



GENETIC DIVERSITY OF MAIZE INBRED LINES BASED ON MORPHOLOGICAL TRAITS AND ITS ASSOCIATION WITH HETEROISIS

A.M.M. AL-NAGGAR^{1*}, A.M. SOLIMAN¹, M.H. HUSSIEN², and A.M.H. MOHAMED³

¹Department of Agronomy, Faculty of Agriculture, Cairo University, Egypt

²Department of Genetics, Faculty of Agriculture, Cairo University, Egypt

³Department of Agronomy, Faculty of Agriculture, Omar El-Mokhtar University, Libya

*Corresponding author's email: medhatalnaggar@agr.cu.edu.eg

Email addresses of co-authors: ahmonged@gmail.com, monahashim64@gmail.com, homajore66@gmail.com

SUMMARY

In any breeding program, the creation of high-yielding maize hybrids with the best possible heterosis expression depends on the genetic diversity of the parental inbred lines. This study aimed to quantify the genetic diversity of eight inbred lines of maize using morphological features and determine the relationship between heterosis in grain yield per hectare and distance matrices of morphological variables. The principal component analysis (PCA) determined the morphological genetic diversity among the eight inbred lines based on 22 variables. The study assessed heterosis in their diallel crossings in a two-year field experiment utilizing a randomized complete block design with three replications. The dissimilarity Euclidean coefficients among the eight maize inbred lines ranged from 0.08 (between L21 and L28) to 0.69 (between L21 and IL80), with an average of 0.38. The results revealed that dissimilarity values based on morphological traits showed a low, positive, and non-significant relationship with mid-parent heterosis, better-parent heterosis, and mean grain yield ha⁻¹. To fully comprehend the genetic diversity of maize inbred lines, an extensive analysis of a vast collection of inbred lines from various populations using a variety of morphological traits is necessary.

Keywords: *Zea mays*, genetic diversity, inbred lines, PCA, heterosis, clustering analysis

Key findings: The results will help maize breeders choose parental inbred lines efficiently to produce F₁ cross hybrids with a high yield and the maximum heterosis possible.

Communicating Editor: Prof. Dr. Clara R. Azzam

Manuscript received: August 5, 2022; Accepted: August 21, 2022.

© Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO) 2022

INTRODUCTION

In terms of overall production and cultivated area, maize (*Zea mays* L.) is Egypt's second-largest cereal crop after wheat. Egypt produced 7.50 million t of grain in 2020 on 1,458,881 ha of maize, with an average yield of 5.14 t/ha (FAOSTAT, 2022). With the insufficient local maize output to meet demand, Egypt imported 7.88 million t of maize grains in 2020 with an

import value of USD1,880,862,000 (FAOSTAT, 2022). Maize producers should increase the grain yield productivity of the recently produced hybrids in order to close the gap between local production and consumption of maize grains in Egypt. The Egyptian breeders have focused their efforts here on creating various inbred lines that can be used in the breeding programs to utilize heterosis better.

To cite this manuscript: Al-Naggar AMM, Soliman AM, Hussien MH, Mohamed AMH (2022). Genetic diversity of maize inbred lines based on morphological traits and its association with heterosis. *SABRAO J. Breed. Genet.* 54(3): 589-597. <http://doi.org/10.54910/sabrao2022.54.3.11>

The knowledge of the genetic diversity of the available germplasm greatly influenced crop plant development and was applied successfully for genotype selection and germplasm management for various breeding goals (Fufa *et al.*, 2005; Boonlertnirun *et al.*, 2012). The performance of the resulting hybrid depends on how genetically divergent the two inbred lines are (Pajic *et al.*, 2010). Higher heterosis results from more diverse parents and vice versa (Duvick, 1999; Dermail *et al.*, 2018). The production of a novel, versatile hybrid with greater levels of heterosis expression requires inbred parental lines with substantial genetic variation in maize breeding programs (Hallauer *et al.*, 2010). Generally, assessing genetic diversity uses phenotypic variables and molecular markers (Govindaraj *et al.*, 2015). Many limitations for using phenotypic data to evaluate genetic divergence exist, i.e., the environmental impact on morphological expression (Beyene *et al.*, 2005), still these serve as a worthy preliminary assessment of maize genetic diversity and provide needed information to evaluate available germplasm (Al-Naggar *et al.*, 2020).

The exploitation of heterosis is very successful in maize as a cross-pollinated crop, which is one of the best technologies to increase the grain yield of this important crop. The value of any inbred line of maize in heterosis breeding ultimately depends on its ability to combine well with other inbreds to produce superior F1 progeny (Adetimirin *et al.*, 2008; Arifin *et al.*, 2018). Information on genetic diversity is crucial for a more successful hybrid breeding program since it is helpful to choose optimal parental inbred lines for heterosis breeding (Bhusal and Lal, 2017). Studies applied a diallel mating design in breeding to find the best-inbred parents for developing cross hybrids (Miranda *et al.*, 2008;

Kumar *et al.*, 2015). In calculating heterosis and mean hybrid performance, it would be helpful to understand the relationship between the genetic diversity of the parents' inbred lines and the performance of their hybrids.

Although many researchers ventured to investigate the relationship between the genetic diversity of inbred lines and the heterosis of their hybrids, as well as, to predict hybrid performance based on the level of genetic diversity of parental inbred lines, this problem remains not fully resolved (Dhliwayo *et al.*, 2009; Devi and Singh, 2011; George *et al.*, 2011; Ndhlela *et al.*, 2015; Singh, 2015). Some researchers found a strong link between genetic distance and heterosis (Spooner *et al.*, 1996; Amorim *et al.*, 2006; George *et al.*, 2011). But others found no link or a non-significant association with heterosis (Balestre *et al.*, 2008; Legesse *et al.*, 2008; Dhliwayo *et al.*, 2009; Devi and Singh, 2011; Bhusal and Lal, 2017).

This study's goals aimed: (1) to use morphological traits to gauge the degree of genetic diversity among eight inbred lines of maize; (2) to use cluster analysis to gauge the genetic separation between these genotypes; and (3) to identify correlations between distance matrices based on morphological traits and heterosis of grain yield/ha.

MATERIALS AND METHODS

Plant material

This work used eight maize (*Zea mays* L.) inbred lines in the S9 generation, originating from various populations and their 28 F₁ hybrids produced in the 2019 growing season, using a half-diallel mating design (Table 1).

Table 1. Origin and parentage of the eight inbred lines used in this investigation.

Inbred line designation	Parental source	Origin
L 14-Y	Population Gemmeiza	ARC-Egypt
L 17-Y	SC30 N 11	DuPont Pioneer-Egypt
L 21-Y	SC 72012	GWS-Egypt
L28-Y	Population 59	ARC-Thailand
IL51W	L-296 A Locally developed	ARC-Egypt
IL53W	Rg-8 G.S. [(Sanjuan × Ci64) (SC.14)]	ARC-Egypt
IL80W	Rg-37 G.S. [(PI221866×307A) (SC.14)]	ARC-Egypt
IL84W	Rg-41 G.S. [(Sanjuan × 307) (SC.14)]	ARC-Egypt

Y=Yellow, W=White, ARC=Agricultural Research Center

Field experiment

The Agricultural Experiment and Research Station of the Faculty of Agriculture, Cairo University, Giza, Egypt (30° 03'N latitude and 31° 13'E longitude at an altitude of 18.60 masl), provided the site of the field assessment trials in the 2020 and 2021 seasons. The experiment used a randomized complete block design (RCBD) with three replications. A total of 36 genotypes (eight inbred lines and 28 F₁s) consisted of each duplicate. Each genotype was given a two-row plot 4 m long, 60 cm apart, and a 25 cm space between hills (one plant per hill). Each experimental plot had a 4.8 m² area. All other agricultural procedures, including irrigation, fertilization, weed and insect control, were carried out based on the requirements of ARC, Egypt to produce healthy plants.

Data recorded

The study recorded data on days to 50% anthesis (DTA), days to 50% silking (DTS), anthesis silking interval (ASI), plant height (PH), ear height (EH), leaf angle (LANG), leaf area index (LAI), leaf area required to produce one-gram grain (LA 1gG⁻¹), chlorophyll concentration index (CCI), number of ears plant⁻¹ (EPP), number of rows ear⁻¹ (RPE), number of kernels row⁻¹ (KPR), number of kernels plant⁻¹ (KPP), 100-Kernel weight (100KW), grain yield plant⁻¹ (GYPP), grain yield ha⁻¹ (GYPH), grain starch content (GSC), grain protein content (GPC), grain oil content (GOC), grain fiber content (GFC), grain ash content (GAC), and grain moisture content (GMC). Using an INSTALAB 600 Near Infrared (NIR) Product Analyzer made by DICKEY-john Corporation, Auburn, Illinois, USA, samples collected from the seed bulk of each genotype were used to measure the seed quality traits (SPC, SSC, SOC, SAC, SFC, and SMC) in both seasons.

Biometrical analyses

SAS software was used to analyze the data. Each year's variance analysis of the RCBD was done separately. If the homogeneity test returned a non-significant result, a combined analysis of the variance of the RCBD over the two years was also carried out. Heterosis (H) relative to the mid parent (MP) and better parent (BP) for each cross combination (F₁ hybrid) was calculated as follows: Mid-parent heterosis MPH = $([F_1 - MP] / MP) \times 100$, where F₁ is the mean of the F₁ hybrid performance and MP is the mean performance of the two

parental inbred lines $([P_1 + P_2] / 2)$. Better-parent heterosis (BPH) = $([F_1 - BP] / BP) \times 100$, where BP = mean of the better parent.

Morphological evaluations

An essential concern in plant breeding is how to best use the data's morphological characterization information. The trait-standardized database was then broken down into its constituent parts (principal components) (PC).

Cluster analysis of morphological data

The study created dendrograms of phenotypic variation for the eight genotypes, using data for all traits averaged across two years. Performing aggregative hierarchical clustering (AHC) of genotypes used morphological data scaled through XLSTAT (2014) software. AHC was based on standard Euclidean distances. Computations on the percentage contribution of various morphological qualities to genetic diversity used XLSTAT to identify the morphological traits that explained the variation across the genotypes using principal component analysis (PCA). Further using XLSTAT's complete linkage method, dendrograms got created using normalized Euclidean distance matrices. Pearson's correlation coefficients were calculated between dissimilarity Euclidean coefficients and heterosis values (MPH and BPH).

RESULTS AND DISCUSSION

Phenotypic identification and variation

Analysis of variance of RCBD across two years indicated that the mean squares (MS) due to genotype (G) were significant ($P \leq 0.01$) for all studied traits. With exceptions to the grain content of starch (GSC), fiber (GFC), ash (GAC), and moisture (GMC), it suggested notable differences among the eight maize inbred lines for most of the studied traits (Table 2). Results of the study suggest good experiment precision with the coefficient of variation (CV) generally low (<10) for all studied traits. Except for the anthesis-silking interval (ASI), leaf area produced one gram grain (LA 1gG⁻¹), leaf area index (LAI), number of ears plant⁻¹ (EPP), number of kernels plant⁻¹ (KPP), grain oil content (GOC), and GFC. The coefficient of determination (R²) for most studied traits was very high (close to unity). It indicates that variables explained a high

Table 2. Summary data for 22 phenotypic traits of eight maize inbred lines tested in the field across two seasons (2020 and 2021).

Variable	Minimum	Maximum	Mean	MS (G)	SD	CV%	R ²
DTA	60.08	60.83	60.46	**	0.29	1.37	0.78
DTS	62.67	63.58	63.13	**	0.38	1.49	0.81
ASI	2.5	3.0	2.67	**	0.17	18.37	0.60
PH	192.3	219.3	204.1	**	9.79	5.24	0.83
EH	87.85	106.58	97.59	**	6.62	9.04	0.72
LA 1gG ⁻¹	0.98	1.26	1.15	**	0.1	21.26	0.99
LAI	2.25	2.74	2.5	**	0.17	15.15	0.97
LANG	23.88	28.33	26.09	**	1.23	6.53	0.75
CCI	32.47	39.26	36.25	**	2.04	7.89	0.88
EPP	1.18	1.64	1.47	**	0.19	19.7	0.75
RPE	13.54	14.62	14.21	**	0.34	6.75	0.77
KPR	37.54	39.39	38.48	**	0.66	7.77	0.57
KPP	629	916.9	803.3	**	106.8	22.24	0.83
HKW	22.82	26.18	24.59	**	1.34	6.28	0.93
GYPP	95.59	176.82	127.18	**	27.89	8.17	0.97
GYPH	2.93	5.75	3.98	**	0.96	9.04	0.97
GSC	63.97	65.27	64.47	Ns	0.51	2.46	0.47
GPC	8.15	8.67	8.43	**	0.16	5.73	0.88
GOC	3.21	3.53	3.3	**	0.11	16.35	0.68
GFC	1.65	2.08	1.87	Ns	0.16	38.71	0.43
GAC	10.19	10.47	10.33	Ns	0.1	10.37	0.43
GMC	11.55	12.21	11.77	Ns	0.21	3.48	0.82

** indicates significant ($P \leq 0.01$), ns indicates not significant. MS=Mean squares, SD=Standard deviation, CV=Coefficient of variation, R²= Coefficient of determination, DTA = Days to anthesis, DTS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, LA 1gG⁻¹ = Leaf area produced 1 g grain, LAI = Leaf area index, LANG = Leaf angle, CCI = Chlorophyll concentration index, EPP = Ears plant⁻¹, RPE = Rows ear⁻¹, KPR = Kernels row⁻¹, KPP = Kernels plant⁻¹, HKW = Hundred kernel weight, GYPP = Grain yield plant⁻¹, GYPH = Grain yield ha⁻¹, GSC = Grain starch content, GPC = Grain protein content, GOC = Grain oil content, GFC = Grain fiber content, GAC = Grain ash content, GMC = Grain moisture content.

variability in the characteristic performance. Several researchers noticed comparable outcomes in maize (Asare *et al.*, 2016; Twumasi *et al.*, 2017; Al-Naggar *et al.*, 2020).

Mean grain yield ha⁻¹ (GYPH) ranged from 2.93 to 5.75 t, with an average of 3.98 t. Mean grain yield plant⁻¹ ranged from 95.59 to 176.82g, with an average of 127.18g. Hundred kernel weight (100-KW) ranged from 22.82g to 26.18g, with an average of 24.59g. The number of days to silking (DTS) ranged from 62.67 to 63.58, with an average of 63.13. Plant height (PH) ranged from 192.3 to 219.3 cm, with an average of 204.1 cm. The LAI ranged from 2.25 to 2.74, with an average of 2.50. The chlorophyll concentration index (CCI) ranged from 32.47% to 39.26%, with an average of 36.25%. The KPP ranged from 629 to 916.9, with an average of 803.3. Seed starch content (SSC) ranged from 63.97% to 65.27%, with an average of 64.47%. Seed protein content (SPC) ranged from 8.15% to 8.67%, with an average of 8.43%. Seed oil content (SOC) ranged from 3.21% to 3.58%, with an average of 3.3%. Grain yield and its

related traits showed genetic variation among the inbred lines, suggesting that significant genetic progress could be made in selecting enhanced grain yield and other traits (Oyekunle and Badu-Apraku, 2018; Al-Naggar *et al.*, 2020).

Principal component analysis

A principal component analysis of standardized data was used to highlight the correlations between maize traits and their use in genotype characterization and comparison to show the genetic diversity among maize inbred lines (Table 3). Data standardization is required to eliminate the units because distinct qualities use various units. The values of the principal components, PC1, and PC2, were scaled to have an equilateral distribution between genotype and trait scores.

According to the principal component analyses of morphological traits, the first principal component (PC1), accounting for 41.33% of the total variation among inbred lines, suggested the value of distinguishing

Table 3. Principal component analysis (PCA) for morphological data, combined across two seasons (2020 and 2021).

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DTA	-0.25	0.23	0.01	-0.11	-0.14	0.18	0.18
DTS	-0.28	0.19	0.06	0.09	-0.08	0.00	0.06
ASI	-0.21	0.03	0.12	0.39	0.07	-0.30	-0.19
PH	0.25	0.13	0.03	0.29	-0.03	-0.24	0.06
EH	0.26	-0.27	0.04	-0.10	-0.01	0.03	0.09
LA 1gG ⁻¹	0.24	0.19	0.08	0.33	-0.04	0.11	-0.11
LAI	0.24	0.16	0.04	-0.11	-0.25	0.33	-0.17
LANG	0.06	0.06	0.32	-0.24	-0.35	-0.34	-0.34
CCI	0.20	0.13	0.30	-0.12	-0.16	0.29	-0.20
EPP	-0.19	0.32	-0.09	-0.06	-0.29	-0.04	0.07
RPE	0.07	-0.05	0.35	0.14	0.28	0.46	-0.04
KPR	0.09	0.30	-0.32	-0.20	0.11	0.17	0.16
KPP	-0.16	0.36	-0.09	-0.05	-0.26	0.05	0.10
HKW	0.22	0.23	0.06	0.29	-0.06	0.04	0.37
GYPP	0.28	0.18	0.05	0.14	-0.11	-0.08	0.07
GYPH	0.28	0.16	0.06	0.14	-0.09	-0.12	0.07
GSC	0.29	-0.06	-0.06	-0.13	0.17	-0.11	0.27
GPC	-0.03	0.08	0.49	-0.10	0.12	-0.14	0.32
GOC	-0.06	0.26	0.19	-0.33	0.36	0.07	-0.21
GFC	-0.13	-0.24	0.28	0.11	-0.36	0.12	-0.06
GAC	-0.11	0.28	-0.06	0.32	0.32	0.15	-0.34
GMC	0.28	0.08	0.00	-0.26	0.06	-0.08	-0.09
Eigenvalue	9.92	4.39	3.54	2.29	2.00	1.42	0.44
Variability (%)	41.33	18.30	14.73	9.54	8.34	5.92	1.84
Cumulative %	41.33	59.63	74.37	83.90	92.24	98.16	100.00

PC1-PC7= Principal components, DTA = Days to anthesis, DTS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, LA 1gG⁻¹ = Leaf area produced 1 g grain, LAI = Leaf area index, LANG = Leaf angle, CCI = Chlorophyll concentration index, EPP = Ears plant⁻¹, RPE = Rows ear⁻¹, KPR = Kernels row⁻¹, KPP = Kernels plant⁻¹, HKW = Hundred kernel weight, GYPP = Grain yield plant⁻¹, GYPH = Grain yield ha⁻¹, GSC = Grain starch content, GPC = Grain protein content, GOC = Grain oil content, GFC = Grain fiber content, GAC = Grain ash content, GMC = Grain moisture content.

maize genotypes jointly by grain yield plant⁻¹, grain yield ha⁻¹, grain starch content, days to silking, grain moisture content, plant height, and 100-kernel weight (Table 3). The second principal component (PC2), which accounted for 18.30% of the overall variability, revealed that grain protein, grain ash, and grain fiber contents, together with ears plant⁻¹, kernels row⁻¹, and kernels plant⁻¹, all played a role in distinguishing inbred lines of maize. The results agreed with Al-Naggar *et al.* (2020), who found that the first two components, PC1, and PC2, accounted for 57.91% of the total variation among 19 maize genotypes.

Dissimilarity Euclidean coefficients based on phenotypic traits

Based on morphological data, the eight maize inbred lines' dissimilarity Euclidean coefficients varied from 0.08 to 0.69, with an average of

0.38 (Table 4). The inbred line L21 was the most, unlike IL80, according to Euclidean distances used to measure dissimilarity; as a result, this pair of genotypes is the most unrelated genotypes in this experiment. The dissimilarity suggests L21 or L28 may cross with IL80 or IL84 to produce high-yielding single-cross hybrids or perform selection in the segregating generations, which could result in transgressive segregation with a higher grain yield than both of its parents. This outcome is consistent with earlier findings (Al-Naggar *et al.*, 2020; Younis *et al.*, 2021). In contrast, dissimilarity Euclidean coefficients revealed the genotypes most similar to one another were those that showed the lowest dissimilarity Euclidean coefficients, based on the phenotypic data. In this experiment were the genotype pairs L21 and L28 (0.08) and L14 and L51 (0.09).

Table 4. Dissimilarity Euclidean coefficients based on phenotypic traits analysis among eight maize inbred lines combined across two seasons (2020 and 2021).

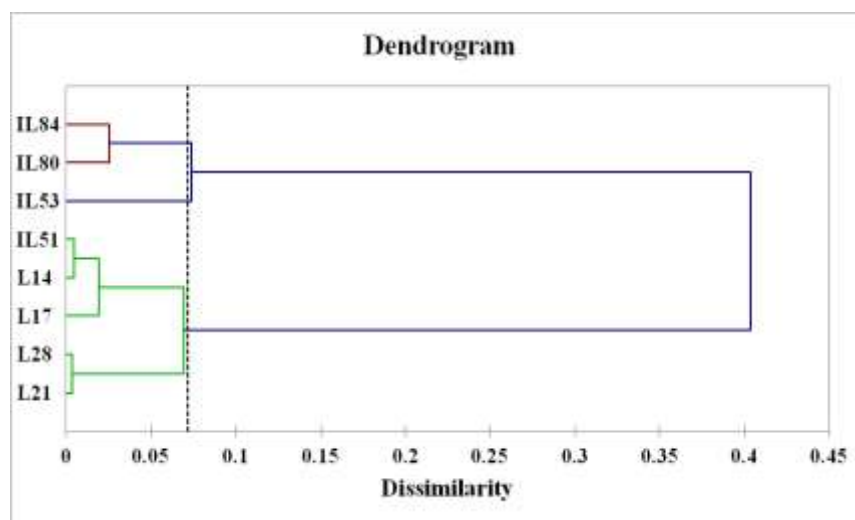
Inbred lines	L14	L17	L21	L28	IL51	IL53	IL80
L17	0.18						
L21	0.24	0.35					
L28	0.23	0.31	0.08				
IL51	0.09	0.17	0.20	0.17			
IL53	0.51	0.36	0.60	0.53	0.46		
IL80	0.51	0.35	0.69	0.63	0.50	0.25	
IL84	0.43	0.31	0.64	0.61	0.45	0.43	0.23

Agglomerative hierarchical clustering (AHC) analysis

Figure 1 shows the dendrogram of the maize inbred lines produced from the complete linkage method's standard phenotypic data collected across two years. The analysis divided the eight inbred lines into two groups. Cluster 1 consisted of five inbred lines, L14, L17, L21, L28, and IL51, while three inbred lines (IL53, IL80, IL84) comprised cluster 2. The first cluster, divided into two groups, consisted of the first group with two inbred lines (L18 and L28)— closely related genotypes. The second group further divides into two subgroups. The first subgroup consists of one inbred (L17) and the second subgroup with two inbred lines (L14, IL51)—closely related genotypes, too. The second cluster also divides into two groups, the first group including only one inbred line (IL53) and the second group two inbred lines (IL80, IL84).

These two inbred lines are closely related genotypes. In conclusion, the most closely related genotypes in the experiment consist of L18 and L21, followed by L14 and IL51. These findings suggest that each pair of these inbred lines may have a common ancestor. This observation is consistent with other earlier findings (Al-Naggar *et al.*, 2020; EL-Harty *et al.*, 2021; Younis *et al.*, 2021).

A technique for categorizing a set of attributes into groups is cluster analysis. The agglomerative hierarchical clustering (AHC) using the unweighted pair group method with arithmetic mean (UPGMA) is the method used for genotypic clustering (Mohammadi *et al.*, 2003; Al-Naggar *et al.*, 2020; El-Harty *et al.*, 2021). The analysis classified the eight maize genotypes into two groups. The clusters reflect uncorrelated groupings that could be helpful for future breeding efforts, since different sets of alleles may control how well the traits perform.

**Figure 1.** Dendrogram of eight maize inbred lines based on 22 morphological characters measured across two seasons (2020 and 2021) using the agglomerative hierarchical clustering.

Correlation of genetic diversity with heterosis and hybrid mean performance

The 28 F₁ hybrids between the eight inbred lines (half-diallel crosses) were tested as mean grain yield ha⁻¹, mid-parent heterosis (MPH), and better-parent heterosis (BPH) (Table 5). Table 6 presents Pearson's correlation coefficients between the morphological genetic diversity matrices (mentioned in Table 4) with MPH, (BPH), and hybrid mean performance (Mean) for grain yield/ha (presented in Table 5). According to Table 6's results, genetic dissimilarity (GD) based on morphological features had weak, positive, and non-significant correlations with BPH (0.11), MPH (0.25), and hybrid mean performance (0.26) for grain yield ha⁻¹.

The findings of many researchers (Balestre *et al.*, 2008; Legesse *et al.*, 2008; Dhliwayo *et al.*, 2009; Devi and Singh, 2011;

Bhusal and Lal, 2017) reported genetic divergence of inbred lines had no significance or association with heterosis. Thus, it validates the study findings regarding the association between genetic diversity based on morphological traits and heterosis. Study results also contradict the findings of other researchers (Spooner *et al.*, 1996; Amorim *et al.*, 2006; George *et al.*, 2011), who claimed that the greater the parental divergence, the greater the likelihood of heterosis. The utilization of distinct parental genetic backgrounds or inbred population sources of non-heterotic patterns may be due to the disparate results of several investigations. To fully comprehend the genetic diversity of the maize crop and its relationship to heterosis, an extensive examination of a broad collection of maize inbred lines from multiple populations utilizing sizable morphological traits needs undertaking.

Table 5. Mean grain yield t/ha⁻¹ (Mean), mid-parent heterosis (MPH) and better-parent heterosis (BPH) of F₁ hybrids across two seasons (2020 and 2021).

F ₁ Hybrids	GYPH (t)	MPH	BPH
L14 × L17	7.552	0.657	0.612
L14 × L21	8.166	1.039	0.690
L14 × L28	8.907	1.213	0.869
L14 × IL51	7.041	0.567	0.496
L14 × IL53	8.211	0.882	0.672
L14 × IL80	7.008	0.520	0.471
L14 × IL84	8.904	0.715	0.545
L17 × L21	7.742	1.033	0.723
L17 × L28	7.433	0.908	0.650
L17 × IL51	7.848	0.730	0.698
L17 × IL53	6.413	0.552	0.414
L17 × IL80	7.248	0.681	0.673
L17 × IL84	7.080	0.322	0.162
L21 × L28	7.657	1.334	1.280
L21 × IL51	8.189	1.245	0.933
L21 × IL53	7.948	1.431	1.245
L21 × IL80	9.582	1.579	1.196
L21 × IL84	8.462	0.888	0.442
L28 × IL51	6.738	0.832	0.610
L28 × IL53	9.389	1.685	1.534
L28 × IL80	7.173	0.865	0.619
L28 × IL84	10.084	1.195	0.705
IL51 × IL53	7.944	1.047	0.897
IL51 × IL80	9.012	0.888	0.862
IL51 × IL84	11.519	1.146	0.857
IL53 × IL80	9.515	1.150	0.968
IL53 × IL84	11.015	1.275	0.846
IL80 × IL84	11.789	1.270	0.987

Table 6. Pearson Correlation Coefficients between morphological genetic dissimilarity (GD), mid-parent heterosis (MPH), better-parent heterosis (BPH), and hybrid mean performance (Mean) for grain yield ha⁻¹.

Parameter	MPH	BPH	Mean
GD (Morph)	0.25	0.11	0.26

CONCLUSIONS

A group of eight maize inbred lines can be characterized and categorized using the principal component analysis (PCA) of phenotypic data allowing researchers to assess the degree of genetic diversity. The farthest related inbred lines used as parents can produce the highest heterosis in the F₁ generation. It is vital for a successful higher-yielding hybrids selection based on morphological data-based agglomerative hierarchical clustering (AHC). The findings showed that heterosis and mean grain yield ha⁻¹ positively correlate with the genetic diversity of the hybrid parents. However, this correlation was not statistically significant. To properly understand the genetic diversity of this valuable crop, an extensive examination of a varied set of maize inbred lines from multiple populations needs execution, using various morphological features.

REFERENCES

- Adetimirin VO, Vroh-Bi, The C, Menkir A, Mitchell SE (2008). Diversity analysis of elite maize inbred lines adapted to west and central Africa using SSR markers. *Maydica* 53: 143-149. <https://www.researchgate.net/publication/242771126>.
- Al-Naggar AMM, Shafik MM, Musa RYM, Younis ASM, Anany AH (2020). Genetic diversity based on morphological traits of 19 maize genotypes using principal component analysis and GT biplot. *Ann. Res. Rev. Biol* 35(2): 68-85. DOI: 10.9734/arrb/2020/v35i230191.
- Amorim EP, Amorim VBO, dos Santos JB, de Souza AP, de Souza JC (2006). Genetic distance based on SSR and grain yield of inter and intra-population maize single cross hybrids. *Maydica* 51: 507-513.
- Arifin NS, Nugraha AA, Waluyo B, Ardiarini NR, Azrai M (2018). Grouping in heterotic pool of maize inbred lines based on numerical and graphical analysis of combining ability. *SABRAO J. Breed. Genet.* 50(4): 475-493.
- Asare S, Tetteh AY, Twumasi P, Adade KB, Akromah R (2016). Genetic diversity in lowland, mid-altitude and highland African maize landraces by morphological trait evaluation. *Afr. J. Plant Sci.* 10: 246-257. DOI:10.5897/AJPS2016.1448.
- Balestre M, Von Pinho RG, Souza JC, Lima JL (2008). Comparison of maize similarity and dissimilarity genetic coefficients based on microsatellite markers. *Genet. Mol. Res.* 7: 695-705. <https://doi.org/10.4238/vol7-3gmr458>.
- Beyene Y, Botha AM, Myburg AA (2005). A comparative study of molecular and morphological methods of describing genetic relationships in traditional Ethiopian highland maize. *Afri. J. Biotechnol.* 4(7): 586-595: 10.5897/AJB2005.000-3107.
- Bhusal TN, Lal GM (2017). Relationship among heterosis, combining ability and SSR based genetic distance in single cross hybrids of maize (*Zea mays* L). *Vegetos* 30(2): 17-26. DOI: 10.5958/2229-4473.2017. 00132.X.
- Boonlertrirun K, Srinives P, Sarithniran P, Jompuk C (2012). Genetic distance and heterotic pattern among single cross hybrids within waxy maize (*Zea mays* L.). *SABRAO J. Breed. Genet.* 44(2): 382-397.
- Dermail A, Suriharn B, Lertrat K, Chankaew S, Sanitchon J (2018). Reciprocal cross effects on agronomic traits and heterosis in sweet and waxy corn. *SABRAO J. Breed. Genet.* 50(4): 444-460.
- Devi P, Singh NK (2011). Heterosis, molecular diversity, combining ability and their interrelationships in short duration maize (*Zea mays* L) across the environments. *Euphytica* 178: 71-81. DOI: 10.1007/s10681-010-0271-3.
- Dhliwayo T, Pixley K, Menkir A, Warburton M (2009). Combining ability, genetic distances and heterosis among elite CIMMYT and IITA tropical maize inbred lines. *Crop Sci.* 49: 1201-1210. DOI: 10.2135/cropsci2008.06.0354.
- Duvick DN (1999). Heterosis: Feeding people and protecting natural resources. In: Coors JG and Pandey S, (eds.), *The Genetics and Exploitation of Heterosis in Crops*, American Society of America, Madison, WI, 19-29.
- EL-Harty EH, Ghazy A, Alateeq TK, AlFaifi SA, Khan MA, Afzal M, Alghamdi SS, Migdadi HM (2021). Morphological and molecular characterization of quinoa genotypes. *Agriculture* 2021: 11:286. <https://doi.org/10.3390/agriculture11040286>.
- FAOSTAT (2022). Food and Agriculture Organization, Statistical Division. Available online: <http://www.fao.org/faostat/en/#data/QC> (accessed on 24 June 2022).
- Fufa H, Baenziger PS, Beecher BS, Dweikat I, Graybosch RA, Eskridge KM (2005).

- Comparison of phenotypic and molecular marker-based classifications of hard red winter wheat cultivars. *Euphytica* 145: 133-46. <https://doi.org/10.1007/s10681-005-0626-3>.
- George MLC, Salazar F, Warbuton M, Narro L, Vallejo FA (2011). Genetic distance and hybrid value in tropical maize under P stress and non-stress conditions in acid soils. *Euphytica* 178(1): 99-109. <https://knowledgecenter.blog.cimmyt.org>.
- Govindaraj M, Vetriventhan M, Srinivasan M (2015). Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. *Genet. Res. Int.* 431-487. DOI: 10.1155/2015/431487.
- Hallauer AR, Carena MJ, Miranda Filho JB (2010). Handbook of plant breeding: Quantitative genetics in maize breeding. Springer, New York, USA.
- Kumar P, Singh NK, Jha SK (2015). Multi-environment evaluation for determining grain yield, combining ability, heterosis and their inter-relationships in maize. *SABRAO J. Breed. Genet.* 47(4): 366-374.
- Legesse BW, Myberg AA, Pixley KV, Twumasi-Afriyie S, Botha AM (2008). Relationship between hybrid performance and AFLP based genetic distance in highland maize inbred lines. *Euphytica* 162: 313-323. <http://hdl.handle.net/2263/9804>.
- Miranda GV, Souza LV, Galvao JCC, Guimarães LJM, Melo AV (2008). Genetic variability and heterotic groups of Brazilian popcorn populations. *Euphytica* 162: 431-440. DOI: 10.1007/s10681-007-9598-9.
- Mohammadi SA, Prasanna BM, Singh NN (2003). Sequential path model for determining interrelationships among grain yield and related characters in maize. *Crop Sci.* 43: 1690-1697.
- Ndhlela T, Herselman L, Semagn K, Magorokosho C, Mutimaamba C (2015) Relationships between heterosis, genetic distances and specific combining ability among CIMMYT and Zimbabwe developed maize inbred lines under stress and optimal conditions. *Euphytica* 204: 635-647. DOI 10.1007/s10681-015-1353-z.
- Oyekunle M, Badu-Apraku B (2018). Assessment of interrelationships among grain yield and secondary traits of early-maturing maize inbred lines under drought and well-watered conditions. *Maydica* 63(18): 1-10 <https://www.researchgate.net/publication/332710305>.
- Pajic Z, Eric U, Drinic SM, Srdic J, Filipovic M (2010). Genetic divergence estimated by RAPD markers and its relationship with hybrid performance in popcorn. *Cereal Res. Commun.* 38: 184-192. <https://doi.org/10.1556/CRC.38.2010.2.4>.
- Singh P (2015). Genetic distance, heterosis and combining ability studies in maize for predicting F₁ hybrid performance. *SABRAO J. Breed. Genet.* 47(1): 21-28
- Spooner DM, Tivang J, Nienhis J, Miller JT, Douches DS (1996). Comparison of four molecular markers measuring relationship among the wild potato relatives (subgenus Potato). *Theor. Appl. Genet.* 92: 532-540. DOI: 10.1007/BF00224555.
- Twumasi P, Tetteh AY, Adade KB, Asare S, Akromah R (2017). Morphological diversity and relationships among the IPGRI maize (*Zea mays* L.) landraces held in IITA. *Maydica* 62: 1-9. <https://www.researchgate.net/publication/323126985>.
- XLSTAT (2014). Statistical and data analysis solution. Boston, USA. Available: <http://www.xlstat.com>.
- Younis ASM, Al-Naggar AMM, Bakry BA, Nassar SMA (2021). Maximizing maize grain, protein, oil and starch yields by using high plant density and stress tolerant genotype. *Asian J. Plant Sci.* 20: 91-101. DOI: 10.3923/ajps.2021.91.101.