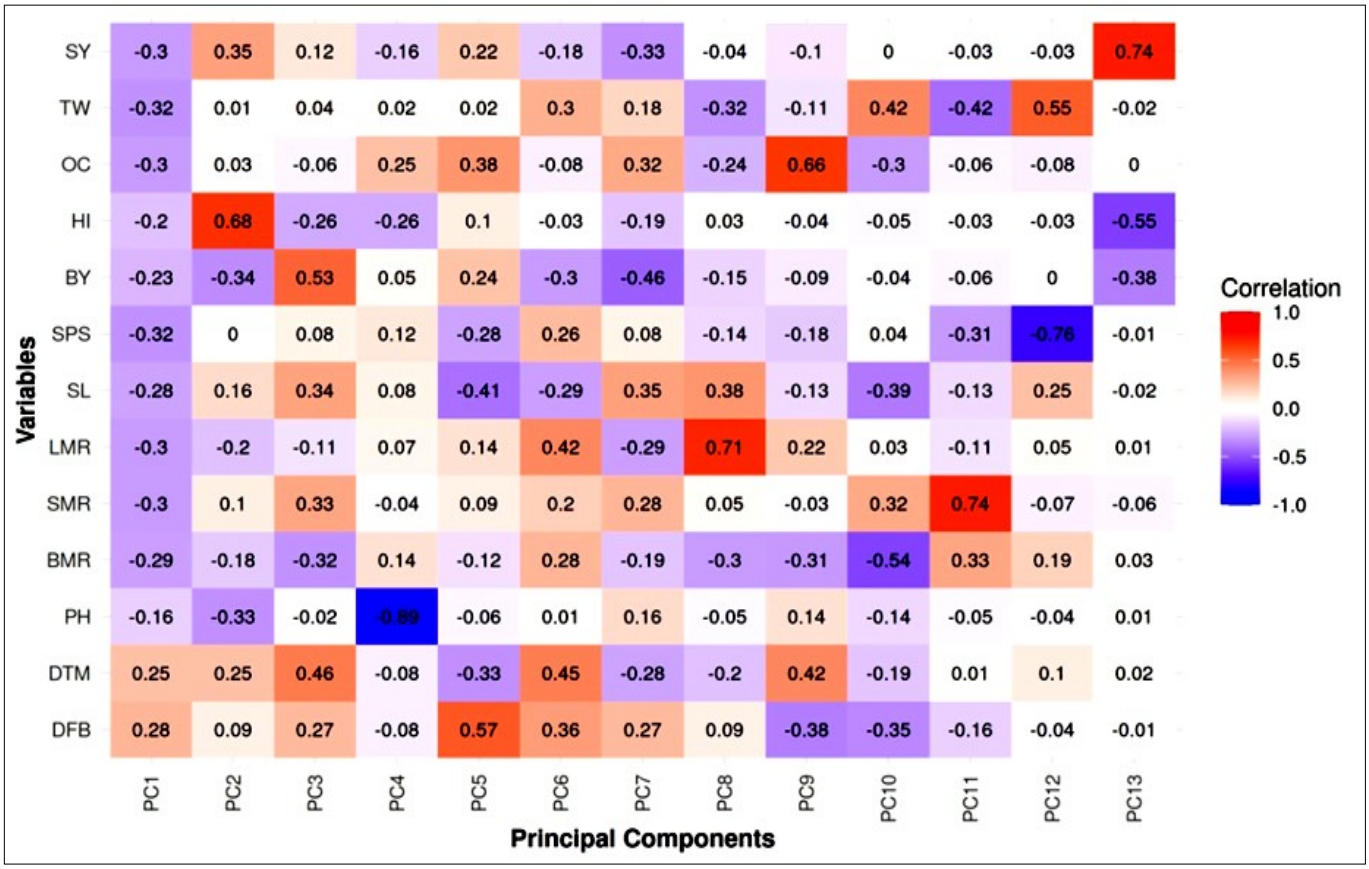

Fig. 3. Correlation of PC with all 13 traits of Indian mustard.

SL (0.16), DFB (0.09), OC (0.03), SMR (0.1) and TW (0.01). Similar results for SY and SL were reported in previous studies (47-48). The PC3 shows a high and positive association with BY (0.53) following DM (0.46), SL (0.34), SMR (0.33), DFB (0.27), SY (0.12), SPS (0.08) and TW (0.04). A similar PC3 correlation observation for DM, SL, SMR and SY were recorded (47, 48). PCA biplot was plotted on the basis of PC1 and PC2 having a percentage of contribution in total variance of 63.66 % and 8.64 %, respectively, indicating the superior genotypes 14 (RH-725 × Pusa Agrani), 17 (RH-725 × Kranti), 37 (Pusa Bold × CS-60) and 42 (Pusa Agrani × CS-60) for SY, as these genotypes aligned near the variable SY in the PCA biplot. It can be selected for further plant breeding programs and selection of superior genotypes. The pictorial representation of 13 variables and 55 genotypes in the PCA biplot based on PC1 and PC2 is represented in Fig. 4.

Radar (spider) plot analysis

The radar chart provides a visual, multivariate comparison of genotypes across yield-related traits. This approach quickly identifies superior genotypes with balanced performance across multiple traits, facilitating informed selection decisions for breeding and improvement programs. The four superior performed genotypes for SY from PCA analysis were selected and subjected to radar analysis revealed considerable variability among genotypes across the observed quantitative traits as represented in Fig. 5. Genotype 14 (RH-725 × Pusa Agrani) exhibited superior performance for DFB, SY, BY, SPS, LMR, SMR and SL indicating its potential for early flowering, seed yield and related traits. Genotype 42 (Pusa Agrani × CS-60) demonstrated high OC, HI, TW, BMR, LMR and PH suggesting its suitability for oil yield improvement. Genotype 17 (RH-725 × Kranti) showed moderate performance across the most traits but excelled slightly in SPS, SY, BY and HI. It appears more balanced but not extreme in any particular trait. Genotype 37 (Pusa Bold × CS-60) stood out in DM, BMR, SMR and HI but showed lower performance in SY. It may be useful for breeding programs targeting biomass traits. The widespread in trait values suggests a significant scope for selection and genetic improvement. Genotype 14 (RH-725 × Pusa Agrani) can be prioritized for seed yield improvement programs, whereas genotype 42 (Pusa Agrani × CS-60) could be valuable for oil quality enhancement. Similar multi-trait evaluation approaches have also been recommended in oilseeds (12, 49).

Conclusion

Variance analysis revealed highly significant results for all 13 traits. The higher PCV compared to the GCV for most traits indicates strong environmental influence, suggesting that direct selection may be misleading. The high heritability with high genetic advance was observed for traits SY, followed by HI, BMR, BY, TW and SL, revealing the additive gene action presence.SY showed significant positive correlations with BMR, SMR, LMR, SL, SPS, BY, HI, OC and TW. The high direct effects of both path coefficients on SY were observed by HI and BY. These positive significant correlations enable the indirect selection of SY through the improvement of these principal traits. PCA allows the selection of the desirable genotypes for variable SY namely RH-725 × Pusa Agrani, RH-725 × Kranti, Pusa Bold × CS-60 and Pusa Agrani × CS-60 whereas the radar chart analysis revealed that genotype (RH-725 × Pusa Agrani) was identified as a promising high-yielding and genotype (Pusa Agrani × CS-60) showed potential for high oil content. Genetic variability, correlation and path coefficient analysis revealed the traits like HI, BMR, TW and SL can be selected for yield improvement in

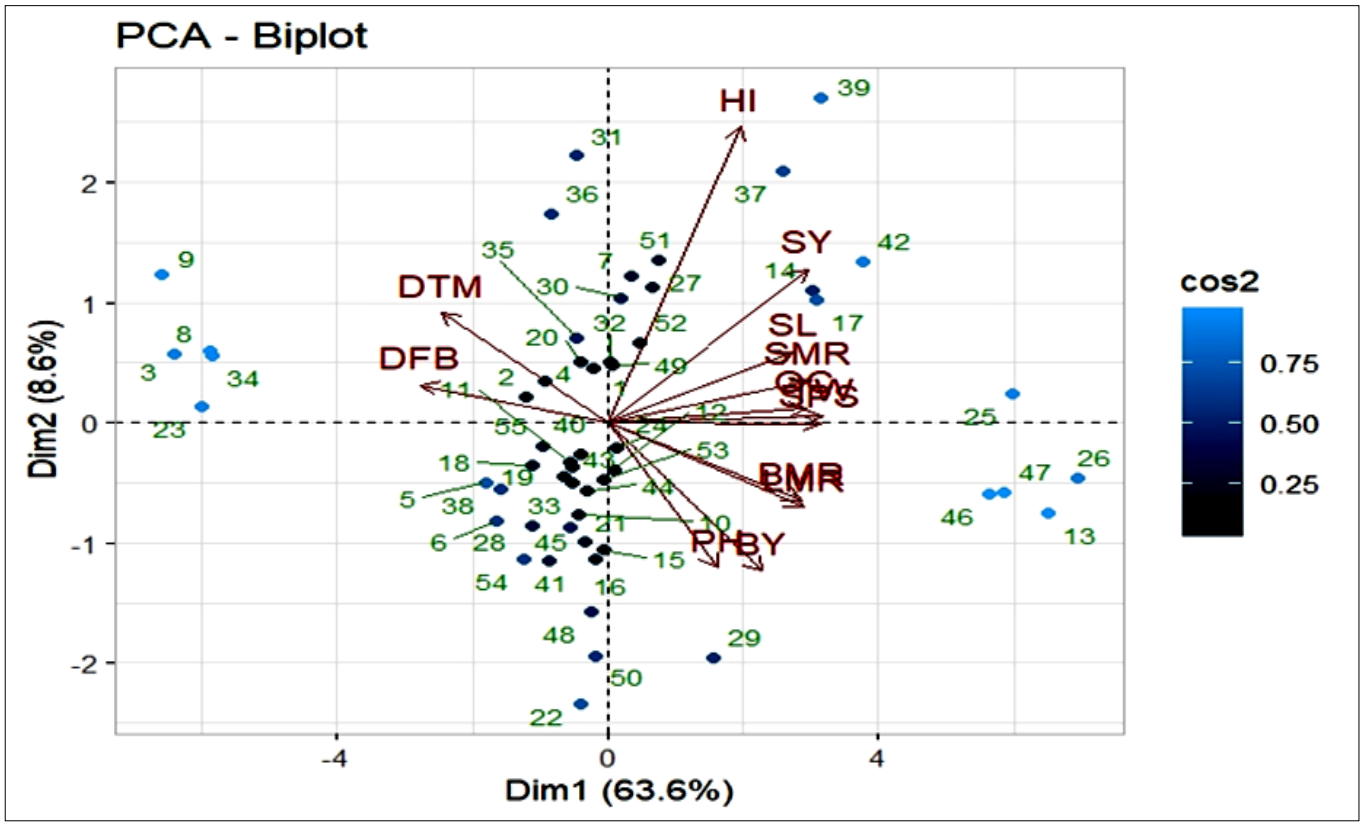

Fig. 4. PCA-biplot representing the variables with genotypes of Indian mustard.

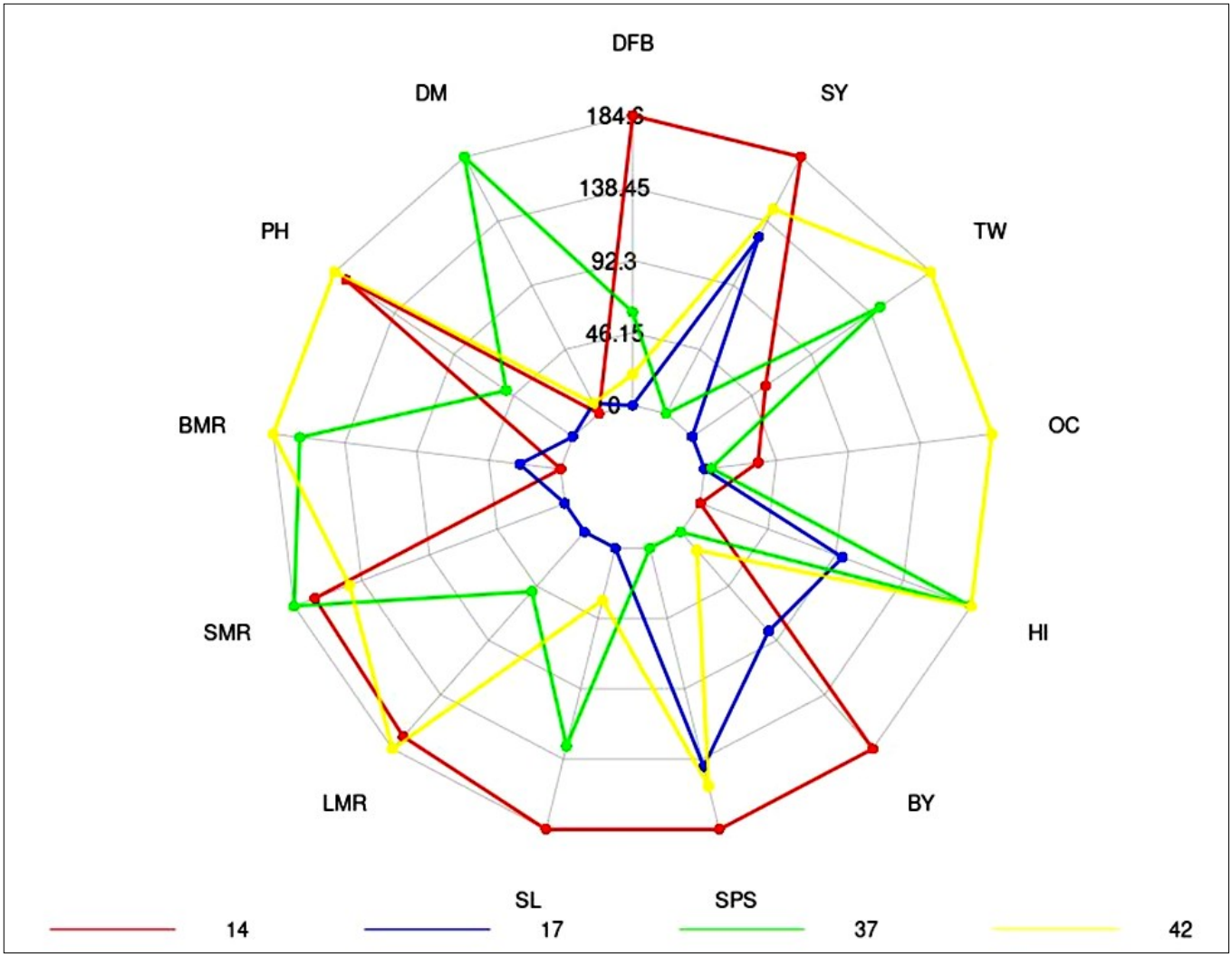

Fig. 5. Radar plot revealing the performance of four genotype 14 (RH-725 × Pusa Agrani), 17 (RH-725 × Kranti), 37 (Pusa Bold × CS-60) and 42 (Pusa Agrani × CS-60) across the traits.

Indian mustard, whereas PCA and radar chart analysis revealed the crosses desirable for the seed yield, viz., RH-725 × Pusa Agrani, RH-725 × Kranti and Pusa Bold × CS-60, can be used in the development of high-yielding varieties.

Acknowledgements

Raj Kumar is thankful to the University Grants Commission for granting the Junior Research Fellowship (Joint CSIR-UGC Fellowship 2023).

Authors' contributions

RK, VK, A and SS carried out conceptualization, data curation, formal analysis, writing original draft, review and editing. MK and LKG carried out investigation, methodology, resources, supervision and validation. NKC, SK and ANY carried out software use, supervision, validation, visualization. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used QuillBot in order to grammar correction. After using QuillBot, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

References

1. Lin LZ, Sun J, Chen P, Harnly J. UHPLC-PDA-ESI/HRMS/MSn analysis of anthocyanins, flavonol glycosides and hydroxycinnamic acid derivatives in red mustard greens (*Brassica juncea* Coss variety). J Agric Food Chem. 2011;59(22):12059-72. https://doi.org/10.1021/jf202 556p
2. Choudhury S, Asrani P, Kashyap A, Rao M, Prasad K, Pant U. Whole genome resequencing of advanced introgression lines of *Brassica juncea* L. Czern. for characterizing alien introgression from *Diplotaxis erucoides* L. DC. Indian J Genet Plant Breed. 2023;83:217-23. https://doi.org10.31742/ISGPB.83.2.7
3. Mei J, Liu J, Yue F, Chen Y, Ming J, Xiong Z, et al. Broadening the genetic base of *Brassica juncea* by introducing genomic components from *B. rapa* and *B. nigra* via digenomic allohexaploid bridging. Crop J. 2022;10(3):672-79. https://doi.org/10.1016/j.cj.2021.09.008
4. Mohd Saad, NS, Severn-Ellis AA, Pradhan A, Edwards D, Batley J. Genomics armed with diversity leads the way in *Brassica* improvement in a changing global environment. Front Genet. 2021;12:600789. https://doi.org/10.3389/fgene.2021.600789
5. Redden R, Vardy M, Edwards D, Raman H, Batley J. Genetic and morphological diversity in the *Brassicas* and wild relative. In: 16th Australian research assembly on Brassicas, Ballarat, Victoria. 2009. p. 1-5.
6. Yu JC, Jiang ZT, Li R, Chan SM. Chemical composition of the essential oils of *Brassica juncea* (L.) Coss. grown in different regions, Hebei, Shaanxi and Shandong of China. J Food Drug Ana. 2003;11 (1):22-26. https://doi.org/10.38212/2224-6614.2729
7. Campbell B, Han DY, Triggs CM. Brassicaceae, nutrient analysis and investigation of tolerability in people with Crohn's disease in a New Zealand study. J Funct Foods Health Dis. 2012;2(11):460-86. https://doi.org/10.31989/ffhd.v2i11.70
8. Jaiswal SK, Prakash R, Acharya R, Reddy AVR, Prakasha NT. Selenium content in seed, oil and oil cake of Se hyper accumulated *Brassica juncea* (Indian mustard) cultivated in a seleniferous region of India. Food Chem. 2012;134(1):401-404. https://doi.org/10. 1016/j. foodchem. 2012.02. 140
9. Tian, Deng F. Phytochemistry and biological activity of mustard (*Brassica juncea*): A review, CyTA. J Food. 2020;18(1):704-18. https://doi.org/10.1080/19476337.2020.1833988
10. Jinks JL, Jones RM. Estimation of the components of heterosis. Genetics. 1958;43:223-34.
11. Shull GH. Beginnings of the heterosis concept. Heterosis.1952;23:31 -33.
12. Kumar A, Singh M, Sharma R. Multivariate analysis of genetic diversity in Indian mustard (*Brassica juncea* L.) based on agro-morphological traits. J Oilseed Brassica. 2021;12(1):34-40. https://doi.org/10.1007/978-3-030-34694-2_11
13. Goyal V, Kumari A, Avtar R, Baliyan V, Mehrotra S. Orthosilicic acid and seaweed extract alleviate the deteriorative effects of high temperature stress in *Brassica juncea* (L.) Czern & Coss. Silicon. 2023;15(11):4909-19. https://doi.org/10.1007/s12633-023-02376-9
14. MOA, FW. State-wise varieties of rapeseed: Mustard crop notified under seed act from 2008-2019. Directorate of oilseeds development, Government of India. [cited 2025 May 21], Available from: https://oilseeds.dac.gov.in/Rapeseed.aspx
15. RMselect Farmer's Choice. [cited 2025 May 21], Available from: https://www.drmr.in/rmv/selectRMvariety.php
16. Burton GW. Quantitative inheritance in grasses. Proc 6th Int. Grasslar 1 Cong. 1952;1:227-83.
17. Falconer DS, Fctm. Introduction to quantitative genetics, England, UK: Longman Group Ltd, 1996.
18. Robinson HF. Quantitative genetics in relation to breeding of the centennial of Mendalism. Indian J Genet Plant Breed. 1966;26:171-87.
19. Allard RW. Principles of plant breeding. John Wiley and Sons Inc., New York. 1960.
20. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybeans and their implications in selection. Agronomy J. 1955;47(10):477-83. https://doi.org/10.2134/agronj1955.00021962004700100008x
21. Al-Jibouri H, Miller PA, Robinson HF. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. Agron J. 1958;50(10):633-36. https://doi.org/10.2134/agronj1958.00021962005000100020x
22. Dewey DI, Lu KH. A correlation and path-coefficient analysis of components of crested wheat grass seed production. Agron J. 1959;51:515-18.
23. Nakazawa M. Functions for medical statistics book with some demographic data. R package version 0.7.6. 2024.
24. Kumar A, Singh RS, Kumar M, Kumari J, Kishore C. Genetic variability, correlation and path analysis in Indian mustard under late sown condition. Annals Plant Soil Res. 2023;25(4):681-87. https://doi.org/10.47815/apsr.2023.10322
25. Singh S, Dwivedi AK, Ashutosh OM, Kumar K. Genotypic variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L. Czern & Coss) genotypes. J Pharmacog Phytochem. 2018;7(3):350-52.
26. Gupta A, Chauhan S, Tyagi SD, Singh S. Genetic variability, heritability, genetic advance and cluster analysis in Indian mustard (*Brassica juncea* L. Czern & Coss.) under timely and late sown conditions. Int J Plant Soil Sci. 2023;35(19):292-301. https://

doi.org/10.9734/IJPSS/2023/v35i193554

27. Mandal K, Ghosh A, Dasgupta T, Kundagrami S. Genetic variability and trait association in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. Agric Sci Digest. 2022;42(5):580-85.
28. Shrivastava A, Tripathi MK, Solanki RS, Tiwari S, Tripathi N, Singh J, et al. Genetic correlation and path coefficient analysis of yield attributing parameters in Indian mustard. Curr J Appl Sci Tech. 2023;42(7):42-58. https://doi.org/10.9734/IJECC/2023/v13i92298
29. Kumar R, Kaur S, Bala K, Kaur S, Sharma L. Assessment of genetic variability, correlation and path analysis for yield traits in F1 hybrids of Indian mustard (*Brassica juncea* L.). Agriways. 2019;7(1):1-7.
30. Rathore RK. Path coefficient analysis in mustard (*Brassica juncea* L.). Int J Phytology Res. 2023;3(3):01-03.
31. Sikarwar RS, Satankar N, Kushwah MK, Singh AK. Genetic variability, heritability and genetic advance studies in yellow sarson (*Brassica rapa* var. Yellow Sarson). Int J Agric Innov Res. 2017;5(5):831-33.
32. Devi SA, Barua PK, Phukan A. Assessment of genetic variability for seed yield and related traits in some mutant and non-mutant lines of Indian mustard (*Brassica juncea* L.). J Exp Agric Int. 2024;46(4):48-55.
33. Gadi J, Chakraborty R, Imam Z. To study the genetic variability, heritability and genetic advance for different quantitative characters in Indian mustard (*Brassica juncea* L. Czern & Coss). Int J Curr Microbiol Appl Sci. 2020;9(10):1557-63. https://doi.org/10.20546/ijcmas.2020.910.186
34. Priyamedha ZA, Kumar A, Ram B, Kumar A, Singh VV, Rai PK. Analysis of genetic parameters and correlation for yield and quality traits in Indian mustard (*Brassica juncea* L.). J Oilseed Brassica. 2018;9(2):146-50. http://srmr.org.in/ojs/index.php/job/article/view/310
35. Kumar A, Chauhan R, Singh KP. Genetic variability, heritability and genetic advance among Indian mustard (*Brassica juncea*) genotypes. Annals Plant Soil Res. 2020;22(1):92-95.
36. Sowmya D, Delvadiya IR, Ginoya AV. Genetic variability, correlation, path coefficient and cluster analysis in Indian mustard (*Brassica juncea* L.). Electron J Plant Breed. 2024;15(1):201-208. https://doi.org/10.37992/2024.1501.019
37. Awasthi D, Tiwari V, Kandalkar VS. Evaluation of heritability and genetic advance for morphological traits of Indian mustard germplasms. Curr J Appl Sci Tech. 2020;39(21):39-47. https://doi.org/10.9734/cjast/2020/v39i2130820
38. Yan W, Rajcan I. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci. 2002;42(1):11-20. https://doi.org/10.2135/cropsci2002.1100
39. Evangelin KM, Mawlong I, Kumar A, Yadav AP. Studies on inter-relationship and path coefficient analysis for seed yield/plant and qualitative traits in Indian mustard (*Brassica juncea* L. Czern and Coss). Int J Plant Soil Sci. 2022;34(24):869-74. https://doi.org/10.9734/ijpss/2022/v34i242712
40. Nandi S, Rout S, Sur B, Chakraborty M, Hijam L, Roy SK, Gupta A. Assessment of genetic parameters, trait association and diversity analysis in Indian mustard (*Brassica juncea* L. Czern. and Coss.). Biol Forum-An Int J. 2021;13(2):95-109.
41. Kaur RKR, Kaur L. Genetic variation for yield characters of F1 hybrids in Indian mustard (*Brassica juncea* L.). J Oilseed Brassica. 2019;10 (2):117-21. https://epubs.icar.org.in/index.php/JOB/article/view/158558
42. Dawar S, Kumar N, Mishra SP. Genetic variability, correlation and path coefficient analysis in the Indian mustard (*Brassica juncea* L. Czern. and Coss.) varieties grown in Chitrakoot, India. Int J Curr Microbiol Appl Sci. 2018;7(03):883-90. https://doi.org/10.20546/ijcmas.2018.703.103
43. Devi B. Correlation and path analysis in Indian mustard (*Brassica juncea* L.) in agro-climatic condition of Jhansi (UP). J Pharmacog Phytochem. 2018;7(1):1678-81.
44. Rout S, Kerkhi SA, Chauhan C. Character association and path analysis among yield components in Indian mustard (*Brassica juncea* L. Czern. and Coss.). Int J Curr Microbiol Appl Sci. 2017;7 (1):50-55. https://doi.org/10.20546/ijcmas.2018.701.007
45. Dwivedi S, Singh M, Yadav RK, Saini PK, Tripathi H. Correlation and path analysis for seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern and Coss.). Int J Environ Clim Change. 2023;13(11):1044-54. https://doi.org/10.9734/ijecc/2023/v13i113253
46. Adhikari A, Punetha H, Pant U. Genetic diversity analysis using agro-morphological traits of *Brassica juncea* subspecies *rugosa* (Pahari rai) from North-Eastern Himalayan region. Electron J Plant Breed. 2022;13(3):790-99.
47. Ghosh S, Avinashe H, Dubey N, Sharadhi GP, Danalakoti K, Sachan S, et al. PCA-based multivariate approach for segmentation of variance in Indian mustard [*Brassica juncea* (L) Czern & Coss]. SABRAO J Breed Genet. 2023;55(6):1963-71. https://doi.org/10.54910/sabrao2023.55.6.10
48. Neeru N, Thakral NK, Avtar R, Singh A. Evaluation and classification of Indian mustard (*Brassica juncea* L.) genotypes using principal component analysis. J Oil Seed Brassica. 2015;6(1):167-74.
49. Zhu R, Sun K, Yan Z, Yan X, Yu J, Shi J, et al. Analysing the phenotype development of soybean plants using low-cost 3D reconstruction. Sci Rep. 2020;10(1):7055. https://doi.org/10.1038/s41598-020-63720-2

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.