Genetic variability for drought tolerance in maize using germination and seedling traits under different PEG treatments

Oluwatoyin Sunday Osekita*, Abiola Toyin Ajayi, Oloruntoba Emmanuel Oladipo and Oluwafisayomi Ifeoluwani Ofakunrin

Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba Akoko, Nigeria

*Corresponding author's email: oluwatoyin.osekita@aaua.edu.ng

Key Message: Treating maize seeds with polyethylene glycol (PEG) enhances germination and lateral root growth for assessing moisture during water stress. This scenario extends the number of periods the maize plant can withstand acute water shortage in the soil therefore leading to the development of drought resilient maize genotypes.

Abstract

Drought stress significantly affects maize productivity, necessitating the development of drought-tolerant varieties. This research was carried out to identify drought-tolerant maize genotypes using polyethylene glycol (PEG) treatments which were achieved through estimation of genetic parameters for drought related traits. A completely randomized design was employed by exposing the maize genotypes to 0%, 5%, and 10% PEG treatments. This was carried out by using 5% of PEG dissolved in water to moisten the seeds sown in petri dishes, similar procedure was carried out for 10% PEG treatment and distilled water was only used to moisten the seeds sown in petri dishes as control. The petri dishes were replicated three times and the sowed seeds were kept in the incubator for 48 hours. Data were collected on the following germination traits such as; germination energy, germination capacity, root length (lateral and tap root), shoot height, number of roots, fresh shoot, and dry shoot weights. Stress tolerance indices (STIs) ranked genotypes based on drought tolerance. The results showed that there were significant genetic variation among the maize genotypes, Tap root length in the control had 2.99 cm while it is lowest in 10 % PEG with 1.36 cm therefore, selection based on rank mean with values in parenthesis identified genotypes 2 (2.5), 5 (3.38), 6 (3.88), 8 (4.13), and 9 (1.75) lower than the grand mean rank mean of 4.69 as drought-tolerant and those with higher values identified genotypes 1 (7.75), 3 (5.38), 4 (5.75), and 7 (7.75) as susceptible. The findings based on the identified drought tolerant maize genotypes can aid in the development of drought resilient maize genotypes which would enhance food security and sustainability. © 2025 The Author(s)

Keywords: Drought, Genetic variability, Germination capacity, Germination energy, Polyethylene glycol, Seedling traits

Introduction

Maize (*Zea mays*) serves as the main staple food for over 900 million people worldwide and is the third largest source of calories after rice and wheat (Abbas et al., 2025; Abdullah et al., 2025), supplying at least 30% of the food calories to more than 4.5 billion people in 94 developing nations, where one-third of children suffer from malnutrition (Hoisington et al., 1996; McMillen et al., 2022). However, various environmental stresses severely impact global maize productivity. Among these, drought stress stands out as one of the most critical abiotic factors, significantly reducing plant growth, development, and production. It is widely regarded as one of the most devastating environmental stresses (Xiong et al., 2006; Waqas et al., 2021). Plants experience drought stress when an inadequate supply of water is available for normal physiological processes, leading to various physiological, chemical, and molecular changes in plant cells and tissues (Farooq et al., 2009). An estimated 15% to 20% of maize grain yield is lost each year due to drought, and these losses are expected to rise as droughts become more frequent and severe due to the effects of climate change (FAOSTAT, 2010; Maazou et al., 2016). Due to maize yield loss from drought, developing countries experienced a revenue loss of up to USD 29 billion between 2005 and 2015 (McMillen et al., 2022).

Drought stress affects nearly all stages of plant development, with its detrimental effects being particularly pronounced when it occurs during critical growth phases such as germination, seedling shoot and root elongation, and flowering (Partheeban et al., 2017; Raj et al., 2020). Additionally, water stress hinders seed emergence and prolongs the mean germination time (Raj et al., 2020). During the reproductive phase, severe water deficits from a few days before silking to approximately 25 days can drastically reduce yield by delaying ear growth and silking, thereby increasing the anthesis-silking interval (ASI) and inhibiting fertilization. This results in kernel abortion, a reduced number of kernels, and significantly lower kernel weight due to decreased photosynthate accumulation. Additionally, drought-induced premature leaf senescence and reduced ear growth further compound the loss in yield,

highlighting the vulnerability of plants to water scarcity during these crucial developmental stages (McMillen et al., 2022).

Plants adapt to and survive drought stress by activating various morphological, biochemical, and physiological mechanisms (Anjum et al., 2011). Physiologically, they regulate the stomatal aperture to reduce water loss through transpiration (Flexas & Medrano, 2002), engage in osmotic adjustment by accumulating compatible solutes such as proline and sugars to sustain cellular turgor (Farooq et al., 2009), and optimize water absorption and retention through root system modifications and reduced cuticular transpiration (Chaves et al., 2009). At the molecular level, plants utilize signaling molecules like abscisic acid to trigger stomatal closure and activate stress-responsive genes (Fujita et al., 2005). Over the years, various approaches have been employed to identify drought-tolerant genotypes, including conventional breeding techniques. However, these methods are often time-consuming and face significant limitations, such as inadequate screening techniques and insufficient understanding of the genetic mechanisms underlying drought tolerance (Bawa et al., 2015). To address these limitations, *in vitro* selection techniques using PEG have emerged as reliable alternatives for identifying desirable genotypes and studying the impacts of water scarcity on plant germination indices (George et al., 2013). Keeping in view these facts, the present study was conducted to evaluate nine genotypes of maize for drought-tolerant and intercharacter association under PEG-stimulated water stress.

Materials and Methods

Plant materials

Nine genotypes of maize were obtained from the National Centre for Genetic Resources and Biotechnology (NACGRAB) in Ibadan, Oyo State, Nigeria. The specific details of the genotypes are presented in Table 1.

Table 1 List of genotypes used in the study

Sr. No.	Genotype code	Genotypes
1	GEN1	NGB02910
2	GEN2	NGB02864
3	GEN3	NGB02895
4	GEN4	NGB02346
5	GEN5	NGB03254
6	GEN6	NGB02900
7	GEN7	NGB02248
8	GEN8	NGB02868
9	GEN9	NGB02870

Experimental procedure

The experiment was conducted at the laboratory of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba Akoko, in 2024, using nine genotypes of maize as listed in Table 1 above. The seeds were surface sterilized before being planted in sterilized plastic containers, each containing two pieces of sterilized filter paper and 5 ml of PEG at three concentration levels (0%, 5%, and 10%). Thirty seeds from each genotype were placed on the filter papers in each container, with the experiment replicated three times for each treatment arranged in a Completely Randomized Design (CRD). Each of the replicated trials was treated with the two concentrations of PEG i. e., 5% and 10% and the control (0%), and is allowed to stay for 48 hours before data taken commenced. The study was terminated at the seedling stage after observation and collection of germination traits.

Data collection

Data on germination energy, germination capacity, root length, number of roots, shoot length, and both fresh and dry shoots and root weights were collected. During data collection, germination energy, representing the percentage of germinated seeds on day four after sowing, was determined by dividing the number of germinated seeds by the total planted and multiplying by 100. Similarly, germination capacity, calculated on day ten, followed the same formula. Other measurements included shoot length, assessed from the base of the plant to the tip of the shoot, and the length of the main root per shoot, measured from the base to the tip of the taproot at the same period. Leaf length, number of roots, and leaves per shoot were also recorded. Furthermore, fresh shoot weight was determined by separating seedlings into shoots and roots and recording the shoot weight, while fresh root weight was measured by weighing the separated fresh roots. Dry shoot and root weights were obtained after oven-drying plant shoots and roots for 48 hours at 60 °C.

Data analysis

Analysis of variance (ANOVA) using SPSS version 22 was carried out on the collected data, and mean values were separated utilizing Duncan's multiple range test (DMRT) at a significance level of $P \leq 0.05$. Drought tolerance indices for all traits were determined using the stress tolerance index (STI) according to Ajayi (2021) as follows:

$$STI = \frac{c*s}{(GM)2}$$

Where C, S, and GM represent the mean values for a genotype under control, mean value under stress, and grand mean over all genotypes under control, respectively. Accessions were ranked into different classes of drought tolerance ranging from 1 (most tolerant) to 8 (least tolerant) for each trait. Ranking of the genotypes was also determined using the procedure of Ajayi et al. (2023).

Estimate of genetic parameters

This was estimated according to the procedure of Ajayi et al. (2024) for genotypic and phenotypic variance, genotypic and phenotypic coefficients of variance, broad sense heritability, genetic advance, and as percent of mean.

Results

The ANOVA results in Table 2 reveal that the effect of genotype, treatment, and the genotype × treatment interaction was significant for all the studied traits. Among the traits, fresh root weight exhibited the highest coefficient of variation (17%), while germination capacity showed the lowest coefficient of variation (0.12%).

Table 2 Analysis of variance on measured morphological growth parameters

Parameter	Genotype	Treatment	Treatment × Genotype	Error	CV
DF	9	2	16	52	
GE	2678.16*	3690.57*	498.56*	151.92	0.14
GC	2580.29*	3585.27*	555.2*	204.49	0.12
SH	1.39*	5.54*	0.66*	0.215	3.26
LRL	3.41*	35.93*	3.38*	0.87	1.22
TRL	8.77*	18.8*	10.55*	0.75	2.13
NR	19.79*	101.34*	10.65*	6.22	0.56
FSW	0.057*	0.61*	0.26*	0.01	17.00
DSW	0.66*	0.29*	0.11*	0.01	14.00

*: significant at $p \leq 0.05$; DF: Degree of freedom; CV: Coefficient of variation; GE: Germination energy; GC: Germination capacity; SH: Shoot height; LRL: Lateral root length; TRL: Tap root length; NR: Number of roots; FSW: Fresh shoot weight; DSW: Dry shoot weight.

Mean performance for germination and seedling traits among maize genotypes

The mean performance for germination and seedling traits among maize genotypes evaluated for drought tolerance under differential PEG treatments is presented in Table 3. Under control conditions, germination energy ranged from the lowest (10%) in GEN4 to the highest (80%) in GEN2. In terms of germination capacity, 80% in GEN9 and 10% in GEN4 displayed the highest and lowest mean values, respectively. Concerning shoot height, 2.73 cm in GEN9 and 1.30 cm in GEN6 were observed as the highest and lowest mean values, respectively. Lateral root length had the highest mean value at 6.17 cm in GEN4 and the lowest mean value at 1.03cm in GEN6. Concerning tap root length, the highest mean value of 8.73 cm was recorded in GEN9, while the lowest value of 1.33 cm was recorded in GEN6. The number of roots ranged from the lowest value (3.67) in GEN8 to the highest value (13.67) in GEN1. Concerning the fresh shoot weight, the highest mean value was 0.67 g in GEN2, while the lowest mean value was observed in GEN4 with a value of 0.20 g. Regarding the dry shoot weight, the mean value ranged from the lowest (0.07 g) in GEN4 to the highest (0.54 g) in GEN7.

Under 5% PEG treatment, germination energy had 60% in GEN2 and 13.32% in GEN3 and GEN8, observed as the lowest and the highest mean values, respectively. In terms of germination capacity, GEN2 had the highest mean value with 63.33%, while GEN1 and GEN8 had the lowest value with 13.33%. Shoot height ranged from the lowest 0.97 cm in GEN8 to the highest (1.87 cm) in GEN4. Concerning lateral root length, 2.97cm in GEN5 and 1.17 cm in GEN8 were observed as the highest and lowest means. In terms of tap root length, 5.30 cm in GEN5 and 1.17 cm in GEN8 were observed as the highest and lowest mean values, respectively. Regarding the number of roots, the highest mean value, 8.00, was observed in GEN6, while the lowest mean value, 3.33, was observed in GEN8. Concerning fresh shoot weight, the highest mean value was observed in GEN9 with a value of 0.20 g, and the lowest mean value was observed in GEN1 and GEN8 with a value of 0.10 g. Regarding the dry shoot weight, 0.77 g in GEN6 and 0.59

g in GEN1, 2, and 9 were observed as the highest and the lowest.

Under 10% PEG treatment, germination energy ranged from the lowest 2.33% in GEN4 to the highest 36% in GEN5. In terms of germination capacity, 50% in GEN5 was observed as the highest mean value, while 3.33% in GEN4 was observed as the lowest mean value. Shoot height from the lowest value (0.40 cm) in GEN4 to the highest (1.53 cm) in GEN5. Concerning lateral root length, GEN6 had the highest mean value of 2.20 cm, and GEN4 had the lowest mean value of 0.4 cm (Fig. 1). Regarding tap root length, GEN3 had the highest mean value of 3.67 cm, and GEN4 had the lowest mean value at 0.53 cm. In the number of roots, 7.00 in GEN2 and 2.67 in GEN4 were observed as the highest and the lowest mean values, respectively. The highest mean value for fresh shoot weight was observed in GEN6 0.35 g, while the lowest mean values were observed in GEN4 and GEN5 with 0.13 g each. For the dry shoot weight, the highest mean value (0.14 g) was observed in GEN6, and the lowest mean value (0.04 g) was observed in both GEN2 and GEN5.

Stress tolerance indices for germination and seedling traits among maize genotypes at 10% PEG treatment

The stress tolerance indices (STI) and ranking for germination traits among genotypes of maize evaluated for drought tolerance in 10% PEG treatment are presented in Table 4. Regarding treatment three (10% PEG), the STI value was the same for all genotypes under germination energy. Germination capacity had 1.1) as the highest value in GEN3 and the lowest in GEN5, 6, and 7, with (0). Under shoot height, (0.72) was the highest value, and (0) was the lowest in GEN5, 6, and 7. STI values (1.96, 1.11, 0.67, and 6) in root length in GEN3, number of roots in GEN9, fresh shoot weight under GEN3, 9, and 10, and lastly dry shoot weight also in GEN3 were all observed as the highest STI values, respectively. The lowest values were observed in GEN5, 6, and 7 under root length, number of roots, fresh shoot weight, and dry shoot weight, with all having a value (0) respectively under the germination parameters. Concerning the 10% PEG

treatment, GEN2, 5, 6, 8, and 9 exhibited are highly tolerant to drought stress with STI rank values 2.50, 3.38, 3.88, 4.13, and 1.75 below the grand mean (4.69). In contrast, GEN1, 3, 4, and 7 are susceptible to drought stress, possessing a rank mean value (7.75, 5.38, 5.75, and 7.75) above the grand mean.

Table 3 Mean performance for germination and seedling traits among maize genotypes under different PEG treatments

0% PEG treatment								
Genotype	GE	GC	SH	LRL	TRL	NR	FSW	DSW
G1	60.00 ± 5.77^{bc}	66.67 ± 66.67^{cd}	1.77 ± 0.07^{ab}	3.89 ± 0.47^{cd}	2.40 ± 0.06^{a}	8.00 ± 0.58^{bc}	0.37 ± 0.03^{abc}	0.25 ± 0.02^{d}
G2	80.00 ± 11.55^{c}	56.67 ± 24.04^{bcd}	2.47 ± 0.38^{ab}	5.31 ± 0.31^{de}	$2.90 \pm 0.29a$	6.00 ± 0.58^{ab}	0.67 ± 0.07^{d}	0.42 ± 0.02^{f}
G3	23.33 ± 13.33^{a}	23.33 ± 13.33^{ab}	1.31 ± 0.07^{a}	1.95 ± 0.10^{ab}	1.47 ± 0.26^{a}	9.33 ± 1.67^{bc}	$0.30 \pm 0.00a^{b}$	0.09 ± 0.1^{ab}
G4	10.00 ± 0.00^{a}	10.00 ± 0.00^{a}	2.00 ± 2.89^{abc}	6.17 ± 0.78^{e}	3.17 ± 0.20^{a}	13.67 ± 2.03^{d}	0.20 ± 0.00^{a}	0.07 ± 0.01^{a}
G5	40.00 ± 15.28^{ab}	50.00 ± 15.28^{abcd}	1.71 ± 0.09^{ab}	2.75 ± 0.49^{abc}	2.13 ± 0.47^{a}	7.00 ± 0.58^{abc}	0.53 ± 0.07^{cd}	0.18 ± 0.01^{c}
G6	16.67 ± 6.67^{a}	20.00 ± 10.00^{ab}	1.30 ± 0.06^{a}	1.33 ± 0.34^{a}	1.33 ± 0.33^{a}	7.00 ± 0.00^{abc}	0.47 ± 0.09^{bc}	0.12 ± 0.01^{b}
G7	16.67 ± 6.67^{a}	$16.67 \pm 6.67a^{b}$	1.67 ± 0.33^{ab}	1.80 ± 0.51^{ab}	1.90 ± 0.46^{a}	6.67 ± 0.88^{abc}	0.30 ± 0.06^{ab}	0.52 ± 0.01^{g}
G8	26.67 ± 12.02^{a}	30.00 ± 10.00^{abc}	1.87 ± 0.41^{abc}	3.23 ± 0.78^{bc}	2.87 ± 0.85^{a}	3.67 ± 1.20^{a}	0.37 ± 0.09^{abc}	0.24 ± 0.01^{d}
G9	70.00 ± 5.77^{bc}	80.00 ± 5.77^{d}	2.73 ± 0.39^{c}	5.43 ± 0.33^{de}	8.73 ± 1.63^{b}	9.67 ± 0.33^{c}	$.47 \pm 0.07^{ab}$	0.35 ± 0.01^{e}
Grand mean	38.15 ± 5.47	39.26 ± 5.67	1.87 ± 0.12	3.54 ± 0.35	2.99 ± 0.46	7.89 ± 0.60	0.41 ± 0.03	0.25 ± 0.03

GE: Germination energy; GC: Germination capacity; SH: Shoot height; LRL: Lateral root length; TRL: Tap root length; NR: Number of roots; FSW: Fresh shoot weight; DSW: Dry shoot weight; Mean values followed by similar subscripts within a column are not significantly different from one another at $p \leq 0.05$ using DMRT.

Table 3 continue

5% PEG treatment								
Genotype	GE	GC	SH	LRL	TRL	NR	FSW	DSW
G1	13.33 ± 3.33^{a}	13.33 ± 3.33^{a}	1.47 ± 0.18^{bc}	1.63 ± 0.15^{b}	2.27 ± 0.09^{b}	5.00 ± 1.53^{bc}	0.10 ± 0.00^{ab}	0.05 ± 0.00^{a}
G2	60.00 ± 10.00^{b}	63.33 ± 6.67^{b}	1.57 ± 0.19^{bc}	1.47 ± 0.18^{b}	2.03 ± 0.34^{b}	4.33 ± 0.88^{bc}	0.17 ± 0.03^{b}	0.05 ± 0.00^{a}
G3	20.00 ± 5.77^{a}	20.00 ± 5.77^{a}	1.40 ± 0.12^{bc}	1.77 ± 0.19^{b}	1.73 ± 0.07^{b}	5.33 ± 1.76^{bc}	0.13 ± 0.03^{ab}	0.26 ± 0.01^{a}
G4	0.00 ± 0.0^{a}	13.33 ± 3.33^{a}	1.87 ± 0.12^{c}	1.67 ± 0.07^{b}	4.83 ± 1.28^{c}	6.33 ± 1.45^{bc}	0.17 ± 0.03^{b}	0.06 ± 0.00^{a}
G5	53.33 ± 8.82^{b}	56.67 ± 12.02^{b}	1.83 ± 0.15^{c}	2.97 ± 0.32^{c}	5.30 ± 0.76^{c}	5.33 ± 0.88^{bc}	0.17 ± 0.03^{b}	0.21 ± 0.01^{a}
G6	16.67 ± 3.33^{a}	16.67 ± 3.33^{a}	1.07 ± 0.07^{b}	1.90 ± 0.35^{b}	2.27 ± 0.09^{b}	8.00 ± 1.15^{c}	0.20 ± 0.06^{b}	0.77 ± 0.01^{b}
G7	0.00 ± 0.00^{a}	0.00 ± 0.00^{a}	0.00 ± 0.00^{a}	0.00 ± 0.00^{a}	0.00 ± 0.00^{a}	0.00 ± 0.00^{a}	0.00 ± 0.00^{a}	0.00 ± 0.00^{a}
G8	13.33 ± 8.82^{a}	13.33 ± 8.82^{a}	0.97 ± 0.49^{b}	1.17 ± 0.58^{b}	1.17 ± 0.59^{ab}	3.33 ± 1.76^{ab}	0.10 ± 0.06^{ab}	0.54 ± 0.27^{b}
G9	50.00 ± 5.77^{b}	53.33 ± 3.33^{b}	1.53 ± 0.07^{bc}	1.40 ± 0.12^{b}	2.07 ± 0.18^{b}	3.67 ± 0.88^{ab}	0.20 ± 0.10^{b}	0.05 ± 0.00^{a}
Grand mean	25.19 ± 4.60	27.78 ± 4.63	1.30 ± 0.12	1.55 ± 0.16	2.41 ± 0.34	4.59 ± 0.54	0.14 ± 0.02	0.22 ± 0.06

GE: Germination energy; GC: Germination capacity; SH: Shoot height; LRL: Lateral root length; TRL: Tap root length; NR: Number of roots; FSW: Fresh shoot weight; DSW: Dry shoot weight; Mean values followed by similar subscripts within a column are not significantly different from one another at $p \leq 0.05$ using DMRT.

Table 3 continue

Genotype	GE	GC	SH	LRL	TRL	NR	FSW	DSW
10% PEG Treatment								
G1	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a
G2	20.00 ± 5.77^{cd}	20.00 ± 5.77^{cd}	1.50 ± 0.06^d	1.40 ± 0.12^{bc}	2.20 ± 0.12^c	7.00 ± 0.58^c	0.15 ± 0.03^a	0.04 ± 0.0^{ab}
G3	3.33 ± 3.33^{ab}	10.00± 0.00^{abc}	1.30 ± 0.29^{cd}	1.97 ± 0.32^{cd}	3.67 ± 0.09^d	4.67 ± 0.33^{bc}	0.15 ± 0.03^a	0.07 ± 0.01^{ab}
G4	3.33 ± 3.33^{ab}	3.33 ± 3.33^{ab}	0.47 ± 0.47^{ab}	0.40 ± 0.40^a	0.53 ± 0.53^{ab}	2.67 ± 2.67^{ab}	0.13 ± 0.13^a	0.05 ± 0.05^{ab}
G5	36.67 ± 8.82^e	50.00 ± 5.77^e	1.53 ± 0.13^d	1.83 ± 0.15^{cd}	2.33 ± 0.59^c	3.67 ± 0.67^{bc}	0.13 ± 0.03^a	0.04 ± 0.00^{ab}
G6	15.00 ± 2.89^{bc}	15.00 ± 2.89^{bcd}	1.30 ± 0.06^{cd}	2.20 ± 0.12^d	1.40 ± 0.35^{bc}	6.00 ± 1.15^{bc}	0.35 ± 0.03^b	0.14 ± 0.00^c
G7	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a	0.00 ± 0.00^a
G8	13.33 ± 3.33^{abc}	13.33 ± 3.33^{bcd}	0.73 ± .29^{bc}	1.10 ± 0.26^b	1.20 ± 0.12^b	4.33 ± 0.88^{bc}	0.17 ± 0.3^a	0.10 ± 0.3^{bc}
G9	30.00 ± 0.00^{de}	23.33 ± 6.67^d	1.20 ± 0.6^{cd}	1.13 ± 0.29^{bc}	0.93 ± 0.18^{ab}	4.00 ± 1.15^{bc}	0.17 ± 0.3^a	0.06 ± 0.10^{ab}
Grand mean	13.52 ± 2.72	15.00 ± 3.08	0.89 ± 0.13	1.13 ± 0.17	1.36 ± 0.24	3.59 ± 0.54	0.14 ± 0.02	0.6 ± 0.01

GE: Germination energy; GC: Germination capacity; SH: Shoot height; LRL: Lateral root length; TRL: Tap root length; NR: Number of roots; FSW: Fresh shoot weight; DSW: Dry shoot weight; Mean values followed by similar subscripts within a column are not significantly different from one another at P ≤ 0.05 using DMRT.
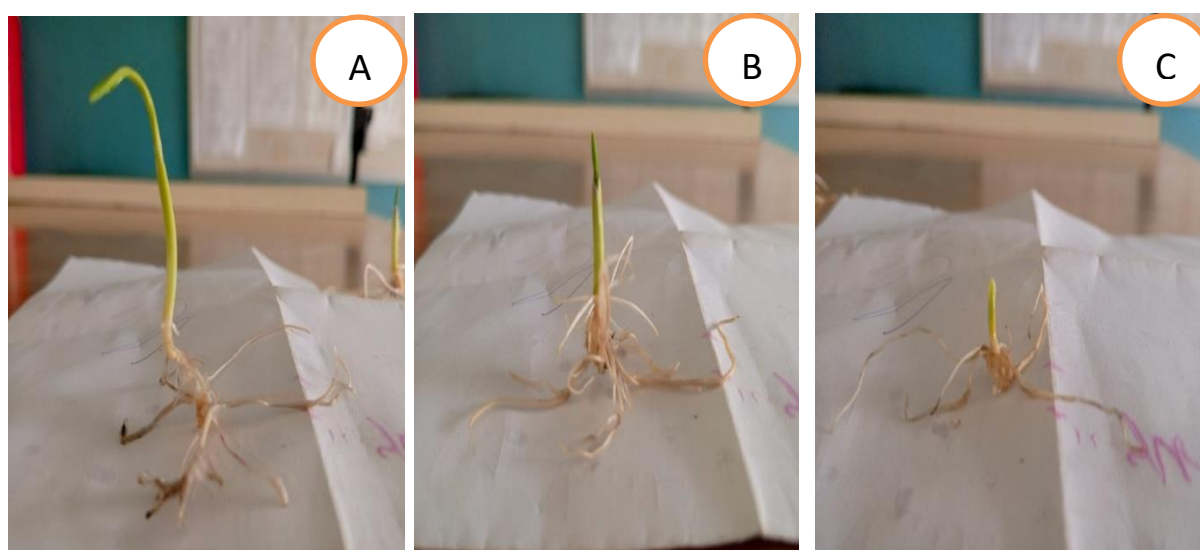

Fig. 1 Variation in lateral root length under different PEG treatments. With specific reference to genotype 6 (NGB02900) for lateral root growth under control condition and drought stress induced by PEG. (A) NGB02900 with lateral root length of 1.33 cm under 0% PEG treatment. (B) NGB02900 with lateral root length of 1.90 cm under 5% PEG treatment. (C) NGB02900 with lateral root length of 2.20 cm under 10% PEG treatment. Fig. 1 shows variability in root length of NGB 02900 with strong tolerance ability to drought. The genotype had the lowest lateral root length in the control treatment, second highest length in 5% PEG treatment and the highest for 10% PEG treatment. Therefore, 10% PEG treatment enhances lateral root growth for tapping moisture far away from the plant in order to sustain drought stress in case of moisture shortage.

Combined estimates of genetic parameters on germination traits of maize genotypes

The combined estimate of genetic parameter results presented in Table 5 revealed that genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PVC) were high for all (≥20). It was also revealed that heritability was high ≥ 60% for all traits observed except lateral root length, tap root length, and number of roots, which had heritability to be moderate at 42.91, 43.19, and 56.03% respectively, furthermore low heritability low for at 15.31%. But for genetic advance as a percent of mean (GAM), all traits were also observed to be high (≥20)

indicating significant impact of PEG for drought tolerance in maize.

Table 4 Stress tolerance indices (STI) and ranking for germination and seedling traits among maize genotypes evaluated for drought tolerance at 10% PEG treatment

Genotype	GE	GC	SH	LRL	TRL	NR	FSW	DSW	RK M
G1	0 (8)	0 (8)	0 (8)	0 (8)	0 (8)	0 (7)	0 (8)	0 (7)	7.75
G2	1.1 (2)	0.74 (3)	1.06 (1)	0.59 (1)	0.71 (2)	0.67 (1)	0.6 (7)	0.27 (3)	**2.5**
G3	0.05 (7)	0.15 (6)	0.49 (4)	0.31 (3)	0.6 (7)	0.7 (6)	0.27 (5)	0.1 (5)	5.38
G4	0.25 (4)	0.02 (7)	0.27 (7)	0.2 (7)	0.19 (6)	0.59 (3)	0.15 (6)	0.06 (6)	5.75
G5	1.01 (3)	1.62 (1)	0.75 (3)	0.4 (6)	0.56 (3)	0.41 (4)	0.41 (3)	0.12 (4)	**3.38**
G6	0.17 (6)	0.19 (5)	0.48 (5)	0.23 (5)	0.21 (5)	0.67 (1)	0.56 (1)	0.27 (3)	**3.88**
G7	0 (8)	0 (8)	0 (8)	0 (8)	0 (8)	0 (7)	0 (8)	0 (7)	7.75
G8	0.24 (5)	0.26 (4)	0.39 (6)	0.28 (4)	0.38 (4)	0.26 (5)	0.37 (4)	0.38 (1)	**4.13**
G9	1.44 (1)	1.21 (2)	0.94 (2)	0.49 (2)	0.91 (1)	0.62 (2)	0.48 (2)	0.34 (2)	**1.75**
GM	0.47	0.47	0.49	0.28	0.4	0.44	0.32	0.17	4.69

Genotype with Rank Mean (RKM) below the Grand Mean (GM) is highly tolerant; RKM is moderately tolerant if equals to GM, while the RKM above the GM is highly susceptible to drought stress; GE: Germination energy; GC: Germination capacity; SH: Shoot height; LRL: Lateral root length; TRL: Tap root length NR: Number of roots; FSW: Fresh shoot weight; DSW: Dry shoot weight.

Table 5 Combined estimates of genetic parameters on germination traits of maize genotypes evaluated for drought tolerance under differential PEG treatments

Parameter	GE	GC	SH	LRL	TRL	NR	FSW	DSW
GM	25.62	27.35	1.35	2.07	2.25	5.36	0.23	0.36
GVT	115.55	116.90	0.15	0.84	3.27	1.48	0.08	0.03
GV	421.04	395.97	0.20	0.42	1.34	2.26	0.01	0.11
PV	504.13	488.50	0.31	0.99	3.10	4.04	0.05	0.13
GCV (%)	80.09	72.77	32.70	31.38	51.31	28.07	38.48	92.28
PCV (%)	87.64	80.82	40.86	47.91	78.07	37.51	98.35	99.79
H2B (%)	83.52	81.06	64.03	42.91	43.19	56.03	15.31	85.53
GA	38.63	36.91	0.73	0.88	1.57	2.32	0.07	0.63
GAM (%)	150.78	134.96	53.90	42.34	69.46	43.29	31.02	175.81

GM: Grand mean; GVT: Genotype × treatment variance; GV: Genotypic variance; PV: Phenotypic variance; GCV: Genotypic coefficient of variance; PCV: Phenotypic coefficient of variance; H^{2}B: Heritability; GA: Genetic advance; GAM: Genetic advance as percentage of mean; GE: Germination energy; GC: Germination capacity; SH: Shoot height; LRL: Lateral root length; TRL: Tap root length NR: Number of roots; FSW: Fresh shoot weight; DSW: Dry shoots weight.

Discussion

The ANOVA results from the current study demonstrated significant effects of genotype on all germination and seedling traits, highlighting substantial genetic variation among the genotypes evaluated across treatments. Additionally, PEG treatment and the interaction between treatment and genotype were significant for all germination and seedling traits, suggesting genotype-specific responses to varying treatments. These findings align with those of Abdel-Ghani et al. (2015), who reported significant effects of treatment, genotype, and genotype × treatment interactions on germination traits in spring barley (*Hordeum vulgare* L.)

In this study, drought conditions simulated using polyethylene glycol (PEG) treatment led to reduce germination energy and germination capacity across all genotypes as the PEG concentration increased. Sharma et al. (2022) also observed similar results, reporting a significant decline in germination percentage and seedling growth as the concentration of PEG treatment increased. The importance of germination traits in affecting seedling performance under drought stress has also been highlighted in previous studies on wheat (Khan et al., 2013) and on tomatoes (Ajayi, et al., 2025). Further, key traits such as germination capacity, germination energy, root length,

number of roots, fresh shoot weight, and dry shoot weights showed substantial genetic variability and high heritability indicating strong genetic influence and stable inheritance under drought conditions. However, under 5% PEG treatment, the negative effects were minimal for certain genotypes, especially in GEN2, GEN3, GEN5, and GEN9, suggesting a higher level of tolerance in these genotypes compared to others. Root elongation is an important adaptive mechanism for plants facing abiotic stresses like drought, salinity, and nutrient deficiencies. This morphological adaptability enables plants to enhance their root systems, boosting their ability to absorb water and nutrients efficiently (Smith, 2023). In this study, genotype GEN5 exhibited drought tolerance, as reflected in its increased lateral root length (LRL) of 2.97 cm and tap root length (TRL) of 5.30 cm under 5% PEG treatment, compared to an LRL and TRL of 1.33 cm under control conditions. Similar results were also reported by (Smith, 2023) through extended lateral root growth for water and nutrient absorption.

Under the highest concentration of PEG (10% PEG), GEN2, 5, 6, 8, and 9 exhibited are highly tolerant to drought stress with STIs rank values 2.50, 3.38, 3.88, 4.13, and 1.75 below the grand mean (4.69). Similarly, Sharma et al. (2022) utilized STI assessment to evaluate drought tolerance in newly developed maize (*Zea mays* L.) hybrids.

Heritability alone does not indicate the extent of genetic improvement achievable through the selection of individual genotypes. Therefore, combining heritability estimates with genetic advance as a percentage of the mean (GAM) provides more meaningful insights (Abebe et al., 2017) by showcasing the potential of roots in drawing water to the plants in order to withstand drought stress in periods of limited moisture availability for plant growth and productivity. In this study, high heritability coupled with high GAM was observed for traits such as germination energy, germination capacity, shoot height, and dry shoot weight. This suggests that these traits are predominantly influenced by genetic factors, likely governed by additive gene action, and have a strong potential for transmission to the next generation. Consequently, selection based on these traits could be an effective approach for genetic improvement. Similar findings were reported by Abebe et al. (2017), who assessed genetic variability, heritability, and genetic advance in yield and related traits of rainfed lowland rice (*Oryza sativa* L.).

Conclusion

This study without prejudice successfully estimated genetic variability for drought tolerance on maize germination and seedling characteristics under different exposure to PEG treatments. Notably, screening nine genotypes of maize under three different treatments in the laboratory revealed significant genetic variations across all traits. Fresh shoot weight exhibited the highest coefficient of variability while the lowest was observed in germination capacity. From the study, genotypes 2, 5, 6, 8, and 9 are the most tolerant genotypes in 10% concentration of PEG treatment but the other genotypes are susceptible to drought stress. Estimate of genetic parameters indicated high heritability and genetic advance for all traits except fresh shoot weight which had low heritability value but the following traits stand out; dry shoot weight, germination energy, germination capacity, shoot height and number of roots. This study underscores the importance of identifying resilient traits and genotypes to improve drought stress tolerance in maize, ultimately contributing to food security and productivity.

Authors' Contributions: A.T.A. designed and supervised the research study. O.S.O. performed the experiments. O.E.O. performed statistical analysis. O.I.O. wrote the first draft of the manuscript. All authors read and approved the final manuscript.

Data availability: The data that support the findings of this study are available from the corresponding author upon reasonable request

Declarations

i. Ethics approval and consent to participate: Ethical approval and informed consent were not required for this study as it did not involve human participants, human data, or animals. The data used in this study were publicly available and did not contain any identifiable personal information.

ii. Competing interest: Authors have declared that no competing interests exist.

Publisher's note: All claims shared in this article are entirely those of the authors and do not reflect the positions of their affiliated institutions, AgriBio e-Spectrum (the publisher), editors, or reviewers. Any mention or assessment of a product, as well as any claims made by its manufacturer, are not endorsed or guaranteed by the publisher.

References

Abbas, R., Hussain, I., Baloch, M. S., Saddozai, U. K., Khan, A. A., Khan, B., & Khan, R. (2025). Allelopathic effect of *Moringa oleifera* on germination and physiology of seedlings in maize (*Zea mays* L.). *Journal of Plant Production and Sustainability, 1*(1), 61–69.

Abdel-Ghani, A. H., Neumann, K., Wabila, C., Sharma, R., Dhanagond, S., Owais, S. J., & Kilian, B. (2015). Diversity of germination and seedling traits in a spring barley (*Hordeum vulgare* L.) collection under drought-simulated conditions. *Genetic Resources and Crop Evolution*, *62*, 275-292.

Abdullah, Zia, M. A., Shoukat, S., Aziz, S., Khan, I. U., Khan, A., Maab, H., & Zaib, S. (2025). Co-expression of *ZmVPP1*, *ZmNAC111*, and *ZmTIP1* confers enhanced drought tolerance in maize (*Zea mays*). *Journal of Plant Production and Sustainability*, *1*(1), 12–19.

Abebe, T., Alamerew, S., & Tulu, L. (2017). Genetic variability, heritability, and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, Ethiopia. *Advances in Crop Science and Technology*, *5*(2), 272.

Ajayi, A. (2021). Genotypic differences in aluminum tolerance of cowpea accessions utilizing germination parameters. *International Journal of Life Sciences and Biotechnology*, *4*(2), 254–273.

Ajayi, A. T., Gbadamosi, A. E., Daodu, E. O., & Osekita, O. S. (2023). Genetics of aluminum tolerance in cowpea accessions screened in pots under field conditions. Proceedings 45th Annual Conference of Genetics Society of Nigeria. pp. 23-28.

Ajayi, A. T., Oladipo, O. E., Adelakin, D. A., & Badmus, M. B. (2025). Genetic diversity and drought tolerance in M7 Ethidium bromide-derived tomato genotypes. *International Journal of Plant and Soil Science*, *37*(9), 182-195.

Ajayi, A. T., Osekita, O. S., Oladipo, O. E. & Akinola, J. A. (2024). Estimates of genetic variability and interplay of germination and seedling traits conferring salinity tolerance in rice (*Oryza sativa* L.).

International Journal of Life Sciences and Biotechnology, 7(3), 149-160.

Anjum, S. A., Xie, X. Y., Wang, L. C., Saleem, M. F., Man, C., & Lei, W. (2011). Morphological, physiological, and biochemical responses of plants to drought stress. *African Journal of Agricultural Research, 6*(9), 2026-2032.

Bawa, A., Addai, A. K., & Abdulai, M. S. (2015). SSR markers as tools for screening genotypes of maize (*Zea mays* L.) for tolerance to drought and *Striga hermonthica* (Del.) Benth in the Northern Guinea Savanna Zone of Ghana. *Research in Plant Biology, 5*(5), 17–30.

Chaves, M. M., Flexas, J., & Pinheiro, C. (2009). Photosynthesis under drought and salt stress: Regulation mechanisms from whole plant to cell. *Annals of Botany*, *103*(4), 551-560.

Faostat (2010). Statistical database of the Food and Agriculture Organization of the United Nations. Rome: FAO.

Farooq, M., Wahid, A., Kobayashi, N., Fujita, D., & Basra, S. M. A. (2009). Plant drought stress: Effects, mechanisms, and management. *Agronomy for Sustainable Development*, *29*(1), 185-212.

Flexas, J., & Medrano, H. (2002). Drought-inhibition of photosynthesis in C3 plants: Stomatal and non-stomatal limitations revisited. *Annals of Botany*, *89*(2), 183-189.

Fujita, Y., Fujita, M., Satoh, R., Maruyama, K., Parvez, M. M., Seki, M. & Shinozaki, K. (2005). AREB1 is a transcription activator of novel ABRE-dependent ABA signaling that enhances drought stress tolerance in Arabidopsis. *The Plant Cell*, *17*(12), 3470-3488.

George, S., Jatoi, S. A., & Siddiqui, S. U. (2013). Genotypic differences against PEG simulated drought stress in tomato. *Pakistan Journal of Botany, 45*(5), 1551–1556.

Hoisington, D., Khairallah, M., Reeves, T., Ribaut, J.M., Skovmand, B., Taba, S., & Warburton, M. (1996). Plant genetic resources: What can they contribute toward increased crop productivity? *Proceedings of the National Academy of Sciences of the United States of America*, *96*, 5937-5943.

Khan, M. I., Shabbir, G., Akram, Z., Shah, M. K. N., Ansar, M., Cheema, N. M., & Iqbal, M. S. (2013). Character association studies of seedling traits in different wheat genotypes under moisture stress conditions. *SABRAO Journal of Breeding and Genetic*, *45*(3), 458-467.

Maazou, A. R. S., Tu, J., Qiu, J., & Liu, Z. (2016). Breeding for drought tolerance in maize (*Zea mays* L.). *American Journal of Plant Sciences*, *7*(14), 1858.

McMillen, M. S., Mahama, A. A., Sibiya, J., Lübberstedt, T., & Suza, W. P. (2022). Improving drought tolerance in maize: Tools and techniques. *Frontiers in Genetics*, *13*, 1001001. https://doi.org/10.3389/fgene.2022.1001001

Partheeban, C., Chandrasekhar, C. N., Jeyakumar, P., Ravikesavan, R., & Gnanam, R. (2017). Effect of PEG-induced drought stress on seed germination and seedling characters of maize (*Zea mays* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences, 6*(5), 1095–1104.

Raj, R. N., Gokulakrishnan, J., & Prakash, M. (2020). Assessing drought tolerance using PEG-6000 and molecular screening by SSR markers in maize (*Zea mays* L.) hybrids. *Maydica*, *64*(2), 1-7.

Sharma, V., Kumar, A., Chaudhary, A., Mishra, A., Rawat, S., B., B. Y., Shami, V., & Kaushik, P. (2022). Response of wheat genotypes to drought stress stimulated by PEG. *Stresses, 2*(1), 26-51.

Smith, J. (2023). Root adaptations in plants: Mechanisms and implications. *Journal of Plant Biology*, *45*(2), 123-134.

Waqas, M. A., Wang, X., Zafar, S. A., Noor, M. A., Hussain, H. A., Azher Nawaz, M., & Farooq, M. (2021). Thermal stresses in maize: Effects and management strategies. *Plants*, *10*(2), 293.

Xiong, L., Wang, R., Mao, G., & Koczan, J. M. (2006). Identification of drought tolerance determinants by genetic analysis of root response to drought stress and abscisic acid. *Plant Physiology*, *142*, 1065-1074.