

Multivariate Characterization and Genetic Divergence of Maize (*Zea mays* L.) Germplasm for Dual-Purpose Improvement under Indo-Gangetic Conditions

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Abstract

The present study evaluated genetic divergence among 35 maize (*Zea mays* L.) genotypes to identify promising material for dual-purpose use, with emphasis on fodder yield, grain yield, and quality-related traits. The experiment was conducted during Kharif 2025 at Demonstration Farm Unit-III, Integral Institute of Agricultural Science and Technology, Integral University, Lucknow, India, using a randomized complete block design with three replications. Observations were recorded for phenological, morphological, fodder, grain yield, and quality traits, and the data were analyzed using ANOVA, principal component analysis, path coefficient analysis, hierarchical clustering, dendrogram analysis, and heatmap analysis.

The genotypes showed appreciable variation for the studied traits, indicating the presence of useful genetic diversity. Among the evaluated lines, HAMIRPUR-1 produced the highest green fodder yield and dry matter yield, followed by IULYM-16 and INDORA-1, suggesting their suitability for fodder biomass improvement. For grain yield, IULYM-15 performed best, followed by IULYM-13 and SHIMLA-1. Principal component analysis showed that PC1 and PC2 accounted for 25.31% and 18.47% of the total variation, respectively, together explaining 43.78% of the total variability. Fresh stem weight, green fodder yield, and dry matter yield were the major contributors to PC1, whereas grain yield, harvest index, ear length, and 100-grain weight contributed mainly to PC2. Cluster analysis separated the genotypes into three distinct groups, supporting the existence of meaningful genetic divergence.

Based on mean performance and multivariate grouping, IULYM-15, IULYM-13, IULYM-16, IULYM-4, HAMIRPUR-2, INDORA-1, IULYM-12, and SHIMLA-2 were identified as useful parental lines. These genotypes may be used in future breeding programs aimed at developing high-yielding dual-purpose maize cultivars adapted to Indo-Gangetic conditions.

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops worldwide and is widely grown for food, feed, fodder, and industrial uses. Its high productivity, wide adaptability, and efficient biomass production make it an important crop in both grain-based and crop-livestock production systems [1]. In India, maize is also gaining importance as a dual-purpose crop because it can provide grain for human and animal consumption as well as green biomass for livestock feeding [2]. The growing demand for quality fodder and the need to improve farm-level productivity have increased the importance of identifying maize genotypes that perform well for both grain and fodder traits [3,4].

Genetic diversity is an essential requirement for any crop improvement program. In maize breeding, diverse germplasm enables breeders to select suitable parents for hybridization and to develop improved cultivars with better yield, adaptability, and heterotic potential [5]. For dual-purpose maize improvement, selection cannot be based on a single trait because grain yield, fodder yield, and quality traits are controlled by several interrelated characters [3]. Therefore, traits such as plant height, leaf length, leaf width, stem girth, green fodder yield, dry matter yield, grain yield, harvest index, crude protein content, neutral detergent fiber, and acid detergent fiber need to be evaluated together [6].

Multivariate statistical techniques provide a useful approach for studying complex trait relationships. Principal component analysis helps identify the major traits contributing to total variation, whereas cluster analysis groups genotypes according to similarity or divergence [7]. These methods are particularly useful in germplasm evaluation because they allow the simultaneous assessment of several traits and help identify superior and genetically diverse parents for breeding programs [8]. Previous studies have also reported the usefulness of PCA and cluster analysis in maize for assessing genetic divergence, identifying important yield-contributing traits, and selecting promising genotypes [9].

Although several studies have evaluated maize germplasm for grain yield or fodder yield separately, limited work has focused on the combined assessment of fodder, grain, and quality traits for dual-purpose improvement [5]. This gap is particularly relevant under Indo-Gangetic conditions, where maize is grown in fertile alluvial soils but faces challenges such as climate variability, increasing fodder demand, and the need for locally adapted cultivars. Identifying genotypes that combine high biomass production, good grain yield, and acceptable quality traits can contribute to the development of improved dual-purpose maize cultivars for this region [10].

Therefore, the present study was conducted to assess genetic divergence among maize genotypes using phenological, morphological, fodder, grain yield, and quality traits. The study also aimed to identify promising and genetically diverse genotypes that may be used as parental material in future breeding programs for dual-purpose maize improvement under Indo-Gangetic conditions.

Materials and Methods

Experimental site and plant material

The field experiment was conducted during Kharif 2025 at Demonstration Farm Unit-III, Integral Institute of Agricultural Science and Technology (IIAST), Integral University, Lucknow, India. The site is located in the Indo-Gangetic plains of northern India at 26.95° N latitude and 80.99° E longitude, with an elevation of about 123 m above mean sea level. The area has a subtropical climate and fertile alluvial soil suitable for maize cultivation.

The experimental material consisted of 35 maize (*Zea mays* L.) genotypes obtained from the Department of Genetics and Plant Breeding, IIAST, Integral University. These genotypes were evaluated for phenological, morphological, fodder, grain yield, and quality traits to study genetic divergence and identify promising material for dual-purpose maize improvement.

Experimental design and crop management

The experiment was laid out in a randomized complete block design with three replications under open-field conditions. The total experimental area was 600 m², measuring 40 m × 15 m. Each genotype was sown in rows with a spacing of 78 cm between rows and 30 cm between plants. Standard agronomic practices and plant protection measures were followed uniformly throughout the crop season to maintain healthy crop growth and reduce non-genetic variation.

Observations recorded

Observations were recorded on five randomly selected competitive plants from each genotype in each replication. Days to 50% tasseling and days to 50% silking were recorded on a plot basis. The traits studied included days to 50% tasseling, days to 50% silking, plant height, number of leaves per plant, leaf length, leaf width, stem girth, fresh leaf weight per plant, fresh stem weight per plant, leaf:stem ratio, green fodder yield per plant, dry matter yield per plant, grain yield per plant, 100-grain weight, ear height, number of cobs per plant, days to 50% brown husk, ear length, ear girth, number of grain rows per ear, shelling percentage, harvest index, crude protein content, neutral detergent fiber, acid detergent fiber, and moisture content.

Statistical and multivariate analysis

The recorded data were analyzed using analysis of variance for a randomized complete block design as described by [11]. Genotypic coefficient of variation, phenotypic coefficient of variation, broad-sense heritability, and genetic advance as a percentage of the mean were estimated using standard biometrical methods [12]. Correlation analysis was performed to examine trait associations [13].

For multivariate analysis, principal component analysis was used to identify the major traits contributing to total variability among the genotypes [14]. Hierarchical cluster analysis was performed using Euclidean distance to classify the genotypes into groups based on similarity and divergence [15]. These analyses were used to identify genetically diverse and agronomically promising genotypes for dual-purpose maize breeding.

Results and Discussion

Multivariate Analysis of Genetic Divergence in Maize Germplasm

Mean performance of genotypes

Considerable variation was recorded among the 35 maize genotypes for phenological, morphological, fodder, grain yield, and quality traits, showing that the experimental material possessed useful genetic diversity. Among the evaluated genotypes, HAMIRPUR-1, IULYM-16, and INDORA-1 performed better for fodder-related traits, particularly fresh stem weight, green fodder yield, and dry matter yield. HAMIRPUR-1 produced the highest green fodder yield (441.10 g plant⁻¹) and dry matter yield (123.58 g plant⁻¹), followed by IULYM-16, which recorded 409.76 g plant⁻¹ green fodder yield and 123.06 g plant⁻¹ dry matter yield. INDORA-1 also showed good biomass performance, with 375.52 g plant⁻¹ green fodder yield.

For grain yield and associated traits, IULYM-15 was the best-performing genotype, recording the highest grain yield per plant (175.80 g). It was followed by IULYM-13 (151.34 g) and SHIMLA-1 (124.07 g). Higher 100-grain weight was observed in genotypes such as SHIMLA-1, CHAMBA-1, and NURPUR-1, indicating better grain boldness and grain-filling ability. Overall, the variation observed for both fodder and grain traits suggests that the evaluated germplasm provides useful breeding material for developing dual-purpose maize genotypes.

Table 1
Mean performance of maize genotypes for phenological, morphological, fodder,

GENOTYPE/TRAIT	D to 50% T	D to 50% S	P H (cm)	N of L	L L(cm)	L W (cm)	S G(cm)	FL W(g)	FS W(g)	L:S R	GF Y(g)	DM Y(g)	GY (g)	100-G W (g)
IULYM-1	57.33	61.33	182.8	8.73	61.28	7.53	2.61	18.19	50.39	0.36	68.58	19.99	27.63	86.52
IULYM-2	56.33	60.33	175.27	8.2	59.81	6.97	2.62	42.01	132.22	0.32	174.23	52.4	21.98	89.62
IULYM-3	56.33	60.33	177.67	7.8	57.19	6.51	2.62	16.8	42.28	0.4	59.08	18.17	27.63	90.23
IULYM-4	55.67	58.67	173.13	7	59.75	6.3	2.57	76.04	267.16	0.29	343.2	98.1	23.57	83.36
IULYM-5	55.33	59	169.33	6.93	59.36	7.13	2.57	21.44	164.46	0.13	185.9	56.08	24.59	83.32
IULYM-6	56.67	60.67	181.8	10.2	64.4	7.22	2.48	59.14	149.39	0.4	208.52	64.32	25.67	93.55
IULYM-7	54.67	59	171.47	10.07	62.65	7.24	2.65	35.92	124.43	0.29	160.35	51.59	28.26	86.04
IULYM-8	55.67	58.33	166.47	6.6	56.63	6.12	2.28	62.2	143.31	0.44	205.51	60.02	24.87	81.96
IULYM-9	55.67	59	160.6	6.53	54.11	5.38	2.53	19.91	98.6	0.2	118.51	37.52	26.51	79.36
IULYM-10	54.67	57.67	171.8	7.07	56.42	7.63	2.45	12.97	42.71	0.3	55.68	16.75	28.63	86.96
IULYM-11	56	59	164.07	7	55.52	5.39	2.59	30.18	91.99	0.33	122.17	34.9	22.91	81.81
IULYM-12	53.67	57.33	161.87	7.33	52.59	5.37	2.44	37.6	154.62	0.24	192.22	54.09	26.61	81.24
IULYM-13	56	59.67	177.07	9.4	60.47	6.84	2.48	12.88	38.04	0.34	50.92	14.7	30.52	88.06
IULYM-14	56.67	60	167.6	9.27	55.6	6.78	2.59	18.13	94.94	0.19	113.07	35.31	24.04	83.07
IULYM-15	55.33	59	166.93	8.47	60.23	7.45	2.4	30.84	109.29	0.28	140.14	42.23	29.37	79.75
IULYM-16	55.67	59.67	166.53	8	58.46	7.2	2.43	111.24	298.51	0.37	409.76	123.06	27.1	84.75
IULYM-17	58.67	62	196.8	8.87	58.65	6.72	2.74	34.91	173.58	0.2	208.49	56.53	23.98	98.22
IULYM-18	57.33	61.33	228.47	10.2	79.8	7.15	2.93	17.19	56.32	0.31	73.52	22.4	26.06	114.18
INDORA-2	58.67	61.67	218.13	11.27	74.96	8.71	2.94	18.65	36.19	0.52	54.84	16.48	26.25	106.08
JAWALI-1	58	62	215.67	10.93	74.71	7.9	2.78	24.86	82.14	0.3	107	32.85	20.44	110.69
MANDI-2	57	61.67	215.53	10.6	80.04	7.95	2.8	26.32	107.81	0.24	134.12	38.81	21.22	107.71
NURPUR-3	59.67	63	229.2	10.53	83.28	7.07	2.86	23.58	56.98	0.41	80.56	24.02	24.87	119.36
CHAMBA-1	58	61.67	223.13	10.87	82.37	6.86	2.87	65.55	145.79	0.45	211.34	65.72	24.96	113.64
HAMIRPUR-1	58.67	62.67	228.07	10.67	83.41	7.13	2.75	107.15	333.95	0.32	441.1	123.58	25.35	118.36
CHAMBA-3	57.33	61.33	244	11.6	88.52	8.37	2.95	26.87	88	0.31	114.87	33.14	20.78	123.44
JAWALI-2	58	61.67	226.6	11.4	83.36	8	2.52	33.57	168.4	0.2	201.97	64.28	22.17	107.32
CHAMBA-2	58.33	61.33	231.27	11.4	85.68	7.1	3.09	35.46	107.73	0.33	143.18	43.92	18.82	120.59
HAMIRPUR-2	58	61	226.2	10.8	87.76	6.85	2.86	15.25	88.76	0.17	104.01	29.57	20.65	113.4
MANDI-1	59	63.67	230.27	11.27	87.37	6.81	2.96	63.61	180.93	0.35	244.53	73.78	22.91	117.35
SHIMLA-1	58	60.67	237.27	11.33	88.24	6.68	2.84	22.58	64.44	0.35	87.02	27.46	22.77	124.29
INDORA-1	59.33	63	233.67	11.4	86.89	6.82	2.84	85.44	290.08	0.3	375.52	110.79	17.9	107.49
HAMIRPUR-3	58.33	61.67	228.2	11	88.12	6.51	2.86	17.87	87.73	0.21	105.59	32.74	19.58	117.91
NURPUR-2	56.33	59	222.87	11.07	87.07	6.95	2.92	29.01	102.32	0.28	131.33	41.4	24.15	109.05
SHIMLA-2	58.33	63.33	232.8	11.33	88.32	6.98	2.98	34.77	77.47	0.45	112.24	31.56	19.48	118.4
NURPUR-1	58.67	61.33	238.23	11.67	88.72	6.61	3.09	26.1	141.29	0.19	167.4	51.08	25.52	119.82

D to 50% T = days to 50% tasseling; D to 50% S = days to 50% silking; PH (cm) = plant height; N of L = number of leaves per plant; LL (cm) = leaf length; LW (cm) = leaf width; SG (cm) = stem girth; FLW (g) = fresh leaf weight; FSW (g) = fresh stem weight; L:SR = leaf:stem ratio; GFY (g) = green fodder yield per plant; DMY (g) = dry matter yield per plant; GY (g) = grain yield per plant; 100-GW (g) = 100-grain weight; EH (cm) = ear height; Cs/P = cobs per plant; D to BH = days to brown husk; EL (cm) = ear length; EG (cm) = ear girth; GRs/E = grain rows per ear; S% = shelling percentage; HI = harvest index; CP (%) = crude protein; NDF (%) = neutral detergent fiber; ADF (%) = acid detergent fiber; MC (%) = moisture content.

Principal Component Analysis (PCA)

Principal component analysis was carried out to identify the traits that contributed most to the overall variation among maize genotypes. The first few principal components explained a major share of the total variability, showing that PCA was useful in reducing the complex trait data into fewer meaningful components.

PC1 was mainly associated with fodder and biomass traits, including fresh stem weight, fresh leaf weight, green fodder yield, and dry matter yield. In contrast, PC2 was more strongly influenced by grain yield, harvest index, ear traits, and 100-grain weight. This pattern indicates that the major variation among genotypes was largely explained by differences in biomass production and vegetative growth, whereas the second component separated genotypes on the basis of grain productivity and reproductive traits.

Thus, PCA helped identify the key traits responsible for genetic divergence and provided a clear basis for distinguishing genotypes with better fodder potential, grain performance, or dual-purpose suitability.

Table 2
Eigenvalues and percentage contribution of principal components.

PC	Eigenvalue	Variance	Cumulative
PC1	6.580628	25.31011	25.31011
PC2	4.803087	18.47341	43.78352
PC3	2.227363	8.566779	52.3503
PC4	1.652375	6.355289	58.70559
PC5	1.279373	4.920664	63.62625
PC6	1.232282	4.739544	68.3658
PC7	1.159824	4.460862	72.82666
PC8	1.067169	4.104495	76.93115
PC9	0.999009	3.842344	80.7735
PC10	0.861147	3.312102	84.0856
PC11	0.8136	3.129232	87.21483
PC12	0.706056	2.715602	89.93043
PC13	0.660674	2.541055	92.47149
PC14	0.480097	1.846528	94.31802
PC15	0.337455	1.297906	95.61592
PC16	0.268933	1.034358	96.65028
PC17	0.237793	0.91459	97.56487
PC18	0.204964	0.788324	98.35319
PC19	0.145488	0.559571	98.91276
PC20	0.099797	0.383833	99.2966
PC21	0.083185	0.319944	99.61654
PC22	0.053715	0.206596	99.82314
PC23	0.029693	0.114203	99.93734
PC24	0.01226	0.047154	99.98449
PC25	0.004031	0.015505	100
PC26	2.01E-31	7.73E-31	100

Trait contribution to principal components

Green fodder yield, fresh stem weight, dry matter yield, fresh leaf weight, and harvest index showed high positive loadings in PC1, indicating that these traits contributed strongly to the total variation among the maize genotypes. In PC2, major contributions were observed from grain yield, ear length, number of grain rows per ear, and 100-grain weight, suggesting their importance in separating genotypes on the basis of grain productivity and yield components.

Phenological traits, such as days to tasseling and days to silking, contributed relatively less to overall divergence. This suggests that biomass and grain yield-related traits were more effective in distinguishing the genotypes. Therefore, traits such as green fodder yield, dry matter yield, fresh stem weight, grain yield,

harvest index, ear length, and 100-grain weight may be considered useful selection criteria for dual-purpose maize improvement.

Table 3
Path analysis showing direct and indirect effects of component traits on green fodder yield in maize genotypes.

Traits	Direct Effect	Total Correlation	Indirect Effect
D to 50% T	0.330158	-0.02928	-0.35944
D to 50% S	-0.2641	-0.13312	0.130977
P H (cm)	0.320758	0.032164	-0.28859
N of L	0.141125	0.055245	-0.08588
L L(cm)	-0.64688	-0.00398	0.642895
L W (cm)	-0.05406	-0.0492	0.004867
S G(cm)	0.320125	0.12279	-0.19734
F L W(g)	-0.18644	0.007199	0.193636
F S W(g)	-1.00901	-0.00287	1.006136
L:S R	-0.03681	0.0212	0.058007
G F Y(g)	NA	-0.00032	NA
D M Y(g)	1.463483	0.01199	-1.45149
G Y (g)	0.106245	0.027785	-0.07846
100-G W (g)	-0.22116	-0.05927	0.161889
E H (cm)	-0.02028	0.053138	0.073422
Cs/P	-0.1662	-0.16667	-0.00047
D to B H	-0.28931	-0.17729	0.112019
E L (cm)	0.04938	0.002239	-0.04714
E G (cm)	-0.07647	-0.05717	0.019295
G Rs/E	-0.06159	-0.00222	0.059376
S %	-0.04064	0.007482	0.048123
H I	0.237402	0.013149	-0.22425
C P (%)	0.017104	0.071187	0.054084
NDF (%)	0.012776	0.012983	0.000207
ADF (%)	0.074163	0.138887	0.064725
M C (%)	0.130146	-0.03954	-0.16968

Path analysis scatter plot interpretation

The path analysis scatter plot showed the relationship between direct effects and total correlation of different component traits with green fodder yield. Traits located in the positive direct-effect region, including dry matter yield, stem girth, plant height, harvest index, grain yield, crude protein content, NDF, and ADF, showed favorable direct contributions to green fodder yield. Among these traits, dry matter yield had the highest positive direct effect, suggesting its strong role in improving fodder yield.

In contrast, fresh stem weight, leaf length, days to 50% silking, days to brown husk, and 100-grain weight showed negative direct effects. The distribution of traits across the four quadrants indicates that selection for fodder yield should consider both direct effects and indirect contributions through associated traits.

Cluster analysis

Hierarchical cluster analysis grouped the 35 maize genotypes into distinct clusters based on Euclidean distance, indicating clear genetic divergence among the germplasm lines. The clustering pattern showed that the genotypes differed considerably for fodder, grain yield, and quality traits. Genotypes within the same cluster had relatively similar trait performance, whereas genotypes placed in different clusters showed greater divergence.

One cluster mainly included fodder-type genotypes with higher fresh stem weight, green fodder yield, and dry matter yield. Another cluster contained grain-oriented genotypes with better grain yield, harvest index, and ear-related traits. This grouping suggests that crossing genotypes from different clusters may be useful for generating wider variability, better recombination, and possible heterosis in future breeding programs.

Table 4
Cluster composition of maize
genotypes based on multivariate
analysis.

S. No.	Genotype	Cluster
1	IULYM-1	I
2	IULYM-10	I
3	IULYM-13	I
4	IULYM-14	I
5	IULYM-15	I
6	IULYM-3	I
7	IULYM-5	I
8	IULYM-7	I
9	IULYM-9	I
10	IULYM-11	II
11	IULYM-12	II
12	IULYM-16	II
13	IULYM-17	II
14	IULYM-2	II
15	IULYM-4	II
16	IULYM-6	II
17	IULYM-8	II
18	IULYM-18	III
19	INDORA-2	III
20	JAWALI-1	III
21	MANDI-2	III
22	NURPUR-3	III
23	CHAMBA-3	III
24	HAMIRPUR-2	III
25	CHAMBA-2	III
26	JAWALI-2	III
27	CHAMBA-1	III
28	HAMIRPUR-3	III
29	MANDI-1	III
30	SHIMLA-1	III
31	INDORA-1	III
32	HAMIRPUR-1	III
33	NURPUR-2	III
34	SHIMLA-2	III
35	NURPUR-1	III

Dendrogram and heatmap analysis

The dendrogram further supported the clustering pattern and provided a clearer view of the genetic relationships among the maize genotypes. Genotypes such as HAMIRPUR-1, IULYM-16, and INDORA-1 were separated mainly because of their superior fodder performance, whereas IULYM-15 and IULYM-13 were grouped according to their higher grain yield potential.

The heatmap also showed clear differences in trait expression among the genotypes. Fodder-performing genotypes showed higher values for biomass-related traits, whereas grain-oriented genotypes showed stronger expression for grain yield and harvest index. Overall, the dendrogram and heatmap together

provided a useful visual summary of genetic diversity, genotype grouping, and trait association in the evaluated maize germplasm.

Identification of superior and divergent genotypes

Based on multivariate characterization, PCA, cluster analysis, and mean trait performance, several genotypes were identified as promising material for dual-purpose maize improvement. HAMIRPUR-1, IULYM-16, and INDORA-1 showed superior fodder performance, mainly due to their higher green fodder yield, fresh stem weight, and dry matter yield. In contrast, IULYM-15, IULYM-13, and SHIMLA-1 performed better for grain yield and related yield-contributing traits.

The genetic divergence observed among these genotypes indicates their possible use as parental lines in future hybridization programs. Crosses between genetically diverse and agronomically superior genotypes may help generate wider variability and improve the chances of selecting lines with better grain yield, fodder yield, and adaptability under Indo-Gangetic conditions.

Table 5
Superior and genetically divergent maize genotypes identified for dual-purpose breeding.

Genotype	Cluster	Superior Traits Identified	Breeding Importance
IULYM-15	I	High grain yield, high HI	Grain improvement
IULYM-13	I	High grain yield and shelling %	Yield breeding
IULYM-16	II	Highest GFY and DMY	Fodder breeding
IULYM-4	II	High biomass production	Silage/fodder
HAMIRPUR-1	III	Very high biomass and plant height	Dual-purpose hybridization
INDORA-1	III	High fodder yield and divergence	Broad genetic base
IULYM-12	II	High protein content	Quality improvement
SHIMLA-2	III	Low ADF content	Better digestibility

Conclusion

The multivariate analysis revealed considerable genetic divergence among the 35 maize genotypes for fodder, grain yield, and quality traits. Variation observed in mean performance, PCA, path analysis scatter plot, dendrogram analysis, and heatmap analysis showed that the evaluated germplasm contains useful diversity for dual-purpose maize improvement. HAMIRPUR-1, IULYM-16, and INDORA-1 were identified as superior fodder-type genotypes because of their higher fresh stem weight, green fodder yield, and dry matter yield. In contrast, IULYM-15, IULYM-13, and SHIMLA-1 showed better performance for grain yield and related yield traits.

PCA showed that PC1 and PC2 explained 25.31% and 18.47% of the total variation, respectively, with a cumulative contribution of 43.78%. Fodder biomass traits contributed mainly to PC1, whereas grain yield-related traits contributed largely to PC2. This indicates that green fodder yield, dry matter yield, fresh stem weight, grain yield, harvest index, ear length, and 100-grain weight may serve as useful selection criteria for dual-purpose maize breeding.

Cluster analysis grouped the genotypes into three distinct clusters, confirming genetic diversity among the germplasm lines. Cluster I included promising grain-oriented genotypes such as IULYM-15 and IULYM-13, whereas Cluster II contained important fodder and quality genotypes such as IULYM-16, IULYM-4, and IULYM-12. Cluster III included divergent and high-biomass genotypes such as HAMIRPUR-1, INDORA-1, SHIMLA-1, and HAMIRPUR-2.

Based on overall performance and genetic divergence, IULYM-15, IULYM-13, IULYM-16, IULYM-4, HAMIRPUR-2, INDORA-1, IULYM-12, and SHIMLA-2 may be considered useful parental material for future breeding programs. Crosses between genetically diverse grain-type and fodder-type genotypes may help generate wider variability, improve recombination, and support the development of high-yielding dual-purpose maize cultivars suitable for Indo-Gangetic conditions.

Declarations

Author's contributions

Conceptualization and study design were carried out by Ali Mohammed Jidda, Prof. Saba Siddiqui, and Dr. Akshay Kumar Singh, while overall supervision and academic guidance were provided by Prof. Saba Siddiqui (Adviser) and Dr. Akshay Kumar Singh (Co-adviser). Methodology development was undertaken by Ali Mohammed Jidda, Manasi Singh, Ravi Pratap Singh and Yusuf Abba Asheikh. Field experimentation and data collection were performed by Ali Mohammed Jidda, Umar Musa, Arshi Fatima, Alok Dubey, and Dev Tyagi.

Formal analysis and data interpretation were conducted by Ali Mohammed Jidda, Muhammad Goni, Abdullahi Usman Largema, and Rohimat Mustapha, whereas software support, tools, and visualization were handled by Yusuf Abba Asheikh, Ravi Pratap Singh and Manasi Singh. The original draft of the manuscript was prepared by Ali Mohammed Jidda, and review and editing were carried out by Saba Siddiqui, Akshay Kumar, and all co-authors. All authors read and approved the final manuscript.

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Clinical Trial Number

Not applicable

Ethics Approval and Consent to Participate

Not applicable. This study did not involve human participants, animal experimentation, or clinical trials requiring ethical approval or informed consent.

Consent for Publication

Not applicable.

Availability of Data and Materials

The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request.

Competing Interests

The authors declare that they have no competing interests.

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Figures

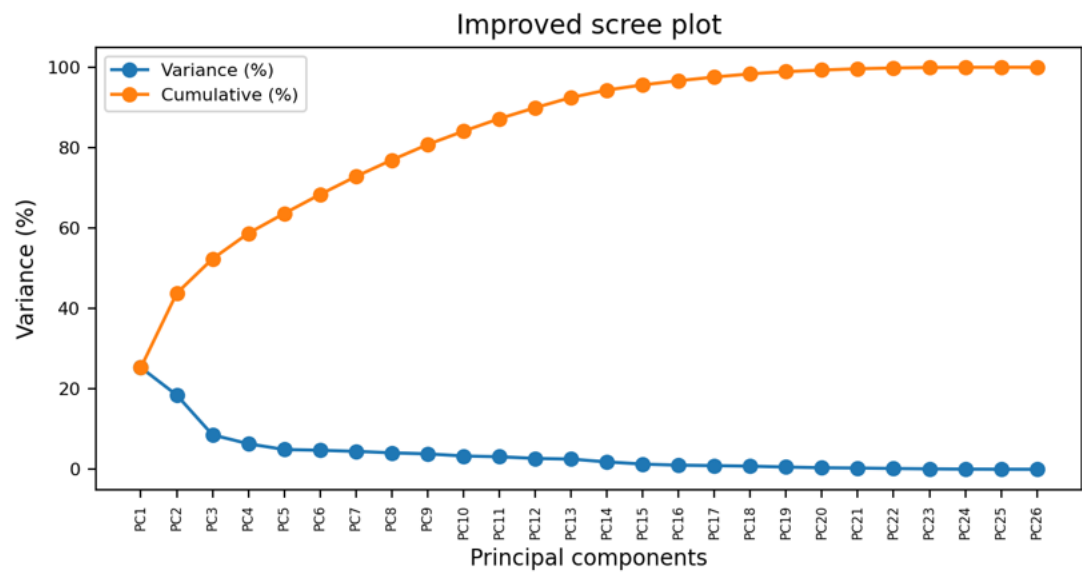


Figure 1

Scree plot showing the percentage contribution of principal components.

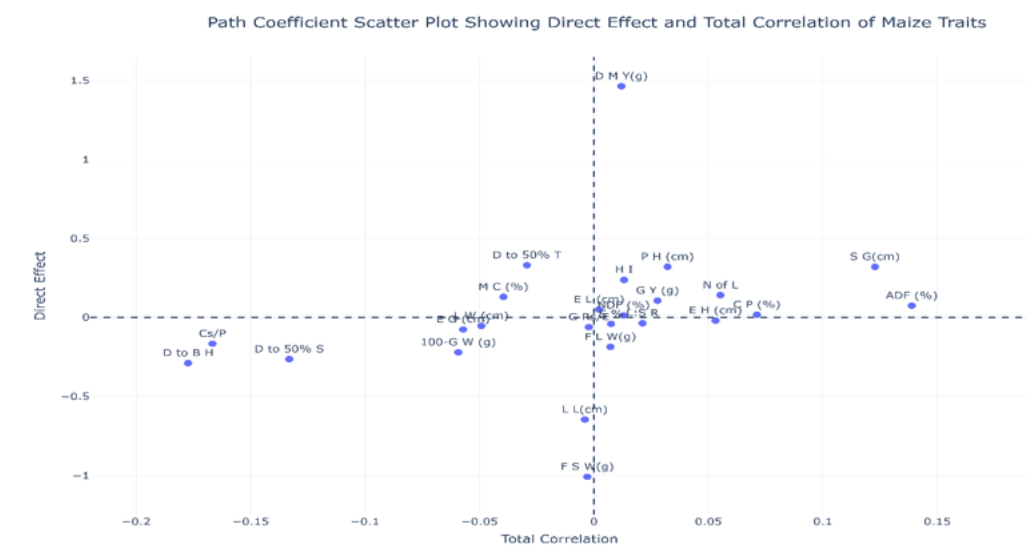


Figure 2

Path coefficient scatter plot showing direct effects and total correlation of maize traits.

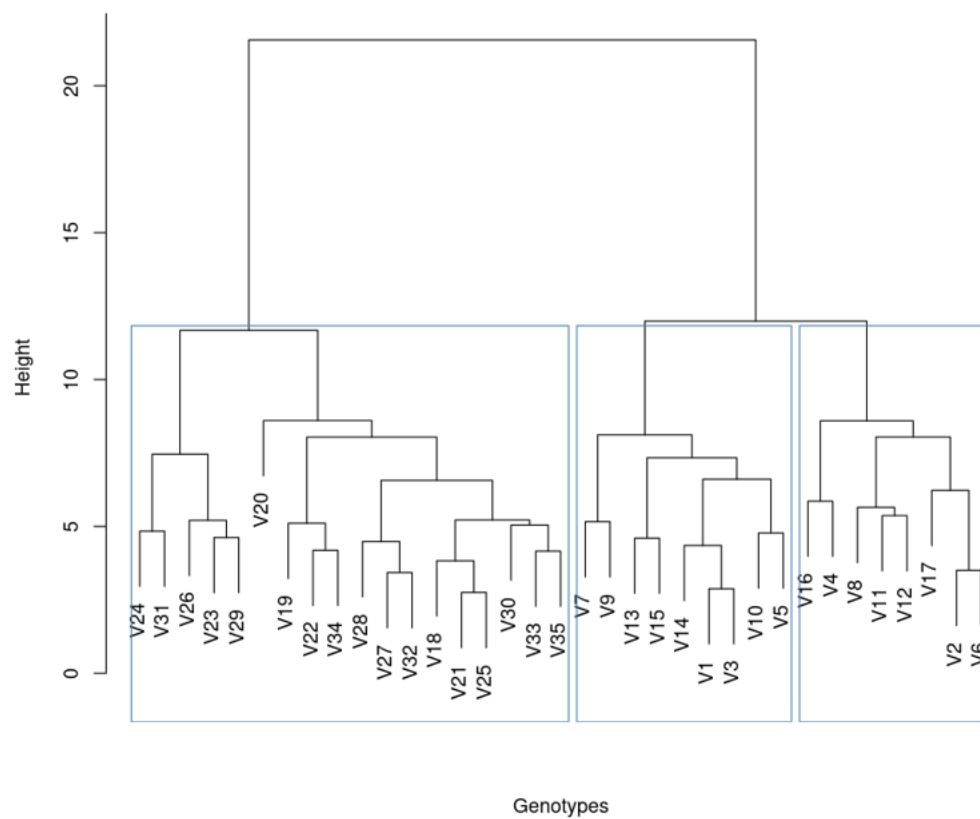


Figure 3
Hierarchical clustering dendrogram of maize genotypes.

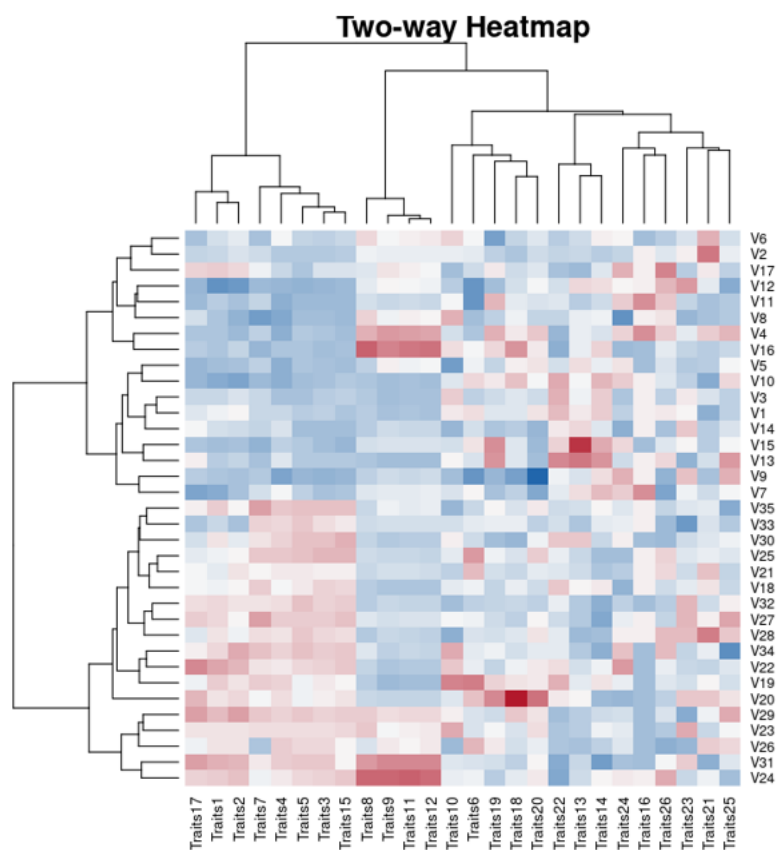


Figure 4

Heatmap showing the trait expression pattern among maize genotypes.