



GENETIC VARIABILITY AND CORRELATION STUDIES IN SELECTED MAIZE (*ZEA MAYS* L.) GENOTYPES DURING THE SEEDLING STAGE IN JOS, NIGERIA

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Abstract

The study aimed to determine the extent of genetic variability and diversity for drought tolerance traits present in 24 maize genotypes in order to aid parents in selecting superior recombinant F1 genotypes. Six seeds of each maize genotype were sown in 45cm x 10cm polyvinyl chloride (PVC) pipes filled with a loamy soil potting mixture. Before seeding, moisture was kept at field capacity. Seedlings were thinned to four per pot after emergence and arranged in a Complete Randomized Design that was replicated three times. The experiment was adequately watered daily for the first 15 days, after which watering was discontinued. Morphophysiological data on seedling water use efficiency was collected and analyzed. For all traits studied, there were significant differences between genotypes. Cluster analysis using Morphophysiological traits separated genotypes into three distinct groups. The genotypic and phenotypic coefficients of variation revealed a high degree of variability. Very high genetic advance and heritability values were observed. The above results indicated that there was enough genetic variability and diversity among the genotypes. As a result, these genotypes may be useful in drought-tolerant crop improvement programs.

Keywords: Maize, Drought, Tolerance, Variance, Heritability, Genetic Advance

Introduction

Maize provides food and economic security to an estimated 208 million people in Sub-Saharan Africa (Grote *et al.*, 2021). The crop has been projected to become the most important crop by 2030 (Salvi *et al.*, 2007). Maize is a C4 plant and is physiologically adapted to diverse environments making it unmatched by any other cereal crop (Izhar and Chakraborty, 2013). According to the Information and communication support for agricultural growth in Nigeria (2017), Nigeria presently produces about 8 million tons annually with yield per hectare ranging between 2000 to 6000 kg/ha depending on

the agroecological zone. Despite extensive heterosis exploitation and extensive improvement research in maize, limiting factors such as low seed yield, poor resistance to biotic and abiotic stressors, poor adaptation to various agro-ecologies, and low tolerance to draughts appear to persist. Drought, the devastating effects of parasitic weeds, tolerance to low nitrogen, salinity, high and low temperatures, and soil nutrient deficiencies have all been blamed for high yield losses. (Banziger *et al.*, 2000; Olaokojo and Olaoye, 2005; BaduApraku *et al.*, 2010; Badu-apraku *et al.*, 2011; Ogunniyan and Olakojo, 2014). Due to

higher evapotranspiration and rising temperatures, the occurrence and severity of drought episodes has increased as a result of global climate change. Drought stresses have been shown to affect maize yield through a variety of mechanisms throughout the maize plant's life cycle. (Leach *et al.*, 2011; Li *et al.*, 2015).

One of the most important recent breeding strategies for crops like maize is to find new varieties with higher grain yields and better nitrogen- and water-use efficiencies. An increasing body of evidence suggests that root system architecture engineering has the potential to support a second green revolution aimed at crop performance under suboptimal water and nutrient supply. Any genetic progress for resistance to abiotic stressors will be long-lasting, indicating that the distribution of roots, particularly those that can penetrate deeper into the soil, is critical in determining plants' ability to capture key resources such as water and mobile nutrients such as nitrate. As a result, root architecture has a significant impact on crop plant growth and yield (Fenta *et al.*, 2014). As a result, the root system is widely regarded as the most critical organ for improving crop adaptation to water stress. (Vadez, 2014). Drought stress causes maize to redirect root growth and dry matter accumulation away from the shoot and toward the root (Sharp *et al.*, 2004; Ribaut *et al.*, 2009). In the face of decreased water potential, these modifications result in sustained root growth and inhibit shoot growth (Ober *et al.*, 2005; Ober and Sharp, 2007; Li *et al.*, 2015).

Drought can cause crop field damage at any time during the growing season. According to the "stress gradient hypothesis," the fate of seedlings will determine the structure and dynamics of the majority of plant populations. (Kitajima and Fenner, 2000; De La Cruz *et al.*, 2008; Li *et al.*, 2015). Thus, phenotypical evaluation at the seedling stage is regarded as an attractive approach because it is a high throughput and low-cost method that saves space and time (Meeks *et al.*, 2013). This approach has been

successfully used to develop drought-tolerant varieties in cowpea (Singh and Matsui 2002), cotton (Longenberger *et al.*, 2006), wheat (Tomar and Kumar, 2004), and maize (Ruta *et al.*, 2010; Meeks *et al.*, 2013; Pace *et al.*, 2014). Another advantage of using seedling drought screens, where young seedlings undergo cycles of water stress in the greenhouse, is that phenotypical variations caused by experimental errors can be controlled better because the plants are much more uniform at the early seeding stage, compared to other periods of plant development (Wang *et al.*, 2015). All plant breeding programmes involving selection and hybridization are aimed at concentrating the different useful genes existing in a pooled genetic diversity to create the much desired superior F1 plant ideotype (Mustafa *et al.*, 2014).

Correlation analysis is used to assess the relative magnitude of influence of an independent variable on a dependent variable in most polygenic traits, such as drought and yield. Drought tolerance, as well as other yield component characters that influence yield, should be used to select desirable genotypes. It is widely accepted that correlation between different character pairs represents a coordination of physiological processes, which is frequently accomplished through advantageous gene linkages (Mather and Harrison, 1949 in Premlatha and Kalamani, 2010). Furthermore, understanding the strength and type of association is necessary for developing breeding procedures. Premlatha and Kalamani (2010), reported that Knowing the extent to which drought affects yield component characters will assist breeders in launching successful crop improvement programs.

The concept of heritability which specifies the proportion of the total variation among a species due to genetic components combined with genetic advance. These are good parameters for determining gene action involved in the inheritance of any trait and by extension help in deciding the best breeding method to apply for improving

such trait. High heritability indicates less environmental influence in the observed variation (Songsri *et al.*, 2008; Eid, 2009), while high heritability accompanied by high genetic advance is an indication of additive gene action for such trait, making it most amenable to selection (Mohsin *et al.*, 2009). Determining the variability of yield and yield related components will enable the plant researcher to deduce the extent of environmental influence on yield, considering that yield and its components are quantitative characters and are affected by the environment.

This study was carried out to show the extent of variability existing in 24 maize genotypes for selection as parents to facilitate the exploitation of maximum genetic variability for the production of superior recombinant genotypes using best options in diallel mating designs as the main aim. However, the specific objective was to use suitable genetic parameters such as phenotypic and genotypic variances, heritability values, phenotypic and genotypic coefficients of variation and genetic advance in selecting best genotypes for incorporation as parents in future maize improvement breeding programme for drought stress tolerance at seedling stage.

Materials and Methods

This research was conducted at the teaching and research screen house of Forestry Research Institute of Nigeria- Federal College of Forestry, Jos. located in Nigeria's Northern Guinea Savanna ecological zone at 09°56'N, 08°53'E at an elevation of 1,217M. Six seeds from each of the 24 maize genotypes were sown in uniformly cut polyvinyl chloride (PVC) pipes at 45cm x 10 cm as pots. Before seeds were sown, each pot was filled with 4.0 kg of loamy soil textural class and adequately irrigated to its field capacity daily for three days. Seedlings were thinned to four per pot after emergence and arranged in a Completely Randomized Design with three replications. For the first 10 days, the experiment was adequately watered at a rate of 0.6 litres per pot daily,

and then watering was discontinued. The experiment was monitored for 45 days. Morphophysiological data on seedling water use (WU) response efficiency was collected and analyzed. The number of leaves (NOL), number of shed leaves (NSL), plant seedling height (PSH), leaf area (LA), plant collar girth (PCG) was determined using Mckee's (1964) procedures. The belowground measurement was carried by modifying the described procedure by Harrington *et al* (1994) and Obeng-Bio *et al* (2011). Each pot containing the seedlings with the ball of soil was carefully lowered into a 2000 litre capacity bowl filled with water to remove the roots carefully which were washed free of sand, and each was transferred to another 25 litre capacity container of water to ensure total removal of sand. The shoot's roots were severed at the cotyledonary node. Using a meter rule, observations and data on the length of the primary root (LPR in cm) were recorded. The sensitive digital Metler weighing balance was used to measure seedling fresh shoot weight (g), fresh root weight (g), dry shoot weight (g), and dry root weight (g). Plant tissue samples were oven-dried at 80°C until a constant weight was obtained. Moisture content was calculated by subtracting the sample's dry weight from its fresh weight. Seedling aspect (SA) score was graded on a scale of 1 to 9 as described by Akinwale *et al* (2017) and other observations were recorded using descriptors for maize (IBPGR, 1997). Quantitative data obtained were subjected to Analysis of variance and significance means were separated using Least significant difference (LSD) using PBTtools (PBTtools, 2014). Mean values were used to estimate Genotypic and Phenotypic coefficients of variation as by Singh and Chaudhury (1985). The broad sense heritability and genetic advance were calculated as proposed by Johnson *et al.* (1955) and simple linear correlation coefficient was determined according to Snedecor and Cochran (1967). A correlation matrix was drawn up using the linear correlation coefficients. UPGMA cluster analysis was used to construct a dendrogram to ascertain the genetic relationships among the tomato accessions.

Results

Genetic Diversity

Significant differences were shown among the genotypes for the morphophysiological characterizers measured, with genetic distance ranging from 0.01 to 0.38 (Fig. 1a, 1.b and table 2). In this study, the cluster analysis based on 12 traits separated genotypes into three distinct clusters. Cluster 1 included 12 genotypes of which are from Kaduna, Oyo, Yobe and Plateau state, while Cluster 2 had 6 genotypes from Oyo, Kaduna and Nassarawa state and Cluster 3 had 6 from Nassarawa, Kaduna and Plateau state respectively (Table.1). The maize germplasm used in this experiment were collected from five states in Nigeria. Kaduna state has the highest collection of a third of the collections made. Followed by Oyo with seven collections. Yobe, Plateau and Nasarawa states each had five, three and one collections respectively. There was no clear morphological variation in the genotypes under study according to the 12 attributes used for this classification. However, the seed showed phenotypical variations (figure 2).

Genetic Variability

The Analysis of variance (ANOVA) revealed highly significant differences ($P \leq 0.005$) among the 24 genotypes for all the characters studied (Table 3,5). Values of genotypic and phenotypic variances were lowest in number of shade leaves and highest in leaf area plant (0.77, 1664.87). Higher values of genotypic and phenotypic variances were observed for plant seedling height (121.48, 127.48), Leaf area (1664.8, 1678.58), Fresh shoot weight (451.19, 467.00), length of primary root (40.26, 44.49) respectively. The genotypic coefficient of variation (GCV) ranged from 16.35 in number of leaves per plant to 68.04 in fresh shoot weight per plant. Similarly, PCV ranged from 19.93 in number of leaves per plant to 72.42 in number of shade leaves per plant (Table 4).

Estimates of broad sense heritability (H^2b) and genetic advance

Estimates of heritability in the broad sense were very high for seedling aspect and leaf area (99%) each, fresh shoot weight (97%), fresh root weight (96%), root volume (96%), plant collar girth (93%), dry shoot weight (92%), length of primary root (90%), dry shoot weight (88%) and number of number of leaves had low to moderate heritability of (67%) (Table 4). Very high genetic advance estimates were recorded for fresh shoot weight (137.76), dry shoot weight (134.39) fresh root weight (130.46) root volume (111.52) while the least value was recorded for number of leaves (27.64) (Table 4).

Character association

The correlation analysis revealed a significant positive association for seedling number of leaves with plant leaf area index ($r = 0.47$), plant collar girth association with leaf area index and fresh shoot weight ($r = 0.47$; $r = 0.51$), the leaf area index correlated significantly with plant seedling height ($r = 0.62$), fresh shoot weight (0.59), dry shoot weight (0.47), fresh root weight (0.50), and dry root weight (0.50). (0.49). Plant height was found to be significantly related to fresh shoot weight ($r = 0.51$), dry shoot weight ($r = 0.75$), and dry root weight ($r = 0.76$). Root volume correlated significantly with fresh root weight ($r = 0.63$). Dry root weight significantly correlated with fresh shoot weight ($r = 0.55$) and dry shoot weight ($r = 0.92$). Fresh root weight correlated significantly with plant seedling height ($r = 0.67$), plant collar girth ($r = 0.40$), fresh shoot weight ($r = 0.61$) and dry shoot weight ($r = 0.59$). The fresh shoot weight correlated significantly with a dry root biomass weight ($r = 0.51$). Root volume and fresh root weight correlated significantly ($r = 0.63$). Dry root weight ($r = 0.55$) and dry shoot weight ($r = 0.92$) were significantly correlated. Fresh root weight ($r = 0.67$), plant collar girth ($r = 0.40$), fresh shoot weight ($r = 0.61$), and dry shoot weight ($r = 0.59$) all had significant correlations. Fresh shoot weight was significantly correlated with dry root biomass weight ($r = 0.51$).(table 6).

Table 1: Genotypes and their origin/ source used for the study

S/N0	Germplasm Identification Name	Code	Source	Classification	State/ location
1.	SAMMAZ 24	A6	IAR-Zaria	OPV	Kaduna
2.	SAMMAZ 32	A10	IAR-Zaria	OPV	Kaduna
3.	SUWAN -1-SR-Y	B6	SSLTD – Ibadan	Accessions	Oyo
4.	SAMMAZ -52	B8	IAR-Zaria	OPV	Kaduna
5.	TZE – WDTSTRC ₄	C2	SSLTD – Ibadan	Accessions	Oyo
6.	MARA -AURE- W (Goniri- Gujba) -2	C3	Goniri- Gujba	Accessions	Yobe
7.	DMR-ESR-Y	C8	NACGRAB-Ibadan	Accessions	Oyo
8.	MARA- AURE- Y (Kilbiri- Gujba-) 1	C9	Kilbiri- Gujba	Accessions	Yobe
9.	TZM -129	D10	SSLTD – Ibadan	Accessions	Oyo
10.	OBA SUPER II F2	E1	SSLTD – Ibadan	OPV	Oyo
11.	PVA SYN -14	E3	SSLTD – Ibadan	OPV	Oyo
12.	PVA-SYN –F0	E7	NACGRAB-Ibadan	OPV	Oyo
13.	MARA AURE –Y (Mamudo- Damagun) -1	E8	Mamudo- Fune	Accessions	Yobe
14.	MARA AURE-W (Bindari – Damagun) -2	F1	Bindari- Fune)	Accessions	Yobe
15.	MARA AURE –W (Indiski- Potiskum) - 2	F2	Indiski- Potiskum	Accessions	Yobe
16.	Kaf- 15 -W (Gueli-2)	F5	Gueli – Akwanga	Accessions	Nasarawa
17.	KAF-3-Y	J5	Abyin-Kafanchan	Accessions	Kaduna
18.	KAF- 4 -W	K3	Abyin-Kafanchan	Accessions	Kaduna
19.	KAF-21	K8	Fantswam -Kafanchan	Accessions	Kaduna
20.	KAF-16	K9	Mangyang-Kafanchan	Accessions	Kaduna
21.	KAF-22 -W- kagoro	L2	Kagoro -Kafanchan	Accessions	Kaduna
22.	TZM-FOB -L	L3	Angware - Jos East	Accessions	Plateau
23.	TZM-DAFFO –L	L4	Daffo – Bokkos	Accessions	Plateau
24.	Kierkier	L7	Angware -Jos East	Accessions	Plateau

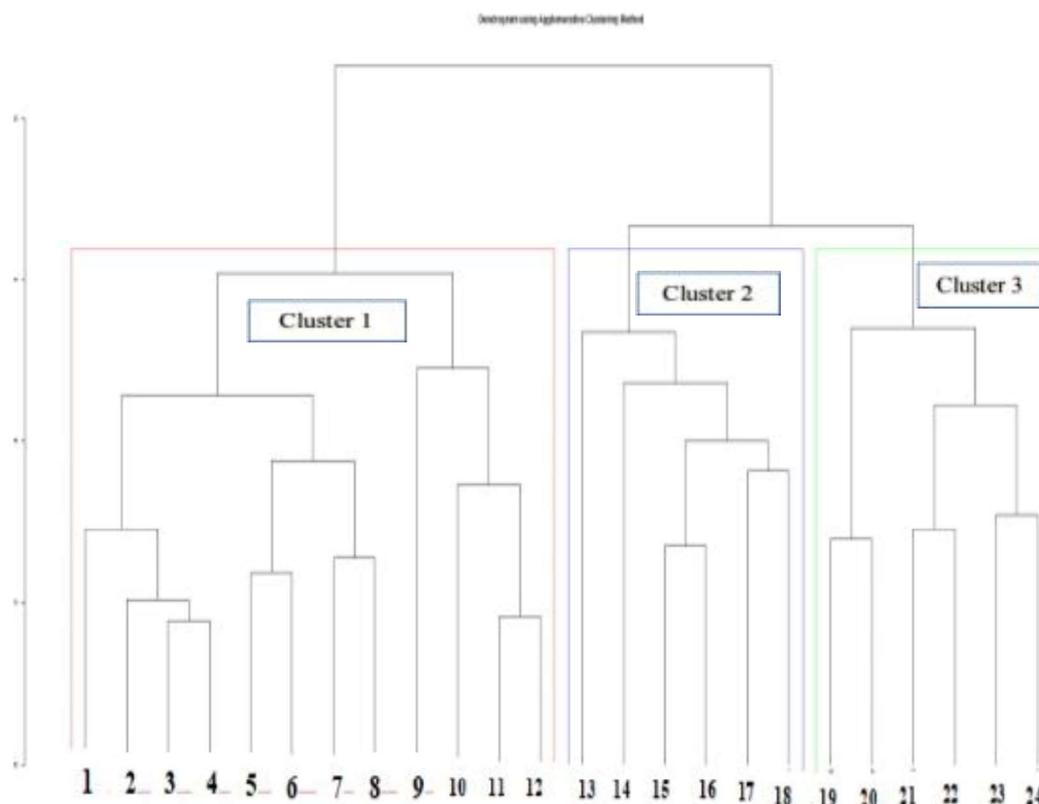


Figure 1a: Dendrogram of 24 Maize Genotypes Based on 12 Agro-Morphological Attributes and Generated From Average Taxonomic Distance Matrix By Upgma In Nysyspc.

S/N	Accession	S/N	Accession
1	KAF- 4 -W	13	PVA-SYN -F0
2	MARA AURE-W (Bindari-Damagun) -2	14	MARA -AURE- W (Goniri-Gujba) -2
3	TZM DAFFO-L	15	KAF-3-Y
4	TZM -129	16	MARA- AURE- Y (Kilbiri- Gujba-) 1
5	SAMMAZ -52	17	KAF-22 -W- kagoro
6	DMR-ESR-Y	18	KAF-21
7	PVA SYN -14	19	Kaf- 15 -W (Gueli-2)
8	TZM-FOB -L	20	TZE – WDTSTRC4
9	SUWAN -1-SR-Y	21	KAF-16
10	SAMMAZ 32	22	Kierkier
11	OBA SUPER II F2	23	MARA AURE –W (Indiski- Potiskum) -2
12	SAMMAZ 24	24	MARA AURE –Y (Mamudo- Damagun) -1

Figure 1b: Dendrogram of 24 Maize Genotypes Based on 12 Agro-Morphological Attributes and Generated From Average Taxonomic Distance Matrix By Upgma In Nysyspc .

Table 2: Cluster Mean for Different Maize Plant Seedling Traits Among 24 Maize Genotypes

Traits		PSH	LA	PCG	NOL	NSL	FSW	DSW	FRW	DRW	LPR	RV	SA
I		0.3844	0.3322	0.2348	0.2016	0.0549	0.3510	0.3785	0.3742	0.3726	0.2073	0.2290	0.0478
II		-0.1098	-0.1633	0.1393	0.0170	0.6094	0.1364	0.0958	-1.1106	0.0955	-0.0320	-0.0728	0.6446
III		0.11829	-0.2551	-0.4423	-0.5369	-0.1799	-0.2249	0.2537	0.0814	0.2738	-0.0320	0.3523	0.2542

Key:

Plant Seedlings Height- (PSH): Leaf Area- (LAjoi): Plant Collar Girth - (PCG): Number of leaves per plant- (NOL): Number of Shed leaves (NSL): Fresh shoot weight (FSW): Dry Shoot Weight (DSW) : Fresh root weight- (FRW) : Dry Root Weight - (DRW): Length of primary root (LPR) : Root volume (RV): Seedling Aspect (AS).

Table 3: - Analysis of variance for different traits for the 24 Maize Genotypes.

S/No	Traits	Accession mean	F – value	P-value ≤ 0.005	Coefficient of variation
1	Plant Seedlings Height- PSH):	50.13	0.06	0.9436	4.89
2	Leaf Area- (LAI)	95.08	1.58	0.2178	3.89
3	Plant Collar Girth - (PCG)	12.22	1.01	0.3704	5.92
4	Number of leaves per plant- (NOL)	8.85	0.70	0.5034	11.40
5	Number of Shed leaves (NSL)	1.89	0.84	0.4372	55.64
6	Fresh shoot weight (FSW)	12.74	0.32	0.7303	31.22
7	Dry Shoot Weight (DSW)	2.54	1.78	0.1799	20.11
8	Fresh root weight- (FRW)	14.00	1.27	0.2906	8.15
9	Dry Root Weight - (DRW)	2.52	0.49	0.6153	25.09
10	Length of primary root (LPR)	32.85	2.14	0.1296	6.33
11	Root volume (RV)	7.40	3.38	0.0427	10.99
12	Seedling Aspect (AS).	3.39	1.00	0.3757	3.48

Table 4: Estimates of phenotypic variance (σ^2_p), genotypic variance (σ^2_g), heritability (H^2_b), genotypic and phenotypic coefficients of variability and genetic advance for various traits of the Maize accessions.

S/NO	Traits	σ^2_g	σ^2_p	σ^2_e	H^2_b (%)	GCV	PCV	GA
1	Plant Seedlings Height- (PSH):	121.48	127.48	6.00	0.95	21.99	22.52	44.21
2	Leaf Area- (LAI)	1664.87	1678.58	13.71	0.99	42.91	43.09	88.04
3	Plant Collar Girth -(PCG)	6.97	7.50	0.52	0.93	21.61	22.41	42.94
4	Number of leaves per plant-NOL)	2.09	3.11	1.02	0.67	16.35	19.93	27.64
5	Number of Shed leaves (NSL)	0.77	1.87	1.10	0.41	46.39	72.42	61.22
6	Fresh shoot weight (FSW)	451.19	467.00	15.81	0.97	68.04	69.22	137.76
7	Dry Shoot Weight (DSW)	2.99	3.25	0.26	0.92	68.03	70.93	134.39
8	Fresh root weight- (FRW)	27.88	29.19	1.30	0.96	64.79	66.29	130.46
9	Dry Root Weight -(DRW)	2.90	3.30	0.40	0.88	67.56	72.07	130.47
10	Length of primary root (LPR)	40.26	44.49	4.23	0.90	19.43	20.43	38.08
11	Root volume (RV)	16.69	17.36	0.67	0.96	55.21	56.31	111.52
12	Seedling Aspect (AS).	1.02	1.03	0.01	0.99	29.74	29.94	60.85

σ^2_g = genotypic variance, σ^2_p = phenotypic variance, σ^2_e = environmental variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, GA = Genetic advance, H^2_b = heritability in broad sense

Table 5: Means Traits of Twenty-Four (24) Genotypes Evaluated In The Screen House Under Imposed Drought Stress At Seedling Stage At The Forestry Research Institute of Nigeria- Federal College of Forestry, Jos.

S/no	Genotypes	PSH	LA	PCG	NOL	NSL	FSW	DSW	FRW	DRW	LRP	RV	AS
1	SAMMAZ 24	35.2	67.5	9.8	8	1	13.6	0.1	1.9	0.4	22.0	7.3	3
2	SAMMAZ 32	41.7	65.1	13.3	5	2	14.8	0.6	4.1	0.6	28	4	4
3	SUWAN-1-SR-Y	31.2	101.1	13.0	10	4	30.5	0.1	2	0.1	16	3.4	4
4	SAMMAZ 52	40.8	71.8	8.1	9	2	10.4	0.63	2.2	0.7	34	2	2
5	TZE-WDTSTR C4	66.3	118.4	12.8	9	3	50.0	7.5	6.8	7.5	31	8	4
6	MARA AURE-W(Goniri-Gujba)-2	42.4	66.1	12.9	10	4	27.4	3.1	10.1	3.1	33	7	5
7	DMR-ESR-Y	39.9	69.1	8.7	10	2	14.6	1.55	5	1.6	44	6	3
8	MARA AURE-Y (Kilbiri-Gujba)-1	51.2	99.6	14.7	10	2	17.9	1.5	6.2	1.5	32	6.4	2
9	TZM-129	49.6	52.2	13.6	10	4	60.2	3.1	11.7	2.5	44	10	4
10	OBA SUPER 11 F2	41.2	70.5	13.4	9	2	36.8	1.5	5.6	1.2	31	4	3
11	PVA -SYN-14	30.2	40.0	8.3	7	1	7.3	0.4	1.6	0.4	27	4.8	3
12	PVA -SYN-F0	52.7	48.2	8.3	6	1	18.3	2.1	8.2	2.1	30.7	8	3
13	MARA AURE-Y (Mamudo-Damagun)-1	50.1	86.2	9.9	8	2	23.9	3.2	16.2	3.2	31	21.9	3
14	MARA AURE -W (Bindari-Damagun)-2	60.1	185.3	17.2	10	2	100.7	3.7	16.6	3.7	36	12	3
15	MARA AURE -W (Indiski-Potiskum)-2	65.6	144.6	14.4	12	2	66.7	4	13.3	4.0	35	6	4
16	KAF-15-W (Gueli-2)	55.4	158.4	10.2	9	2	36.5	5.3	10	5.3	32	8	4
17	KAF-3-Y	44.9	44.4	11.7	8	2	23.8	2.4	5.6	2.3	33	4.2	5
18	KAF-4-W	51.2	131.5	17.6	9	1	9.3	1.7	6	1.7	32.8	6	3
19	KAF -21	66.0	140.8	15.1	10	1	46.7	4.3	22	4.3	36	8.4	2
20	KAF -16	65.7	71.2	13.5	7	2	25.2	4	12.8	4.2	31	10	5
21	KAF-22-W-Kagoro	58.3	122.6	10.3	10	1	28.2	1.9	5.7	1.9	31	12	5
22	TZM -FOB-L	60.0	99.6	10.6	7	1	24.3	2.6	4.6	2.6	38	4	3
23	TZM-DAFFO -L	43.7	70.7	13.5	9	1	28.4	2.5	4.8	2.5	34	4.2	2
24	KIERKIER	59.9	156.7	12.2	10	2	33.7	3.1	12.7	3.1	46	10	2
MEAN		50.13	95.08	12.22	8.85	2.07	31.22	2.54	8.15	2.52	32.85	7.40	3.39
CV%		4.90	3.90	5.90	11.40	38.5	12.70	20.10	14.00	25.10	6.30	11.00	3.50
SE		1.41	2.14	0.42	0.58	0.46	2.30	0.29	0.66	0.37	1.20	0.47	0.07
F-test		*	*	*	*	*	*	*	*	*	*	*	*
5%LSD		4.03	6.09	1.19	1.66	1.31	6.53	0.84	1.88	1.04	3.42	1.34	0.19

*Significant at $p = 0.005$ levels of probability. Number of Leaf (NOL), Number of Dead /Shade Leaf (NODL/NOSL), Plant Seedling eight (PSH), Leaf Area (L.A), Plant Collar Girth (PCG), Seedling Aspect (SA); Root Volume (RV); Length of Primary Root (LPR); Dry Root Weight (DRW); Fresh Root Weight (FRW); Fresh Shoot Weight (FSWT); Dry Shoot Weight (DSWT); Leaf Area (L.A).

Table 6: Correlation coefficient for twenty-four genotypes evaluated in the screen house under imposed drought stress at the seedling stage at the Forestry Research Institute of Nigeria Federal College of Forestry, Jos

	PSH	LA	PCG	NOL	NSL	FSW	DSW	FRW	DRW	LPR	RV	SA
PSH	1											
LA	0.62*	1										
PCG	0.36*	0.47*	1									
NOL	0.18	0.47*	0.32	1								
NSL	-0.08	-0.08	0.19	0.20	1							
FSW	0.51*	0.58*	0.51*	0.43*	0.21	1						
DSW	0.75*	0.47*	0.25	0.21	0.12	0.55*	1					
FRW	0.67*	0.50*	0.40*	0.27	0.04	0.61*	0.59	1				
DRW	0.76*	0.49*	0.25	0.18	0.11	0.51	0.92	0.57*	1			
LPR	0.41	0.19	0.08	0.27	-0.02	0.28	0.33	0.40	0.29	1		
RV	0.38	0.27	0.02	0.06	-0.01	0.28	0.35	0.63*	0.36	0.16	1	
SA	0.09	-0.12	0.04	-0.06	0.35	0.15	0.21	-0.02	0.21	-0.22	0.10	1

*Significant at $p = 0.05$ levels of probability. Number of Leaf (NOL), Number of Dead /Shade Leaf (NODL/NOSL), Plant Seedling eight (PSH), Leaf Area (LA), Plant Collar Girth (PCG), Seedling Aspect (SA); Root Volume (RV); Length of Primary Root (LPR); Dry Root Weight (DRW); Fresh Root Weight (FRW); Fresh Shoot Weight (FSWT); Dry Shoot Weight (DSWT); Leaf Area (LA).

Discussion

Measuring morphological characteristics enables one to compute genetic diversity. This is a simple method for determining the amount of genetic variation and evaluating genotype performance in suitable growing environments (Fufa *et al.*, 2005; Shuaib *et al.*, 2007, Nwosu *et al.*, 2018). Locating traditional and improved crop varieties that are adapted to diverse environments and shifting biotic and abiotic stresses is one way that farmers and breeders can use biodiversity (Dwivedi *et al.*, 2016). For agricultural and plant breeding purposes, accurate, quick, and trustworthy plant variety identification is crucial (Weising *et al.*, 2005). The clustering of the accessions used in this study is comparable to that reported by Wali, *et al.* (2019), who used maize germplasm divided into twelve clusters based on the twelve characters they examined for their genetic diversity analysis results. As evidenced by the grouping of the materials KAF -4-W (Kaduna), SUWAN-1-SR-Y (Oyo), Daffo local (Plateau), and MARA -AURE- W (Goniri- Gujba) -2 (Yobe), the clustering pattern and geographic origin of these materials are not significantly associated. The same cluster contained KAF-16, Kaf-15-W (Gueli-2), TZE-WDTSTRC4, which were all collected from Kaduna, Nasarawa, and Oyo, respectively. This finding is consistent with the findings of Islam *et al.* 2020 in their study on maize genetic diversity using plant traits that contribute to grain yield of 19 genotypes. Some of the genotypes discovered may be considered distinct varieties. This finding could, however, be confirmed through molecular characterization using SSR markers.

Highly significant differences among accessions for all attributes measured indicate that the genotypes have sufficient genetic variability and diversity, implying that there is room for improvement in this crop. Nwadike *et al* (2022) and Wali. *et al* (2019) in Maize reported similar findings in 24 maize accessions. The presence of sufficient genetic variability among the

experimental materials is required for the hybrid breeding program.

The slightest variations between the attribute PCV and GCV values suggest that environmental factors have a smaller impact on how they manifest. It is most likely to be successful to select these genotypes to improve for attributes related to drought tolerance. However, relative larger differences between PCV and GCV values found for plant seedling height suggest that environmental factors have a greater influence than other studied attributes.

The proportion of phenotypic variation that can be attributed to genetic variation is known as heritability. All studied characters in the current study had high heritabilities (greater than 80%), with the exception of the quantity of leaves per plant and the quantity of shed leaves per plant. The degree of environmental influence on characters is low, according to high heritability. According to Parnse (1957), the greater utility of taking into account estimate of genetic advance as a useful selection tool lies in accompanied heritability estimates, any of the characters can therefore be used for selection. Therefore, a straightforward inheritance system for these traits is suggested by the extremely high genetic progress and high heritability estimates for all studied traits.

The greater photosynthetic products available for partitioning and plant growth under applied drought stress may account for the significant positive correlations between seedling number of leaves and plant leaf area index, plant collar girth association, fresh shoot weight, plant seedling height, fresh shoot weight, dry shoot weight, fresh root weight, and dry root weight, respectively. Fresh shoot weight was discovered to be significantly correlated with plant height because growing plants produce more biomass, particularly above ground, as their height increases. In a similar way, dry root weight, root volume, and fresh root weight all showed positive correlations. Significant correlations were found between dry root weight and fresh and dry shoot

weight. Significant relationships were found between fresh root weight and plant seedling height, plant collar girth, fresh shoot weight, and dry shoot weight.

Conclusion

The presence of adequate genetic variability in the material studied was revealed by this study. Indicating that genetic diversity and strong genetic associations between traits would aid in indirect selection, allowing breeders to develop maize genotypes for a future breeding program. Because the genetic parameters discussed here are functions of environmental variability, estimates in other environments may differ. However, based on the high genetic advance accompanied by high heritability estimates for various attributes studied, with the exception of the number of shed leaves and plant collar girth. We conclude that traits with high heritability estimates are inherited via additive gene action. Therefore, choosing traits with strong associations will also enhance traits related to drought tolerance. Furthermore, it may be possible to determine whether selection for one trait has any impact on another by looking at genetic parameters with highly heritable traits. After several selection cycles, a high response rate ought to be possible. For the majority of the inter-character associations, coefficients of variation at the genotypic level were, on average, lower than those at the phenotypic level. These imply a predominance of environmental factors that may have prevented character expression.

Conflict of Interest

The authors declare that there was no conflict of interest.

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