

GENETIC DIVERGENCE AND YIELD POTENTIAL OF MUSTARD (BRASSICA JUNCEA L.) GENOTYPES UNDER THE AGRO-CLIMATIC CONDITIONS OF SOUTH PUNJAB, PAKISTAN

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Abstract

Mustard (*Brassica juncea* L.) is an important oilseed crop; however, its productivity is constrained by limited genetic improvement and environmental stresses. The present study was conducted to evaluate the genetic variability, trait associations, and genetic divergence among twenty-five mustard genotypes under the agro-climatic conditions of South Punjab, Pakistan. Field experiment was carried out at the Regional Agriculture Research Institute (RARI), Bahawalpur using a randomized complete block design with three replications. Data were recorded for days to 50% flowering, days to maturity, plant height, leaf area, primary branches per plant, silique length, number of siliques per plant, number of seeds per silique, thousand-grain weight, and seed yield. Analysis of variance revealed highly significant differences among genotypes for most traits, indicating substantial genetic variability. Correlation analysis showed that seed yield was strongly and positively associated with the number of seeds per silique ($r=0.997^{**}$), thousand-grain weight ($r = 0.961^{**}$), number of siliques per plant ($r = 0.955^{**}$), and plant height ($r = 0.944^{**}$), suggesting these traits as reliable indirect selection criteria. Principal component analysis demonstrated that the first two principal components explained 79.35% of the total variation, with yield-related traits contributing most to genetic divergence. Cluster analysis grouped the genotypes into two distinct clusters, where Cluster-2 exhibited superior performance for plant height, siliques per plant, seeds per silique, thousand-grain weight, and seed yield. The study confirmed the existence of considerable genetic diversity among the evaluated germplasm and identified promising genotypes and key yield-contributing traits that can be effectively utilized in future mustard breeding programs aimed at improving productivity and adaptation.

Introduction

Mustard is often known as rai or raya. It belongs to the family Cruciferae, is a premier oil-seed crop, adds considerable value in global vegetable oil production, and has an impact on agricultural economics. Mustard is a natural amphidiploid with a chromosome number ($2n=36$) (Deewan et al. 2024). In Pakistan, Rapeseed and mustard contribute the second domestic source of edible oil after cottonseed (Saleem et al. 2017). As a primary source of dietary fats and an industrial raw material, the oil palm is crucial to meeting the rising demand for edible oil (Pua 2000). Mustard is cultivated as a rubi crop in Pakistan, particularly in the arid and semi-arid regions of Punjab and Sindh. Pakistan is facing urgent economic pressure, relying on imports to meet roughly 80% of domestic consumption, thereby draining substantial foreign exchange reserves annually (Khan et al. 2025). The crop is facing extreme environmental volatility, which critically limits plant growth, physiological functioning, and seed yield. The terminal heat stress exceeding 30°C during the critical flowering stage severely impacts pod formation and reduces seed filling capacity. (Sakpal et al. 2023) Moreover, changing monsoon patterns and prolonged droughts result in severe soil moisture deficits in huge farming zones (Deewan et al. 2024). To overcome these challenges, characterizing diverse germplasm lines under field screening is essential. Yield determination under stress is a complex phenomenon controlled by polygenic traits that interact with environmental conditions ($G \times E$ interactions). Evaluating genotypes under real-world environmental conditions ensures reliable and real-world agronomic results (Guguloth et al. n.d.; Kashyap et al. 2023). This research utilizes 23 distinct genotypes of mustard with a standard check to find out genetic diversity and determine how different genetic lines respond to different stresses under field conditions. Therefore, screening a wide range of genotypes through agromorphological traits helps in the selection of promising germplasm that can be used in future breeding programs (Gp et al. 2026).

Materials and Methods

Experimental locations

The study was conducted at Regional Agriculture Research Institute, Bahawalpur. The environmental and soil conditions (Soil analysis, Table 2) of the experimental site are suitable for the evaluation and cultivation of mustard crop.

Experimental material and design

There were 25 mustard genotypes evaluated in the experiment shown in Table 1. The experiment was laid out following a Randomized Complete Block Design (RCBD) with three replications at this location.

Crop husbandry

The crop was planted in rows with row-to-row spacing of 90 cm and plant-to-plant spacing of 45 cm. Each plot consisted of six rows with a plot length of 6 m. The net plot size was $6.0 \text{ m} \times 2.7 \text{ m}$. All recommended agronomic practices, including land preparation, fertilization, irrigation, and plant protection measures, were applied uniformly to all treatments throughout the cropping period.

Data collection

Data were recorded on important morphological, phenological, physiological, and yield-related traits, including days to 50% flowering, days to maturity, plant height, siliqua length, number of seeds per siliqua, number of siliqua per plant, primary branches per plant, thousand seed weight, leaf area, and yield (Ponniyath et al. 2026). Observations were recorded at appropriate growth stages. For each trait, ten plants were randomly selected and tagged from each plot, and mean values were computed for analysis.

Statistical analysis

Data collected from all three locations over two years were pooled and analyzed statistically. Analysis of variance was performed to determine the significance of differences among genotypes and environments. Mean comparisons and multivariate analyses were conducted where applicable to assess genotypic performance and trait associations. Statistix 8.1, XLSTAT, and R/RStudio software were used for statistical analysis, while Microsoft Excel was utilized for data compilation and graphical representation.

Table 1: *List of mustard genotypes evaluated in this study*

Sr No.	Name of the Genotypes	Sr No.	Name of the Genotypes
G1	Emp-1	G14	SI-12
G2	Emp-2	G15	Emp-12
G3	Amp-1	G16	Emp-14
G4	SI-21	G17	Emp-16
G5	Emp-3	G18	Emp-17
G6	SI-3	G19	Emp-18
G7	IUB-007	G20	SI-20
G8	Emp-5	G21	SI-21
G9	Emp-6	G22	Emp-23
G10	SI-7	G23	IUB-23
G11	HB-1	G24	SI-24
G12	HB-2	G25	IUB-25
G13	IUB-13		

Table 2: *Physiochemical properties of the soil at the experimental site.*

Sr. No.	Soil Property	Value/Reading
1	Soil Texture	Clay Loamy
2	pH	7.9
3	EC	4.9 dSms
4	Organic Matter	0.74
5	Available P	7.6 ppm
6	Available K	84 ppm
7	Zinc	1.36 ppm

Results and Discussion

ANOVA

The analysis of variance (ANOVA) was conducted to assess the extent of genetic variability among twenty-five mustard (*Brassica juncea* L.) genotypes for yield and associated agronomic traits. The ANOVA results revealed highly significant differences among genotypes for days to 50% flowering (340.11**), days to maturity (416.80**), number of seeds per siliqua (52.67**), number of siliqua per plant (5759.17**), plant height (1643.90**), siliqua length (0.98**), thousand-grain

weight (3.61**), and seed yield (323018**) (Table 3) (Yadav et al. 2025) (Katara et al. 2025). Leaf area (20.11*) exhibited significant variation at the 5% probability level, but primary branches per plant (11.95^{NS}) showed non-significant differences among genotypes (Tiwari et al. 2025). These findings indicate the presence of substantial genetic diversity for most of the studied traits and suggest considerable opportunities for selection and genetic improvement in mustard breeding programs.

Table 3: *Analysis of variance (ANOVA) revealed significant to highly significant genotypic differences for most agronomic and yield-related traits, indicating substantial genetic variability among the evaluated mustard genotypes.*

SOV	Replication	Genotype	Error
Df	2	24	48
Days to Flowering (DT)	3.77	340.11**	0.47
Days to Maturity (DTMA)	6.49	416.80**	0.54
Leaf Area (LA)	41.81	20.11*	10.81

Number of Seeds per Siliqua (NOSPS)	31.41	52.67**	3.25
Number of Siliquas per Plant (NSPP)	560.65	5759.17**	50.43
Primary Branches per Plant (PBPP)	3.89	11.95 ^{NS}	8.14
Plant Height (PH)	289.44	1643.90**	4.27
Siliqua Length (SL)	0.26	0.98**	0.14
Thousand-Grain Weight (TGW)	0.70	3.61**	0.05
Seed Yield per Plant	15122.00	323018.00**	1548.00

The highly significant genotypic effects observed for flowering and maturity traits demonstrate the existence of considerable variability in crop duration among the evaluated mustard genotypes, providing opportunities for selecting early- and late-maturing cultivars suitable for diverse agro-climatic conditions (Choudhary et al. 2025). Similarly, the significant variation detected for plant height, siliqua length, seeds per siliqua, and siliquas per plant indicates the availability of exploitable genetic diversity for important yield-contributing components.

The highly significant differences recorded for thousand-grain weight and seed yield suggest that the studied genotypes possess substantial variability for productivity-related traits. Since seed yield is a complex trait governed by several interacting components, the observed variability in siliqua number, seed number, and seed weight can be effectively utilized in breeding programs focused on

developing high-yielding mustard cultivars. The significant variation observed for leaf area further indicates differences in photosynthetic surface and growth potential among genotypes, which may indirectly influence biomass accumulation and final yield performance.

In contrast, primary branches per plant exhibited non-significant variation among genotypes, suggesting a relatively narrow genetic base for this trait within the evaluated germplasm (Kumar et al. 2025). Such traits may require the incorporation of diverse breeding materials or wider germplasm collections to broaden variability and enhance selection efficiency. Overall, the significant to highly significant variation observed for most agronomic and yield-related traits confirms that the evaluated mustard genotypes constitute a valuable genetic resource for future breeding efforts focused on improving seed yield, adaptability, and overall crop performance.

Descriptive Analysis

Table 4: Descriptive statistics indicating substantial phenotypic variability among twenty-five mustard genotypes for yield and associated agronomic traits.

Trait	Mean	Minimum	Maximum	Range
Days to 50% Flowering (DT)	96.87	80.00	114.33	34.33
Days to Maturity Attain (DTMA)	172.03	154.00	190.33	36.33
Leaf Area (LA)	15.85	12.00	22.33	10.33
Number of Seeds per Siliqua (NOSPS)	25.46	19.17	32.57	13.40
Number of Siliquas per Plant (NSPP)	354.41	300.67	443.67	143.00
Primary Branches per Plant (PBPP)	10.29	6.00	13.33	7.33
Plant Height (PH, cm)	166.92	126.00	204.33	78.33
Siliqua Length (SL, cm)	4.87	3.83	5.83	2.00
Thousand-Grain Weight (TGW, g)	7.90	6.07	9.70	3.63
Seed Yield (kg ha ⁻¹)*	1597.10	1172.30	2248.70	1076.40

The descriptive statistics revealed considerable variability among the evaluated mustard genotypes for all studied traits. Days to 50% flowering ranged from 80.00 to 114.33 days, while days to maturity varied from 154.00 to 190.33 days, indicating the presence of both early- and late-maturing genotypes. Plant height exhibited a wide range from 126.00 to 204.33 cm, reflecting substantial variation in vegetative growth (Reddy et al. 2025). Similarly, the number of siliques per plant ranged from 300.67 to 443.67, and seed yield varied from 1172.30 to 2248.70, suggesting significant differences in yield potential among genotypes (Table 4). The observed variability in yield contributing traits such as seeds per silique, silique length, and thousand-grain weight indicates the availability of valuable genetic resources for selection and improvement. The broad phenotypic variation observed among genotypes highlights their potential utility in mustard breeding programs aimed at developing high-yielding varieties.

Correlation Coefficient Analysis

The correlation coefficient analysis revealed the relationships among traits as, days to 50% flowering (DT 50% F), days to maturity (DTMA), plant height (PH), number of siliques per plant (NOSPS), silique length (SL), number of seeds per pod (NSPP), thousand-grain weight (TGW), seed yield (Yield), primary branches per plant (PBPP), and leaf area (LA) in the evaluated mustard genotypes. Seed yield exhibited strong and positive correlations with number of seeds per silique ($r = 0.997^{**}$), thousand-grain weight ($r = 0.961^{**}$), number of siliques per plant ($r = 0.955^{**}$), and plant height ($r = 0.944^{**}$) (Table 5) (Kaur et al. 2025). Positive associations were also observed between yield and days to 50% flowering ($r = 0.656$), days to maturity ($r = 0.527$), and silique length ($r = 0.524$). However, yield showed negative

correlations with primary branches per plant ($r = -0.561$) and leaf area ($r = -0.433$).

Similarly, plant height exhibited exceptionally strong positive correlations with thousand-grain weight ($r = 0.995$), number of siliques per plant ($r = 0.970$), and number of seeds per pod ($r = 0.934$). A very high positive association was also observed between the number of seeds per pod and thousand-grain weight ($r = 0.952$), while the number of siliques per plant was strongly correlated with thousand-grain weight ($r = 0.978$) and the number of seeds per pod ($r = 0.941$). In contrast, primary branches per plant and leaf area showed negative relationships with most of the agronomic and yield-related traits.

The correlation analysis demonstrated strong and meaningful associations among flowering, morphological, and yield-related traits in the evaluated mustard genotypes. Seed yield exhibited highly positive correlations with the number of seeds per pod, thousand-grain weight, number of siliques per plant, and plant height, indicating that these traits are the major contributors to enhanced seed productivity. The exceptionally high association between seed yield and number of seeds per pod suggests that seed set is the most influential determinant of yield under the prevailing agro-climatic conditions. Likewise, the strong positive relationships of yield with thousand-grain weight and number of siliques per plant indicate that improved seed size and greater reproductive capacity substantially enhance productivity. These findings are consistent with previous reports that siliques number, seed number, and seed weight are the principal yield-contributing traits in mustard and can be effectively utilized as indirect selection criteria in breeding programs (Singh et al. 2025) (Pradhan et al. 2021).

Table 5: Pearson's correlation coefficients among the studied quantitative traits.

Variables	DT 50% F	DTMA	PH	NOSPS	SL	NSPP	TGW	Yield	PBPP	LA
DT 50% F		0.802	0.777	0.785	0.605	0.642	0.767	0.656	-0.201	-0.353
DTMA			0.627	0.623	0.596	0.505	0.61	0.527	-0.107	-0.484
PH				0.97	0.545	0.934	0.995	0.944	-0.335	-0.395
NOSPS					0.588	0.941	0.978	0.955	-0.415	-0.455

SL	0.506	0.568	0.524	-0.253	-0.353
NSPP		0.952	0.997	-0.579	-0.423
TGW			0.961	-0.376	-0.404
Yield				-0.561	-0.433
PBPP					0.354
LA					

The strong positive correlations among plant height, thousand-grain weight, number of siliquae per plant, and number of seeds per pod further indicate that vigorous plant growth promotes reproductive development and ultimately increases seed yield. Positive associations of days to 50% flowering and days to maturity with most yield-contributing traits suggest that relatively longer-duration genotypes accumulated greater biomass and produced superior yield. In contrast, primary branches per plant and leaf area exhibited negative correlations with yield and several yield components, indicating that excessive vegetative growth may reduce assimilate partitioning toward reproductive structures. These findings suggest a possible trade-off between vegetative and reproductive growth, where greater allocation of assimilates to branches and leaf expansion may limit seed production. Overall, the correlation matrix highlights number of seeds per pod, thousand-grain weight, number of siliquae per plant, and plant height as the most reliable

selection criteria for improving seed yield in mustard breeding programs.

Principal Component Analysis

The principal component analysis (PCA) provided a comprehensive understanding of the phenotypic divergence among the mustard genotypes based on days to 50% flowering (DT 50% F), days to maturity (DTMA), plant height (PH), number of siliquae per plant (NOSPS), siliqua length (SL), number of seeds per pod (NSPP), thousand-grain weight (TGW), seed yield (Yield), primary branches per plant (PBPP), and leaf area (LA). The scree plot indicated that the first two principal components (PC1 and PC2) explained 79.35% of the total variability, with PC1 contributing 67.54% and PC2 contributing 11.81% of the total variation (Saroj et al. 2021a). The remaining principal components individually accounted for less than 10% of the total variation, indicating that the majority of phenotypic diversity among the evaluated mustard genotypes was effectively explained by the first two principal components (Table 6 and Table 1).

Table 6: Eigenvalues, percentage of variance, and cumulative variance explained by the principal component analysis (PCA).

	Eigenvalue	Variability (%)	Cumulative %
PC1	6.754	67.539	67.539
PC2	1.181	11.806	79.345
PC3	0.902	9.017	88.362
PC4	0.572	5.718	94.08
PC5	0.376	3.761	97.841
PC 6	0.162	1.616	99.457
PC 7	0.027	0.267	99.724
PC 8	0.024	0.235	99.96
PC 9	0.003	0.027	99.987
PC10	0.001	0.013	100

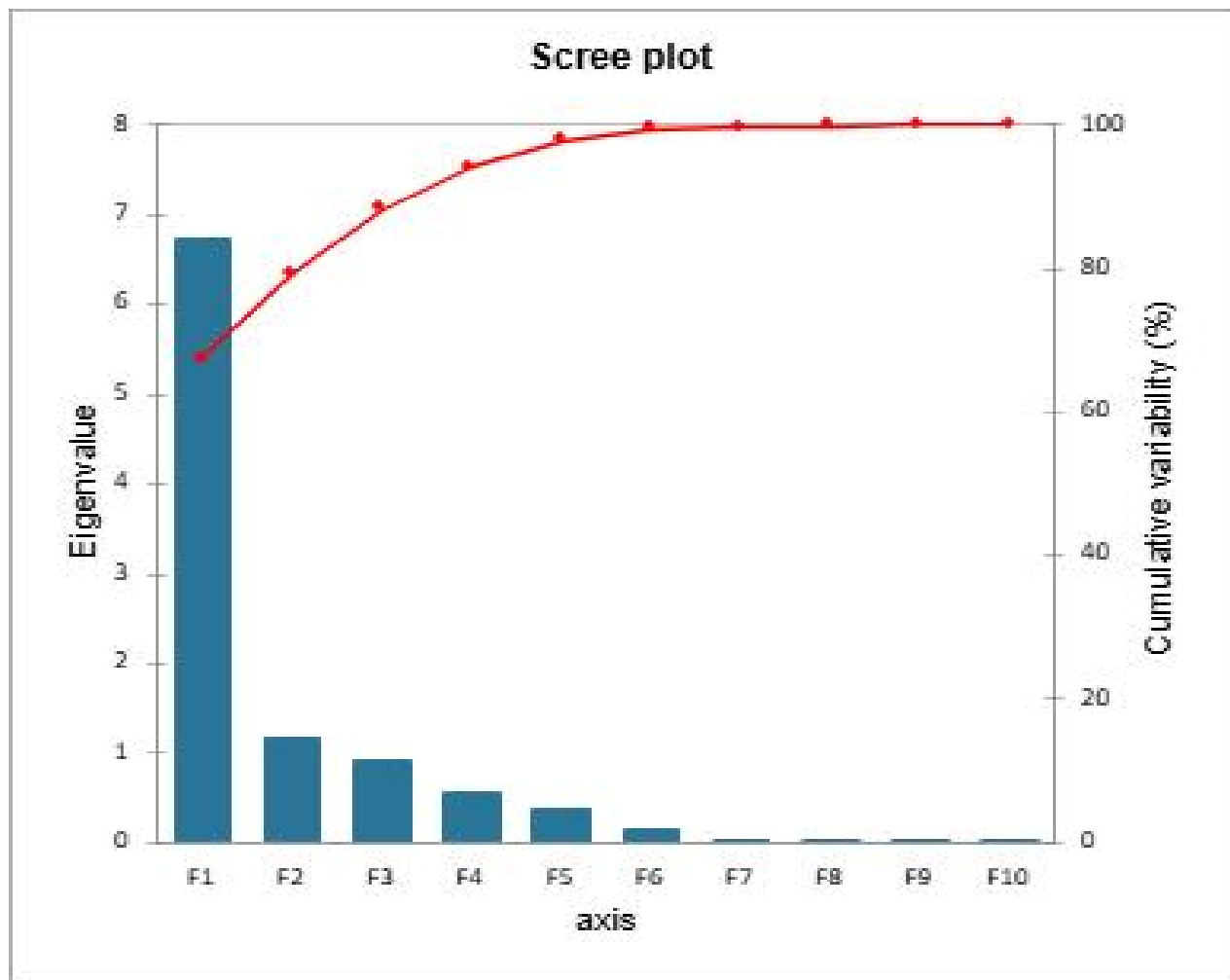


Figure 1. Scree Plot displaying the eigenvalues (blue bars) and cumulative variance percentage (red line) across the extracted principal components (PC1-PC10).

The variable correlation circle revealed that plant height (PH), number of siliquae per plant (NOSPS), number of seeds per pod (NSPP), thousand-grain weight (TGW), and seed yield were strongly associated with the positive direction of the first principal component (PC1), demonstrating their major contribution to overall genetic divergence (Figure 2) (Garg et al. 2026a). Likewise, days to

maturity (DTMA), days to 50% flowering (DT 50% F), and siliqua length (SL) also exhibited positive associations with PC1 and PC2, whereas primary branches per plant (PBPP) and leaf area (LA) were positioned on the opposite side of the correlation circle, indicating negative associations with the major yield-contributing traits.

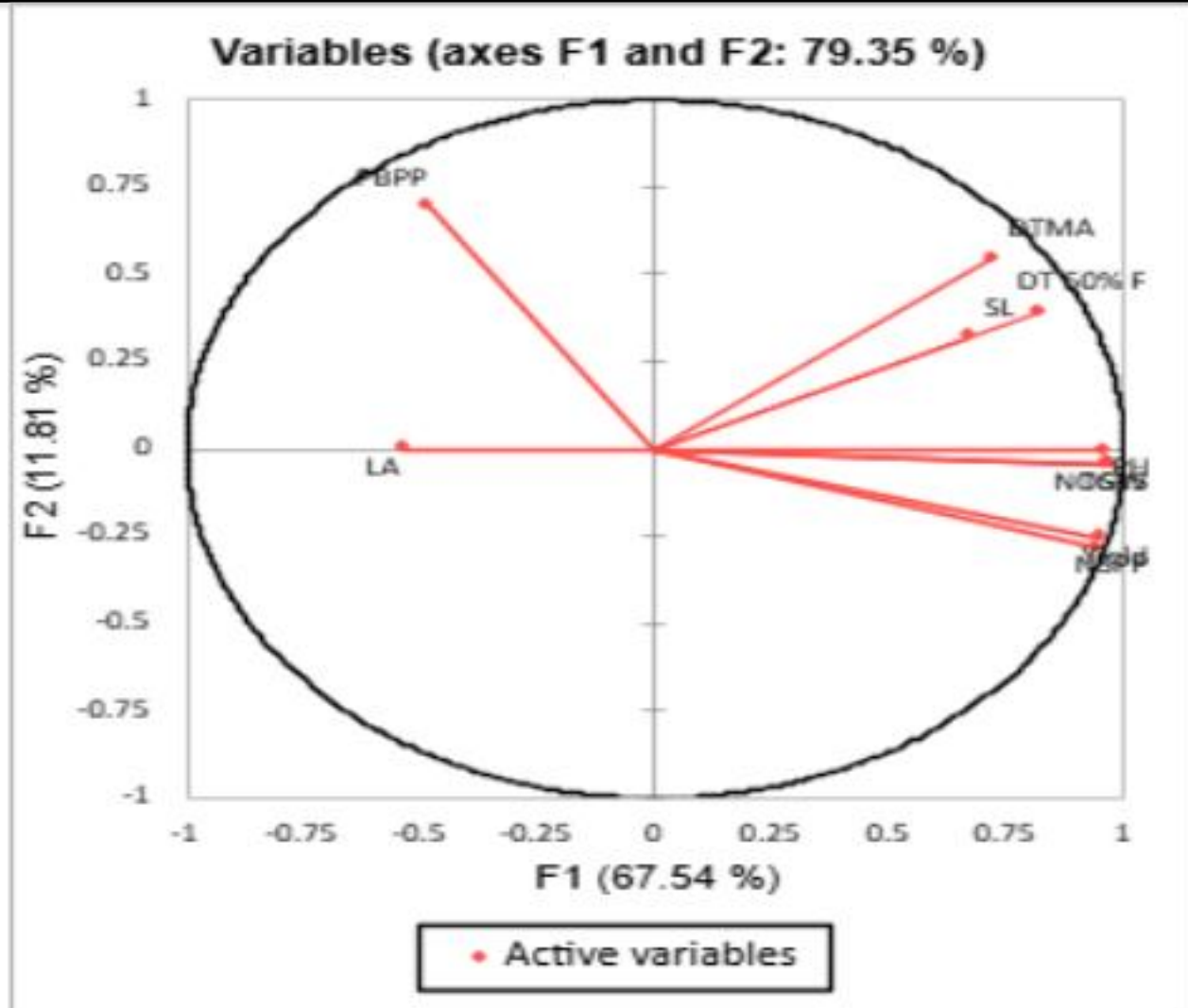


Figure 2. Correlation circle plot showing the relationship and total cumulative variance (79.35%)

Table 7: Contribution of the variables

Variable	PC1	PC2	PC3	PC4	PC5
DT 50% F	10.069	13.09	0.373	0.37	22.418
DTMA	7.679	25.112	4.756	0.168	19.491
PH	13.586	0.002	5.888	2.517	0.941
NOSPS	14.026	0.16	2.116	0.84	0.835
SL	6.654	8.633	4.585	54.658	25.196
NSPP	13.111	6.842	1.8	0.236	0.445
TGW	13.845	0.156	4.952	1.255	1.552
Yield	13.396	5.51	1.731	0.279	0.732

PBPP	3.425	40.495	13.387	15.679	20.945
LA	4.21	0	60.412	23.998	7.446

The PCA biplot effectively differentiated the mustard genotypes according to their agronomic performance and trait associations (Figure 3). Genotypes located along the positive side of PC1 were closely associated with higher seed yield, thousand-grain weight, number of siliquae per plant, and number of seeds per pod, indicating superior yield potential. Conversely, genotypes

positioned on the negative side of PC1 were associated with relatively lower performance for these traits (Md Mahmudul et al. 2023). The biplot further demonstrated considerable phenotypic diversity among the evaluated genotypes, providing an effective basis for identifying promising parental materials for future breeding programs.

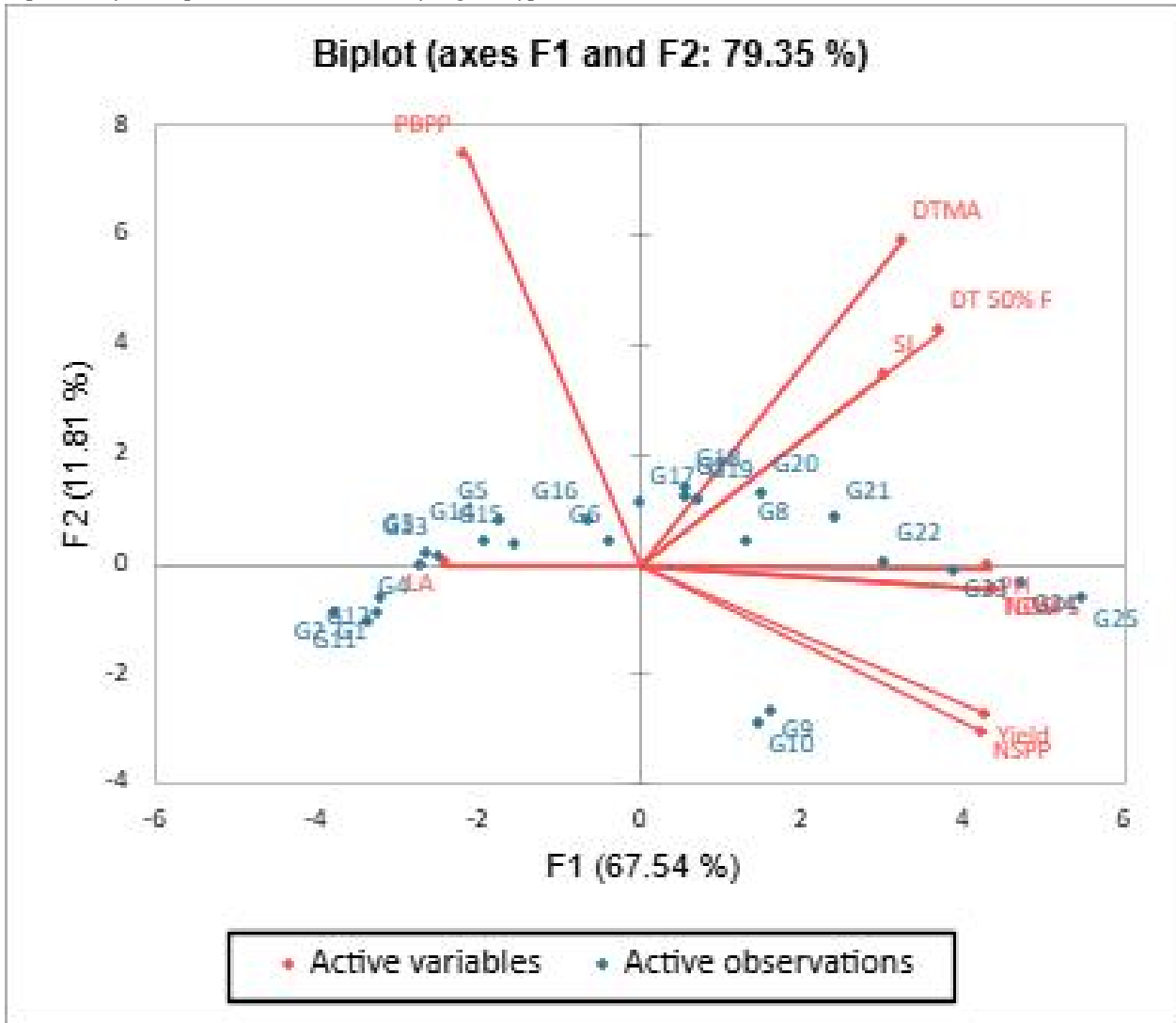


Figure 3. Principal component analysis (PCA) biplot demonstrating the distribution of active observations and variables across axes PC1 (67.54%) and PC2 (11.81%).

The PCA results demonstrated substantial phenotypic divergence among the mustard genotypes, confirming the presence of considerable

genetic variability for economically important traits. The first principal component primarily represented yield and its associated components,

indicating that seed yield, thousand-grain weight, number of siliquae per plant, and number of seeds per pod were the major contributors to overall variability. These findings suggest that selection based on these traits would be highly effective for improving seed yield in mustard. (Hariom Kumar Sharma and Bhagirath Ram 2021). The positive grouping of flowering and maturity traits with yield-related characters further indicates that relatively longer-duration genotypes accumulated greater biomass and reproductive capacity under the agro-climatic conditions of South Punjab. In contrast, the negative association of primary branches per plant and leaf area with the major yield components suggests that excessive vegetative growth may reduce assimilate partitioning toward reproductive development. Overall, principal component analysis successfully identified the key traits responsible for phenotypic divergence and facilitated the identification of superior genotypes for future breeding and varietal improvement programs (Saroj et al. 2021b).

Cluster Analysis

The cluster analysis classified the twenty-five mustard genotypes into two distinct clusters based on their performance for days to 50% flowering (DT 50% F), days to maturity (DTMA), plant height (PH), number of siliquae per plant (NOSPS), siliqua length (SL), number of seeds per pod

(NSPP), thousand-grain weight (TGW), and seed yield (Yield). The dendrogram generated using Euclidean distance and Ward's hierarchical clustering method clearly separated the genotypes into two major clusters (Figure 4). Cluster-1 consisted of 18 genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G11, G12, G13, G14, G15, G16, G17, G18, G19, and G20), whereas Cluster-2 comprised 7 genotypes (G9, G10, G21, G22, G23, G24, and G25) (Table 8) (Table 1) (Ankur Adhikari, Himanshu Punetha, and Usha Pant 2025a).

Cluster-2 exhibited superior mean performance for almost all agronomic and yield-related traits compared with Cluster-1. The genotypes in Cluster-2 recorded higher values for days to 50% flowering (104.000 days), days to maturity (177.714 days), plant height (193.714 cm), number of siliquae per plant (30.448), siliqua length (5.238 cm), number of seeds per pod (415.667), thousand-grain weight (9.219 g), and seed yield (2052.143 kg ha⁻¹) (Chauhan et al. 2023). In contrast, Cluster-1 showed comparatively lower mean values for days to 50% flowering (94.093 days), days to maturity (169.815 days), plant height (156.500 cm), number of siliquae per plant (23.513), siliqua length (4.733 cm), number of seeds per pod (330.593), thousand-grain weight (7.391 g), and seed yield (1420.204 kg ha⁻¹) (Table 9).

Table 8: Cluster classification of evaluated genotypes based on phenotypic similarity.

Cluster	No. of Genotypes	Genotypes under Respective Cluster
Cluster-1	18	Emp-1, Emp-2, Amp-1, SI-21, Emp-3, SI-3, IUB-007, Emp-5, HB-1, HB-2, IUB-13, SI-12, Emp-12, Emp-14, Emp-16, Emp-17, Emp-18, SI-20
Cluster-2	7	Emp-6, SI-7, SI-21, Emp-23, IUB-23, SI-24, IUB-25

Table 9: Cluster mean values of morphological and yield-related traits of the studied genotypes.

Cluster	DT 50% F	DTMA	PH	NOSPS	SL	NSPP	TGW	Yield
1	94.093	169.815	156.5	23.513	4.733	330.593	7.391	1420.204
2	104	177.714	193.714	30.448	5.238	415.667	9.219	2052.143

The cluster statistics further revealed that Cluster-1 contained the largest number of genotypes (18), whereas Cluster-2 contained seven superior-performing genotypes. The within-cluster variance was 28,464.41 for Cluster-1 and 18,125.34 for Cluster-2, indicating relatively greater variability among the genotypes grouped in Cluster-1. The dendrogram also demonstrated considerable

dissimilarity between the two clusters, confirming substantial phenotypic divergence among the evaluated mustard genotypes (Figure 4).

The cluster analysis confirmed the presence of considerable phenotypic diversity among the mustard genotypes evaluated under the agro-climatic conditions of South Punjab. The clear separation of genotypes into two distinct clusters

indicates substantial genetic divergence, suggesting that the evaluated germplasm possesses broad variability for important agronomic and yield-related traits. The superior performance of Cluster-2 for plant height, number of siliques per plant, number of seeds per pod, thousand-grain weight, and seed yield indicates that genotypes grouped in this cluster possess desirable genetic combinations for enhanced productivity. These findings suggest that the genotypes included in Cluster-2 represent valuable genetic resources for future varietal development and breeding programs (Chauhan et al. 2023).

The relatively higher within-cluster variability observed in Cluster-1 indicates the presence of greater phenotypic heterogeneity, providing

opportunities for selection within the cluster. Conversely, the compact nature of Cluster-2 reflects greater uniformity among the high-performing genotypes. The large inter-cluster distance observed in the dendrogram suggests that hybridization between genotypes belonging to different clusters may generate greater genetic recombination and transgressive segregants, thereby increasing the probability of developing superior mustard cultivars (Garg et al. 2026b). Similar observations have been reported in multivariate diversity studies of mustard, where cluster analysis effectively distinguished genetically diverse genotypes and facilitated the identification of promising parental lines for crop improvement (Kang et al. 2021).

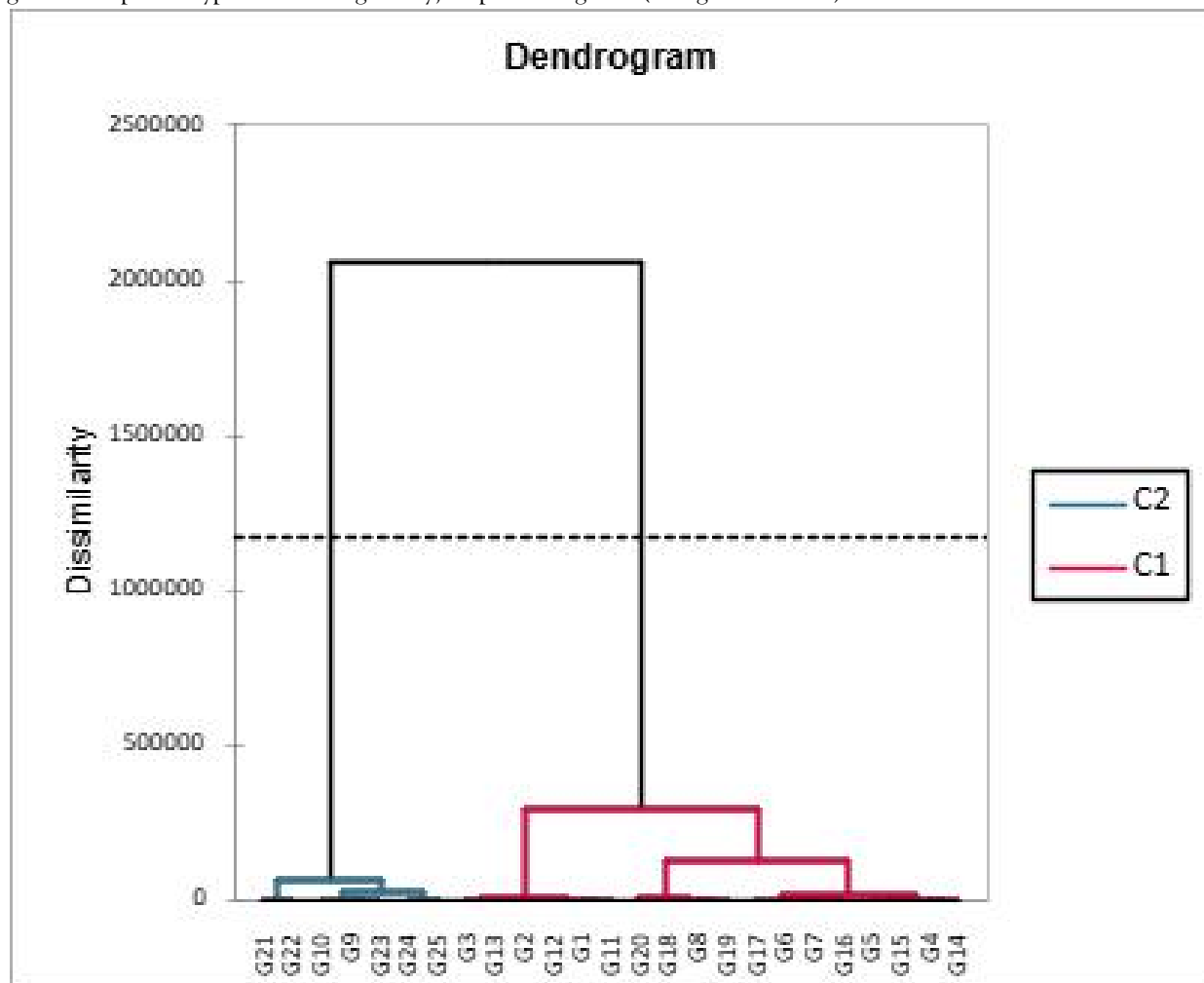


Figure 4. Dendrogram showing hierarchical cluster analysis of 25 groups (G1-G25). A vertical dashed threshold line separates the data into two distinct clusters. C1 (large, red) and C2 (small, blue).

Conclusion

The present study demonstrated substantial genetic variability among the twenty-five mustard genotypes, indicating the availability of valuable genetic resources for crop improvement. Significant differences observed for most agronomic and yield-related traits confirmed the effectiveness of selection for developing superior cultivars. Correlation analysis identified the number of seeds per silique, thousand-grain weight, number of siliques per plant, and plant height as the major determinants of seed yield, suggesting that these traits should receive priority in selection programs. Principal component analysis revealed that yield and its associated components accounted for the majority of phenotypic variation, while cluster analysis successfully differentiated the genotypes into distinct groups and identified Cluster-2 as the most promising group for high yield performance. The considerable inter-cluster divergence indicates that hybridization between genetically distant genotypes may enhance genetic recombination and facilitate the development of high-yielding mustard cultivars. Overall, the findings provide valuable information for parent selection, germplasm utilization, and future breeding strategies aimed at improving mustard productivity and adaptability under the agro-climatic conditions of Pakistan.

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Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have influenced the work reported in this study.

Author's Contribution

Atufa Batool and Muhammad Noman Manzoor conceived and designed the study. Muhammad Ajmal Iqbal, Muhammad Faizan, and Muhammad Hamza saeed, contributed to experimental data collection and analysis. Muhammad Abdullah, and

Qasim Ram contributed to data interpretation, manuscript review, and editing. All authors read and approved the final manuscript.

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