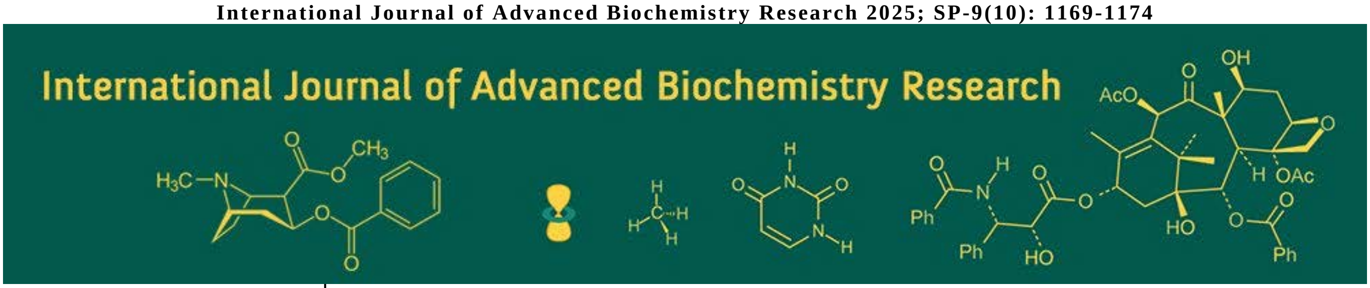
International Journal of Advanced Biochemistry Research 2025; SP-9(10): 1169-1174



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(10): 1169-1174
www.biochemjournal.com
Received: 02-07-2025
Accepted: 05-08-2025

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Genetic diversity studies of inbred lines for grain yield and its traits

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i10So.5975

Abstract

The genetic divergence among 80 maize (*Zea mays* L.) genotypes was assessed at experimental field of Agricultural Research Station (ARS), Karimnagar, Telangana, during *kharif* 2024 using Mahalanobis D^2 statistics based on fourteen traits. The genotypes were categorized into eleven distinct clusters. Largest was the Cluster I, comprising 61 genotypes, indicates high degree of genetic similarity followed by clusters II each with 7 genotypes and clusters V and VIII, each with 5 genotypes, Cluster X with 2 genotypes and remaining clusters contained a single genotype. Inter-cluster distances were notably higher than intra-cluster distances, indicating substantial genetic variability among genotypes from different clusters. The maximum inter-cluster distance (693.37) was recorded between clusters X and XI, followed by distances between clusters IX and XI (568.26), IV and X (551.47), VI and XI (503.64), II and X (493.13), VIII and X (474.44), V and XI (461.06), VII and IX (441.45) and VIII and XI (430.76). These high values reflect significant genetic divergence among the respective clusters. The highest intra-cluster distance (191.94) was recorded in cluster V, while clusters III, IV, VI, VII, and IX had zero intra-cluster distance, as each consisted of only one genotype. Among all clusters, cluster IX had the highest mean grain yield per plant, followed by clusters X and I. Hence, crosses made between clusters X and XI which improve hybrid production. Based on the magnitude of inter-cluster distances, genotypes from clusters V, IX, X and XI can be considered promising parents for hybridization programs aimed at developing superior hybrids. The characters like ear girth, ear height, number of kernels per row, number of kernel rows per ear are positively correlated with grain yield. The characters ear girth, test weight, number of kernels per row, ear length show highest positive direct effect on grain yield at genotypic level and test weight ear length, number of kernels per row, number of kernel rows per ear sow highest positive direct effect on grain yield at phenotypic level.

Keywords: Maize Inbreds, D^2 statistics, Genetic diversity, Inter-cluster distance, correlation, path analysis

Introduction

Maize (*Zea mays* L.), the third most important crop in India, and a member of the Poaceae family, is highly adaptable, thriving from sea level up to 3000 meters in altitude and across latitudes ranging from 58°N to 40°S. As a C4 plant, it is fertilizer-responsive, has high yield potential, and extensive cross-pollination, making it ideal for genetic improvement by plant breeders. Most maize cultivation occurs in warmer temperate regions and humid subtropical climates, with peak production in areas where the warmest month temperatures range from 20 °C to 27 °C and frost-free periods last between 120 and 180 days. Maize originated approximately 9,000 years ago through a single domestication event from its wild ancestor, teosinte, in southern Mexico (Matsuoka *et al.*, 2002). Among grain crops, maize displays the widest range of morphological variation (Kuleshov, 1933) and is widely grown across temperate, subtropical, and tropical regions worldwide. It serves as a dependable source of nutrition for humans, poultry, animals, and livestock, with its demand steadily rising due to its diverse applications, such as starch and ethanol production. This growing demand can be met, at least in part, by either expanding the area under maize cultivation or by enhancing crop productivity through the development and adoption of high-yielding hybrids.

Maize breeders consistently emphasize the importance of maintaining genetic diversity among parental genotypes, as it is vital for developing heterotic hybrids. Consequently, assessing the genetic divergence of maize germplasm is a key step in hybrid breeding programs aimed at producing high-yielding hybrids.

The extent of genetic diversity among germplasm can be effectively estimated using advanced biometrical tools such as multivariate analysis based on Mahalanobis D² statistics. This method is highly valuable for quantifying the level of divergence among inbred lines or any biological population at the genotypic level. It also aids in determining the relative contribution of various traits to overall divergence, both within and between clusters. Clustering techniques are employed to categorize genotypes into subgroups, aiming for maximum homogeneity within groups. The choice of clustering method depends on the approach best suited to the dataset. Information derived from these clusters can then be utilized to identify potential parents for developing heterotic maize hybrids.

In this context, the present study was conducted to assess the genetic diversity among 80 maize inbred lines, with the aim of identifying superior and genetically diverse parents for the development of heterotic hybrids. Knowing the favourable direct and indirect effects of component traits on grain yield will aid breeders in designing an effective selection strategy.

Material and Methods

The present study was carried out during kharif 2024 at Agricultural Research Station (ARS), Karimnagar, Telangana. The experimental material comprised of 80 inbred lines, including four checks (BML-6, BML-7, LM-13 and LM-14). The genotypes were sown in Augmented block Design with replicated checks. Each genotype was planted in two rows of 3m length each in each block, with a spacing of 60 cm between rows and 20 cm within row. The crop was raised as per the recommended package of practices. Observations on various pre and postharvest parameters were recorded on five plants selected at random from each entry in each block for days to 50 per cent anthesis, days to 50 per cent silking, anthesis silking interval, days to maturity, plant height (cm), ear length (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, grain yield per plant (g), test weight (g), shelling (%) and starch content (%). The collected data was analysed using standard statistical procedures. Genetic divergence was assessed using the D² statistics proposed by Mahalanobis (1928) [13] and outlined by Rao (1952) [17]. The percentage contribution of each trait to the total genetic divergence was calculated following the method described by Singh and Choudhary (1977) [20].

Results and Discussion

Analysis of variance based on fourteen quantitative characters showed significant variance among the evaluated genotypes of maize (Table 1). Significant variation across the genotypes showed that there were enough genotypic variations to improve the selection potential.

Table 1: Analysis of variance of augmented block design

Source	Mean Sum of Squares				
	Block (Ignoring treatments)	**Treatment (eliminating blocks)**	**Checks**	**Checks+ Varieties vs. varieties**	**Error**
Df	3	83	3	80	9
Days to 50 per cent anthesis	9.083**	2.320	4.333	2.245	1.278
Days to 50 per cent silking	10.583***	2.291*	4.563*	2.206*	0.674
Anthesis silking interval (ASI)	1.139	0.492	2.063	0.433	1.451
Days to maturity	10.583***	2.291*	4.563*	2.206*	0.674
Plant height (cm)	92.344*	377.574***	213.167**	383.739***	17.667
Ear height (cm)	380.750***	132. 368 ***	166.063 ***	131.104 ***	6.063
Ear length (cm)	8.885***	5.212***	10.809***	5.002***	0.066
Ear girth (cm)	5.392*	17.214***	8.332**	17.547***	0.980
Number of kernel rows per ear	0.344	3.149***	2.250**	3.183***	0.250
Number of kernels per row	34.382***	20.648***	16.167**	20.816***	1.778
Test weight (g)	12.565***	9.741***	7.631**	9.820***	0.753
Shelling (%)	19.157	13.364	9.400	13.512	14.956
Starch Content (%)	37.362***	2.562**	0.243	2.649**	0.569
Yield (g)	139.686***	321.427***	151.735***	327.790***	3.698

* Significant at 5 per cent level; ** Significant at 1 per cent level

The highest days to 50 percent anthesis and days to 50 percent silking was observed in KML-119, maximum plant height was seen in KML-105, more ear girth in KML-11, number of kernels per row in KML-33, highest grain yield is seen in KML-60. Eighty genotypes were grouped into 11 clusters as presented in Table 3. Cluster I was the largest, containing 61 genotypes whereas cluster III, IV, VI, VII, and IX were the smallest cluster containing only one genotype. Average intra and inter cluster distance of eleven clusters are presented in Table 2. The magnitude of the intra-cluster distances reflects the level of genetic diversity among genotypes within the same cluster. The inter-cluster distances were greater than the intra-cluster distances, indicating that genetic diversity between clusters was higher than within clusters. The intra cluster distances shown by inbred lines from cluster V (191.94) to cluster X (85.55). cluster V (191.94) followed by cluster II (142.15), cluster I (107.26), cluster VIII (97.25), cluster X (85.55) and remaining clusters III, IV, VI, VII, IX, XI shown zero intra cluster distances. indicating comparatively similar nature of the genotype within the cluster as proposed by (Arunachalam, 1981) [3], Bhusal *et al.* (2016) [4], Alam *et al.* (2013) [2] and Mani and Deshpande (2016) [14]. The high intra-cluster distance values indicated considerable genetic diversity among the genotypes grouped within the same clusters. This suggests significant potential for gene exchange among genotypes within these clusters as reported by Jakhar *et al.* (2018) [8]. The maximum inter cluster distance found between cluster X and XI (693.37) which indicates more diversity achieved between the genotypes of the clusters which leads to parental selection in hybridization programmes and lowest in between cluster III and VI (20.14). Although the genotypes were not extremely divergent between clusters having less inter cluster distance, they could not be grouped together based on the evaluated traits. Several researchers have recommended that crossing genotypes from clusters with high inter-cluster distances may produce promising segregants for selection as suggested by Lahane *et al*. (2016) [12], Matin *et al*. (2017) [16], Jakhar *et al*. (2018) [8], Kumar *et al*. (2014a) [10], Marker and Krupakar (2009) [15], Kumawat *et al* (2020) [11].

Table 2: Intra and inter cluster distances within and between clusters of 80 inbred lines

Clusters	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**	**Cluster XI**
Cluster I	107.26	178.11	165.79	149.58	251.72	213.27	193.87	166.66	181.17	347.00	331.54
Cluster II		142.15	329.63	246.57	319.88	391.71	313.31	312.75	294.14	493.13	288.89
Cluster III			0.00	58.53	308.63	20.14	20.39	76.09	356.54	367.69	386.42
Cluster IV				0.00	374.78	87.15	48.42	67.38	377.04	551.47	289.57
Cluster V					191.94	346.78	360.97	355.62	329.10	306.42	461.06
Cluster VI						0.00	37.99	83.95	441.07	434.71	503.64
Cluster VII							0.00	97.74	441.45	429.22	349.43
Cluster VIII								97.25	326.17	474.44	430.76
Cluster IX									0.00	239.26	568.26
Cluster X										85.55	693.37
Cluster XI											0.00

The data indicated that the cluster mean presented in Table 3. for Days to 50% anthesis is highest for cluster IV (66.00) and lowest for cluster III, VI, IX, X and XI (61.00). Days to 50 percent silking highest for cluster IV (68.00) and lowest for cluster XI (63.00). Anthesis silking interval highest for cluster V (5.00) and lowest for cluster IV and XI (2.00). Days to maturity is highest and lowest for cluster IV (108.00) and XI (103.00) respectively. Longest plant height is observed in cluster XI (195.00) and shortest plant height is observed in cluster VI (69.44). Ear height is high in cluster II (74.43) and lowest in cluster VIII (38.40). Ear length is more in cluster IX (23.50) and less in cluster VI (13.00). Ear girth is observed to be high in cluster IX (39.45) and low in cluster VI (30.08). Number of kernel rows per ear is high in cluster V (15.60) and low in cluster IV and VII (10.00). Cluster V (31.10) is having high number of kernels per row and cluster VII (17.00) have least number of kernels per row. Means of genotypes present in cluster IX (32.53) have high test weight when compared to remaining clusters and lowest test weight observed in genotypes of clusters VI (20.12). Shelling percentage is highest in clusters IV (79.20) and lowest shelling percentage is observed in cluster X (66.45). Percentage of high starch content is recorded in cluster V (80.10) and low starch in cluster III (60.12). Yield is highest in cluster IX (113.00) and lowest in cluster VII (44.60).

Parents for hybridization programmes could be chosen based on large inter-cluster distance to isolate useful recombinants in the segregating generations. A greater parental distance increases the likelihood of incorporating a higher number of desirable alleles at target loci. When these loci recombine in the F_2 and F_3 generations, following a cross between distantly related parents, the chances of successful selection for any trait of interest are enhanced (Ghaderi *et al*., 1984) [7].

Table 3: Cluster means of genotypes

Clusters	**Days to 50% anthesis**	**Days to 50% silking**	**Anthesis silking interval**	**Days to maturity**	**Plant height (cm)**	**Ear height (cm)**	**Ear length (cm)**	**Ear girth (cm)**	**Number of kernel rows per ear**	**Number of kernels per row**	**Test weight (g)**	**Shelling (%)**	**Starch content (%)**	**Yield (g)**
Cluster I	62.80	65.24	2.46	105.24	97.25	53.47	16.76	36.24	12.86	23.75	26.57	72.77	62.73	80.92
Cluster II	62.86	65.00	2.14	105.00	117.35	74.43	17.64	34.70	11.71	25.00	28.78	71.70	62.00	76.49
Cluster III	61.00	64.00	3.00	104.00	83.00	40.00	15.00	32.12	12.00	19.00	20.45	78.20	60.37	51.40
Cluster IV	66.00	68.00	2.00	108.00	90.00	43.00	15.00	30.13	10.00	20.00	23.01	79.20	63.11	54.00
Cluster V	62.20	65.20	3.40	105.20	111.00	55.80	18.28	35.29	15.60	31.10	27.12	72.76	80.10	64.68
Cluster VI	61.00	64.00	3.00	104.00	69.44	40.00	13.00	30.08	12.00	20.00	20.12	70.10	61.22	45.60
Cluster VII	63.00	66.00	3.00	106.00	92.00	47.00	14.00	30.12	10.00	17.00	21.34	77.20	60.82	44.60
Cluster VIII	62.20	64.60	2.40	104.60	74.76	38.40	15.40	30.67	10.80	22.20	23.89	72.14	62.86	60.44
Cluster IX	61.00	64.00	3.00	104.00	83.89	49.00	23.50	39.45	14.00	25.00	32.53	68.80	60.12	113.00
Cluster X	61.00	66.00	5.00	106.00	102.50	55.50	21.13	38.17	13.00	25.00	26.56	66.45	63.58	92.40
Cluster XI	61.00	63.00	2.00	103.00	195.00	52.00	16.00	32.12	12.00	20.00	24.12	74.00	61.55	62.00

Based on range of means, it is possible to know the characters influencing divergence. The results showed that the anthesis silking interval contributed 25.42% to the divergence of inbred lines. It was followed by grain yield per plant (24.07%), ear height (22.60%), number of kernel rows (10.70%), plant height (4.88%), number of kernel rows per ear (3.44%), starch content (3.18%), ear length (2.50%), ear girth (1.61%), test weight (1.43%), shelling percentage (0.17%) ranked least, contributed very less divergence. These findings were in line with Rathod *et al*. (2021) [18], Ganeshan *et al*. (2010) [6].

Correlation studies, presented in table 4, 5 describe degree and direction of characters towards grain yield per plant. Genotypically, grain yield was positively significant with days to 50 percent anthesis, days to 50 percent silking, ear height, ear length, ear girth, number of kernel rows per ear, kernels per row, test weight and negatively significant with starch content and positive and significant with ear height, ear length, ear girth, number of kernel rows per ear, kernels per row, test weight and negatively significant with starch content phenotypically. The findings were similar with ear height, ear length, ear girth, number of kernel rows per ear, kernels per row, test weight Dar *et al*. (2015), Reddy *et al*.

(2022) [19], Kovačević *et al.* (2024) [9], SC% was positive in findings of Saleem *et al.* (2008).

Among the various evaluated characters, ear girth recorded highest positive significant association with grain yield followed by test weight, ear length, number of kernel rows per ear, ear height, number of kernels per row, days to 50 percent silking followed by days to 50 percent anthesis at genotypic level and ear girth, test weight, ear length, number of kernel rows per ear, number of kernels per row at phenotypic level.

Table 4: Genotypical correlation studies for 14 characters of maize genotypes

Character	DFA	DFS	ASI	DM	PH (cm)	EH (cm)	EL (cm)	EG (cm)	NKRE	NKR	TW (g)	Shelling (%)	SC (%)	Yield (g)
DFA	1.0000	0.7819***	-0.3309***	-0.5319***	0.0637	0.3787***	-0.0979	0.3173***	-0.0065	0.0742	0.1587*	0.1907***	0.1608*	0.2351***
DFS		1.0000	0.3664***	-0.7085***	-0.0098	0.4403***	0.0524	0.3189***	0.0347	0.1342*	0.1928***	-0.0400	0.2260***	0.2634***
ASI			1.0000	-0.2044***	-0.0301	-0.0291	0.2005***	-0.0461	0.0714	0.1078	-0.0139	-0.3410***	0.2633***	-0.0963
DM				1.0000	-0.0211	-0.2014***	-0.0231	-0.1581*	-0.0184	-0.0413	-0.1039	0.0678	-0.1092	-0.1054
PH (cm)					1.0000	0.5496***	0.2381***	0.1399*	0.1589*	0.1955***	0.2346***	0.0778	0.3194***	0.0924
EH (cm)						1.0000	0.3787***	0.4208***	0.2868***	0.3217***	0.5078***	0.0192	0.0770	0.4175***
EL (cm)							1.0000	0.4368***	0.4073***	0.6574***	0.5492***	-0.1233	0.1285*	0.5709***
EG (cm)								1.0000	0.6996***	0.2783***	0.6717***	0.0446	0.0601	0.7391***
NKRE									1.0000	0.3938***	0.4342***	-0.0061	0.2356***	0.5302***
NKR										1.0000	0.4392***	0.0015	0.3333***	0.4188***
TW											1.0000	-0.1253*	0.0663	0.7210***
Shelling (%)												1.0000	-0.0219	-0.0537
SC (%)													1.0000	-0.2224***

Table 5: Phenotypical correlation studies for 14 characters of maize genotypes

Character	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	Test weight (g)	Shelling (%)	Starch Content (%)	Yield (g)
DFA	1.0000	0.3846***	-0.1469*	0.2400***	0.0165	0.1487*	-0.0272	0.0983	0.0209	0.0340	0.0744	0.0523	0.0803	0.0992
DFS		1.0000	0.1105	0.3511***	-0.0056	0.1389*	0.0179	0.1023	0.0101	0.0409	0.0507	-0.0280	0.1101	0.0734
ASI			1.0000	0.0662	-0.0270	-0.0276	0.1954**	-0.0509	0.0675	0.1008	-0.0060	-0.2783***	0.2481***	-0.0961
DM				1.0000	-0.0268	0.1229	0.0163	0.0791	0.0069	0.0539	0.0329	0.0151	0.0850	0.0800
PH (cm)					1.0000	0.5289***	0.2185***	0.1258*	0.1520*	0.1808**	0.2201***	0.0494	0.2982***	0.0902
EH (cm)						1.0000	0.3604***	0.3982***	0.2688***	0.3142***	0.4826***	0.0179	0.0638	0.4068***
EL (cm)							1.0000	0.4029***	0.3744***	0.6248***	0.5186***	-0.1138	0.1300*	0.5416***
EG (cm)								1.0000	0.6422***	0.2585***	0.6197***	0.0228	0.0487	0.6956***
NKRE									1.0000	0.3663***	0.4043***	0.0000	0.2057**	0.5069***
NKR										1.0000	0.4095***	0.0065	0.3155***	0.4062***
TW											1.0000	-0.0966	0.0608	0.6788***
Shelling (%)												1.0000	-0.0030	-0.0436
SC (%)													1.0000	-0.2064***

* Significant at 5 per cent level; ** Significant at 1 per cent level, DFA= Days to 50% anthesis, DFS= Days to 50% silking, ASI= Anthesis silking interval, DM= days to maturity, PH= Plant height, EH= Ear height, EL= Ear length, EG= Ear girth, NKRE= No. of kernel rows per ear, NKR= No. of kernels per row, TW= test weight, SC=starch content.

Table 6: Path analysis of various characters in maize inbred lines

Characters		DFA	DFS	ASI	DM	PH (cm)	EH (cm)	EL (cm)	EG (cm)	NKRE	NKR	Test weight (g)	Shelling (%)	Starch Content (%)	GYP (g)
DFA	G	-0.0232	-0.0645	0.0077	0.0355	-0.0015	-0.0088	0.0023	-0.0074	0.0001	-0.0017	-0.0037	-0.0044	-0.0037	0.2351
	P	0.0410	0.0158	-0.0060	0.0098	0.0007	0.0061	-0.0011	0.0040	0.0009	0.0014	0.0030	0.0021	0.0033	0.0992
DFS	G	-0.1005	-0.0361	-0.0132	0.0617	0.0004	-0.0159	-0.0019	-0.0115	-0.0013	-0.0048	-0.0070	0.0014	-0.0082	0.2634
	P	0.0096	0.0251	0.0028	0.0088	-0.0001	0.0035	0.0004	0.0026	0.0003	0.0010	0.0013	-0.0007	0.0028	0.0734
ASI	G	0.0252	-0.0279	-0.0762	0.0156	0.0023	0.0022	-0.0153	0.0035	-0.0054	-0.0082	0.0011	0.0260	-0.0201	-0.0963
	P	0.0086	-0.0064	-0.0582	-0.0039	0.0016	0.0016	-0.0114	0.0030	-0.0039	-0.0059	0.0004	0.0162	-0.0144	-0.0961
DM	G	0.2338	0.2608	0.0312	-0.1526	0.0032	0.0307	0.0035	0.0241	0.0028	0.0063	0.0159	-0.0104	0.0167	-0.1054
	P	0.0112	0.0164	0.0031	0.0466	-0.0013	0.0057	0.0008	0.0037	0.0003	0.0025	0.0015	0.0007	0.0040	0.0800
PH (cm)	G	0.0004	-0.0001	-0.0002	-0.0001	0.0060	0.0033	0.0014	0.0008	0.0010	0.0012	0.0014	0.0005	0.0019	0.0924
	P	0.0001	0.0000	-0.0001	-0.0001	0.0041	0.0022	0.0009	0.0005	0.0006	0.0007	0.0009	0.0002	0.0012	0.0902
EH (cm)	G	-0.0042	-0.0049	0.0003	0.0022	-0.0061	-0.0111	-0.0042	-0.0047	-0.0032	-0.0036	-0.0057	-0.0002	-0.0009	0.4175
	P	-0.0006	-0.0005	0.0001	-0.0005	-0.0021	-0.0039	-0.0014	-0.0016	-0.0011	-0.0012	-0.0019	-0.0001	-0.0002	0.4068

EL (cm)	G	-0.0139	0.0075	0.0286	-0.0033	0.0339	0.0540	0.1425	0.0622	0.0580	0.0937	0.0783	-0.0176	0.0183	0.5709
	P	-0.0044	0.0029	0.0320	0.0027	0.0357	0.0590	0.1636	0.0659	0.0613	0.1022	0.0848	-0.0186	0.0213	0.5416
EG (cm)	G	0.1259	0.1265	-0.0183	-0.0627	0.0555	0.1670	0.1733	0.3968	0.2776	0.1104	0.2666	0.0177	0.0239	0.7391
	P	0.0331	0.0344	-0.0171	0.0266	0.0423	0.1340	0.1356	0.0065	0.2161	0.0870	0.2085	0.0077	0.0164	0.6956
NKRE	G	-0.0006	0.0032	0.0066	-0.0017	0.0147	0.0264	0.0375	0.0645	0.0922	0.0363	0.0400	-0.0006	0.0217	0.5302
	P	0.0027	0.0013	0.0087	0.0009	0.0196	0.0346	0.0483	0.0828	0.1289	0.0472	0.0521	0.0000	0.0265	0.5069
NKR	G	0.0140	0.0253	0.0204	-0.0078	0.0369	0.0607	0.1241	0.0525	0.0744	0.1888	0.0829	0.0003	0.0629	0.4188
	P	0.0055	0.0067	0.0164	0.0088	0.0295	0.0512	0.1018	0.0421	0.0597	0.1629	0.0667	0.0011	0.0514	0.4062
TW(g)	G	0.0428	0.0520	-0.0037	-0.0280	0.0633	0.1369	0.1481	0.1811	0.1171	0.1184	0.2696	-0.0338	0.0179	0.7210
	P	0.0208	0.0142	-0.0017	0.0092	0.0615	0.1348	0.1448	0.1731	0.1129	0.1144	0.2793	-0.0270	0.0170	0.6788
Shelling (%)	G	-0.0077	0.0016	0.0138	-0.0027	-0.0031	-0.0008	0.0050	-0.0018	0.0002	-0.0001	0.0051	-0.0404	0.0009	-0.0537
	P	-0.0014	0.0007	0.0073	-0.0004	-0.0013	-0.0005	0.0030	-0.0006	0.0000	-0.0002	0.0025	-0.0262	0.0001	-0.0436
SC (%)	G	-0.0569	-0.0800	-0.0932	0.0386	-0.1130	-0.0272	-0.0455	-0.0213	-0.0833	-0.1179	-0.0235	0.0078	-0.3438	-0.2224
	P	-0.0270	-0.0370	-0.0833	-0.0285	-0.1001	-0.0214	-0.0436	-0.0163	-0.0690	-0.1059	-0.0204	0.0010	-0.3355	-0.2064

Diagonal values are direct effects

Path coefficient analysis of study presented in table 6, further indicated that ear girth (0.3968) has the highest positive direct effect on grain yield per plant, followed by test weight, number of kernels per row, ear length, plant height is positive genotypically and phenotypically same as findings of Damtie *et al*. 2021 [5], while starch content is negative and indirect effect towards yield genotypically. However, phenotypically test weight (0.2793) has strongest positive direct effect on grain yield per plant followed by number of kernels per row, ear length, number of kernel rows per ear this in line with Hamad *et al*. (2024), days to maturity, days to 50 percent anthesis, days to 50 percent silking while starch content is negative and indirect effect towards yield. Ear girth, days to 50 percent anthesis, ear length are in line with Akshaya *et al*. (2022) [1].

Conclusion

Most of the maize inbred lines showed significant differences for all the characters under study indicating the presence of considerable variability among them. The large number of clusters and their genetic divergence values further confirmed substantial genetic diversity. Inbred lines with higher genetic divergence can be effectively utilized in crossing programs to develop high-yielding maize hybrids. Grain yield is significantly correlated and have direct effects with ear girth, ear length, number of kernel rows per ear, number of kernels per row, test weight and negatively significant and show indirect effect with starch content.

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