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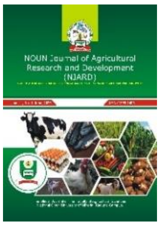

Original Article

Genetic Variability and Correlation Studies in Selected Maize (zea mays l.) Genotypes during the Seedling Stage in Jos, Nigeria.

Nwadike, C [1*]., Ochigbo, E.A [2]., Ojo, G. O. S [3]. & Vange, T [2].

[1]Forestry Research Institute of Nigeria (FRIN) Forest Hill-Jericho, Ibadan - Oyo State, Nigeria.
[2]Department of Plant Breeding and Seed Science, University of Agriculture, Makurdi-Benue State, Nigeria.
[3]Department of Crop Production, University of Agriculture, Makurdi-Benue State, Nigeria.
**Corresponding Author: 08060761175: chrisnwadike1@gmail.com*

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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. Before conducting ANOVA, data normality and variance homogeneity were assessed using the Shapiro-Wilk and Levene's tests, respectively. For all traits studied, there were significant differences between genotypes. Cluster analysis using Morphophysiological traits separated genotypes into three distinct groups while Pearson correlation method was used for the correlation analysis. The genotypic and phenotypic coefficients of variation revealed a high degree of variability. Very high genetic advance and heritability values were observed. The results indicate sufficient genetic variability and diversity among the genotypes. Integrated analysis of genetic parameters and trait performance identified several promising parental lines for drought tolerance improvement, including KIERKIER, TZM-DAFFO–L, KAF-16, MARA AURE–W, SAMMAZ-52, OBA SUPER II, and PVA–SYN lines. These genotypes hold potential for use in future drought-tolerant crop improvement programs.

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

Introduction

Maize (*Zea mays* L.) is a cornerstone food crop that offers food and economic security to more than 208 million people in sub-Saharan Africa (Grote *et al.,* 2021). Worldwide, by 2030, it is anticipated to be the most significant cereal crop (Salvi *et al.,* 2007), which is primarily due to environmental adaptation as a C4 plant across a wide range of habitats (Izhar and Chakraborty, 2013). In Nigeria, where maize is cultivated at about 8 million tons per year with the yield varying from 2,000 to 6,000 kg/ha depending on the agro-ecological zone (Information and Communication Support for Agricultural Growth in Nigeria, 2017).

Despite significant genetic improvements through heterosis exploitation and modern breeding techniques, maize productivity continues to be constrained by several biotic and abiotic stressors. These include drought, parasitic weeds, poor tolerance to low nitrogen, salinity, temperature extremes, and nutrient-deficient soils (Banziger *et al.,* 2000; Olaokojo and Olaoye, 2005; Badu-Apraku *et al.,* 2010, 2011; Ogunniyan and Olakojo, 2014). Among these, drought remains one of the most significant threats, particularly as climate change exacerbates the frequency and intensity of drought events due to rising temperatures and increased evapotranspiration (Leach *et al.,* 2011; Li *et al.,* 2015).

Modern breeding strategies are increasingly focused on developing varieties with improved water- and nutrient-use efficiency. A growing body of evidence supports the role of root system architecture as a key trait in enhancing drought adaptation. Traits such as deeper root penetration and efficient soil resource capture are critical under water-limited conditions (Fenta *et al.,* 2014). The root system, widely recognized as central to plant adaptation under drought (Vadez, 2014), enables the plant to redirect resources under stress—sustaining root growth while limiting shoot development (Sharp *et al.,* 2004; Ribaut *et al.,* 2009; Ober *et al.,* 2005; Ober and Sharp, 2007).

Drought stress can impact maize throughout its life cycle, but early-stage drought tolerance is particularly crucial. According to the stress-gradient hypothesis, seedling survival often determines the long-term structure and dynamics of plant populations (Kitajima and Fenner, 2000; De La Cruz *et al.,* 2008). Consequently, phenotypic evaluation at the seedling stage offers an efficient, cost-effective approach to screening large numbers of genotypes for drought tolerance (Meeks *et al.,* 2013). This approach has already proven successful in breeding programs for cowpea, cotton, wheat, and maize (Singh and Matsui, 2002; Tomar and Kumar, 2004; Longenberger *et al.,* 2006; Ruta *et al.,* 2010; Pace *et al.,* 2014). Early-stage screening also reduces phenotypic variation due to environmental noise, leading to more reliable selection (Wang *et al.,* 2015).

To develop superior genotypes under stress conditions, breeders rely heavily on genetic variability and trait heritability. Variability analysis helps assess the extent of genetic versus environmental contributions to trait expression. Heritability estimates, particularly when coupled with high genetic advance, indicate traits governed predominantly by additive gene action and therefore suitable for improvement through selection (Songsri *et al.,* 2008; Mohsin *et al.,* 2009; Eid, 2009). Correlation analysis further informs breeding by identifying relationships among traits, which can reflect either physiological coordination or beneficial gene linkages (Mather and Harrison, 1949, in Premlatha and Kalamani, 2010). Understanding such relationships is critical when selecting for drought tolerance, especially when dealing with polygenic traits like yield.

This research was therefore conducted to evaluate the extent of genetic variability and inter-trait relationships among some 24 maize genotypes at the seedling stage under drought conditions. The overarching goal was to identify promising parental lines for inclusion in future breeding programs. Specifically, this study aimed to estimate genetic parameters including phenotypic and genotypic variances, heritability, coefficients of variation, and genetic advance. These parameters will guide the selection of genotypes with favorable drought-tolerant traits for incorporation into diallel crossing schemes aimed at producing superior recombinant lines.

Materials and Methods

The study was conducted in the teaching and research screen house of the Forestry Research Institute of Nigeria–Federal College of Forestry, Jos, located in the Northern Guinea Savanna zone (09°56'N, 08°53'E; 1,217M elevation). A total of 103 maize genotypes were screened at the seedling stage under moisture-stressed and non-stressed conditions to evaluate seedling traits and other parameters. Twenty-four top-performing genotypes were selected. Six seeds from each of the 24 maize genotypes were sown in uniformly cut polyvinyl chloride (PVC) pipes at 45cm x10 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 (Table 1). 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). Before conducting ANOVA, data normality and variance homogeneity were assessed using the Shapiro-Wilk (Shapiro and Wilk,1965) and Levene's tests (Levene,1960), respectively. Both tests showed $p > 0.05$, confirming that ANOVA assumptions were met and the analysis appropriate. Quantitative data obtained were subjected to Analysis of variance and significance means were separated using Least significant difference (LSD) using PBTools (PBTools, 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 Cochram (1967). A correlation matrix was drawn up using the linear correlation coefficients. UPGMA cluster analysis was used to construct a dendogram to ascertain the genetic relationships among the tomato accessions.

Table 1. The Physico-chemical property of the soil used at the start of the experiment

Parameter	Value
Particle size distribution (%)	
Coarse sand	14.2
Fine sand	66.1
Clay	3.6
Silt	16.4
Textural class	Loamy
pH(H20)	6.47
pH(KCL)	5.04
Organic Carbon (%)	0.81
Total Nitrogen (%)	0.08
Total Phosphorus (mg/kg)	6.2
Base saturation (%)	48.6
Organic matter (%)	1.54
Exchangeable cations (c mol / kg)	
K	0.11
Mg	1.9
Ca	2.7
Na	0.06
Al	1.4
H	2.2
CEC	8.35
Zn (ppm)	6.27
Fe (ppm)	5.11
Cu (ppm)	3.69
Mn (ppm)	1.78
S (ppm)	0.69

Soil Analysis Values were obtained from a predetermine potting mixture ratio.

Results

Genetic Diversity

The maize germplasm used in this study was sourced from different location of the country. This geographic variation likely contributed to the genetic diversity observed due to differing agro-ecological conditions and farming practices (Table 2).

Significant differences were shown among the genotypes for the morphophysiological characterizers measured, with genetic distance ranging from 0.01 to 0.38 (Fig. 1a,1b and Table 3). 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.

Genetic Variability

The ANOVA results in Table 4 reveal that among the 12 traits evaluated across 24 maize genotypes was significant but only Root Volume (RV) exhibited highly significant variation (F = 3.38, P = 0.0427), indicating genotypic differences for this trait at the 5% significance level. All other characteristics, including seedling height, leaf area, collar girth, number of leaves, shoot and root weights, and seedling aspect, showed significant differences ($P > 0.05$) (Table 4).

The results showed that the 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 shad leaves per plant (Table 5).

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 5).

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 2: 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

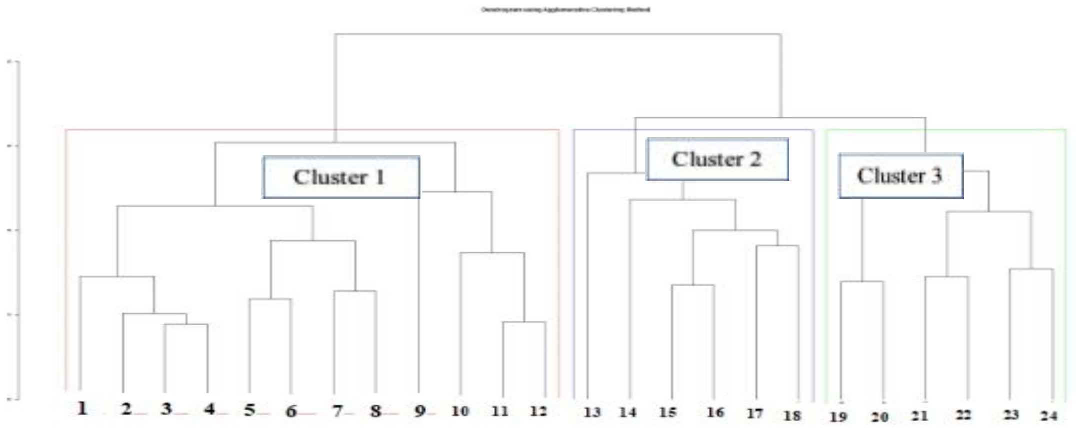

Figure 1a: Dendogram of 24 Maize Genotypes Based on 12 Agro-Morphological Attributes and Generated from Average Taxonomic Distance Matrix by Upgma in Nysyspc.

Dendogram Table: 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

.

Table 3: Cluster Mean for Different Maize Plant Seedling Traits among 24 Maize Genotypes

	Traits											
Cluster	PSH	LA	PCG	NOL	NSL	FSW	DSW	FRW	DRW	LPR	RV	SA
I	0.384	0.3322	0.2348	0.2016	0.0549	0.3510	0.3785	0.3742	0.3726	0.2073	0.2290	0.0478
II	-0.110	-0.1633	0.1393	0.0170	0.6094	0.1364	0.0958	-.11106	0.0955	-0.0320	-0.0728	0.6446
III	0.1830	-0.2531	-0.442	-0.537	-0.180	-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 4: - Analysis of variance for different traits for the 24 Maize Genotypes.

S/No	Traits	Accession means	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)	3.85	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	3.15
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	5.33
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 5: Estimates of phenotypic variance (σ^2p), genotypic variance (σ^2g), heritability (H^2b), genotypic and phenotypic coefficients of variability and genetic advance for various traits of the Maize genotypes.

S/N	Traits	σ^2g	σ^2p	σ^2e	H^2b (%)	GCV	PCV	GA
1	Plant Seedlings Height- PSH):	121.48	127.48	5.00	0.95	21.99	22.52	44.21
2	Leaf Area- (LAI)	1664.87	1678.58	13.71	0.99	42.91	43.09	38.04
3	Plant Collar Girth -(PCG)	5.97	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	51.22
6	Fresh shoot weight (FSW)	451.19	467.00	15.81	0.97	58.04	59.22	137.76
7	Dry Shoot Weight (DSW)	2.99	3.25	0.26	0.92	58.03	70.93	134.39
8	Fresh root weight- (FRW)	27.88	29.19	1.30	0.96	54.79	56.29	130.46
9	Dry Root Weight -(DRW)	2.90	3.30	0.40	0.88	57.56	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	50.85

Note: σ^2g = genotypic variance, σ^2g = phenotypic variance, σ^2e = environmental variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, GA= Genetic advance, H^2b = 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

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

Note**:** *Significant at p = 0.05 levels of probability. Number of Leaf (NOL), Number of Shade Leaf (NSL,) 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 (FSW); Dry Shoot Weight (DSW); Leaf Area (LA).

Discussion

Genetic Variability

The primary source of genetic diversity is likely attributable to geographic variation, which reflects differences in agro-ecological conditions and farming practices across the locations from which the genotypes were sourced. The observed significant differences among genotypes for all measured traits indicate the presence of substantial genetic variability. Addition to other traits root volume is shown to display high significant variation and most promising trait of consideration for selecting genotypes with drought tolerance potentials. These suggest considerable potential for improvement through selection and hybridization, a prerequisite for effective breeding programs (Nwadike *et al.,* 2022; Wali *et al.,* 2019). Morphological characterization, as employed in this study, remains a practical and reliable approach for estimating genetic diversity and evaluating genotype performance in a given environment (Fufa *et al.,* 2005; Shuaib *et al.,* 2007; Nwosu *et al.,* 2018). Such diversity is crucial for developing maize cultivars adaptable to diverse and changing agroecological conditions (Dwivedi *et al.,* 2016). The clustering pattern observed, where genotypes from geographically distinct regions are grouped, reflects a weak association between geographical origin and genetic relatedness. This is consistent with findings by Islam *et al.* (2020) and Wali *et al.* (2019), who reported similar patterns using morphological traits. Genotypes like KAF-4-W (Kaduna) and MARA AURE-W (Goniri-Gujba) clustered with others from distant regions, indicating gene flow or shared ancestry beyond geographic boundaries. While these groupings provide preliminary insights, molecular characterization using SSR markers to confirm the distinctiveness of these genotypes is recommended

Phenotypic and Genotypic Coefficients of Variation

The relatively narrow differences between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for most traits suggest minimal environmental influences on these traits. This enhances the efficiency of selection for improvement, especially for traits contributing to drought tolerance. However, larger disparities between PCV and GCV observed for seedling height imply greater environmental influence, which may complicate selection based on phenotypic performance alone.

Heritability and Genetic Advance

Heritability estimates were generally high (>80%) for most traits, except for the number of leaves and shed leaves per plant. High heritability indicates that much of the phenotypic variation is attributable to genetic factors, suggesting that these traits are under additive gene control and are amenable to selection (Songsri *et al.,* 2008; Eid, 2009). The combination of high heritability with high genetic advance observed for several traits such as root and shoot biomass-indicates that genetic gains through selection would likely be substantial (Parnse, 1957; Mohsin *et al.,* 2009). These findings affirm that traits can be improved in early-generation selection schemes targeting drought stress tolerance.

Trait Associations and Implications for Drought Tolerance

Correlation analysis revealed strong, positive relationships among key morpho-physiological traits. Traits such as number of leaves, leaf area index, collar girth, and biomass components (fresh and dry weights of shoot and root) were positively associated. These interrelationships imply shared genetic control or physiological coordination under drought conditions. For instance, the significant correlation between plant height and fresh shoot weight suggests that taller seedlings tend to accumulate more biomass-a trait advantageous under limited water availability. Similarly, strong positive correlations between fresh and dry root weights, root volume, and shoot biomass imply that coordinated growth is essential for sustaining resource acquisition and plant vigour during early drought stress (Sharp *et al.,* 2004; Fenta *et al.,* 2014). These correlations are particularly relevant for indirect selection, as improving one trait could positively influence others. For example, selection for increased collar girth or root biomass may enhance shoot development and overall plant resilience under drought. The findings support the view that targeting seedling-stage traits can lead to improved drought adaptation in maize, as demonstrated in previous studies (Meeks *et al.,* 2013; Li *et al.,* 2015).

Conclusion

The findings from this study revealed a wide range of genetic variability among the maize genotypes evaluated, indicating a substantial pool of genetic resources that can be exploited in breeding programs. Strong genetic associations among traits suggest that indirect selection will be a valuable strategy for improving complex traits such as drought tolerance. Although environmental factors may influence genetic parameter estimates across locations, the high heritability and genetic advance observed for most of the studied traits—excluding the number of shed leaves and plant collar girth—suggest that these traits are predominantly governed by additive gene action. This implies that recurrent selection and pedigree breeding methods can achieve significant genetic progress. Traits with strong heritability and favourable genetic associations should be prioritized in selection, as they are more likely to confer stable improvements under drought stress. The generally lower genotypic coefficients of variation compared to phenotypic coefficients indicate a notable environmental influence, which may mask the true expression of certain traits. Nevertheless, the genetic architecture revealed in this study provides a strong foundation for informed selection decisions. Based on the integrated analysis of genetic parameters and trait performance, several genotypes emerged as promising candidates for use as parental lines in drought tolerance improvement programs. These include KIERKIER, TZM-DAFFO–L, KAF-16, MARA AURE–W (Bindari), SAMMAZ-52, TZM-FOB–L, KAF-4–W, OBA SUPER II, KAF-21, MARA AURE–Y (Mamudo-Damagun)-1, MARA AURE–W (Bindari-Damagun)-2, PVA–SYN-F0, PVA–SYN-14, SAMMAZ-24, DMR-ESR-Y, and MARA AURE–Y (Kilbiri-Gujba)-1. These genotypes exhibit desirable genetic attributes and consistent performance across key drought-related traits, making them suitable for future crossing schemes and population development aimed at enhancing drought resilience in maize.

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