

Multivariate Cluster and PCA Biplot Analysis of Yield and Oil Quality Traits in *Brassica juncea*

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Abstract

Indian mustard (*Brassica juncea*) is a major oilseed crop in India, contributing significantly to edible oil production and nutritional security. Despite its importance, productivity remains below the global average, necessitating genetic improvement for both yield and oil quality traits. In this study, 25 genotypes of *B. juncea* were evaluated during Rabi 2025 for seven quantitative traits, including plant height (PH), number of siliquae per plant (NSPP), seeds per silique (SPS), biological yield per plant (BYPP), harvest index (HI), seed yield per plant (SYPP), and erucic acid (EA). Erucic acid content was estimated using GC-FID, while multivariate statistical approaches such as cluster analysis and principal component analysis (PCA) were employed to assess genetic divergence and trait associations. Cluster analysis revealed three distinct groups, with Cluster III showing the highest NSPP (185.70) and SYPP (22.87), along with the lowest EA (27.18), making it the most promising for simultaneous yield and oil quality improvement. Cluster I exhibited the highest HI (39.88) but elevated EA (50.16), suggesting its utility as a donor for partitioning efficiency. PCA indicated that the first three components explained 75.25% of the total variation, with PC1 dominated by PH, NSPP, and SYPP, while PC2 highlighted HI and SPS. Erucic acid loaded strongly on PC4, confirming its independence from yield-related traits. The PCA biplot further demonstrated clear differentiation among genotypes, with yield traits clustering together and EA positioned separately. Overall, the combined application of cluster analysis and PCA provided robust insights into trait architecture, confirming that yield efficiency can be enhanced through silique traits and harvest index, while oil quality improvement via reduced erucic acid can be achieved independently. These findings offer valuable guidance for breeding strategies aimed at developing high-yielding, low-erucic mustard varieties suitable for diverse agro-ecological zones.

1. Introduction

The genus *Brassica* encompasses a diverse group of economically important oilseed crops, including *Brassica juncea*, *Brassica napus*, and *Brassica rapa*, which together contribute substantially to global vegetable oil production. These crops play a critical role in ensuring food and nutritional security, as well as supporting industrial sectors through the supply of renewable raw materials. In India, *B. juncea* constitutes the principal oilseed *Brassica* species, occupying a dominant share of the rapeseed–mustard production system due to

its wide adaptability, resilience under marginal conditions, and suitability for diverse agro-ecological zones (Shekhawat *et al.*, 2012; Yadava *et al.*, 2022). Despite its importance, the productivity of Indian mustard remains below the global average, underscoring the need for sustained genetic improvement focusing on both yield and quality traits.

Oil quality in *Brassica* is largely governed by fatty acid composition, among which erucic acid (EA; cis-13-docosenoic

acid, 22:1) is of primary significance. From a nutritional standpoint, elevated levels of EA are considered undesirable due to associated health concerns, leading to internationally accepted standards that define low-erucic (canola-quality) oils as containing less than 2% EA, whereas high-erucic types typically exceed 35–40% of total fatty acids (Codex Alimentarius Commission, 2019; Rakow & Raney, 2003). Traditional germplasm of *B. juncea* and related species often exhibits high EA content in the range of 30–50%. However, systematic breeding efforts have led to the development of low-erucic genotypes through the introgression and selection of alleles governing fatty acid elongation. Improved Indian mustard varieties such as Pusa Mustard 30, Pusa Mustard 27, and NRCDR 2 represent significant progress toward enhancing oil quality. Conversely, high-erucic germplasm, including *Brassica carinata* and selected breeding lines, continues to be of industrial relevance due to its suitability for the production of lubricants, polymers, and specialty chemicals (Kumar *et al.*, 2023; Taylor *et al.*, 2010).

Reliable estimation of erucic acid content is essential for both breeding and quality assurance. Gas chromatography (GC) of fatty acid methyl esters remains the standard analytical method due to its high accuracy and reproducibility. In parallel, rapid and non-destructive techniques such as near-infrared spectroscopy (NIRS) have gained prominence for large-scale screening, particularly in early-generation selection. Recent advancements in spectroscopic and chemometric approaches, including hyperspectral imaging and direct analytical techniques, have further improved the efficiency and

throughput of fatty acid profiling in *Brassica* seeds (Hamad & Chakraborty, 2024; Velasco & Becker, 1998).

Given the polygenic nature of yield and its interaction with quality traits such as erucic acid content, the evaluation of genetic variability requires robust multivariate statistical approaches. Principal component analysis (PCA) is widely employed to reduce dimensionality and identify the principal sources of variation within a dataset by transforming correlated variables into orthogonal components. To enhance biological interpretability, rotated component matrices commonly obtained through varimax rotation are used to maximize the contribution of individual variables to specific components, thereby facilitating clearer trait associations. In addition, cluster analysis enables the classification of genotypes into distinct groups based on multivariate similarity, providing insights into genetic divergence and aiding in the selection of parents for hybridization programs. The combined application of these analytical tools allows for a comprehensive understanding of trait architecture and supports the identification of superior genotypes for targeted breeding objectives.

2. Material methods

The present study comprised of 25 genotypes of *Brassica juncea* (Table 1). The experiment was conducted during *Rabi* 2025 in Randomized Block Design with three replications at the Research Farm of the Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology,

Kumarganj, Ayodhya (Uttar Pradesh), India.

2.1 Morphological traits phenotyping

The morphological traits of *Brassica juncea* genotypes, observations on yield and yield related traits were recorded from five randomly selected plant per genotypes including plant height (PH), number of siliquae per plant (NSPP), seeds per siliqua (SPS), biological yield per plant (BYPP), harvest index (HI), erucic acid (EA), and seed yield per plant (SYPP).

2.2 Erucic acid estimation by GC-FID

Erucic acid estimation of seed samples was determined by GC-FID following acid-catalyzed transmethylation.

2.3 Statistical analysis

Qualitative and quantitative data analysed using R software (v4.5.2).

Intact seeds (~50 mg) were treated with methanolic sulphuric acid (1.5% v/v) at 80 °C for 1 h to generate fatty acid methyl esters (FAMES), which were extracted with n-hexane and used for analysis.

FAMES were analyzed using an Agilent 8890 GC equipped with a flame ionization detector and a DB-FATWAX UI column under standard temperature and gas flow conditions. Fatty acids were identified by comparing retention times with known FAME standards.

Quantification was performed by peak area normalization, and results were expressed as relative percentage of total fatty acids, enabling precise lipid profiling of mustard seed samples.

Table 1 Details of *Brassica juncea* varieties, including pedigree, specific attributes, suitable areas of cultivation and source.

Name of varieties	Pedigree	Specific attributes	Suitable area of cultivation	Source
Pusa Mustard-22 (PM-22)	Pusa Barrani x ZEM 2	Low erucic acid	Zone II (Delhi, Haryana, Jammu & Kashmir, Panjab, Parts of Rajasthan)	ICAR-IARI, New Delhi
Pusa Mustard-31	PDZ-1 x PDZ-2	Double zero	Zone II (Punjab, Haryana, Delhi, Jammu, Northern Rajasthan) under timely sown irrigated conditions	ICAR-IARI, New Delhi
Pusa Mustard-28 (PM-28)	SEJ-2 x LES-39	Early maturing, Moderate resistance to Alternaria blight and white rust	Delhi, Haryana, Punjab, Rajasthan, and Western Uttar Pradesh.	ICAR-IARI, New Delhi
Pusa Mustard-30 (PM-30)	SEJ-2 x LES-1-27	LEA, Moderate resistance to Alternaria blight and white rust	North Indian	ICAR-IARI, New Delhi
Maya	Varuna x KRV 11	Resistant to white rust	Uttar Pradesh, Madhya Pradesh, South Rajasthan and parts of Bihar	CSAUA&T, Kanpur
Pusa Bold	Varuna x BIC 1780	Suitable for rainfed areas, early as well as late sown, bold seeded	Delhi, Uttar Pradesh and Eastern India	ICAR-IARI, New Delhi
RGN-229	Varuna x RGN-73	Heat stress tolerance, Late sowing in arid zone	Rajasthan	SKRAU, Bikaner, Rajasthan
Giriraj	HB-9908 x Hb-9916	Tolerant to Alternaria blight and powdery mildew	Rajasthan, Haryana	ICAR-DRMR, Bharatpur
PM-27	Selection form EJ-17	Moderately tolerant to Alternaria blight and powdery mildew	Delhi, Haryana, Punjab, Rajasthan, Western Uttar Pradesh	ICAR-IARI, New Delhi

Shivani	Selection from local germplasm	Short-duration, rainfed variety	Jharkhand, Bihar, Eastern Uttar Pradesh, parts of West Bengal	BAU, Ranchi, Jharkhand
RH-749	Varuna x Rohini	High yield stability across environments	Haryana, Punjab, Delhi, Western Uttar Pradesh, Rajasthan	CCSHAU, Hisar, Haryana
NDR-2005-1	Selection from local germplasm	Alternaria blight and white rust	Uttar Pradesh (eastern districts), Bihar, Jharkhand	ANDUAT, Ayodhya
NDR-8501	Selection line	Highly salt tolerance	Uttar Pradesh (eastern districts), Bihar, Jharkhand	ANDUAT, Ayodhya
CS-60	Varuna x CS-52	Highly salt tolerance	Haryana, Punjab, Uttar Pradesh, Rajasthan	ICAR-CSSRI, Karnal
Varuna	T-59 x indigenous line	Widely adapted across India	Haryana, Punjab, Delhi, Rajasthan, Uttar Pradesh, Bihar, Jharkhand	ICAR-IARI, New Delhi
Heera	Eastern European line	Low erucic acid	-	East Europe
RLC-3	Selection line	Low erucic acid, Resistant to powdery mildew	Punjab, Haryana, Delhi, Western Uttar Pradesh, parts of Rajasthan	PAU, Ludhiana
Pant Toria -3 (PT-3)	Selection line from local toria germplasm	Resistant to powdery mildew	Uttar Pradesh, Bihar, Uttarakhand, Jharkhand	GBPUAT, Pantnagar
Bioseed Y43	-	irrigated farming systems	Uttar Pradesh, Bihar, Uttarakhand, Jharkhand	Bioseed, RSM, Bihar
Donskaza	Exotic introduction	Low erucic acid	-	Russia
Jawahar Mustard-3	Varuna x YRT 3	Tolerant to Alternaria blight	Madhya Pradesh	JNKVV, Jabalpur
Gujrat Mustard-2	Varuna x Gujrat local	Alternaria blight and white rust	Gujarat, Rajasthan, Haryana (semi-arid irrigated areas)	SDAU, Gujrat
PBR-97	Varuna x PBR-91	Moderately resistant to Alternaria blight and powdery mildew	Punjab, Haryana, Delhi, Western Uttar Pradesh, parts of Rajasthan	PAU, Ludhiana
BR-40	T-59 x indigenous germplasm	Moderately resistant to Alternaria blight, white rust, and aphids	Bihar, Jharkhand, Eastern Uttar Pradesh	BAU, Ranchi, Jharkhand-
EC-399294	Exotic collection	White rust resistance	-	UK

3. Results and Discussion

Cluster analysis

Cluster analysis of 25 genotypes of *Brassica juncea* based on yield and quality traits revealed clear genetic divergence among the three clusters. The average intra-cluster distances were lowest in Cluster II (2.20) and Cluster III (2.45) (Table 1), indicating higher homogeneity and genetic similarity among genotypes within these groups. In contrast, Cluster I showed the highest intra-cluster distance (3.14), reflecting greater variability among its members. Inter-cluster distances were highest between Cluster I and Cluster II (3.39), followed by Cluster I and Cluster III

(3.22), suggesting that genotypes in Cluster I are genetically more distinct from those in Clusters II and III. The relatively lower inter-cluster distance between Cluster II and Cluster III (2.32) indicates closer genetic relationships among these groups. These results highlight that genotypes in Cluster I can serve as potential parents for hybridization with those in Cluster II or III to maximize heterosis and genetic gain. Similar findings have been reported in mustard breeding, where divergent clusters were exploited to enhance yield and oil quality traits (Kumar *et al.*, 2019; Singh *et*

al., 2021). Moreover, the presence of erucic acid variation across clusters supports earlier reports that oil quality improvement

can be achieved independently of yield components (Saklani *et al.*, 2023).

Table 2. Estimates of average intra and inter-cluster distance for 3 cluster in *Brassica juncea*.

Cluster	I	II	III
I	3.14	3.39	3.22
II		2.20	2.32
III			2.45

Hierarchical cluster analysis of 18 *Brassica juncea* genotypes based on yield and quality traits revealed clear genetic divergence (Figure 1). The dendrogram grouped the genotypes into distinct clusters, reflecting similarity patterns among them. Varieties such as 'Varuna', 'Pusa Bold', and 'Giriraj' clustered together, indicating close genetic relationships and similar trait performance. In contrast, genotypes like 'RLC-3' and 'EC-399294' formed separate branches at higher linkage distances, suggesting greater genetic diversity. The clustering pattern also highlighted that genotypes with high harvest index and biological yield tended to group together,

while those with elevated erucic acid content were placed in distinct clusters, confirming independence of oil quality traits from yield components. The presence of divergent clusters suggests that crossing genotypes from genetically distant groups (e.g., Cluster I vs. Cluster III) can maximize heterosis and genetic gain. These findings are consistent with earlier reports that cluster analysis is an effective tool for identifying diverse parents in mustard breeding (Kumar *et al.*, 2019; Singh *et al.*, 2021), while oil quality improvement through reduction of erucic acid can be achieved without compromising yield potential (Saklani *et al.*, 2023).

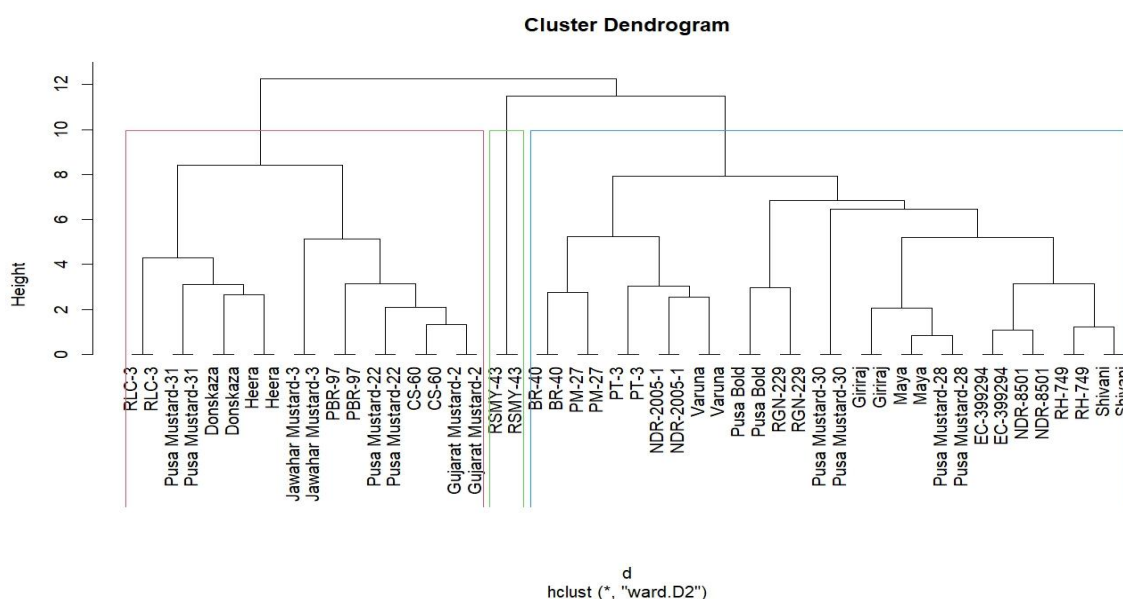


Figure 1. Dendrogram for yield and yield components of *Brassica juncea* genotypes.

Cluster mean values

Cluster mean analysis of yield and quality traits in *Brassica juncea* revealed distinct genetic groupings (Table 3). Cluster III recorded the highest mean values for number of siliquae per plant (NSPP, 185.70) and seed yield per plant (SYPP, 22.87), indicating its superiority for yield potential. Cluster I showed moderate NSPP (94.98) but the highest harvest index (HI, 39.88), suggesting efficient biomass partitioning and yield efficiency. Cluster II exhibited the highest biological yield per plant (BYPP, 63.52) but comparatively lower HI (31.10), reflecting that higher biomass does not necessarily translate into higher seed yield. Quality trait analysis revealed that erucic acid (EA) content was

maximum in Cluster I (50.16), moderate in Cluster II (43.43), and lowest in Cluster III (27.18), highlighting Cluster III as the most promising group for oil quality improvement. These results suggest that genotypes from Cluster III can be prioritized for simultaneous improvement of yield and oil quality, while Cluster I genotypes may serve as donors for high harvest index. The divergence among clusters supports earlier findings that siliqua traits and harvest index are key drivers of yield efficiency (Kumar et al., 2019; Singh et al., 2021), while erucic acid reduction can be achieved independently without major yield penalty (Saklani et al., 2023).

Table 3. Cluster mean values of seven traits including yield, yield related traits and quality traits in *Brassica juncea* genotypes.

Cluster	NSPP	SPS	BYPP	HI	EA	SYPP
I	94.98	22.07	54.48	39.88	50.16	21.75
II	124.22	13.38	63.52	31.10	43.43	19.76
III	185.70	13.75	63.33	36.11	27.18	22.87

Principal Component Analysis

Principal component analysis (PCA) of seven quantitative traits in *Brassica juncea* revealed that the first three components accounted for 75.25% of the total variation (Table 4). PC1 explained the maximum variance (31.23%), with high positive loadings for plant height (PH, 0.551), number of siliquae per plant (NSPP, 0.499), and seed yield per plant (SYPP, 0.383), indicating that these traits are the primary contributors to overall genetic variability. PC2 contributed 26.34% of the variance, with strong positive associations for harvest index (HI, 0.664), seeds per siliqua (SPS, 0.454), and SYPP (0.479), highlighting the role of reproductive

efficiency and biomass partitioning in yield determination. PC3 explained 17.69% of the variance, dominated by negative loadings of biological yield per plant (BYPP, -0.808) and SYPP (-0.433), suggesting that excessive biomass may not always translate into higher seed yield. Interestingly, erucic acid (EA) showed a strong positive loading in PC4 (0.902), which accounted for 11.96% of the variance, confirming that oil quality variation is largely independent of yield-related traits. These results emphasize that yield improvement in mustard can be achieved through selection for NSPP, SPS, HI, and SYPP, while oil quality

improvement (low erucic acid) can be targeted separately without compromising yield. Similar findings have been reported

in earlier studies on mustard variability and trait associations (Kumar et al., 2019; Singh et al., 2021; Saklani et al., 2023).

Table 4. Principal component analysis for seven quantitative traits in *Brassica juncea* genotypes.

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigenvalue	2.186	1.844	1.238	0.837	0.574	0.318	0.002
Variance. Percent	31.226	26.340	17.687	11.963	8.207	4.549	0.028
Cumulative. Variance (%)	31.226	57.565	75.252	87.216	95.422	99.972	100.000
Eigen Vectors							
PH	0.551	-0.001	0.285	0.252	-0.164	0.723	-0.036
NSPP	0.499	-0.166	0.009	0.039	0.823	-0.211	0.012
SPS	-0.344	0.454	-0.174	-0.348	0.462	0.557	-0.009
BYPP	0.172	-0.249	-0.808	0.005	-0.104	0.138	-0.475
HI	0.235	0.664	0.170	-0.005	-0.077	-0.292	-0.620
EA	-0.311	0.184	-0.139	0.902	0.190	0.020	0.001
SYPP	0.383	0.479	-0.433	0.006	-0.174	-0.131	0.623

Biplot analysis

Principal component biplot analysis of *Brassica juncea* genotypes revealed clear differentiation among yield and quality traits (Figure 2). The first two principal components (Dim1 = 31.2%, Dim2 = 26.3%) together explained 57.6% of the total variation, providing a reliable visualization of trait associations. Traits such as plant height (PH), number of siliquae per plant (NSPP), and seed yield per plant (SYPP) showed strong positive loadings along Dim1, indicating their major contribution to yield variability. Harvest index (HI) and seeds per siliqua (SPS) were positively associated with Dim2, highlighting their role in reproductive efficiency and biomass partitioning. Erucic acid (EA) was oriented distinctly along

Dim2, away from yield-related traits, confirming that oil quality variation is largely independent of yield components. The distribution of genotypes across quadrants demonstrated that those with high NSPP and SYPP clustered together, while genotypes with elevated EA were separated, suggesting that simultaneous improvement of yield and oil quality is feasible through targeted selection. These findings corroborate earlier reports that siliqua traits and harvest index are key drivers of yield efficiency (Kumar et al., 2019; Singh et al., 2021), while erucic acid reduction can be achieved independently (Saklani et al., 2023).

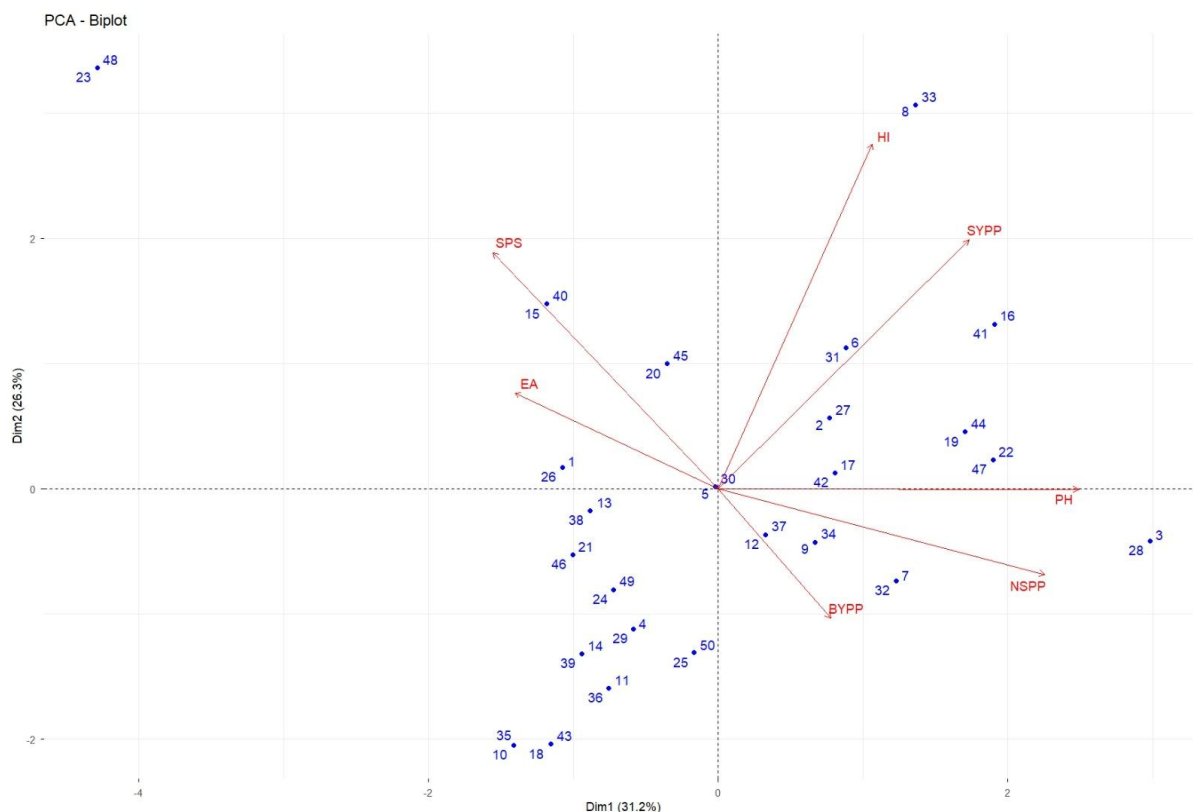


Figure 2. PCA biplot of seven characters of *Brassica juncea* using PC1 and PC2.

Cluster analysis using PCA dimensions

Cluster analysis using PCA dimensions (Dim1 = 30.7%, Dim2 = 28.6%) grouped *Brassica juncea* genotypes into three distinct clusters (Figure 3). Cluster I (blue) contained genotypes with moderate yield and higher erucic acid values, suggesting limited scope for oil quality improvement. Cluster II (yellow) grouped genotypes with relatively higher biological yield but moderate harvest index, indicating that biomass productivity does not always translate into seed yield efficiency. Cluster III (gray) included genotypes with superior number of siliquae per plant (NSPP) and seed yield per plant (SYPP), along with lower erucic acid

content, making this cluster the most promising for simultaneous yield and oil quality improvement. The clear separation among clusters highlights the genetic divergence present in the population, and crossing genotypes from Cluster III with those from Cluster I or II could maximize heterosis and broaden the genetic base. These findings align with earlier reports that cluster analysis is an effective tool for identifying diverse parents in mustard breeding (Kumar et al., 2019; Singh et al., 2021), while oil quality improvement through reduction of erucic acid can be achieved independently (Saklani et al., 2023).

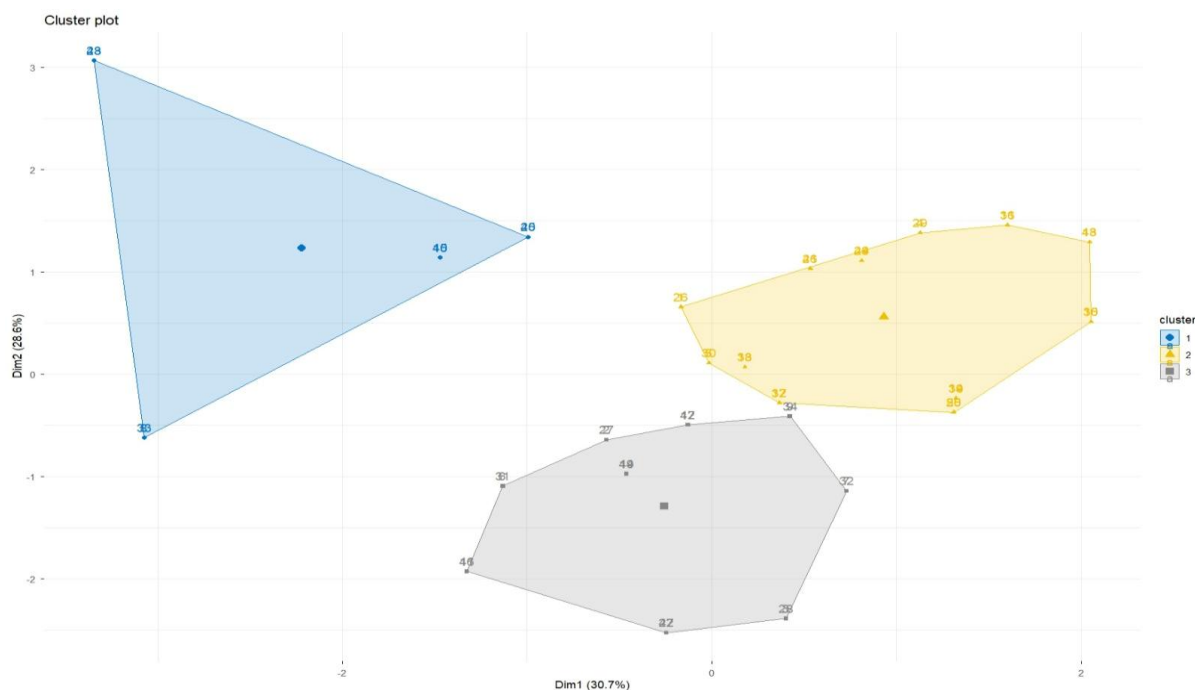


Figure 3 Cluster analysis including PCA of seven characters of *Brassica juncea* using the PC1 and PC2.

The scree plot revealed that the first four principal components together explained over 87% of the total variance (Figure 4). This indicates that most of the genetic variability in *Brassica juncea* can be effectively captured by these components, making them key for trait association studies.

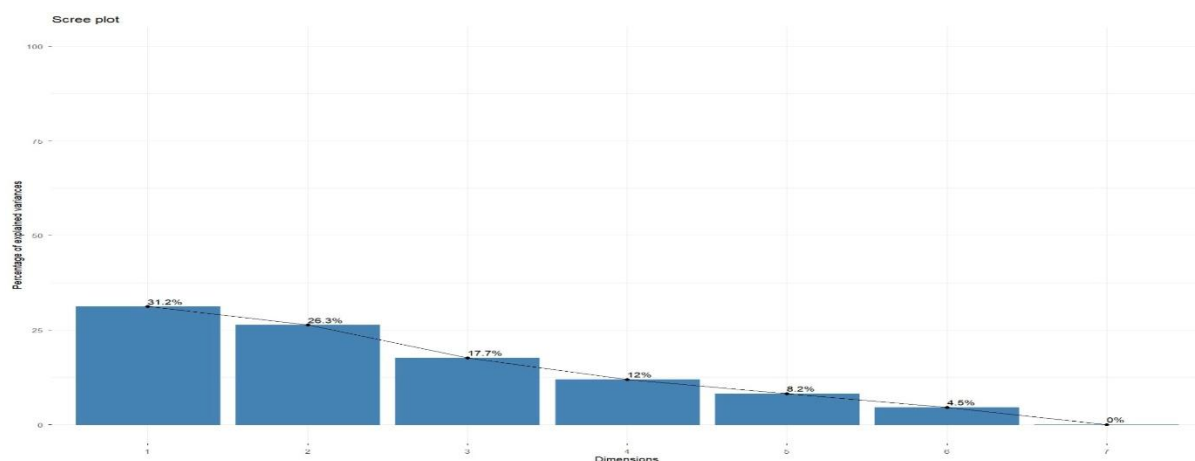


Figure 4. The scree plot shows the eigenvalues of different principal component (bar in finger) as shown by PCA of the *Brassica juncea* genotypes based on yield and yield related traits.

Conclusion:

The present study demonstrated that multivariate approaches such as cluster analysis and principal component analysis

provide robust insights into the genetic variability of *Brassica juncea*. Cluster analysis revealed clear divergence among

genotypes, with Cluster III emerging as the most promising group for simultaneous improvement of yield and oil quality traits due to its high siliqua number, superior seed yield, and low erucic acid content. PCA further confirmed that yield efficiency is primarily governed by siliqua traits, harvest index, and seed yield per plant, while erucic acid variation remains independent of yield components. The biplot analysis highlighted distinct trait associations and genotypic differentiation, supporting the feasibility of targeted selection strategies. Overall, the integration of cluster and PCA analyses underscores that genetic improvement in mustard can be achieved by combining high-yielding genotypes with low-erucic donors, thereby accelerating the development of nutritionally superior and agronomically efficient varieties suitable for diverse agro-ecological zones.

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Disclaimers

The authors present only their finding and erucic acid estimation affiliated organization, National Bureau of Plant Genetics and Resources, New Delhi. In the case of direct or indirect losses resulting from the use of this content, the authors accept responsibility for its accuracy and quality.

Informed consent

No animal used during the research.

Conflict of interest

Neither author has a conflict of interest. No funding or sponsorship was involved in the design or article preparation.

References

- Codex Alimentarius Commission. (2019). *Standard for named vegetable oils (CXS 210-1999)*. FAO/WHO.
- Hamad, R., & Chakraborty, S. K. (2024). A chemometric approach to assess oil composition in *Brassica juncea* using hyperspectral imaging. *Scientific Reports*, 14, 15643.
- Kumar, A., Yadava, D. K., Singh, R., & Kumar, N. (2023). Advances in breeding of Indian mustard (*Brassica juncea*) for yield and quality traits. *Journal of Oilseed Brassica*, 14(1), 1–15.
- Kumar, S., Pal, S., Dubey, N., Avinash, H., Khan, S., & Reddy, J. P. (2019). Estimation of genetic variability, correlation and path analysis for yield and yield contributing characters in Indian mustard (*Brassica juncea* L.). *Journal of Pharmacognosy and Phytochemistry*, Special Issue 1, 102–105.
- Kumar, S., Pal, S., Dubey, N., Avinash, H., Khan, S., & Reddy, J. P. (2019). Estimation of genetic variability, correlation and path analysis for yield and yield contributing characters in Indian mustard (*Brassica juncea* L.). *Journal of Pharmacognosy and Phytochemistry*, Special Issue 1, 102–105.
- Rakow, G., & Raney, J. P. (2003). Present status and future perspectives of breeding for seed quality in Brassica oilseed crops. *Plant Breeding*, 122(3), 183–190.

Saklani, S., Grover, K., Choudhary, M., Sandhu, S. K., & Javed, M. (2023). Fatty acid composition and oxidative potential of food products prepared using low erucic *Brassica* oils. *Proceedings of the National Academy of Sciences, India Section B: Biological Sciences*, 93(1), 107–117.

Shekhawat, K., Rathore, S. S., Premi, O. P., Kandpal, B. K., & Chauhan, J. S. (2012). Agronomic management of Indian mustard (*Brassica juncea*). *International Journal of Agronomy*, 2012, 408284.

Singh, P., Yadav, R., Meena, H. S., & Chauhan, J. S. (2021). Association analysis for yield and quality traits in mustard (*Brassica juncea*). *Plant Archives*, 21(1), 112–118.

Taylor, D. C., Katavic, V., Zou, J., MacKenzie, S. L., & Keller, W. A. (2010). Field evaluation of transgenic *Brassica carinata* with altered seed oil composition. *Crop Science*, 50(2), 564–573.

Velasco, L., & Becker, H. C. (1998). Analysis of erucic acid using NIRS in *Brassica* seeds. *Plant Breeding*, 117(2), 97–102.

Yadava, D. K., Singh, N., & Kumar, R. (2022). Genetic enhancement of Indian mustard: Status and prospects. *Indian Journal of Agricultural Sciences*, 92(2), 123–131.