



SCREENING OF MAIZE GENOTYPES UNDER WATER STRESS CONDITION AT EARLY GROWTH STAGES

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SUMMARY

Water shortage is the most yield-limiting factor in maize (*Zea mays* L.) crops, especially when the crop is at the seedling stage. In a maize breeding program, effective and reliable screening methods for water stress tolerance would be helpful. In this study, maize genotypes totaling 49 underwent evaluation against different water stress levels of 30%, 40%, and 100% field capacity at their early growth stages. The experiment transpired in the greenhouse of the University of Sargodha, Sargodha, Pakistan. The data assessment used completely randomized design (CRD), principal component analysis (PCA), biplot analysis, and correlation matrix to identify the water stress-tolerant genotypes. The significant ($p < 0.05$) differences were evident among the genotypes for all traits. Among principal factors, the first three had eigenvalues greater than one. The components, PC1, PC2, and PC3, accounted for 60%, 80%, and 95.8% of the cumulative variability, respectively. The analysis concluded that the mean emergence time (MET) and desiccation tolerance index (DTI) revealed negative correlations, suggesting their limiting role in early seedling performance. However, the genotypes 15067, Pearl, Sultan, 15023, 14996, 15005, Akbar, Sahiwal-2002, and 14985 proved superiors in performance and behaved as the best possible candidates for future water stress-tolerant breeding programs.

Keywords: Maize (*Z. mays* L.), maize germplasm, water stress conditions, seedling traits, principal component analysis, biplot analysis, correlation

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Key findings: Drought stress at the seedling stage significantly impairs maize (*Z. mays* L.) growth and vigor. In this study, several genotypes demonstrated superior performance under induced water stress, indicating potential water stress tolerance. Notably, genotypes 15067, Pearl, Sultan, 15023, 14996, 15005, Akbar, Sahiwal-2002, and 14985 exhibited enhanced emergence traits, desiccation tolerance, and recovery ability. These genotypes are promising candidates for incorporation into maize drought-resilient breeding programs.

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important cereal crops globally, ranking third after wheat and rice. It is a versatile crop with wide applications in food, feed, biofuel, and various industrial sectors. In developing countries like Pakistan, maize serves as a vital source of food and income, particularly for smallholder farmers. The adaptability of maize to different agro-climatic conditions, coupled with its relatively short growth duration, makes it a favorable crop for farmers. However, despite its genetic potential for high yield, maize remains vulnerable to a range of abiotic stresses, with drought being the most critical.

In Pakistan, maize occupies about 1.44 million hectares, producing 8.24 million tons in FY 2024–2025. This output is 15.4% lower than the previous year, reflecting more frequent and intense drought. Overall, agricultural growth in the same period was only 0.56%, largely due to weather-driven crop shortfalls. Ongoing shifts in weather patterns have made rainfall more erratic, worsened water scarcity, and created serious hurdles for sustainable maize production (Economic Survey of Pakistan, 2025) and critical challenges for sustainable maize production.

Drought stress during early developmental stages, particularly germination and seedling establishment, can have severe consequences on plant morphology, physiology, and, ultimately, yield (Song *et al.*, 2019). At this stage, water deficit impairs seed imbibition, radicle elongation, and leaf expansion, thereby reducing the plant's ability to establish a robust root system and absorb nutrients (He *et al.*, 2018).

Coping with these challenges necessitates screening of maize genotypes under controlled drought conditions at the early growth stage as a practical and essential

strategy. Early-stage screening is cost-effective and enables the rapid identification of tolerant genotypes, which can incur further evaluation under field conditions (Rehman *et al.*, 2023). The use of polyethylene glycol (PEG) solutions allows researchers to assess drought tolerance by evaluating morphological and physiological traits, such as root/shoot length, fresh and dry weight, relative water content (RWC), chlorophyll content, and seedling vigor index (Javaid *et al.*, 2023). The physiological and biochemical responses of maize to water stress are complex and involve various adaptive mechanisms, including stomatal regulation, osmotic adjustment, and antioxidant defense systems. Genotypic variability in drought tolerance has been evident in maize, suggesting that some cultivars possess intrinsic mechanisms to withstand water deficit better than others do (Saba *et al.*, 2022). Identifying and utilizing such genotypes is vital for breeding programs aiming to enhance drought resilience in maize.

The growing demand for maize due to population pressure, feed requirements, and industrial use enhancing its resilience to drought stress is crucial for long-term agricultural sustainability. Therefore, this study sought to evaluate the performance of selected maize genotypes under simulated water stress conditions at the early seedling stage using PEG-induced drought. The findings of this research will contribute to identifying drought-tolerant genotypes, thereby supporting breeding programs aimed at developing climate-resilient maize cultivars.

MATERIALS AND METHODS

This research on maize (*Z. mays* L.) genotypes commenced in a greenhouse at the experimental area of the College of Agriculture,

University of Sargodha, Sargodha, Pakistan. Collected genotypes totaling 49 came from the National Genebank of Pakistan, located at the National Agricultural Research Centre (NARC), Islamabad, Pakistan, and the Maize and Millet Research Institute (MMRI), Yousafwala Sahiwal, Pakistan. Sowing of seeds occurred in circular disposable plastic cups, each measuring approximately 30 cm in depth and 8–10 cm in diameter and containing 450 g of river sand. The river sand, obtained from a local riverbed, was the chosen soil type for its natural drainage capacity, low nutrient content, and uniform texture, making it suitable for controlled plant growth experiments. The use of larger cups ensured adequate space for root development, proper aeration, and effective drainage during the early growth stage. The greater depth minimized the risk of waterlogging, maintained a stable moisture gradient, and reduced root binding, which can occur in shallower containers even with smaller soil volumes. The experiment proceeded following a completely randomized design (CRD) with five replications. Five seeds per genotype sown in each disposable transparent plastic cup ensured a uniform crop establishment. The first irrigation used a freshwater source for both normal and water stress treatments, while the second irrigation, administered 15 days later, applied only to the entries under normal conditions. Allowing the plants to rise for seven more days continued under both conditions. At the three-leaf stage, the researchers withheld irrigation water, with the pots cut and wrapped in muslin cloth and tap water showered to dissolve the sand. Then, the obtained shoots and roots entailed drying on tissue paper and reached evaluation for the following seedling traits.

List of genotypes used in this study

Overall, 49 maize genotypes succeeded in their evaluation in this study. The collection included a wide range of genetic backgrounds, providing a strong basis for assessing variability in traits under the experimental conditions (Table 1).

Experimental location

The geographical location of the research site was at the College of Agriculture, University of Sargodha, in Sargodha, Punjab, Pakistan. The map highlights the spatial position of the study area, providing visual context for the location where the experimental activities progressed. This site became the choice for its significance to agricultural research in the region and its accessibility for data collection (Figure 1).

Data collection and analysis

The data collected for various seedling traits included emergence percentage (%), mean emergence time (MET), emergence index (EI), energy of emergence (EOE), emergence rate index (ERI), desiccation tolerance index (DTI), and percent seedling recovery (PST). The collected data underwent assessment using analysis of variance (ANOVA) as described by Steel *et al.* (1997). Principal component analysis (Sneath, 1973) and correlation analysis, as performed by the study, examined the relationships among various seedling traits using the statistical software R Studio. The discussion on the different traits analyzed follows below.

Emergence (%)

When seeing the first seedling shoot has risen and emerged from the sand, the numbers of seedlings attained counting and recording of the observable seedlings. The logging of data daily took 10 days (Smith and Millet, 1964; Noorka and Khaliq, 2007).

$$EC(\%) = \frac{\text{Total number of seedlings appeared in 10 DAS}}{\text{Total number of seeds sown}} \times 100$$

Where, DAS = days after seedling.

Emergence index (EI)

The estimation of seedlings' emergence rate in each replication followed the procedure

Table 1. List of genotypes used in this study.

No.	Genotype	Source
1	14930	National Genebank of Pakistan (NARC), Islamabad, Pakistan
2	14931	National Genebank of Pakistan (NARC), Islamabad, Pakistan
3	14933	National Genebank of Pakistan (NARC), Islamabad, Pakistan
4	14934	National Genebank of Pakistan (NARC), Islamabad, Pakistan
5	14935	National Genebank of Pakistan (NARC), Islamabad, Pakistan
6	14937	National Genebank of Pakistan (NARC), Islamabad, Pakistan
7	14941	National Genebank of Pakistan (NARC), Islamabad, Pakistan
8	14958	National Genebank of Pakistan (NARC), Islamabad, Pakistan
9	14968	National Genebank of Pakistan (NARC), Islamabad, Pakistan
10	14969	National Genebank of Pakistan (NARC), Islamabad, Pakistan
11	14971	National Genebank of Pakistan (NARC), Islamabad, Pakistan
12	14972	National Genebank of Pakistan (NARC), Islamabad, Pakistan
13	14976	National Genebank of Pakistan (NARC), Islamabad, Pakistan
14	14983	National Genebank of Pakistan (NARC), Islamabad, Pakistan
15	14985	National Genebank of Pakistan (NARC), Islamabad, Pakistan
16	14992	National Genebank of Pakistan (NARC), Islamabad, Pakistan
17	14993	National Genebank of Pakistan (NARC), Islamabad, Pakistan
18	14995	National Genebank of Pakistan (NARC), Islamabad, Pakistan
19	14996	National Genebank of Pakistan (NARC), Islamabad, Pakistan
20	14999	National Genebank of Pakistan (NARC), Islamabad, Pakistan
21	15005	National Genebank of Pakistan (NARC), Islamabad, Pakistan
22	15014	National Genebank of Pakistan (NARC), Islamabad, Pakistan
23	15021	National Genebank of Pakistan (NARC), Islamabad, Pakistan
24	15023	National Genebank of Pakistan (NARC), Islamabad, Pakistan
25	15035	National Genebank of Pakistan (NARC), Islamabad, Pakistan
26	15037	National Genebank of Pakistan (NARC), Islamabad, Pakistan
27	15039	National Genebank of Pakistan (NARC), Islamabad, Pakistan
28	15041	National Genebank of Pakistan (NARC), Islamabad, Pakistan
29	15048	National Genebank of Pakistan (NARC), Islamabad, Pakistan
30	15054	National Genebank of Pakistan (NARC), Islamabad, Pakistan
31	15055	National Genebank of Pakistan (NARC), Islamabad, Pakistan
32	15061	National Genebank of Pakistan (NARC), Islamabad, Pakistan
33	15064	National Genebank of Pakistan (NARC), Islamabad, Pakistan
34	15067	National Genebank of Pakistan (NARC), Islamabad, Pakistan
35	15075	National Genebank of Pakistan (NARC), Islamabad, Pakistan
36	15077	National Genebank of Pakistan (NARC), Islamabad, Pakistan
37	15095	National Genebank of Pakistan (NARC), Islamabad, Pakistan
38	15110	National Genebank of Pakistan (NARC), Islamabad, Pakistan
39	15120	National Genebank of Pakistan (NARC), Islamabad, Pakistan
40	15132	National Genebank of Pakistan (NARC), Islamabad, Pakistan
41	Akbar	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
42	AkhGoti	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
43	Czp-132001	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
44	Desi Fsd	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
45	Golden	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
46	Lala Musa	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
47	MMRI Yellow	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
48	Pearl	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal
49	Sahiwal-2002	Maize and Millet Research Institute (MMRI) Yousafwala Sahiwal

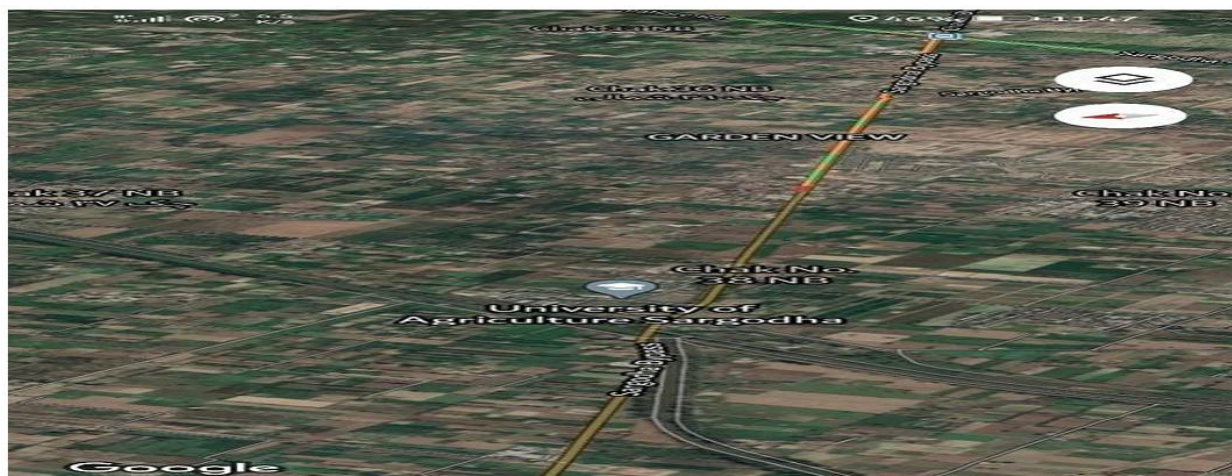


Figure 1. Geographical location of research conducted at the College of Agriculture, University of Sargodha (Courtesy: Google maps).

outlined by the Association of Official Seed Analysts (1983).

$$EI = \frac{\text{No of seeds emerged at first count} + \dots + \text{No. of seeds emerged at final count}}{\text{Days of first count} + \dots + \text{days of final count}}$$

Emergence rate index (ERI)

The recording of the emergence rate index comprised the emergence index divided by the emergence (%) in each replication (Noorka and Khaliq, 2007).

$$ERI = \frac{\text{Emergence Index}}{\text{Emergence}}$$

Energy of emergence (EOE)

The percent of seeds that have emerged by a fixed early day (e.g., 4 DAS) is the energy of emergence, where counting the emerged seedlings in each replication on that day proceeded to compute as follows:

$$EOE(\%) = \frac{\text{Number emerged by day}}{\text{Total seeds sown}} \times 100$$

Mean emergence time (MET)

Mean emergence time for each replication underwent calculation using the formula proposed by Ellis and Roberts (1981) and later adopted by Noorka and Khaliq (2007) as follows:

$$MET = \frac{\sum Dn}{\sum n}$$

Where n denotes the number of seeds that germinated on a particular day, while D corresponds to the number of days elapsed since the onset of germination.

Desiccation tolerance index (DTI)

Plants received adequate watering until the 2–3 leaf stage, which is considerably the appropriate stage for seedling evaluation according to the International Seed Testing Association (ISTA, 1997). After this stage, withholding water ensued, leading most seedlings to the verge of death. The plants then received re-watering, with the survival



Figure 2. Experimental setup showing maize seedlings in disposable plastic cups in the greenhouse.

Table 2. Analysis of variance (ANOVA) for seedling traits under study.

S.O.V.	d.f.	G%	MET	EI	EOE	ERI	DTI	PSR
Genotypes	49	543.18*	2.37**	0.18**	565.38**	1.12**	1.004*	844.4**
Error	100	60	0.57	0.05	229.33	3.14	0.66	384

*Significant at $p < 0.05$, **Significant at $p < 0.01$, NS= nonsignificant, G%= Germination Percentage, MET= Mean Emergence Time, EI= Emergence Index, EOE= Energy of Emergence, ERI= Emergence Rate Index, DTI= Desiccation Tolerance Index, and PSR= Percent Seedling Recovery.

assessed after regrowth in each replication. The logging of the number of live and dead seedlings daily continued during this period (Noorka and Khaliq, 2007).

$$\text{Desiccation tolerance index} = \frac{\text{Final number of dead seedling}}{\text{Final emergence number}}$$

Percent seedling recovery (PSR)

The percentage of seedling recovery or regrowth after desiccation achieved its determination using the formula outlined by Noorka and Khaliq (2007), as illustrated below.

$$\text{Seedling recovery(\%)} = \frac{\text{Number of plants resuming growth}}{\text{Total number of seedlings}} \times 100$$

Experimental setup at the College of Agriculture, University of Sargodha

The experimental setup used for conducting the research appears in Figure 2. The photo illustrates the arrangement of experimental pots and the management practices applied during the experiment. It provides a visual representation of the study's organization,

ensuring clarity in understanding the procedures followed.

RESULTS AND DISCUSSION

Phenotypic variation in germination and seedlings

Analysis of variance demonstrated significant ($p < 0.01$) differences among the 49 maize (*Z. mays* L.) genotypes for all seedling traits, indicating substantial genetic diversity (Table 2). Germination percentage (GP) ranged from 26.67% (genotype 15035) to 93.33% (15067), with several entries exceeding 86% (Pearl, Sahiwal-2002, Sultan, and 15005)—matching the variability seen in other studies that report strong genotype effects on germination rate in maize (Noorka and Khaliq, 2007; Ibirinde *et al.*, 2022a).

Mean emergence time (MET) also varied significantly, from 3.39 days for genotype 15021 to 7.22 days for 14985 (Table 3). This variation aligns with illustrating that differences in seed metabolic activity and coat permeability fundamentally influence

Table 3. Mean values of germination percentage, mean emergence time, emergence index, energy of emergence, emergence rate index, desiccation tolerance index, and percent seedling recovery.

Genotypes	G%	MET	EI	EOE	ERI	DTI	PSR
14930	60.00	4.33	0.77	33.33	0.013	1.11	33.33
14931	60.00	4.69	0.67	6.67	0.011	0.50	40.00
14933	60.00	5.00	0.73	26.67	0.011	0.11	53.33
14934	60.00	5.19	0.67	13.33	0.011	0.08	60.00
14935	60.00	4.56	0.72	26.67	0.013	0.11	53.33
14937	53.33	6.72	0.41	0.00	0.008	1.67	20.00
14941	60.00	6.72	0.45	0.00	0.008	2.00	20.00
14958	73.33	4.50	0.91	33.33	0.013	0.39	53.33
14968	80.00	5.17	0.89	13.33	0.011	0.42	60.00
14969	86.67	5.42	0.92	26.67	0.012	1.08	53.33
14971	73.33	5.09	0.81	20.00	0.011	0.75	53.33
14972	66.67	5.75	0.65	6.67	0.010	1.00	46.67
14976	53.33	4.67	0.67	26.67	0.012	0.67	33.33
14983	80.00	3.41	1.19	46.67	0.015	0.28	66.67
14985	40.00	7.22	0.29	0.00	0.007	0.50	26.67
14992	60.00	4.22	0.76	20.00	0.013	1.33	33.33
14993	60.00	4.75	0.69	13.33	0.011	1.33	40.00
14995	60.00	4.72	0.69	20.00	0.012	0.33	46.67
14996	53.33	4.56	0.62	13.33	0.012	0.00	53.33
14999	73.33	4.83	0.85	20.00	0.011	1.44	40.00
15005	86.67	3.47	1.28	46.67	0.015	0.19	73.33
15014	66.67	4.92	0.73	13.33	0.011	0.33	53.33
15021	80.00	3.39	1.19	46.67	0.015	0.19	66.67
15023	86.67	3.70	1.22	40.00	0.014	0.11	80.00
15035	26.67	6.83	0.19	0.00	0.007	0.33	20.00
15037	73.33	4.89	0.87	26.67	0.012	0.44	53.33
15039	66.67	4.72	0.80	26.67	0.012	1.33	40.00
15041	73.33	4.37	0.93	26.67	0.012	0.19	60.00
15048	66.67	5.00	0.76	26.67	0.012	0.44	46.67
15054	60.00	4.22	0.76	20.00	0.013	0.11	53.33
15055	80.00	4.98	0.88	20.00	0.011	0.50	53.33
15061	73.33	5.15	0.75	6.67	0.010	0.53	53.33
15064	66.67	4.75	0.81	20.00	0.012	0.22	53.33
15067	93.33	3.57	1.36	53.33	0.015	0.19	80.00
15075	66.67	4.67	0.75	6.67	0.011	2.33	20.00
15077	66.67	4.25	0.82	26.67	0.013	1.33	40.00
15095	73.33	4.89	0.83	20.00	0.012	0.11	66.67
15110	53.33	4.33	0.66	13.33	0.012	1.67	20.00
15120	60.00	4.50	0.73	20.00	0.012	1.00	40.00
15132	73.33	4.50	0.91	26.67	0.012	0.22	60.00
Akbar	80.00	3.84	1.12	40.00	0.014	0.25	66.67
AkhGoti	80.00	3.67	1.13	40.00	0.014	0.11	73.33
Czp-132001	40.00	6.61	0.30	0.00	0.008	1.00	20.00
Desi Fsd	73.33	4.75	0.84	20.00	0.012	1.42	40.00
Golden	66.67	4.28	0.84	26.67	0.013	1.44	33.33
Lala Musa	80.00	4.92	0.88	13.33	0.011	0.44	60.00
MMRI Yellow	73.33	4.20	0.97	40.00	0.014	0.39	53.33
Pearl	86.67	5.23	0.91	13.33	0.010	0.19	73.33
Sahiwal -2002	86.67	3.60	1.23	40.00	0.014	0.31	66.67

emergence timing (Khodarahmpour, 2011). Similar conclusions were notable in regional studies involving maize under salinity stress, where MET and germination percentage varied with genotype and environment (Noorka and Khaliq, 2007).

Emergence performance and seedling vigor

Significant variations appeared among the genotypes for emergence index (EI) and energy of emergence (EOE). The EI values ranged from 0.19 (15035) to 1.36 (15067), and EOE ranged from zero to 53.33 (Table 3). Consistent with this, Ibirinde *et al.* (2022a) reported relevant positive associations between EI, root length, and biomass in maize. Additionally, advanced studies indicated that genotypes with higher EI and EOE exhibit better field emergence and yield performance (Gao *et al.*, 2024a).

Emergence rate and drought tolerance

The emergence rate index (ERI) ranged from 0.007 (14985) to 0.015 (15021), while the desiccation tolerance index (DTI) varied from 0.00 (14996) to 2.33 (15075) (Table 3). Genotypes with high ERI and low DTI demonstrated superior survival under drought conditions. This finding confirms previous work showing that rapid emergence paired with moisture retention abilities enhances early-stage drought resilience (Tweddle *et al.*, 2002).

Post-stress/percent seedling recovery

The percent seedling recovery (PSR) contrasted significantly among the maize genotypes, ranging from 20% in five genotypes to 80% in Sultan, 15023, and 15067, indicating a 60% variation (Table 3). This wide range underscores the recovery capacity as a strong marker of genotype resilience. Compared with previous findings that reported a narrower PSR range, the broader variation observed here may refer to differences in environmental conditions or seed lot quality (Rehman *et al.*, 2015).

Integrated performance of traits

Genotypes that demonstrate optimal seedling performance shared a combination of high GP, EI, EOE, ERI, and PSR, coupled with low MET and DTI. This composite trait profile has had associations with improved early stand density, enhanced water-use efficiency, and competitive advantage in field-grown maize.

Correlation of germination (%) with other traits

As illustrated in Figure 3, GP revealed a significant negative correlation with MET, implying that faster-emerging seeds exhibited higher germination rates. This relationship reflects findings by Ibirinde *et al.* (2022b), who emphasized that rapid germination had an association with improved seedling establishment in stress conditions. The GP also showed positive correlations with EI, EOE, ERI, and PSR, indicating that genotypes with strong germination capacity also demonstrated early vigor and resilience (Gao *et al.*, 2024a).

Correlation of emergence time with other traits

MET gave a negative correlation with GP, EI, EOE, ERI, and PSR, while a positive connection with DTI (Figure 3). This suggested that longer emergence time reduced overall seedling vigor and drought resilience. These findings corroborate earlier observations of Zhang *et al.* (2021) and Ngugi *et al.* (2022), who stated that low MET was a key adaptive trait for rapid establishment in stress-prone environments.

Correlation of emergence index with other traits

EI exhibited strong positive correlations with GP, EOE, ERI, and PSR, and negative correlations with MET and DTI (Figure 3). Recent research by Ali *et al.* (2023) also confirmed that higher EI values indicate association with improved emergence uniformity and stress tolerance in maize and other cereals.

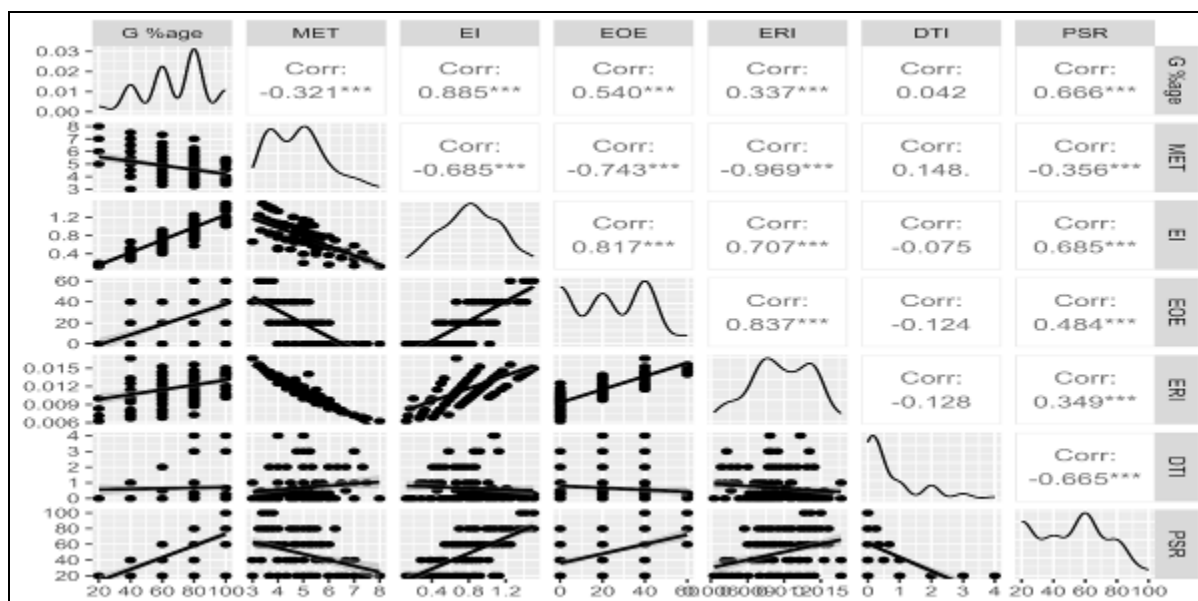


Figure 3. Traits association for different seedling traits under study.

Correlation of emergence energy with other traits

EOE signified negative correlations with MET and DTI and positive associations with GP, EI, ERI, and PSR (Figure 3). This indicated that seeds with higher energy of emergence were more efficient in utilizing internal reserves, leading to faster and more uniform seedling development (Gao *et al.*, 2024a). These results align with trends observed in wheat and rice under abiotic stress conditions, validating EOE as a key physiological trait for seed quality evaluation (Ali *et al.*, 2023).

Correlation of emergence rate index with other traits

ERI provided strong negative correlations with MET and DTI and positive associations with GP, EI, EOE, and PSR (Figure 3). These results agreed with Meeks *et al.* (2013), who identified ERI as a reliable index for seedling vigor across various stress environments. More recently, Oluwasanya *et al.*'s (2022) findings demonstrated ERI's utility in predicting early growth potential in sub-Saharan maize populations, highlighting its breeding relevance.

Correlation of desiccation tolerance index with other traits

DTI had significant negative correlations with EI, EOE, ERI, and PSR, but nonsignificant correlations with GP and MET (Figure 3). These findings suggested that higher DTI indicated lower seedling vigor and stress resilience. This interpretation was consistent with the findings of Zhou *et al.* (2023), who concluded that DTI was an important screening trait for drought-susceptible lines. Additionally, studies in soybean and maize by Rauf *et al.* (2022) further confirmed the inverse relationship between desiccation tolerance and early vigor parameters.

Correlation of percentage seedling recovery with other traits

PSR showed strong negative correlations with MET and DTI and positive linkages with GP, EI, EOE, and ERI (Figure 3). These results aligned with earlier reports by Meeks *et al.* (2013), which had further reinforcement from recent work in maize and sorghum breeding by Gao *et al.* (2024a). High PSR values were indicative of genotypes that recovered better after stress,

Table 4. Standard deviation, variance proportion, and cumulative contribution of principal components for seedling traits.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Standard deviation	2.055	1.177	1.047	0.474	0.199	0.127	0.096
Proportion of Variance	0.603	0.198	0.156	0.032	0.005	0.002	0.001
Cumulative Proportion	0.603	0.801	0.958	0.990	0.996	0.998	1.000

Table 5. Traits contribution for different principal component analysis.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
G %	0.353	-0.092	0.637	-0.163	0.337	-0.328	0.459
MET	-0.402	-0.2699	0.3751	0.497	0.0261	-0.442	-0.42
EI	0.4607	0.035	0.286	-0.0568	0.276	0.405	-0.678
EOE	0.433	0.172	-0.078	0.832	-0.069	0.1280	0.248
ERI	0.414	0.294	-0.358	-0.117	-0.038	-0.7173	-0.288
DTI	-0.130	0.6955	0.4732	-0.067	-0.517	0.028	-0.040
PSR	0.351	-0.563	0.1068	-0.1049	-0.731	-0.009	-0.039

Where G%= Germination Percentage, MET= Mean Emergence Time, EI= Emergence Index, EOE= Energy of Emergence, ERI= Emergence Rate Index, DTI= Desiccation Tolerance Index, and PSR= Percent Seedling Recovery.

making PSR an effective criterion in selection programs for abiotic stress resilience.

Principal component and biplot analyses

Principal component analysis (PCA), performed on seven seedling traits, resulted in three components (PC1, PC2, and PC3) exhibiting eigenvalues greater than one. This suggested their significance in explaining variability among genotypes (Table 4). The cumulative proportion of variability explained by PC1, PC2, and PC3 was 60.3%, 80.1%, and 95.8%, respectively. These components collectively captured most variations among the genotypes, making them critical for trait-based selection.

Each trait contributed differently across components. Germination percentage contributed 0.353 to PC1 but showed a slight negative loading in PC2 (-0.092), indicating variability in how this trait interacts with others across principal axes (Table 5). Mean emergence time (MET) had a strong negative contribution to PC1 (-0.402) and PC2 (-0.269), while its positive contribution to PC3 (0.375) highlighted its distinct influence on variation in later components. Germination index (GI)

consistently exhibited positive correlations across all three components: 0.461 in PC1, 0.035 in PC2, and 0.286 in PC3, implying its strong association with overall seedling performance.

Energy of emergence (EOE) contributed positively to PC1 (0.433) and PC2 (0.172) but negatively to PC3 (-0.078), whereas emergence rate index (ERI) showed positive contributions to PC1 and PC2 but a negative loading of -0.358 in PC3. Desiccation tolerance index (DTI) and percent seedling recovery (PSR) contributed 0.130 and 0.695 to PC1 and 0.473 and 0.351 to PC3, respectively, detailing their substantial roles in seedling vigor and stress resilience.

The biplot derived from PC1 and PC2 visualized the associations among traits and grouped them based on vector angles and lengths (Figure 4). Traits within the same group showed stronger correlations with each other, while those with wider angles exhibited weaker or even negative associations. Group 1 included germination percentage and PSR, suggesting their interrelated performance. Group 2 encompassed GI, EOE, and ERI, all of which were key indicators of seedling vigor. Moreover, Group 3 was limited to DTI,

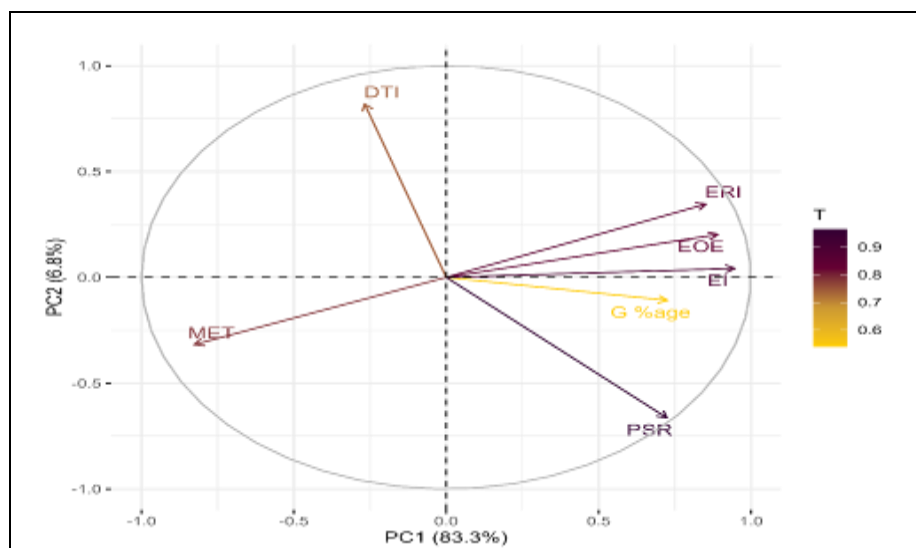


Figure 4. Biplot graph for 49 maize genotypes.

indicating its unique variability, while Group 4 solely contained MET, highlighting its distinct contribution from the other traits.

Traits with longer vector lengths and narrower angles (i.e., higher cosine similarity) specified stronger influence on variation. For instance, PSR and germination percentage had strong correlations in Group 1, while GI, EOE, and ERI showed high interdependence in Group 2. On the other hand, MET had a strong negative correlation with GI, EOE, and ERI, aligning with previous reports on seedling vigor components (Zhou *et al.*, 2023; Gao *et al.*, 2024b).

In maize breeding programs, the identification of drought-tolerant genotypes is vital. PCA has proven to be an effective tool in data reduction and trait prioritization for genotype selection (Molin *et al.*, 2013). This method enables the clustering of genotypes and trait associations, facilitating targeted breeding. In this study, genotypes such as 15067, Pearl, Sultan, 15023, 14996, 15005, Akbar, Sahiwal-2002, and 14985 exhibited superior performance, reaching recommendations for further recombination breeding to develop drought-resilient accessions. The effectiveness of traits, such as germination percentage, EI, MET, EOE, ERI, DTI, and PSR (Hussain, 2009), in

distinguishing genotype performance had achieved well documentation. The study findings reaffirm their significance and potential application in breeding programs under abiotic stress conditions.

CONCLUSIONS

The presented study validated significant genetic variability among 49 maize (*Z. mays* L.) genotypes for key seedling traits within stress conditions. Traits such as germination percentage (GP), emergence index (EI), energy of emergence (EOE), emergence rate index (ERI), and percent seedling recovery (PSR) displayed positive interrelations and served as reliable indicators of seedling vigor and stress resilience. However, mean emergence time (MET) and desiccation tolerance index (DTI) revealed negative correlations, suggesting their limiting role in early seedling performance. Principal component and biplot analyses took the variation and proved GP, EI, EOE, ERI, and PSR as the most prominent traits, signifying genotypes 15067, Pearl, Sultan, 15023, 14996, 15005, Akbar, Sahiwal-2002, and 14985 as superior genotypes, as favorable for use in targeted breeding programs.

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