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RESEARCH ARTICLE

Exploring genetic diversity in quality protein maize and selection of genotypes by MGIDI index

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Abstract

Genetic diversity is a fundamental requirement for the development of high-yielding and resilient maize hybrids. In this context, the present study was undertaken to evaluate the genetic variability for 15 traits among 25 maize inbred lines during *Rabi* 2021 at the Maize Research Farm, TCA, Dholi, DR.P.C.A.U., Pusa, Samastipur, Bihar, with the objective of identifying genetically diverse and agronomically superior lines for future breeding programs**.** The principal component analysis (PCA) identified first six principle components with more than 1.0 eigenvector and cumulatively explained 85.06 % of the total variance. The Tocher's cluster analysis was worked out where the 25 inbred lines were grouped into seven different clusters. Cluster I had a maximum of five inbred lines, while cluster V, VI, VII had only one entry. Mahalanobis D^2 analysis was performed to know inter and intra cluster distances. Cluster IV displayed maximum intra cluster distance of 63.86 among the clusters. The inter-cluster D^2 values also ranged widely with a minimum value of 91.29 between clusters VI and VII to a maximum value of 285.05 between clusters 91.29 VI and V indicating high diversity among the genotypes of different clusters. It was suggested to intercross inbred lines from diverse cluster IV and V in order to develop superior hybrids with maximum heterosis. Among the fifteen traits studied, Harvest index contributed maximum of 12.9 % to the total divergence followed by followed by ear length (11.2 %), no. of kernels per row (10.5 %). Multi trait Genotype – Ideotype Distance Index (MGIDI) selection index results figured out that 15 traits were separated as 6 factors and superior genotypes G8, G9, G15, G24 were selected. The findings of this study provide valuable insights for maize breeders by identifying promising parent lines and trait contributions for maximizing heterosis and genetic gains. The diverse inbred lines identified in this study serve as critical resources for hybrid development and strategic breeding in maize improvement programs.

Keywords: MGIDI index; PCA; protein maize; quality; selection index

Introduction

Maize (*Zea mays* L.) is one of the leading food, feed and industrial crop in the world as well as in India and has shown wider adaptability across majority of the environments, because of its broad genetic base (1). Because maize is a highly cross-pollinated crop, breeders have been able to exploit heterosis commercially (2). They have also demonstrated heterosis benefits for increasing corn yield (3). The development of high-yielding single cross hybrids resistant to biotic and abiotic stresses is the main priority area of maize breeding and it is a continuous process. The hybrids generated from the diverse parents exhibit high heterosis (4). Thus, the selection of diverse inbred lines is a fundamental step in the development of hybrids. Knowledge of diversity in the germplasm lines has a significant impact on crop improvement (5). The genetic diversity helps to identify diverse inbred lines and assist maize breeders to formulate the hybrid breeding programme to maximize the heterosis.

Multivariate analysis such as cluster analysis and Principal Component Analysis (PCA) has been extensively used in diversity study (6). Genetic clustering of germplasm lines helps breeders to identify diverse lines. Usually, maximum diversity is expected between the lines which belong to different clusters, while inbred lines from the same cluster are expected to have low diversity (7). D^2 analysis is the most useful technique in the analysis of genetic divergence among the inbred lines, which provides the estimation of inter and intra-cluster distances.

In PCA, observations are analyzed by several inter-correlated quantitative variables (6). The aim of PCA is to extract the essential details from the table, to represent it as a set of new orthogonal variables called the principal components and to display the pattern of similarity of the observations and of the variables as points. PCA is a method of describing the pattern of variation among characters in an individual. This method eliminates inter-correlation among variables in multivariate data and plots a multi-dimensional relationship on two or three principal axes (8). The present investigation was carried out to estimate the magnitude of the genetic diversity among 25 maize inbred lines using cluster and the PCA.

Material and Methods

The present experiment was performed during *Rabi* 2021 in Randomised Block Design by 3 replications with size of the plot is 1.5 x 4 = 6 m^2 at Maize research farm TCA, Dholi (Fig. 1). Every plot having two rows with 4m length and spacing is 75 cm x 20 cm former is between rows and later is between plants. Experimental material comprised 25 QPM inbred lines were obtained from "TCA, Dholi, DR.P.C.A.U., Pusa, Samastipur, Bihar". Brief discussion of inbred lines was shown in Table 1. The observations were recorded from each inbred lines for eleven quantitative traits viz., days to 50 % tasseling, days to 50 % silking, days to 75 % dry husk, plant height (cm), ear height (cm), number of kernel rows per ear, number of kernels per row, ear girth (cm), ear length (cm), hundred grain weight (g), protein content (%), lysine content (%), tryptophan content (%) harvest index (%) and grain yield (q/ha). The data was analyzed using Mahalanobis D^2 statistic using dist function in R studio. All the genotypes were grouped into different clusters with the help of Tocher's method using toc function (8) The grapes function was used to perform, the PCA and the biplot function was used to plot PC1 vs PC2.

Results and Discussion

Cluster analysis

Several studies on maize have shown that inbred lines from diverse genetic bases to be more productive than crosses of inbred lines derived from closely related stocks. Genetic diversity is a prerequisite for any crop improvement programme because hybrids between genotypes with diverse genetic backgrounds show greater heterosis and produce a greater proportion of recombinants than those between closely related parents (9). Further, the study of genetic divergence in the maize inbred lines will help to determine the real potential of the genotype (10). The diversity analysis among these twenty-five genotypes was able to group these genotypes into 7 different clusters. Cluster I consists maximum of 12 inbred lines, followed by cluster II of 5 inbred lines, cluster IV of 3 inbred lines, cluster III of 2 inbred lines and V, VI, VII are solitary (Table 2). The study found that inbred lines possessed considerable genetic diversity among themselves, as they were distributed among eight different clusters. These eight clusters were differing genetically among themselves, even within the cluster inbred lines were varying genetically which is indicated by their inter and intra cluster distance calculated by Mahalanobis D^2 statistics (11). Intra-cluster distance ranged from 0 (Cluster V, VI, VII) to 63.86 (Cluster IV) the intra-cluster distance is maximum in cluster IV (D^2 = 63.86) followed by cluster I (D^2 = 57.29), cluster II (D^2 =55.40). This suggests the presence of significant variability within some clusters, particularly Cluster IV, which can be further exploited for selection of promising lines within the same genetic group. The inter-cluster D^2 values also ranged widely with a minimum value of 91.29 between clusters VI and VII to a maximum value of 285.05 between clusters 91.29 VI and V indicating high diversity among the genotypes of different

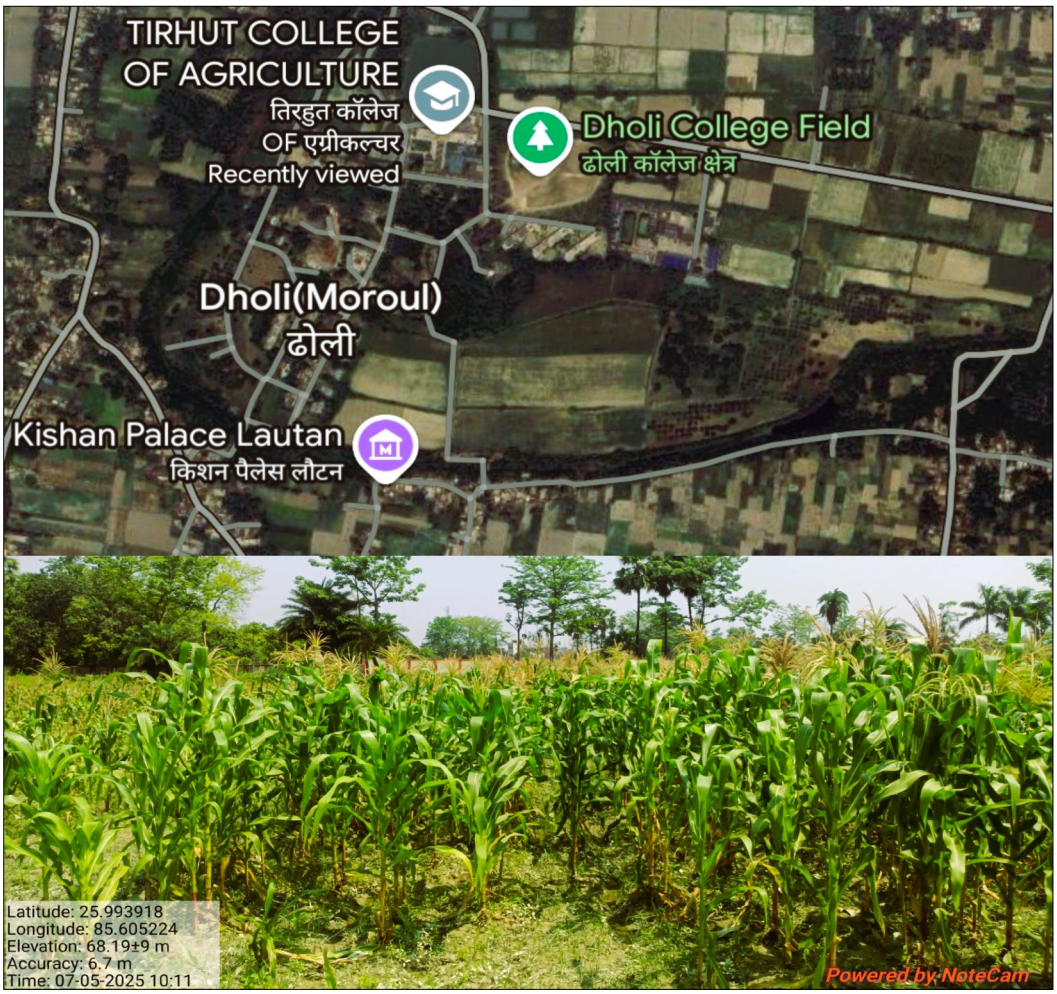

Fig.1. Geo-location map of College fields, Tirhut College of Agriculture (TCA), Dholi.

Table 1. List and source of inbred lines

Sl.No	Inbred line	Source
1	CML-161	Dholi centre
2	CML-163	Dholi centre
3	CML-165	Dholi centre
4	CML-169	Dholi centre
5	(CLQ-RCYQ31XCLO-RCYQ35)	Dholi centre
6	(CML-161XCLQ-RCYQ31)-B-10-3-BB	Dholi centre
7	Pool-17 QPM-S_6	Dholi centre
8	(CML-161/CML-165)-B-B-B-11/CML-193	Dholi centre
9	(VERA-193XG18)HS#16-7-2-4-1-1D/CML-193	Dholi centre
10	Sgg TLYQ(HG-AB)-B-B-B-36-BBB/CML-193	Dholi centre
11	Pool34C24(DQPM)-B-20-BB	Dholi centre
12	Pop-61C_1QPMTEYF-51-2-1-2-2-B-1-B/CML-193	Dholi centre
13	(CML-176XCLG2501)-B55-1-5-2-BBB-#	Dholi centre
14	(CLQ.6601XCL.0243)-B-26-1-BB-1.B6-#	Dholi centre
15	(CL.G2501XCML170)-B-24-1-1-2-BBB/CML150XCLO3618)-B-16-1-1-1B5).B.4-BB(Q)-BB.B1-B1-BB#	Dholi centre
16	CLQ-RCYQ41-BB-2-B*6-#	Dholi centre
17	CLQ-RCYQ035- B*11-#	Dholi centre
18	CML-161 XCML-165.B-2-3- B*4#B1	Dholi centre
19	(CLQ-RCYQXCLQ.RCYQ35)-B-36-2-B*5-5	Dholi centre
20	G33MQH103-3-1-5-1-B*14	Dholi centre
21	CLQ-RCYQ31XCLO-RCYQ49(CML-176XCL-G2501)-B-55-2-1-B)-B-10-3-B5	Dholi centre
22	Sgg S_1YQ-BBB-12-BBB/CML-193	Dholi centre
23	CML-161XCLO.RCYQ49-CML-176/CLG 250)-B-5-5-2-1-B)-B-19-1-B10	Dholi centre
24	CLQ-RCYQ31XCLQ-RCYQ49=(CML-176XCLG-2501-B-55-2-1-BB/CML-193	Dholi centre
25	VPQM-9-1-2-1-1 AAA	Dholi centre

Table 2. Grouping of genotypes into clusters

Cluster	Genotypes
I	16, 22, 12, 3, 1, 4, 7, 20, 9, 23, 15, 19
II	2, 6, 18, 11, 5
III	17, 21
IV	8, 13, 25
V	10
VI	14
VII	24

clusters (Table 3). Such wide inter-cluster distances are indicative of potential heterotic combinations, making them valuable for use in hybrid breeding programs aimed at maximizing genetic gain (12). Based on the inter cluster values nearest and farthest clusters were worked out and listed in Table 4. The inbred in cluster VI was most divergent with many inbred lines, especially with inbred lines of cluster V (285.05), cluster III (252.91) and cluster IV (172.83), as the genotypes from these three clusters were farther from cluster VI. Similarly, cluster V is the farthest cluster from cluster I (215.52). While the genotypes from cluster VII were more diverse from cluster III (174.82) and cluster V (173.55) were more diverse. These findings highlight the uniqueness of solitary clusters (V, VI, VII), suggesting that the inbred lines in these clusters may possess rare or novel alleles contributing to agronomically important traits such as yield stability, abiotic stress tolerance, or resistance to local pests and diseases**.** Hence, crossing the inbred lines from these farthest clusters would result in higher heterosis. These results not only support previous studies but also offer region-specific insights, especially under Rabi season conditions of eastern India, thus providing a practical roadmap for identifying parental combinations in hybrid maize development (13-15).

Among the 15 traits harvest index contributed more to diversity (12.9 %) followed by ear length (11.2 %), no. of kernels per row (10.5 %), ear girth (9.2 %) whereas days to 50 % tasseling and days to 75 % brown husk contributed less to the diversity (Fig. 2).

The cluster mean values are depicted in (Table 5). The mean value of plant height ranged from 92.23 to 165.94. Maximum was recorded in cluster IV and minimum in cluster VII. Hence selection of parents for plant height trait from these two clusters will be beneficial. Ear height cluster mean values are ranged from 81.78 (cluster I) to 45.33 (cluster VII), these two clusters are suitable for selection of parents for ear height character. Days to 50 % tasseling cluster men values ranged from 120 (cluster V, VI, VII) to 116 (cluster II), these

Table 3. Inter and Intra cluster distance of 7 clusters

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	57.29	127.32	110.11	136.22	215.52	129.18	138.75
Cluster 2		55.40	150.38	126.48	126.38	110.04	121.499
Cluster 3			27.06	142.82	141.72	252.91	174.82
Cluster 4				63.86	120.94	172.83	163.17
Cluster 5					0.00	285.05	173.55
Cluster 6						0.00	91.29
Cluster 7							0.00

Table 4. Nearest and farthest cluster based on inter cluster distance (D2)

Cluster	Nearest cluster	Farthest cluster
Cluster I	Cluster III (110.11)	Cluster V (215.52)
Cluster II	Cluster VI (110.04)	Cluster III (150.38)
Cluster III	Cluster I (110.11)	Cluster VI (252.91)
Cluster IV	Cluster V (120.94)	Cluster VI (172.83)
Cluster V	Cluster IV (20.94)	Cluster VI (285.05)
Cluster VI	Cluster VII (91.29)	Cluster V (285.05)
Cluster VII	Cluster VI (91.29)	Cluster III (174.82)

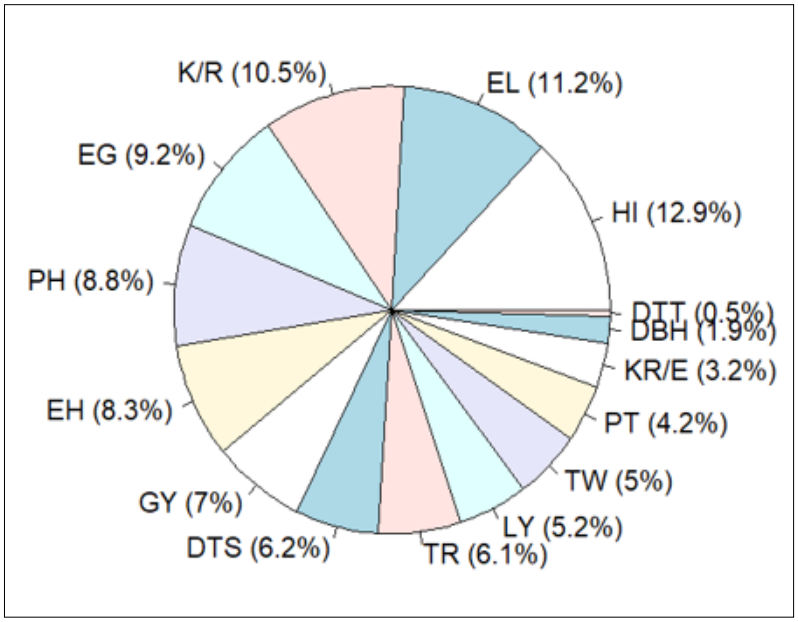

Fig. 2. Percentage contribution of different traits.

Table 5. Cluster mean values of 15 characters

	PH	EH	DTT	DTS	DBH	EL	EG	KR/E	K/R	PT	LY	TP	TW	HI	GY
Cluster 1	131.51	62.13	118.50	121.50	146	12.78	10.72	12.41	29.75	9.20	3.36	0.83	26.08	51	2966.41
Cluster 2	127.05	62.06	116	119	144.50	12.66	11.27	12.80	21.2	9.69	3.29	0.81	21.49	35.99	2611.87
Cluster 3	111.95	53.06	119.50	123.50	148.50	19.33	9.62	14.50	25	9.14	2.98	0.74	22	42.78	3319.8
Cluster 4	165.94	81.78	118.50	121	147	16.14	10.35	12.	27.66	9.19	3.43	0.88	26	34.55	2680.95
Cluster 5	135.40	65.67	120	123.50	148.50	19.10	14	11	25	9.75	2.88	0.74	21.67	31	3068.67
Cluster 6	120.53	59.33	120	123	148.50	8.40	9.93	12	28	10.57	4.08	1.04	22.67	38	2637.46
Cluster 7	92.23	45.33	120	123.50	148	12.77	11.33	13	32	9.04	3.32	1.01	22.13	26.33	3017.77

*PH- plant height, EH- ear height, DTT- days to 50 % tasseling, DTS- days to 50 % silking, DBH- days to 75 % brown husk, EL- ear length, EG- ear girth, KR/E- no. of kernel rows per ear, K/R- no. of kernels per row, PT- protein content, LY- Lysine content, TP-tryptophan content, TW- test weight, HI- harvest index, GY- grain yield.

clusters had potential for parent selection for the days to 50 % tasseling character. Similarly for quality traits clusters I, VI and VII showing high cluster values genotypes in these clusters may be used as parents for further breeding programmes. Whereas clusters I, III, V, VII are showing high cluster mean values for yield contributing traits and yield hence selection of genotypes from these clusters may used as parents for increasing yield in further breeding programmes. Similar findings were reported in early findings (9, 16).

Principal Component Analysis (PCA)

PCA was performed to assess the underlying structure of variability among 25 inbred maize lines based on 15 phenotypic and biochemical traits. The analysis yielded 15 principal components (PCs), equal to the number of traits evaluated, with the first six components exhibiting eigen values greater than 1. These six PCs cumulatively explained 85.06 % of the total variation, indicating that a significant portion of the data's variability can be summarized with relatively few components (Table 6). This dimensionality reduction helps in identifying key traits contributing to genetic divergence, which is essential for effective selection in breeding programs.

The first principal component (PC1), accounting for 23.54 % of the total variability, had high positive loadings for plant height, ear height, ear girth, number of kernel rows per ear, protein content and lysine content, while days to 50 % tasseling, days to 50 % silking, days to 75 % brown husk, ear length, number of kernels per row, tryptophan content, test weight, harvest index and grain yield showed negative loadings. The mixed loading pattern in PC1 suggests a potential trade-off between maturity traits and nutritional quality on one side and agronomic performance traits such as grain yield on the other. This indicates that lines with higher protein and lysine content may tend to have lower yield or later maturity, which poses a challenge in breeding programs aiming to improve both yield and nutritional quality simultaneously. Similar correlations have been reported (17), highlighting the complexity of simultaneous selection for quality and yield traits. PC2, explaining 17.17 % of the variability, revealed an inverse trend compared to PC1. Traits like days to 75 % brown husk, number of kernels per row, protein content, lysine content, tryptophan content and test weight loaded positively, while plant height, ear height and grain yield loaded negatively. This further emphasizes the divergence between grain nutritional quality and yield potential. The grouping of high-quality traits together in PC2 suggests that these characters are interrelated and could be selected collectively. However, their negative association with grain yield implies that breeding for quality may inadvertently reduce productivity if not carefully managed a concern also echoed in previous findings (15).

PC3 (15.66 % variability) showed positive contributions from most traits except for days to 75 % brown husk, number of kernel rows per ear and key protein-related traits. This suggests that PC3 may represent a component capturing

Table 6. Eigen values of principal components

Principal component	Eigen value	Percentage of variance	Cumulative percentage of variance
PC1	3.532	23.546	23.546
PC2	2.576	17.176	40.723
PC3	2.349	15.661	56.384
PC4	1.887	12.58	68.964
PC5	1.382	9.215	78.179
PC6	1.034	6.89	85.069
PC7	0.78	5.197	90.266
PC8	0.517	3.449	93.715
PC9	0.387	2.581	96.296
PC10	0.284	1.892	98.189
PC11	0.187	1.247	99.436
PC12	0.039	0.262	99.698
PC13	0.029	0.194	99.892
PC14	0.013	0.086	99.978
PC15	0.003	0.022	100

general agronomic vigor or developmental traits, rather than quality aspects. The relatively broad positive association indicates that several traits may co-vary positively and could be selected in tandem for overall performance.

PC4 (12.58 %) was negatively associated with traits such as ear girth, number of kernel rows per ear, number of kernels per row, lysine content, tryptophan content, harvest index and grain yield. In contrast, traits like days to tasseling, silking and plant height showed positive loadings. The inverse association of yield and quality traits in this component further underscores the difficulty in selecting genotypes that combine early maturity, high grain quality and high productivity a key breeding challenge (18).

In PC5, which accounted for 9.25 % of the variability, all traits except harvest index exhibited negative loadings. This component appears to isolate harvest index as a potential selection criterion independent of other traits, suggesting its utility in identifying genotypes with efficient biomass partitioning even when other traits are less favorable.

Finally, PC6 contributed 6.89 % of the variation and showed positive associations for most traits except ear girth, number of kernels per row, protein content, test weight and harvest index. This indicates potential variability in resource allocation and trait independence at later PCs, which, although explaining less variation, could still offer unique insights during fine-scale selection. Scree plot (Fig. 3) showing the variance explained by each component.

Overall, the PCA revealed complex interrelationships among agronomic, developmental and nutritional traits. The presence of opposing trait loadings within components highlights the potential for both positive and negative correlations, implying that trait improvement may require compromises or careful balancing. These insights are critical for maize breeding strategies aiming to combine early maturity, high yield and enhanced nutritional value. While these results are generally in agreement with studies some contrasting findings (6), particularly those where grain yield and 100 grains weight loaded strongly in the earlier components (19), may reflect population-specific genetic architecture or environmental influences, reinforcing the need for environment-specific breeding strategies.

The scatter biplot depicts the variability of each trait displayed as blue lines (Fig. 4). In the scatter plot the genotypes which are place towards the better end (*i.e.,* either positive end or negative end depends on the direction in which trait associated with the principal component) of the

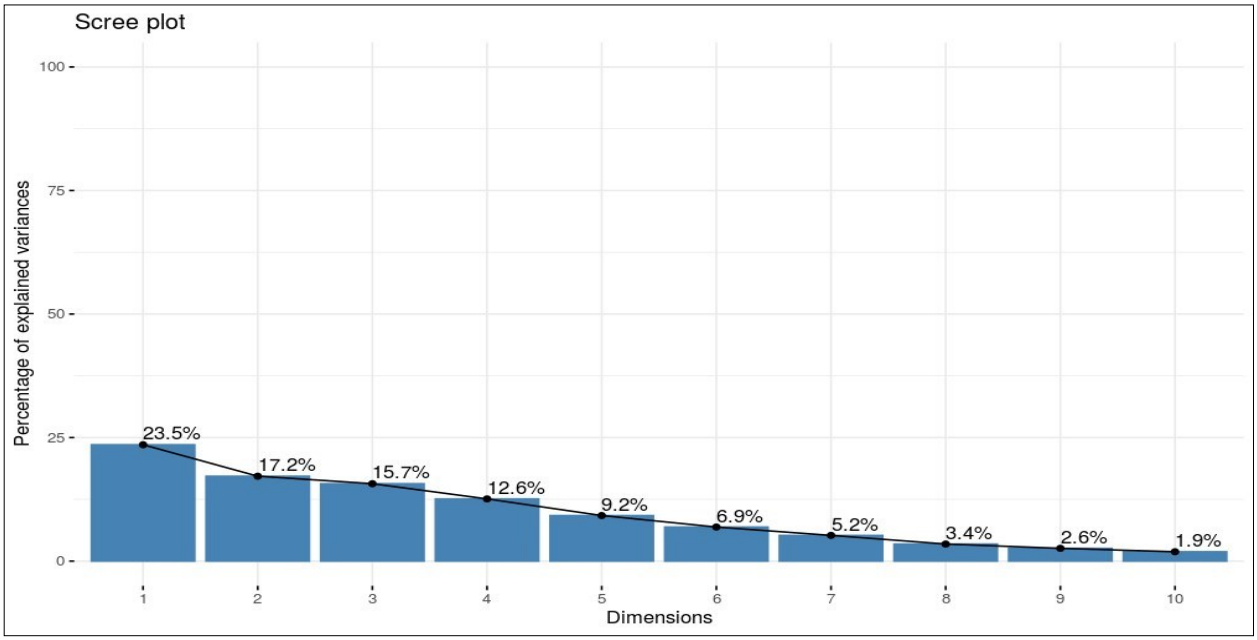

Fig. 3. Screeplot showing percentage of explained variance.

principal components is supposed to be good for those components. Therefore, the inbred lines G1, G7, G11 are good for protein and lysine content. Similarly, the inbred lines G14, G19, G8, G24, G5, G9, G12 and G16 are good for tryptophan content, no.of kernelss per row, test weight, days to 50 % tasseling and days to 75 % brown husk. The genotypes G23, G4, G22, G3, G15, G21, G17, G10 are good for harvest index, grain yield, days to 50 % silking and ear length. Likewise, the genotypes G18, G20, G13, G25, G2, G6 are good for no. of kernel rows per ear, plant height, ear height and ear girth. These results of clustering and principal components of the current study would help in characterizing the genotypes used in the study and utilize them effectively in the further breeding programme.

MGIDI

MGIDI selection index results figured out that 15 traits were separated as 6 factors (FA) and FA1 includes flowering and maturity traits like days to 50 % flowering, days to 50 % silking and days to 75 % brown husk (Table 7). FA2 includes traits like lysine content, tryptophan content and ear length. FA3 includes ear height and plant height whereas FA4 includes yield contributing traits like no. of kernels per row, harvest index and grain yield. FA5 includes ear girth and protein content. Likewise, in FA4, FA6 also includes yield contributing traits like test weight and no. of kernel rows per ear. All the studied traits exerted positive selection gain except for no. of kernel rows per ear and protein content both accounted for about 3.38 negative selection percentage. The selection pressure was used with aim of selection of superior genotypes. It resulted in the identification of 4 inbred lines as best performers (Fig. 5). The MGIDI index not only streamlined trait selection but also revealed meaningful trait groupings relevant to breeding priorities. The association of nutritional traits with ear length suggests potential for simultaneous improvement of quality and structural traits. Similarly, the distribution of yield-related traits across two separate factors reflects the complexity of yield formation and the possibility of targeting specific yield components. The slight negative gains observed in protein content and kernel rows may indicate trade-offs with other prioritized traits, a common challenge in multi-trait

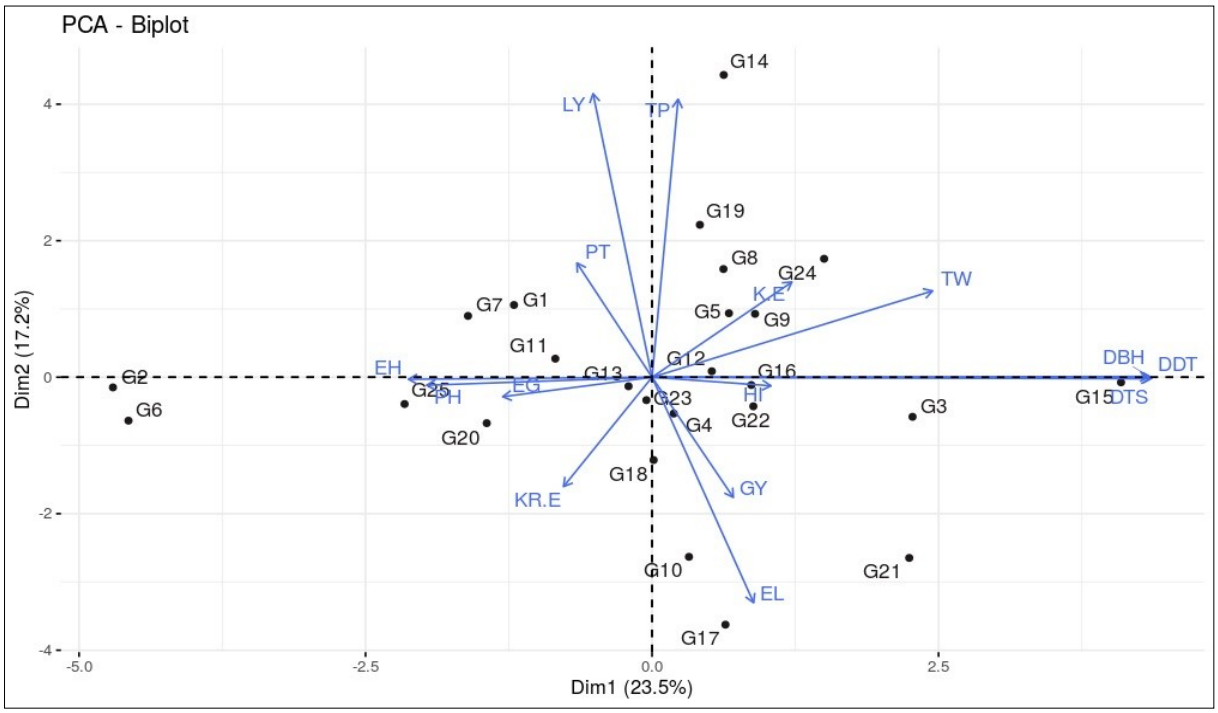

Fig. 4. Scattered diagram of 25 genotypes of maize inbred lines.

Table 7. Factor loadings of each variable

Variables	PC1	PC2	PC3	PC4	PC5	PC6
PH	0.223	-0.016	0.52	0.22	-0.022	0.253
EH	0.241	-0.004	0.485	0.24	-0.028	0.32
DDT	-0.494	-0.001	0.009	0.092	-0.117	0.187
DTS	-0.492	-0.003	0.009	0.116	-0.089	0.197
DBH	-0.491	0.001	-0.009	0.189	-0.029	0.064
EL	-0.1	-0.438	0.002	0.056	-0.317	0.17
EG	0.148	-0.038	0.106	-0.028	-0.686	-0.096
KR/E	0.087	-0.212	-0.231	-0.395	-0.049	0.443
K/R	-0.138	0.185	0.243	-0.406	-0.011	-0.107
PT	0.074	0.222	-0.162	0.196	-0.471	-0.441
LY	0.058	0.551	-0.055	-0.18	-0.087	0.235
TP	-0.026	0.54	-0.063	-0.107	-0.172	0.36
TW	-0.277	0.168	0.438	0.074	-0.003	-0.219
HI	-0.118	-0.017	0.327	-0.435	0.197	-0.288
GY	-0.08	-0.233	0.198	-0.485	-0.323	0.014

*PH- plant height, EH- ear height, DTT- days to 50 % tasseling, DTS- days to 50 % silking, DBH- days to 75 % brown husk, EL- ear length, EG- ear girth, KR/E- no. of kernel rows per ear, K/R- no. of kernels per row, PT- protein content, LY- Lysine content, TP-tryptophan content, TW- test weight, HI- harvest index, GY- grain yield.

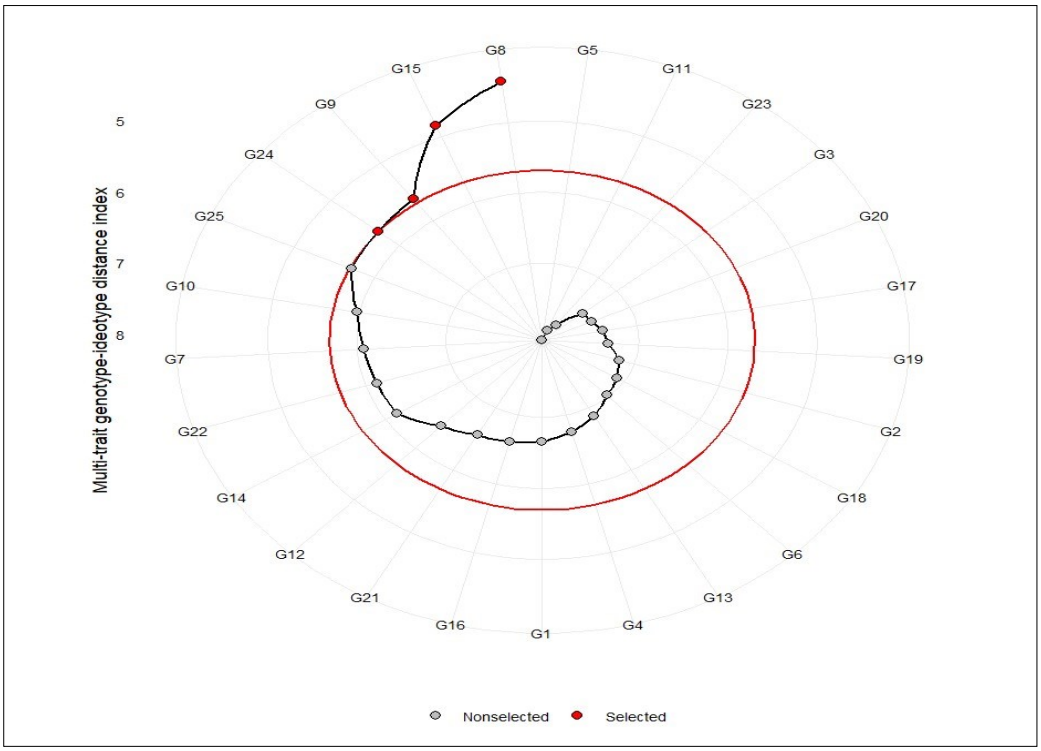

Fig. 5. Selection of genotypes based on MGIDI index.

Table 8. Genetic gain of different traits based on MGIDI index

Sl No.	Traits	Factor	SG (%)
1	DTT	FA1	1.68
2	DTS	FA1	1.72
3	DBH	FA1	0.71
4	EL	FA2	1.69
5	LY	FA2	4.27
6	TR	FA2	9.18
7	PH	FA3	2.97
8	EH	FA3	2.55
9	K/R	FA4	4.83
10	HI	FA4	1.85
11	GY	FA4	3.03
12	EG	FA5	6.98
13	PT	FA5	-1.16
14	KR/E	FA6	-2.22
15	TW	FA6	7.12

selection (Table 8). Overall, MGIDI proved effective in identifying balanced genotypes, supporting its value in advancing multi-trait selection strategies in maize improvement programs (20).

Strength and weakness plot showed that relative contribution of different traits on superior genotypes. The MGIDI was classified into six contributing factors, where the factors that contributed more were plotted near and/ inside the centre whereas factors that contributed less were plotted towards the edge (Fig. 6). FA1 had a higher contribution to the MGIDI of G15 suggesting that this genotype performs poorly for the days to 50 % tasseling, days to 50 % silking and days to 75 % brown husk, FA1 had smallest contribution to genotypes G9, G24, G8 suggesting that these genotypes are good for FA1 characters. FA2 had higher contribution to the MGIDI of G24 and G8 suggesting that these genotypes are poor performing and the genotypes G9 and G15 had less contribution hence these genotypes are good for FA2 traits like ear length, lysine content and tryptophan content. FA3 had higher contribution to the MGIDI of G8 and G9 showing that these genotypes are poor performers. As they are closer to the plot genotypes G24 and G15 are the good performers for the FA3 traits like plant height and ear height. FA4 had a higher contribution to the MGIDI of G9 and G15 suggesting their poor performance for FA4 traits while the genotypes G24 and G8 are the good performers for FA4 traits like no. of kernels per row, harvest index and grain yield. FA5 had a higher contribution to the MGIDI of G9 suggesting that this genotype performs poorly for FA5 traits and the genotypes G8, G15, G28 are the good performers for the traits like ear girth and protein content. FA6 had a higher contribution to the MGIDI of G24 and G15 suggesting that these genotypes perform poorly for the FA6 traits while the genotypes G8 and G9 are the good performers for the traits like no. of kernel rows per ear and test weight. Similar results were reported in previous works (21).

Conclusion

The study comprehensively assessed genetic diversity among 25 maize inbred lines using principal component analysis, cluster analysis, Mahalanobis D^2 statistics and the MGIDI selection index. PCA revealed that six principal components

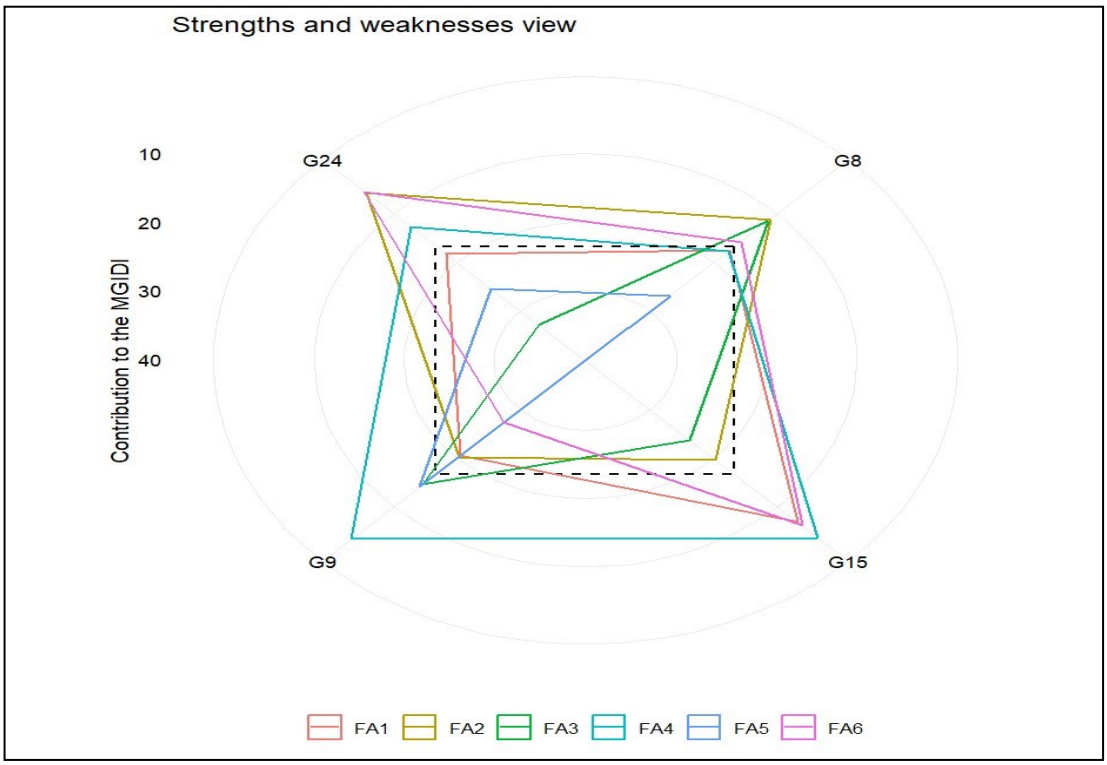

Fig. 6. Strength and weakness view of different traits.

with eigenvalues greater than one explained 85.06 % of the total variability, with key traits such as plant height, ear height, protein content, lysine content and grain yield contributing significantly to diversity. Cluster analysis and Mahalanobis D^2 distances identified genetically distant inbred lines that can be strategically used as parents to maximize heterosis in future hybrid development. The MGIDI index further refined the selection process by identifying four superior genotypes with favorable multi-trait performance, effectively integrating maturity, nutritional quality and yield-related traits. Notably, the study highlighted potential trade-offs between protein content and yield components, emphasizing the need for balanced selection strategies. These findings not only provide a robust framework for selecting diverse and high-performing parental lines but also support targeted breeding for improved grain quality, adaptability and productivity. This work lays a solid foundation for future genomic studies, heterotic grouping and the development of nutritionally enriched, high-yielding maize hybrids.

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Authors' contributions

AE carried out research and written the manuscript, AK, SKS, AN conceptualized the work and provided resources, UK, AS did the statistical work and PP proofread the manuscript.

Compliance with ethical standards

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

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