

Article

Integrated Assessment of Drought Tolerance Indices in Maize Genotype Selection

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Abstract

Drought is a major constraint limiting maize productivity worldwide, highlighting the need for reliable methods to identify drought-tolerant genotypes. This study evaluated the effectiveness of drought tolerance indices and multivariate analyses for discriminating maize genotypes differing in drought adaptation. In total, 20 maize genotypes were assessed under optimal and water-limited conditions using grain yield under non-stress (Y_p) and drought stress (Y_s) together with 15 drought tolerance indices. Correlation analysis, principal component analysis (PCA), clustering, and overlay analysis were applied to identify informative indices and characterize genotype responses. Productivity-oriented indices (STI, GMP, HM, MSTI, REI, and YI) were strongly associated with grain yield and consistently identified superior genotypes, whereas SSI, TOL, and SSPI mainly reflected drought susceptibility. PCA separated productivity and stress susceptibility into two complementary components and showed that five variables (Y_p , Y_s , YI, ATI, and MSTI_K1) retained 99.49% of the variation explained by the complete dataset. Cluster and overlay analyses confirmed stable genotype classification and distinct adaptation strategies. These findings demonstrate that a reduced set of complementary variables provides an efficient framework for drought tolerance assessment and supports the identification of maize germplasm, combining high productivity with stable performance under variable water availability.

Keywords: *Zea mays*; drought tolerance; grain yield; adaptability; drought stress indices; multivariate analysis; PCA; cluster analysis; abiotic stress



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1. Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops globally, serving as a key source of food, feed, and industrial raw materials. However, its productivity is increasingly threatened by climate change, which is characterized by rising temperatures, irregular precipitation patterns, and an increased frequency of extreme weather events. These changes intensify abiotic stresses such as drought, heat, and nutrient deficiency, which frequently occur simultaneously and interactively, leading to significant yield instability [1,2]. In maize, reproductive stages—particularly flowering and grain filling—are highly sensitive to environmental stress, making yield stability a major breeding objective [3].

Drought stress is widely recognized as the most critical factor limiting maize productivity across diverse agroecological zones. It reduces photosynthetic efficiency, disrupts

assimilate partitioning, and impairs reproductive development, ultimately decreasing grain yield [4]. Heat stress further exacerbates these effects by accelerating phenological development and shortening the grain-filling period [2]. In addition, nutrient limitations, particularly nitrogen deficiency, significantly constrain plant growth and interact with drought and heat stress to further reduce productivity [5]. The combined occurrence of these stresses highlights the need for breeding strategies that target multiple stress factors simultaneously rather than individually [6].

Traditional maize breeding approaches have relied primarily on direct selection for grain yield under contrasting environments. However, grain yield is a complex quantitative trait with low heritability under stress conditions due to strong genotype $\times$ environment ($G \times E$) interactions [7,8]. This complexity reduces the efficiency of selection and necessitates the use of indirect selection criteria. Consequently, stress tolerance indices have become essential tools for evaluating genotype performance across stress and non-stress conditions [9,10].

Classical indices such as the stress tolerance index (STI), stress susceptibility index (SSI), mean productivity (MP), and tolerance index (TOL) remain widely used due to their ability to characterize different components of stress response [11,12]. In maize, these indices have been successfully applied for identifying drought-adapted genotypes and selecting materials combining productivity and stress resistance [13].

In recent years, the application of drought tolerance indices has expanded considerably in maize and other cereal crops. Numerous studies have demonstrated that indices such as STI, geometric mean productivity (GMP), harmonic mean (HM), yield index (YI), and yield stability index (YSI) are strongly associated with grain yield under stress conditions and are effective in identifying tolerant genotypes [13]. However, individual indices often provide inconsistent genotype rankings because each index reflects only a specific aspect of stress response. Therefore, recent research emphasizes the combined use of multiple indices to improve selection accuracy and robustness [14].

To overcome the limitations of univariate approaches, multivariate statistical methods have been widely adopted in modern breeding programs. Techniques such as principal component analysis (PCA), cluster analysis, and genotype–trait (GT) biplot analysis enable simultaneous evaluation of multiple traits and indices, providing a more comprehensive understanding of genotype performance [8]. These approaches facilitate the identification of stable and high-yielding genotypes and reveal complex relationships among traits that are not evident in single-variable analyses.

Another important factor influencing genotype performance is genotype $\times$ environment ($G \times E$) interaction. Environmental variability under climate change leads to inconsistent genotype performance across locations and years, necessitating multi-environment trials. Statistical approaches such as GGE biplot analysis, mixed models, and stability analysis are widely used to evaluate adaptability and yield consistency [8]. Recently, environmental characterization approaches have become increasingly important for understanding plant responses to complex environmental conditions [15].

Advances in high-throughput phenotyping and data analytics have further enhanced the capabilities of plant breeding. Technologies such as remote sensing, imaging platforms, and machine learning enable the collection and analysis of large-scale phenotypic data under field conditions. These approaches facilitate the identification of traits associated with stress tolerance and improve the accuracy of selection decisions [15].

Importantly, recent research emphasizes the need to evaluate combined stress scenarios rather than individual stress factors. Under natural field conditions, crops are rarely exposed to a single stress; instead, drought, heat, and nutrient deficiencies often occur simultaneously, leading to complex and nonlinear responses [6]. Studies have shown that

combined stress effects can be more severe than individual stress responses, highlighting the importance of integrated stress evaluation frameworks.

Despite significant progress, several challenges remain in the selection of stress-tolerant genotypes. The inconsistency among stress indices, the complexity of $G \times E$ interactions, and the difficulty of integrating phenotypic, genomic, and environmental data continue to constrain breeding efficiency [3]. Furthermore, the lack of standardized methodologies for multi-stress evaluation complicates comparisons across studies.

Therefore, there is a growing need for integrative breeding approaches that combine stress tolerance indices, multi-trait selection, and advanced statistical tools within a unified framework. Such approaches are essential for improving the accuracy and efficiency of selection and for developing maize varieties that are resilient to climate variability [14].

In this context, the present study aims to evaluate maize genotypes using an integrated approach that combines drought tolerance indices and multivariate analysis to identify stable and high-performing genotypes under contrasting environmental conditions. This approach is expected to contribute to the development of climate-resilient maize cultivars and provide insights into effective breeding strategies under changing environmental conditions.

2. Materials and Methods

The field trials were conducted at the experimental fields of the Yuriev Plant Production Institute, which is located in the Kharkiv Region, Ukraine 49°59'48.29" N, 36°27'53.67" E; elevation 200 m above sea level). The soil at the study site is classified as Chernozem (according to the WRB classification). The soil was characterized by 5.46% humus content (3.17% SOC), total nitrogen content of 0.29% (2.9 g·kg⁻¹), available phosphorus of 0.18% P₂O₅ (0.078% P), exchangeable potassium of 2.0% K₂O (1.66% K), soil pH of 5.8 measured in KCl solution, hydrolytic acidity of 3.28 cmol·kg⁻¹, and a sum of exchangeable bases of 37.4 cmol·kg⁻¹.

The study evaluated the grain yield of 17 new maize hybrids developed at the Yuriev Plant Production Institute. The early-maturing group included three hybrids (G1, G2, G4) and the check hybrid—'KhA Kvinta' (G3). The medium-early group was the most numerous, comprising ten hybrids (G5–G14) and the check hybrid—'Damir' (G15). Additionally, four medium-maturing hybrids (G16, G17, G19, G20) and the check hybrid, 'Arho' (G18), were examined. The yield potential of the new hybrids ranges from 10 to 13 t·ha⁻¹, and the check hybrids are officially listed in the State Register of Plant Varieties of Ukraine.

The field trials followed a randomized complete block design (RCBD) with three replications to account for soil and microclimatic heterogeneity. The four-row plot area was 19.6 m², with a harvested area (two middle rows) of 9.8 m², a row spacing of 70 cm, and a plot length of 7 m. The plant density was maintained at 57,000 plants·ha⁻¹. Yield was measured after threshing of hand-harvested ears, with the determination of grain moisture at harvest. Grain yield was expressed in t·ha⁻¹, adjusted to a standard moisture content of 14%.

The climate in study location is humid continental (Dfb type according to the Köppen classification), with an average annual temperature of approximately +8 °C and annual precipitation ranging from 450 to 550 mm. The hybrids were evaluated in 2023 and 2024, which were contrasting in terms of water availability during the growing period (Figure 1).

In 2023, the air temperatures were generally close to or slightly above the long-term averages, providing a relatively favorable thermal background for plant growth. However, the precipitation distribution was uneven: rainfall exceeded the norm in April, followed by a moisture deficit in May and June. Excess precipitation in July partially compensated for the previous drought, but a shortage was again noted in August and September.

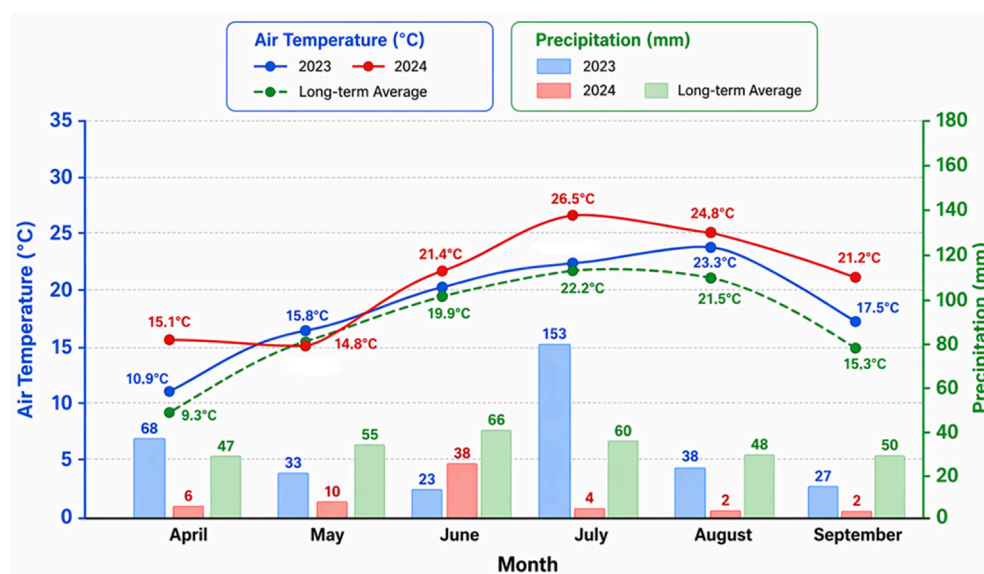


Figure 1. Air temperature and precipitation during the 2023–2024 study period.

In 2024, the weather was more contrasting and less favorable. As early as in April, abnormally high air temperatures were recorded alongside a sharp precipitation deficit. The moisture shortage persisted throughout May and June. The most adverse conditions developed from July to September, as critically low precipitation was associated with high temperatures. Thus, while 2023 was marked by uneven but partially compensated wetting, 2024 was characterized by prolonged drought and elevated thermal stress, which negatively impacted the maize growth and yield formation. No supplemental irrigation was applied in either year. The experiments were conducted under natural rainfall conditions. Based on the contrasting meteorological conditions, the 2023 growing season was regarded as the favorable (non-stress) environment, whereas the 2024 season represented a natural drought-stress environment. The severity of drought was further confirmed by substantial reductions in grain yield, which reached approximately 50–70% in the most susceptible genotypes.

The analysis included standardized values of drought tolerance indices (Table 1) and yields.

Table 1. Name and formulas of drought tolerance indexes used in the experiment.

Abbreviation	Name	Formula	Citation
YI	Yield index	$Y_s/\bar{Y}_s$	[16]
YSI	Yield stability index	Y_s/Y_p	[17]
TOL	Tolerance	$Y_p - Y_s$	[11]
HM	Harmonic mean	$2 \times (Y_p \times Y_s) / (Y_p + Y_s)$	[10]
SSI	Stress susceptibility index	$(1 - \frac{Y_s}{Y_p}) / (1 - \frac{\bar{Y}_s}{\bar{Y}_p})$	[9]
GMP	Geometric mean productivity	$\sqrt{Y_p \times Y_s}$	[10]
STI	Stress tolerance index	$(Y_p \times Y_s) / (\bar{Y}_p)^2$	[10]
MSTI (K1)	Modified stress tolerance index (K1)	$\frac{Y_p^2}{\bar{Y}_p^2} \times STI$	[12]
MSTI (K2)	Modified stress tolerance index (K2)	$\frac{Y_s^2}{\bar{Y}_s^2} \times STI$	[12]
DI	Drought resistance index	$[Y_s \times (\frac{Y_s}{Y_p})] / \bar{Y}_s$	[18]
RDI	Relative drought index	$(\frac{Y_s}{Y_p}) / (\frac{\bar{Y}_s}{\bar{Y}_p})$	[18]
ATI	Abiotic tolerance index	$(\frac{Y_p - Y_s}{Y_p - \bar{Y}_s}) \times \sqrt{Y_p \times Y_s}$	[19]
SNPI	Stress non-stress production index	$\sqrt[3]{\frac{Y_p + Y_s}{Y_p - Y_s}} \times \sqrt[3]{Y_p \times Y_s \times \bar{Y}_s}$	[19]
REI	Relative efficiency index	$\frac{Y_s}{Y_p} \times \frac{Y_p}{\bar{Y}_p}$	[20]
SSPI	Stress susceptibility percentage index	$(\frac{Y_p - Y_s}{2 \times Y_p}) \times 100$	[19]

Y_p —grain yield in the favorable growing season (2023); Y_s —grain yield in the drought-affected growing season (2024); $\bar{Y}_p$ —mean grain yield across all genotypes in the favorable growing season (2023); $\bar{Y}_s$ —mean grain yield across all genotypes in the drought-affected growing season (2024).

To evaluate the relationships between traits, a correlation analysis was performed using Pearson's correlation coefficient. Statistical significance was assessed at the $p < 0.05$ and $p < 0.01$ levels. Principal component analysis (PCA) was performed to investigate the multivariate relationships among drought tolerance indices and yield under optimal (Y_p) and stress (Y_s) conditions. Prior to analysis, all variables were standardized (z-scores) to eliminate scale effects. PCA was conducted using the FactoMineR package version 2.14 in R [21]. Eigenvalues, explained variance, cumulative variance, variable loadings, contributions, squared cosine values ($\cos^2$) were calculated to evaluate the importance and quality of representation of each drought tolerance index in the principal component space. The Kaiser criterion (eigenvalue ≥ 1) were used to assist in determining the number of informative principal components [22]. An integrated ranking score combining variable contributions and $\cos^2$ values was calculated to identify the most informative drought tolerance indices for genotype discrimination. Genotypes were classified by k-means clustering using their scores on the first two principal components (PC1 and PC2). Four clusters ($k = 4$) were identified with 50 random initializations to ensure solution stability. The resulting clusters were used to characterize groups of genotypes with similar drought response profiles. To compare the structural behavior of drought tolerance indices, an overlay analysis was performed using standardized genotype coordinates. Grain yield under optimal (Y_p) and drought (Y_s) conditions was used as the reference coordinate system, and all variables were standardized by z-score transformation ($z = (x - \mu)/\sigma$) to eliminate differences in measurement scale. For each drought tolerance index, genotype positions were projected onto the corresponding Y_p -index space and compared with the original Y_p - Y_s distribution. The displacement of genotype positions relative to the reference distribution was used to evaluate the extent to which individual indices preserved or modified the original relationships among genotypes.

All statistical analyses were performed using R software packages version 4.4.3.

3. Results

3.1. Yield Performance and Drought Tolerance Index Evaluation

The evaluation of 20 maize genotypes under contrasting moisture conditions revealed substantial variation in grain yield performance and drought adaptation characteristics. The studied genotypes demonstrated considerable differences in yield potential under optimal moisture conditions (Y_p), grain yield under drought stress (Y_s), and calculated drought tolerance indices, indicating a diverse genetic response to water limitation. The grain yield under non-stress conditions (Y_p) ranged from 7.06 t ha^{-1} in genotype G19 to 10.46 t ha^{-1} in genotype G3 (Table 2). The highest yield potential was recorded for G3 (10.46 t ha^{-1}), G15 (10.10 t ha^{-1}), and G18 (10.10 t ha^{-1}), demonstrating superior productivity under favorable growing conditions. Genotypes G20 (9.36 t ha^{-1}), G14 (8.88 t ha^{-1}), and G12 (8.84 t ha^{-1}) also showed relatively high yield potential. In contrast, G1, G6, and G19 demonstrated comparatively lower yield performance under optimal conditions.

Under drought stress conditions, genotype responses differed considerably. Grain yield under stress (Y_s) ranged from 3.20 t ha^{-1} in G10 to 8.08 t ha^{-1} in G11. The highest stress yield was recorded for G11, followed by G12 (7.49 t ha^{-1}) and G13 (7.23 t ha^{-1}). These genotypes maintained relatively high productivity under water limitation, indicating improved stress adaptation. Conversely, G8, G9, G10, and G20 exhibited substantial yield reductions under drought conditions. The calculated drought tolerance indices demonstrated different patterns of genotype response depending on whether they emphasized productivity, stability, or stress susceptibility. Yield-based indices, including Stress Tolerance Index (STI), Geometric Mean Productivity (GMP), Harmonic Mean (HM), Yield Index (YI), Modified Stress Tolerance Index (MSTI), Stress Non-Stress Production Index (SNPI),

and Relative Efficiency Index (REI), generally reflected the ability of genotypes to maintain productivity across environments.

Table 2. Grain yield performance and drought tolerance indices of maize genotypes under non-stress and drought conditions.

Genotype	Yp	Ys	YI	YSI	TOL	GMP	HM	SSI	STI	MSTI_K	MSTI_K2	DI	RDI	ATI	SNPI	REI	SSPI
G1	7.19	5.86	1.04	0.82	1.33	6.49	6.46	0.55	0.58	0.42	0.63	0.85	1.23	3.02	13.44	0.88	9.22
G2	7.88	6.55	1.16	0.83	1.33	7.19	7.16	0.50	0.72	0.62	0.96	0.97	1.25	3.34	15.45	1.08	8.41
G3	10.46	6.08	1.08	0.58	4.38	7.97	7.69	1.25	0.88	1.34	1.02	0.63	0.87	12.26	11.34	1.33	20.94
G4	9.62	5.67	1.00	0.59	3.95	7.39	7.13	1.22	0.76	0.97	0.76	0.59	0.89	10.24	10.62	1.14	20.53
G5	8.30	5.56	0.98	0.67	2.74	6.79	6.66	0.99	0.64	0.61	0.62	0.66	1.01	6.54	10.90	0.96	16.53
G6	7.32	4.65	0.82	0.64	2.67	5.84	5.69	1.09	0.47	0.35	0.32	0.52	0.96	5.46	8.93	0.71	18.22
G7	8.45	4.42	0.78	0.52	4.03	6.11	5.81	1.42	0.52	0.51	0.32	0.41	0.79	8.64	8.08	0.78	23.83
G8	7.56	4.32	0.77	0.57	3.24	5.72	5.50	1.28	0.45	0.36	0.26	0.44	0.86	6.50	8.03	0.68	21.42
G9	7.34	3.64	0.65	0.50	3.70	5.17	4.87	1.50	0.37	0.28	0.15	0.32	0.75	6.71	6.61	0.56	25.18
G10	8.10	3.20	0.57	0.40	4.90	5.09	4.59	1.80	0.36	0.33	0.12	0.22	0.60	8.75	5.77	0.54	30.22
G11	8.21	8.08	1.43	0.98	0.13	8.14	8.14	0.05	0.92	0.86	1.88	1.41	1.48	0.37	40.68	1.38	0.79
G12	8.84	7.49	1.33	0.85	1.35	8.14	8.11	0.46	0.92	0.99	1.61	1.12	1.27	3.85	18.17	1.38	7.63
G13	8.66	7.23	1.28	0.84	1.43	7.91	7.88	0.49	0.87	0.90	1.42	1.07	1.26	3.96	17.16	1.31	8.24
G14	8.88	6.86	1.22	0.77	2.02	7.81	7.74	0.68	0.84	0.92	1.25	0.94	1.16	5.53	14.83	1.27	11.37
G15	10.10	6.65	1.18	0.66	3.45	8.20	8.02	1.02	0.93	1.31	1.29	0.78	0.99	9.92	12.94	1.40	17.08
G16	8.15	6.07	1.07	0.74	2.08	7.03	6.96	0.76	0.69	0.63	0.79	0.80	1.12	5.14	12.70	1.03	12.77
G17	8.35	5.18	0.92	0.62	3.17	6.58	6.40	1.13	0.60	0.58	0.50	0.57	0.93	7.31	9.86	0.90	18.97
G18	10.10	5.83	1.03	0.58	4.27	7.68	7.39	1.26	0.82	1.15	0.87	0.60	0.87	11.50	10.87	1.23	21.13
G19	7.06	5.47	0.97	0.78	1.59	6.22	6.17	0.67	0.54	0.37	0.50	0.75	1.17	3.46	11.87	0.81	11.23
G20	9.36	4.10	0.73	0.44	5.26	6.20	5.71	1.67	0.53	0.65	0.28	0.32	0.66	11.43	7.39	0.80	28.08

The highest values of productivity-oriented indices were mainly observed in genotypes G3, G15, and G18. For example, G15 demonstrated the highest GMP (8.20), HM (8.02), STI (0.93), and REI (1.40), reflecting its high productivity under both environments. Similarly, G3 showed high values of GMP (7.97), HM (7.69), STI (0.88), and REI (1.33), confirming its strong performance under contrasting moisture conditions. G18 also exhibited favorable productivity index values, with high GMP (7.68), HM (7.39), and STI (0.82). In addition to highly productive genotypes, several genotypes demonstrated improved stress performance despite moderate yield potential. G11 and G12 showed the highest Yield Stability Index (YSI) values (0.98 and 0.85, respectively), indicating a relatively small reduction in yield under drought conditions. G11 also demonstrated the lowest Tolerance Index (TOL = 0.13) and Stress Susceptibility Index (SSI = 0.05), reflecting minimal yield reduction compared with its performance under optimal conditions.

Stress susceptibility-related indices revealed contrasting genotype responses. Higher values of SSI, TOL, and SSPI were observed in genotypes with greater yield reduction under drought. G10 showed the highest SSI (1.80), SSPI (30.22), and TOL (4.90), followed by G20 and G9, indicating strong sensitivity to drought conditions. These genotypes combined relatively acceptable yield potential with poor yield maintenance under stress.

The ranking analysis based on drought tolerance indices provided an integrated assessment of genotype performance (Table 3).

Genotypes with consistently low mean ranks demonstrated superior performance across multiple criteria. The lowest mean rank values were observed for G15 (5.80), G3 (6.60), G11 (6.73), and G12 (6.53), confirming their favorable combination of yield potential and drought response.

Genotypes with high mean rank values, particularly G9 and G10 (15.27), demonstrated poor performance across most indices. These genotypes showed low rankings for productivity-related indices and unfavorable positions for susceptibility parameters, confirming their limited adaptation under drought conditions.

Table 3. Ranking of maize genotypes based on drought tolerance indices.

Genotype	YI	YSI	TOL	GMP	HM	SSI	STI	MSTI_K1	MSTI_K2	DI	RDI	ATI	SNPI	REI	SSPI	Mean	SD
G1	9	5	19	13	12	16	13	15	11	6	5	19	6	13	16	11.87	4.79
G2	6	4	18	9	8	17	9	11	7	4	4	18	4	9	17	9.67	5.35
G3	7	14	3	4	6	7	4	1	6	11	14	1	10	4	7	6.60	4.12
G4	11	13	6	8	9	8	8	5	10	13	13	4	13	8	8	9.13	2.97
G5	12	9	11	11	11	12	11	12	12	10	9	10	11	11	12	10.93	1.03
G6	15	11	12	17	17	10	17	18	15	15	11	13	15	17	10	14.20	2.81
G7	16	17	5	16	15	4	16	14	16	17	17	7	16	16	4	13.07	5.13
G8	17	16	9	18	18	5	18	17	18	16	16	11	17	18	5	14.60	4.70
G9	19	18	7	19	19	3	19	20	19	18	18	9	19	19	3	15.27	6.27
G10	20	20	2	20	20	1	20	19	20	20	20	6	20	20	1	15.27	8.05
G11	1	1	20	2	1	20	2	8	1	1	1	20	1	2	20	6.73	8.46
G12	2	2	17	3	2	19	3	4	2	2	2	16	2	3	19	6.53	7.06
G13	3	3	16	5	4	18	5	7	3	3	3	15	3	5	18	7.40	5.99
G14	4	7	14	6	5	14	6	6	5	5	7	12	5	6	14	7.73	3.71
G15	5	10	8	1	3	11	1	2	4	8	10	5	7	1	11	5.80	3.75
G16	8	8	13	10	10	13	10	10	9	7	8	14	8	10	13	10.07	2.22
G17	14	12	10	12	13	9	12	13	13	14	12	8	14	12	9	11.80	1.93
G18	10	15	4	7	7	6	7	3	8	12	15	2	12	7	6	8.07	3.99
G19	13	6	15	14	14	15	14	16	14	9	6	17	9	14	15	12.73	3.49
G20	18	19	1	15	16	2	15	9	17	19	19	3	18	15	2	12.53	7.04

Intermediate responses were observed for G2, G5, G14, and G16. These genotypes maintained moderate yield performance and demonstrated balanced index values, suggesting intermediate adaptation characteristics. Their performance indicates that drought response exists as a continuous variation rather than a simple classification between tolerant and susceptible groups.

Overall, the evaluation of yield parameters and drought tolerance indices demonstrated considerable genetic variability among maize genotypes. The results confirmed that drought adaptation involves multiple components, including yield potential, yield stability, and susceptibility to stress-induced reduction.

3.2. Correlation Structure of Drought Tolerance Indices

Correlation analysis was performed to determine the relationships among grain yield parameters and drought tolerance indices and to identify the indices most closely associated with genotype performance under contrasting moisture conditions (Figure 2).

Grain yield under non-stress conditions (Y_p) and drought stress conditions (Y_s) were considered reference parameters for evaluating the effectiveness of drought tolerance indices. The correlation structure revealed distinct groups of indices according to their relationships with yield performance.

Most productivity-based indices demonstrated strong positive associations with both Y_p and Y_s . The Stress Tolerance Index (STI), Geometric Mean Productivity (GMP), Harmonic Mean (HM), Yield Index (YI), Drought Index (DI), Modified Stress Tolerance Index (MSTI_K1 and MSTI_K2), Stress Non-Stress Production Index (SNPI), and Relative Efficiency Index (REI) showed significant positive relationships with grain yield parameters.

The strongest associations were observed for STI, GMP, and HM, which showed high correlation coefficients with both yield environments. This indicates that these indices effectively captured the combined contribution of yield potential and stress performance. Genotypes with high values for these indices generally maintained higher grain yield under drought conditions.

Yield Index (YI) demonstrated a particularly close association with Y_s , reflecting its ability to identify genotypes that maintained productivity under water limitation. Similarly, REI showed stable positive relationships with both yield parameters, supporting its effectiveness in evaluating relative genotype performance.

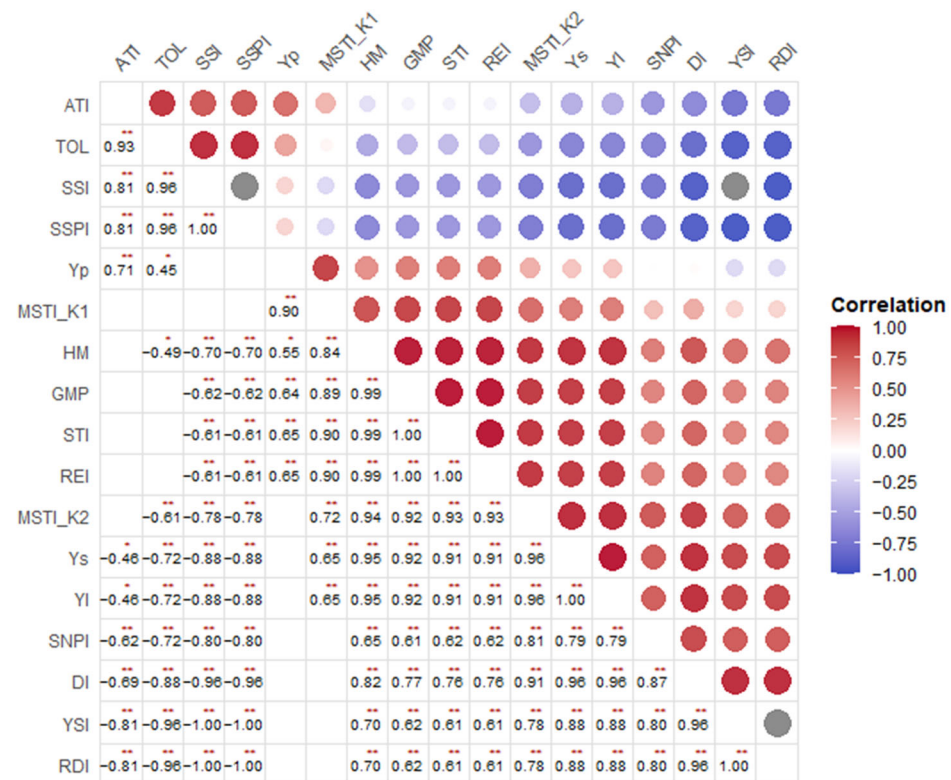


Figure 2. Correlogram showing the relationships between drought tolerance indices and maize yield performance. YI—Yield index; YSI—Yield stability index; TOL—Tolerance; HM—Harmonic mean; SSI—Stress susceptibility index; GMP—Geometric mean productivity; STI—Stress tolerance index; MSTI_K1, MSTI_K2—Modified stress tolerance index (K1); MSTI (K2)—Modified stress tolerance index (K2); DI—Drought resistance index; RDI—Relative drought index; ATI—Abiotic tolerance index; SNPI—Stress non-stress production index; REI—Relative efficiency index; SSPI—Stress susceptibility percentage index. Significant differences at $p < 0.05$ and $p < 0.01$ are marked by * and ** respectively.

The modified stress tolerance indices MSTI_K1 and MSTI_K2 also demonstrated strong positive associations with productivity traits. Their consistent behavior indicates that modification of stress tolerance calculations may improve the integration of yield potential and stress response.

In contrast, susceptibility-related indices showed different correlation patterns. SSI, TOL, and SSPI were negatively associated with drought performance, particularly with Ys. These relationships indicate that these indices primarily reflect the degree of yield reduction caused by stress rather than absolute productivity.

The stronger negative association of SSI and TOL with Ys compared with Yp demonstrates that these indices are more sensitive to drought-induced yield losses. Therefore, they provide complementary information by identifying genotypes with greater sensitivity to water limitation.

The Relative Drought Index (RDI) and Abiotic Tolerance Index (ATI) demonstrated weaker and more variable relationships with yield parameters. Their lower correlation values indicate that these indices may describe additional aspects of genotype response that are not directly represented by grain yield.

The overall correlation pattern confirmed that drought tolerance indices can be divided according to their functional relationships with genotype performance. Productivity-based indices mainly reflected yield maintenance and adaptation, whereas susceptibility indices characterized yield reduction under stress.

3.3. Principal Component Analysis of Drought Tolerance Indices

Principal component analysis (PCA) was performed to identify the major sources of variation among maize genotypes and to determine the relative importance of drought tolerance indices and yield-related traits for genotype discrimination. The first two principal components effectively summarized the multivariate structure of the dataset (Table 4).

Table 4. Summary of principal component analysis and contribution of drought tolerance indices.

Variable	PC1 Loading	PC2 Loading	PC1 Contribution, %	PC2 Contribution, %	PC1 $\cos^2$	PC2 $\cos^2$	Total Contribution, %
Yp	0.19	0.98	0.30	22.29	0.04	0.95	22.60
ATI	−0.54	0.83	2.41	16.11	0.30	0.69	18.52
MSTI_K1	0.57	0.81	2.67	15.46	0.33	0.66	18.13
YI	0.99	0.10	8.03	0.23	0.99	0.01	8.26
Ys	0.99	0.10	8.03	0.23	0.99	0.01	8.26
DI	0.98	−0.18	7.83	0.75	0.96	0.03	8.58
MSTI_K2	0.96	0.21	7.42	1.03	0.91	0.04	8.45
TOL	−0.79	0.61	5.01	8.76	0.62	0.38	13.77
SSI	−0.92	0.39	6.83	3.52	0.84	0.15	10.35
SSPI	−0.92	0.39	6.83	3.52	0.84	0.15	10.35
RDI	0.92	−0.39	6.83	3.52	0.84	0.15	10.35
YSI	0.92	−0.39	6.83	3.52	0.84	0.15	10.35
HM	0.92	0.39	6.83	3.46	0.84	0.15	10.30
STI	0.87	0.49	6.14	5.67	0.76	0.24	11.82
REI	0.87	0.49	6.14	5.67	0.76	0.24	11.82
GMP	0.87	0.48	6.19	5.48	0.76	0.23	11.66
SNPI	0.83	−0.18	5.65	0.78	0.70	0.03	6.43

Grain yield under optimal (Yp) and drought (Ys) conditions was strongly represented in the PCA space. Both variables showed high positive loadings on PC1, whereas Yp contributed most strongly to PC2 (22.29%), indicating that the second component mainly reflected variation associated with yield potential. Among the drought tolerance indices, ATI (18.52%), MSTI_K1 (18.13%), and TOL (13.77%) exhibited the greatest contributions to PC2, whereas YI, DI, and MSTI_K2 were primarily associated with PC1, showing high loadings (>0.96) and excellent representation quality ($\cos^2 > 0.90$). Productivity-oriented indices, including STI, GMP, HM, and REI, also showed strong positive associations with PC1, while susceptibility-related indices (SSI and SSPI) were negatively associated with this component. Conversely, YSI and RDI were positively related to PC1, reflecting their association with yield stability under drought.

To identify the variables contributing most to genotype discrimination, drought tolerance indices were ranked according to their combined contribution and representation quality in the PCA space (Table 5). The integrated PCA score identified Yp, ATI, MSTI_K1, YI, Ys, DI, and MSTI_K2 as the most informative variables, whereas SNPI showed the lowest overall contribution.

The efficiency of variable reduction was evaluated by comparing PCA models constructed using the complete dataset and a reduced dataset containing the five highest-ranked variables (ATI, MSTI_K1, YI, Ys, and Yp) (Table 6). In the full model, the first two principal components explained 97.53% of the total variance, with PC1 and PC2 accounting for 72.33% and 25.20%, respectively. The reduced model retained a comparable multivariate structure, with the first two principal components explaining 99.49% of the total variance. These results indicate that the reduced variable set preserved nearly all of the information contained in the complete dataset despite the substantial decrease in the number of variables.

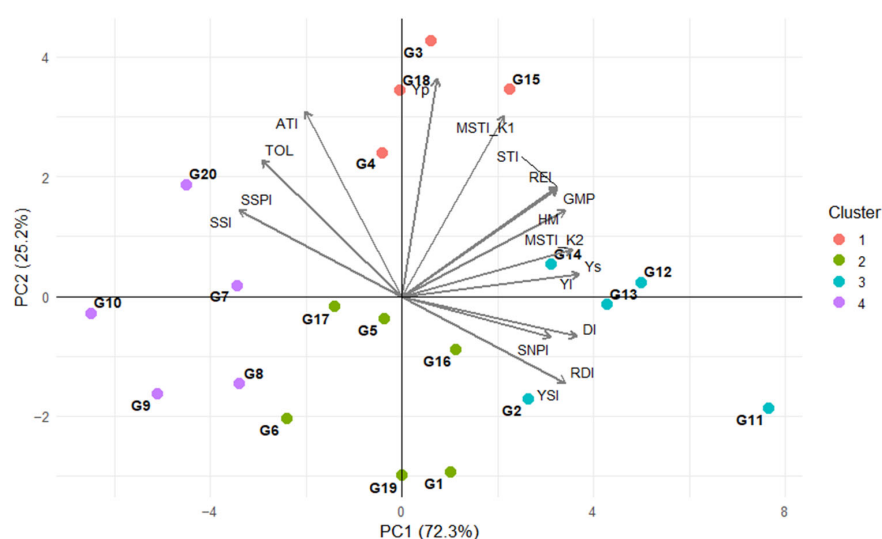
Table 5. PCA-weighted ranking of drought tolerance variables based on contribution and representation quality.

Variable	PC1 Contribution (%)	PC2 Contribution (%)	PC1 $\cos^2$	PC2 $\cos^2$	PCA Score
Yp	0.30	22.29	0.04	0.95	21.30
ATI	2.41	16.11	0.30	0.69	11.83
MSTI_K1	2.67	15.46	0.33	0.66	11.11
YI	8.03	0.23	0.99	0.01	7.93
Ys	8.03	0.23	0.99	0.01	7.93
DI	7.83	0.75	0.96	0.03	7.56
MSTI_K2	7.42	1.03	0.91	0.04	6.82
TOL	5.01	8.76	0.62	0.38	6.38
SSI	6.83	3.52	0.84	0.15	6.27
SSPI	6.83	3.52	0.84	0.15	6.27
RDI	6.83	3.52	0.84	0.15	6.27
YSI	6.83	3.52	0.84	0.15	6.27
HM	6.83	3.46	0.84	0.15	6.26
STI	6.14	5.67	0.76	0.24	6.02
REI	6.14	5.67	0.76	0.24	6.02
GMP	6.19	5.48	0.76	0.23	5.99
SNPI	5.65	0.78	0.70	0.03	3.96

Table 6. PCA eigenvalues and explained variance.

Principal Component	Full Set			Reduced Set		
	Eigenvalue	Variance	Cumulative	Eigenvalue	Variance	Cumulative
PC 1	12.30	72.33	72.33	2.91	58.23	58.23
PC 2	4.28	25.20	97.53	2.06	41.27	99.49
PC 3	0.34	1.99	99.52	0.02	0.31	99.80
PC 4	0.06	0.34	99.86	0.01	0.20	100.00

The PCA biplots generated using the complete and reduced datasets showed highly similar patterns of genotype and variable distribution (Figures 3 and 4). In both analyses, productivity-related indices (STI, GMP, HM, REI, MSTI, YI, DI, and Ys) were closely grouped and oriented in the same direction, indicating strong positive relationships and their common ability to identify high-performing genotypes across contrasting moisture conditions. In contrast, susceptibility indices (SSI, TOL, SSPI, and ATI) were positioned in the opposite direction, reflecting their negative association with yield maintenance under drought.

**Figure 3.** PCA biplot of drought tolerance indices and maize genotypes (full indices set).

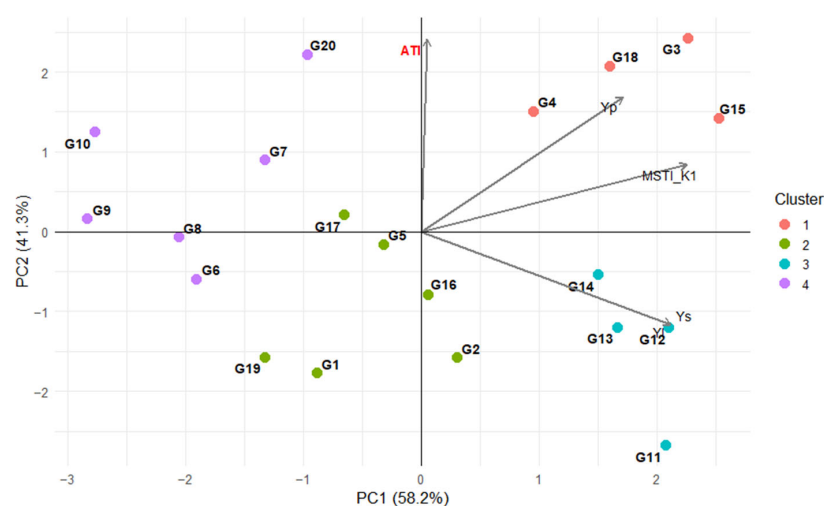


Figure 4. PCA biplot of drought tolerance indices and maize genotypes (reduced indices set).

The spatial distribution of genotypes further illustrates distinct drought response strategies. Genotypes located near the productivity-related indices were characterized by superior yield performance and improved drought adaptation, whereas those positioned closer to susceptibility indices exhibited greater yield reduction under water deficit. The similarity between the full and reduced PCA models confirms that the selected variables adequately describe the principal patterns of variation among maize genotypes and provide a reliable basis for subsequent genotype classification.

3.4. PCA-Based Clustering of Maize Genotypes

To assess the ability of the reduced variable set to preserve the multivariate structure of the original dataset, genotype distributions obtained from the complete and reduced PCA models were compared (Table 7). The comparison revealed a high degree of agreement between the two approaches. Most genotypes retained similar positions within the PCA space after variable reduction, and cluster assignments remained largely unchanged, indicating that the reduced dataset adequately captured the major patterns of variation among maize genotypes.

Table 7. Comparison of PCA-based genotype classification using the full and reduced sets of drought tolerance variables.

Genotype	Yp	Ys	Full Set			Reduced Set		
			PC1	PC2	Cluster	PC1	PC2	Cluster
G1	7.19	5.86	1.02	−2.94	2	−0.89	−1.77	2
G2	7.88	6.55	2.63	−1.71	3	0.30	−1.58	2
G3	10.46	6.08	0.60	4.27	1	2.26	2.42	1
G4	9.62	5.67	−0.42	2.41	1	0.95	1.51	1
G5	8.30	5.56	−0.37	−0.38	2	−0.32	−0.16	2
G6	7.32	4.65	−2.42	−2.04	2	−1.91	−0.59	4
G7	8.45	4.42	−3.45	0.19	4	−1.33	0.90	4
G8	7.56	4.32	−3.41	−1.45	4	−2.06	−0.07	4
G9	7.34	3.64	−5.11	−1.62	4	−2.83	0.16	4
G10	8.10	3.20	−6.49	−0.28	4	−2.77	1.25	4
G11	8.21	8.08	7.65	−1.86	3	2.07	−2.68	3
G12	8.84	7.49	4.99	0.24	3	2.11	−1.20	3
G13	8.66	7.23	4.28	−0.12	3	1.67	−1.20	3
G14	8.88	6.86	3.10	0.54	3	1.50	−0.54	3
G15	10.10	6.65	2.24	3.46	1	2.53	1.42	1
G16	8.15	6.07	1.11	−0.88	2	0.06	−0.79	2
G17	8.35	5.18	−1.40	−0.17	2	−0.65	0.21	2
G18	10.10	5.83	−0.05	3.45	1	1.60	2.07	1
G19	7.06	5.47	−0.01	−2.99	2	−1.33	−1.57	2
G20	9.36	4.10	−4.50	1.87	4	−0.97	2.22	4

The greatest consistency was observed for genotypes representing contrasting drought response strategies. Genotypes G3, G4, G15, and G18 were consistently assigned to Cluster 1 in both analyses, whereas G7, G8, G9, G10, and G20 remained grouped in Cluster 4. Likewise, the drought-adapted genotypes G11, G12, G13, and G14 consistently occupied the same region of the PCA space and were classified into Cluster 3 regardless of the number of variables included in the analysis. Only minor shifts in PCA coordinates were observed for several intermediate genotypes, particularly G2, G6, and G19, but these changes had little influence on the overall classification pattern.

The high similarity between the two PCA solutions demonstrates that the five selected variables (ATI, MSTI_K1, YI, Ys, and Yp) retained the principal information required for genotype discrimination. Consequently, the reduced model substantially decreased data complexity while preserving the biological interpretation of genotype relationships and drought response patterns.

Principal component-based clustering separated the 20 maize genotypes into four distinct groups differing in productivity and drought adaptation (Table 8). The identified clusters reflected contrasting combinations of yield potential under favorable conditions and the ability to maintain productivity under water deficit.

Table 8. Cluster classification of maize genotypes based on drought tolerance indices and yield performance.

Cluster	Number	Genotypes	Mean Yp $\pm$ SD	Mean Ys $\pm$ SD	Ys/Yp
1	4	G3, G4, G15, G18	10.07 $\pm$ 0.34	6.06 $\pm$ 0.43	0.60
2	6	G1, G5, G6, G16, G17, G19	7.73 $\pm$ 0.60	5.47 $\pm$ 0.50	0.71
3	5	G2, G11, G12, G13, G14	8.49 $\pm$ 0.43	7.24 $\pm$ 0.59	0.85
4	5	G7, G8, G9, G10, G20	8.16 $\pm$ 0.80	3.94 $\pm$ 0.51	0.48

Cluster 1 comprised four genotypes (G3, G4, G15, and G18) characterized by the highest grain yield under optimal conditions (mean Yp = 10.07 $\pm$ 0.34 t ha⁻¹). Under drought stress, the average yield declined to 6.06 $\pm$ 0.43 t ha⁻¹, corresponding to a mean Ys/Yp ratio of 0.60. The position of these genotypes within the PCA space, together with their high values of STI, GMP, HM, and REI, indicates that they possess excellent yield potential but only moderate drought adaptation, making them particularly suitable for environments where favorable growing conditions predominate.

Cluster 2 included six genotypes (G1, G5, G6, G16, G17, and G19). This group exhibited lower productivity under optimal conditions (mean Yp = 7.73 $\pm$ 0.60 t ha⁻¹) than Cluster 1, but maintained a relatively stable performance under drought (mean Ys = 5.47 $\pm$ 0.50 t ha⁻¹), resulting in a Ys/Yp ratio of 0.71. These genotypes therefore represent materials with balanced productivity and drought tolerance, although neither trait reached the level observed in Clusters 1 or 3.

Cluster 3 consisted of five genotypes (G2, G11, G12, G13, and G14) and displayed the most favorable drought response among all groups. Although their yield potential under optimal conditions (8.49 $\pm$ 0.43 t ha⁻¹) was intermediate, they achieved the highest grain yield under drought (7.24 $\pm$ 0.59 t ha⁻¹) and the greatest yield retention (Ys/Yp = 0.85). Their close association with productivity-oriented drought indices and separation from susceptibility-related indices in the PCA biplot further confirmed their superior adaptation to water-limited environments. Consequently, this cluster represents the most valuable source of drought-tolerant germplasm for breeding programs.

Cluster 4 comprised five genotypes (G7, G8, G9, G10, and G20) and represented the drought-sensitive group. Although their average yield under optimal conditions (8.16 $\pm$ 0.80 t ha⁻¹) was comparable with that of Cluster 3, grain yield under drought

decreased markedly to $3.94 \pm 0.51 \text{ t ha}^{-1}$, producing the lowest mean Y_s/Y_p ratio (0.48). These genotypes were characterized by high values of susceptibility-related indices (SSI, TOL, and SSPI) and consistently occupied the region of the PCA space associated with drought sensitivity.

Overall, the cluster analysis distinguished four biologically meaningful groups representing different drought response strategies. Cluster 1 consisted of highly productive genotypes with moderate drought tolerance, Cluster 2 included genotypes with intermediate adaptation, Cluster 3 represented drought-adapted and yield-stable materials, whereas Cluster 4 contained drought-sensitive genotypes exhibiting substantial yield reduction under water deficit.

To illustrate the relationship between maize grain yield under optimal (Y_p) and stress (Y_s) conditions, a slightly different visualization approach was used (Figure 5). A scatterplot was constructed to assess the distribution of genotypes according to their yield and level of adaptation to stress.

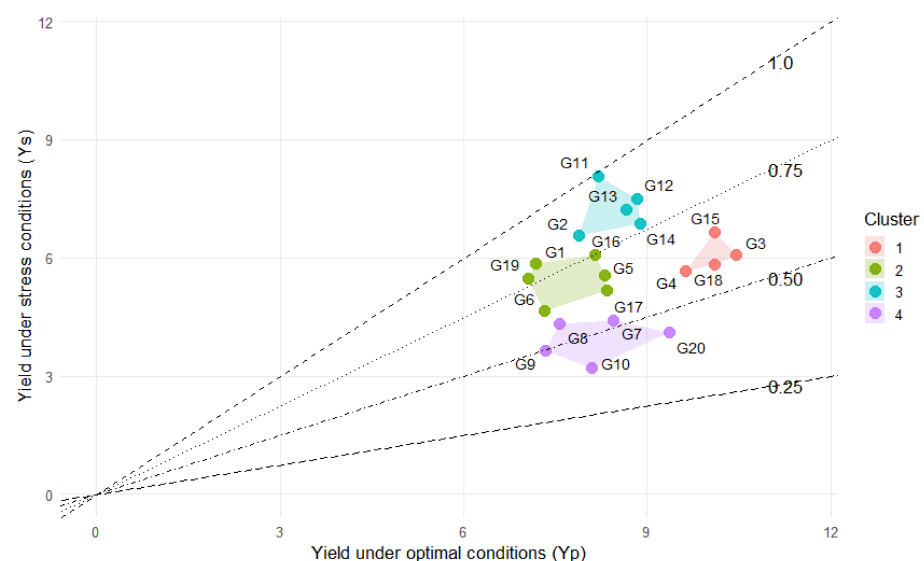


Figure 5. Yield performance of maize genotypes belonging to different clusters under contrasting moisture conditions.

The x -axis represented grain yield under non-stress conditions, and the y -axis represented yield under stress. The graph included several diagonal reference lines to visualize different levels of stress tolerance effectiveness and to facilitate interpretation of genotype responses. The upper diagonal line (1.0) indicated a theoretical situation in which genotypes maintained the same yield level under stress conditions as under optimal conditions, reflecting maximum stress tolerance. Intermediate lines (0.75 and 0.50) represented gradually decreasing levels of yield maintenance under stress, while the lower line (0.25) indicated a significant reduction in productivity due to stress conditions. Thus, genotypes located closer to the upper reference lines were considered more stable and adapted to stress.

3.5. Structural Comparison of Drought Tolerance Indices Using Overlay Analysis

Overlay analysis was performed to compare the extent to which individual drought tolerance indices preserved the original pattern of genotype distribution based on grain yield under optimal (Y_p) and drought (Y_s) conditions (Figure 6). The analysis revealed substantial differences among indices in their ability to maintain the original relationships between genotype productivity and drought response.

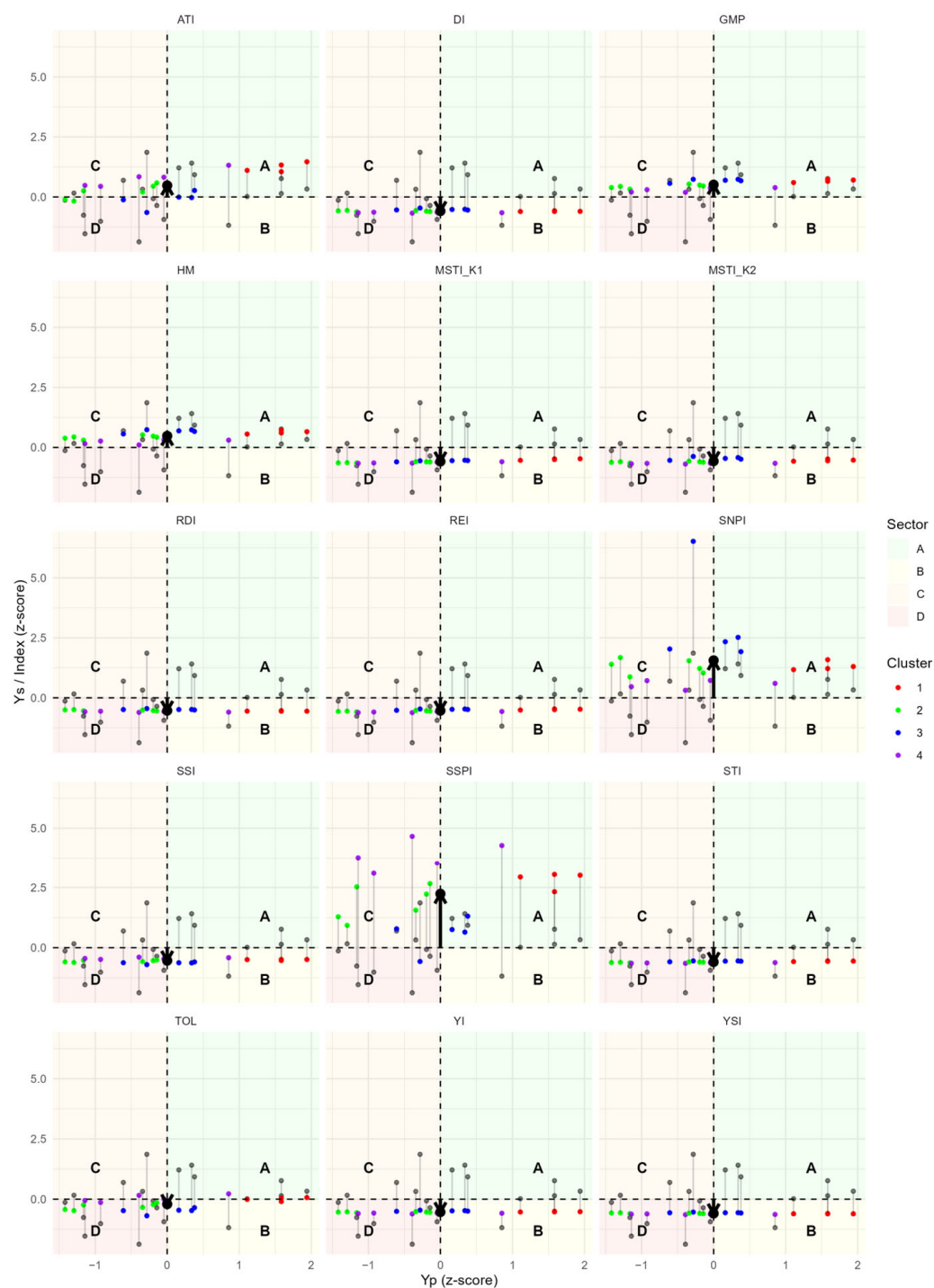


Figure 6. Overlay visualization of genotype distribution based on Yp–Ys and Yp–index relationships.

Productivity-oriented indices, particularly STI, GMP, and HM, produced only minor shifts in genotype positions relative to the reference Yp–Ys distribution. The short displacement vectors observed for these indices indicate that they closely reflected the original yield structure, preserving both genotype ranking and the relative distances among genotypes. Consequently, genotypes identified as superior in the baseline yield space remained associated with the same performance group after projection onto these indices.

A similar pattern was observed for REI, MSTI, and DI, which also maintained a close correspondence with the reference distribution. Although these indices slightly modified genotype positions, the overall clustering pattern remained largely unchanged,

indicating that they integrate drought response without substantially altering the original yield relationships.

In contrast, susceptibility-oriented indices generated markedly larger positional shifts. SSI and TOL displaced genotypes away from the productivity-oriented region, emphasizing differences in yield reduction rather than absolute grain yield. ATI exhibited a similar tendency, producing pronounced separation among genotypes with contrasting drought responses. These transformations indicate that susceptibility indices primarily characterize the magnitude of stress-induced yield loss and therefore provide information complementary to that obtained from productivity-based indices.

The largest deviations from the reference distribution were observed for SNPI and SSPI. These indices generated longer displacement vectors and greater dispersion of genotype positions, resulting in more pronounced changes in genotype ranking relative to the original Y_p – Y_s relationship. Their behavior suggests greater sensitivity to differences in stress response, although at the expense of preserving the original productivity structure.

Overall, the overlay analysis demonstrated that drought tolerance indices differ not only in their numerical values but also in the way they represent relationships among genotypes. Productivity-based indices, including STI, GMP, HM, REI, and MSTI, most closely preserved the original yield structure, whereas susceptibility-related indices, particularly SSI, TOL, ATI, and SSPI, emphasized drought-induced yield losses and altered genotype distribution to a greater extent. These results complement the correlation and PCA analyses and further support the use of productivity-oriented indices as reliable indicators for identifying maize genotypes combining high yield potential with drought tolerance.

4. Discussion

Drought tolerance in maize is a complex quantitative trait resulting from the interaction of genetic background, environmental conditions, and physiological mechanisms controlling plant productivity under water deficit. The considerable variation observed among the evaluated genotypes confirms that adaptation to drought cannot be adequately described by grain yield under either optimal or stress conditions alone. Similar conclusions have been reported in previous studies demonstrating that integrated drought tolerance indices provide a more reliable basis for genotype evaluation than single yield parameters because they simultaneously account for productivity potential and stress response [21–25].

The evaluated drought tolerance indices clearly represented two complementary aspects of genotype performance. Productivity-oriented indices, including STI, GMP, HM, MSTI, REI, and YI, consistently identified genotypes combining high yield potential with relatively stable performance across contrasting environments. In contrast, susceptibility indices (SSI, TOL, and SSPI) primarily reflected the magnitude of yield reduction under drought rather than productive capacity itself. The contrasting behaviour of these index groups indicates that drought adaptation should be interpreted as a balance between maintaining productivity and minimizing stress-induced yield losses. Consequently, susceptibility indices are most informative when interpreted together with productivity-related indices rather than used independently, an observation consistent with previous reports in maize and other cereal crops [24–29].

The multivariate analyses provided additional insight into the biological structure of drought adaptation [30]. Correlation analysis demonstrated that productivity-related indices formed a strongly interconnected group closely associated with grain yield under both optimal and drought conditions, whereas susceptibility indices represented a distinct response component [13,31]. Principal component analysis confirmed this pattern by separating productive performance from stress sensitivity into two complementary dimensions of genotype variation. These results indicate that drought tolerance is governed by mul-

multiple biological processes rather than a single physiological mechanism, reinforcing the importance of integrating complementary indicators when evaluating breeding material.

One of the principal findings of this study is that reliable characterization of drought response can be achieved without calculating a large number of highly correlated indices. The reduced PCA model retained almost all of the information contained in the complete dataset while using only five complementary variables (Yp, Ys, YI, ATI, and MSTI_K1). Because many drought tolerance indices are mathematically derived from the same yield components, they inevitably contain overlapping information. The present results demonstrate that careful selection of informative variables can substantially reduce analytical complexity without compromising genotype discrimination. This approach improves the interpretability of multivariate analyses and provides a more practical framework for routine evaluation of breeding materials.

The robustness of this reduced-variable approach was further supported by the consistency of genotype classification. Similar grouping patterns obtained from the full and reduced datasets indicate that the principal biological relationships among genotypes were preserved despite the reduction in the number of variables. Likewise, overlay analysis showed that productivity-based indices largely maintained the original yield structure, whereas susceptibility indices altered genotype positioning by emphasizing stress-induced yield losses. These complementary analyses demonstrate that different drought tolerance indices describe different aspects of adaptation and that their choice directly influences genotype ranking and selection decisions.

From a breeding perspective, the identified genotype groups represent contrasting adaptation strategies that may be valuable for different production environments. Genotypes characterized by high productivity under favorable conditions constitute promising material for maximizing yield where water availability is generally sufficient, whereas genotypes maintaining relatively high productivity under drought represent valuable sources of stress adaptation for water-limited environments. Consequently, breeding objectives should consider both productivity potential and yield stability to ensure broad adaptation under increasingly variable climatic conditions.

Although the proposed approach proved effective for differentiating maize genotypes, several limitations should be acknowledged. The present study was conducted under a single experimental environment, whereas drought intensity and timing vary considerably among locations and growing seasons. Furthermore, genotype evaluation was based primarily on grain yield and derived drought tolerance indices, without incorporating physiological or molecular traits that could provide additional insight into the mechanisms underlying stress adaptation. Future studies should therefore validate the proposed reduced-variable framework across multiple environments and diverse germplasm collections.

Overall, the integration of drought tolerance indices with correlation analysis, principal component analysis, clustering, and overlay visualization provides a robust and biologically meaningful framework for evaluating maize drought adaptation. More importantly, the results demonstrate that a limited set of carefully selected complementary variables is sufficient to characterize genotype performance, reducing redundancy while preserving the biological interpretation of drought response. Such an approach may improve the efficiency of drought screening and facilitate the identification of maize germplasm combining high productivity with stable performance under increasingly variable water availability.

5. Conclusions

This study provides a comprehensive assessment of drought tolerance in maize by integrating grain yield evaluation with complementary drought tolerance indices and

multivariate statistical analyses. The results demonstrated substantial genetic variation among the evaluated genotypes under contrasting moisture conditions, confirming that drought adaptation is governed by multiple biological processes rather than by grain yield alone. The contrasting performance of genotypes under optimal and drought environments further emphasized that high yield potential does not necessarily confer superior drought adaptation, highlighting the importance of evaluating both productivity and yield stability in breeding programs.

The combined use of productivity-oriented indices (STI, GMP, HM, YI, MSTI, and REI) together with susceptibility-related indices (SSI, TOL, and SSPI) provided a more robust characterization of genotype performance than any individual index. Correlation analysis and principal component analysis consistently separated these indices into two complementary functional groups representing productivity maintenance and drought susceptibility. These findings demonstrate that reliable assessment of drought tolerance requires simultaneous consideration of both components and confirm that no single index is sufficient to characterize the complex nature of genotype adaptation to water deficit.

A major contribution of this study is the demonstration that multivariate evaluation of drought tolerance can be substantially simplified without compromising biological interpretation or selection accuracy. The reduced multivariate model based on only five informative variables (Y_p , Y_s , YI, ATI, and MSTI_K1) retained nearly the entire information contained in the complete dataset and preserved the genotype classification obtained using the full set of drought tolerance indices. This result indicates that many commonly applied indices provide overlapping information and that selecting biologically complementary variables is more informative than simultaneously applying a large number of highly correlated parameters.

Cluster analysis identified four distinct adaptation strategies among the evaluated maize genotypes, ranging from highly productive but moderately drought-sensitive materials to genotypes characterized by superior yield stability under water-limited conditions. The strong agreement between classifications obtained from the complete and reduced datasets confirmed the robustness of genotype discrimination and demonstrated that simplified multivariate approaches can effectively support breeding decisions. Furthermore, the overlay analysis revealed that drought tolerance indices differ not only in their numerical values but also in their influence on the spatial distribution and classification of genotypes. Productivity-based indices largely preserved the original yield relationships, whereas susceptibility-oriented indices altered genotype positioning by emphasizing different biological components of drought response.

Overall, this study demonstrates that integrating complementary drought tolerance indices with correlation analysis, principal component analysis, reduced-variable modelling, cluster analysis, and structural overlay analysis provides a comprehensive and biologically meaningful framework for evaluating drought adaptation in maize. Beyond comparing the performance of individual drought tolerance indices, the study shows that biologically informed reduction in the evaluated variables preserves the essential structure of genotype differentiation while substantially simplifying multivariate analysis. This approach reduces analytical redundancy, improves the biological interpretation of drought tolerance, and offers a practical strategy for large-scale breeding programs aimed at developing maize cultivars with stable productivity under increasingly variable climatic conditions. Moreover, the proposed analytical framework is not restricted to maize and may be adapted for evaluating drought response and optimizing multivariate selection strategies in other cereal crops and under diverse abiotic stress conditions.

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