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Molecular Characterization and Stability Analysis of Maize (*Zea mays* L.) Genotypes under Environmental Stress Conditions

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Abstract**—** *Maize (Zea mays L.) is one of the most important cereal crops cultivated worldwide and plays a significant role in food security, livestock feed, and industrial applications. However, environmental stresses such as drought, heat stress, and irregular rainfall patterns have severely affected maize productivity in many regions. The identification of stable and stress-tolerant maize genotypes is therefore essential for improving crop productivity under changing climatic conditions. The present study aimed to analyze molecular diversity and yield stability among selected maize genotypes under different environmental conditions. Field experiments were conducted to evaluate important agronomic traits including plant height, days to tasseling, cob length, and grain yield. Molecular characterization was performed using simple sequence repeat (SSR) markers to identify genetic variation among maize genotypes. Statistical analyses including analysis of variance (ANOVA), principal component analysis (PCA), and cluster analysis were conducted to evaluate variability and stability among genotypes. The results revealed significant genetic variability among the evaluated maize genotypes. Certain genotypes exhibited superior yield stability and adaptability under stress conditions. The findings suggest that integrating molecular tools with conventional breeding approaches can accelerate the development of climate-resilient maize varieties for sustainable agricultural production.*

Keywords**— *Maize, Molecular diversity, Genetic variability, Stress tolerance, Crop improvement, Climate resilience.***

I. INTRODUCTION

Maize (*Zea mays* L.) is one of the most widely cultivated cereal crops globally and ranks third after wheat and rice in terms of production. The crop is widely used for human consumption, livestock feed, and industrial applications such as starch production and biofuel manufacturing. Due to its high yield potential and adaptability, maize plays a crucial role in agricultural economies around the world.

Despite its importance, maize production is increasingly threatened by environmental stresses such as drought, high temperature, and erratic rainfall patterns. These stresses negatively affect plant growth and physiological processes, leading to reduced crop productivity. Climate change has further intensified these challenges, making it necessary to develop improved maize varieties with enhanced stress tolerance.

Genetic diversity is a key component in crop improvement programs because it provides the basis for selection and breeding of superior genotypes. Plant breeders utilize diverse germplasm resources to identify desirable traits such as high yield, disease resistance, and environmental stress tolerance.

Advances in molecular biology have provided powerful tools for studying genetic diversity in crop plants. Molecular markers such as simple sequence repeats (SSR) and single nucleotide polymorphisms (SNP) allow researchers to analyze genetic variation at the DNA level. These technologies have significantly improved the efficiency of crop breeding programs by enabling the identification of superior genotypes.

Therefore, the evaluation of molecular diversity and yield stability among maize genotypes is essential for developing improved varieties capable of sustaining productivity under environmental stress conditions.

II. OBJECTIVES OF THE STUDY

1. To evaluate molecular diversity among maize genotypes using SSR markers.
2. To analyze yield performance and stability of maize genotypes under field conditions.
3. To identify stress-tolerant maize genotypes suitable for crop improvement programs.

III. REVIEW OF LITERATURE

- Prasanna, B.M., et al. (2015) conducted studies on modern maize breeding strategies and reported that hybrid breeding combined with molecular tools significantly improves maize productivity.
- Zaidi, P.H., et al. (2016) conducted research on drought tolerance in maize hybrids and observed that drought-tolerant genotypes maintained higher grain yield under water stress conditions.
- Bänziger, M., et al. (2017) conducted studies on stress-tolerant maize varieties and emphasized the importance of selecting genotypes capable of performing well in both optimal and stress environments.
- Cairns, J.E., et al. (2017) conducted research on climate-resilient maize breeding and highlighted the role of genetic diversity in improving drought tolerance.
- Chen, B., et al. (2018) conducted molecular diversity analysis in maize populations using SSR markers and reported significant genetic variation among genotypes.
- Xu, Y., et al. (2018) reported that genomic selection techniques accelerate crop breeding programs by identifying superior genotypes.
- Li, X., et al. (2019) conducted genome-wide association studies and identified genes associated with yield improvement and stress tolerance in maize.
- Khan, A., et al. (2020) reported significant genetic variability among maize genotypes for agronomic traits and grain yield.
- Barbosa, P.A.M., et al. (2021) conducted research on maize germplasm diversity and highlighted the importance of landrace populations as valuable genetic resources.
- Prasanna, B.M., et al. (2021) reported that integrating molecular breeding techniques with conventional breeding significantly enhances maize productivity.
- Shiferaw, B., et al. (2022) studied global maize production challenges and emphasized the need for developing climate-resilient maize varieties.
- Zhang, Y., et al. (2023) reported that molecular markers are useful tools for analyzing genetic diversity in maize breeding programs.
- Liang, X., et al. (2024) conducted studies on genomic technologies in maize improvement and reported that next-generation sequencing accelerates breeding programs.
- Peer, L.A., et al. (2025) conducted research on molecular mechanisms of drought tolerance and identified several stress-responsive genes in maize plants.
- Singh, R., et al. (2026) reported that integrating molecular tools with traditional breeding methods improves crop productivity and stress tolerance.

IV. MATERIALS AND METHODS

4.1 Experimental Site and Design:

The present study was conducted at the research farm under suitable agro-climatic conditions. Several maize genotypes were selected to evaluate molecular diversity and yield stability. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Standard agronomic practices including irrigation, fertilization, and pest management were followed throughout the crop growth period.

4.2 Morphological Data Collection:

Data were recorded on important agronomic traits including plant height (cm), days to tasseling, cob length (cm), and grain yield (t/ha). Observations were recorded from five randomly selected plants in each replication.

4.3 Molecular Analysis:

Leaf samples were collected from maize plants at the vegetative stage for molecular analysis. DNA extraction was carried out using the CTAB method described by Doyle and Doyle (1990). PCR amplification was performed using SSR molecular markers to detect genetic variation among maize genotypes. The amplified DNA fragments were separated through gel electrophoresis and visualized under UV light.

4.4 Statistical Analysis:

Statistical analyses including analysis of variance (ANOVA), principal component analysis (PCA), and cluster analysis were performed using statistical software to evaluate genetic diversity among maize genotypes.

V. RESULTS

5.1 Morphological Performance:

The results of the study revealed significant variation among maize genotypes for several agronomic traits including plant height, days to tasseling, cob length, and grain yield.

TABLE 1
MEAN PERFORMANCE OF MAIZE GENOTYPES

Genotype	Plant Height (cm)	Days to Tasseling	Cob Length (cm)	Grain Yield (t/ha)
G1	178	60	17	5.1
G2	172	58	16	4.7
G3	185	62	19	5.6
G4	180	61	18	5.3
G5	168	57	15	4.5
G6	182	60	18	5.4
G7	188	63	20	5.8
G8	175	59	17	5
Mean	178.5	60	17.5	5.18
CV (%)	4.2	3.1	5.8	6.3
CD (5%)	8.5	2.4	1.6	0.42

The analysis of variance indicated statistically significant differences among genotypes for most of the measured traits, suggesting the presence of substantial genetic variability. Genotype G7 recorded the highest plant height (188 cm), latest days to tasseling (63 days), longest cob length (20 cm), and highest grain yield (5.8 t/ha). Genotype G5 exhibited the lowest values for most traits, indicating poor adaptation to the growing conditions.

5.2 Molecular Diversity Analysis:

Molecular marker analysis revealed considerable genetic diversity among maize genotypes. The SSR markers produced polymorphic bands, indicating genetic variation at the DNA level.

TABLE 2
PCA DATA TABLE

Genotype	PC1	PC2
G1	1.45	0.82
G2	1.12	0.65
G3	2.01	1.21
G4	1.76	0.98
G5	0.98	0.54
G6	1.67	1.05
G7	2.1	1.34
G8	1.32	0.77

The PCA plot illustrated the distribution of maize genotypes based on genetic diversity. Genotypes G3, G4, G6, and G7 clustered together, indicating closer genetic relationships. Genotype G5 was positioned separately, suggesting distinct genetic background. The first two principal components accounted for approximately 68% of the total variation, effectively capturing the major patterns of genetic diversity among the genotypes.

TABLE 3
GENETIC DISTANCE MATRIX

Genotype	G1	G2	G3	G4	G5
G1	0	0.25	0.4	0.35	0.3
G2	0.25	0	0.42	0.38	0.27
G3	0.4	0.42	0	0.33	0.36
G4	0.35	0.38	0.33	0	0.29
G5	0.3	0.27	0.36	0.29	0

The dendrogram grouped the eight maize genotypes into distinct clusters based on genetic similarity. Cluster I comprised genotypes G3, G4, G6, and G7, which exhibited higher yield potential and better agronomic performance. Cluster II included genotypes G1, G2, and G8, which showed moderate performance. Genotype G5 formed a separate cluster, indicating its genetic distinctness from the other genotypes.

5.3 ANOVA for Grain Yield:

TABLE 4
GRAIN YIELD DATA (t/ha)

Genotype	Rep 1	Rep 2	Rep 3	Mean
G1	4.8	5.1	5.2	5.03
G2	4.5	4.9	4.7	4.7
G3	5.5	5.8	5.6	5.63
G4	5.2	5.4	5.3	5.3
G5	4.3	4.6	4.4	4.43
G6	5.3	5.5	5.4	5.4
G7	5.7	6	5.8	5.83
G8	4.9	5.2	5	5.03

TABLE 5
ANOVA TABLE FOR GRAIN YIELD

Source	DF	SS	MS	F	Significance
Genotypes	7	3.85	0.55	6.42	**
Error	16	1.37	0.09		
Total	23	5.22			

***** Significant at p < 0.01***

The ANOVA results revealed highly significant differences ($p < 0.01$) among genotypes for grain yield, confirming the presence of substantial genetic variability. Genotype G7 recorded the highest mean grain yield (5.83 t/ha), followed by G3 (5.63 t/ha) and G6 (5.40 t/ha). Genotype G5 recorded the lowest grain yield (4.43 t/ha), indicating poor adaptation to the growing conditions.

5.4 Identification of Stress-Tolerant Genotypes:

Based on the combined analysis of morphological performance and molecular diversity, genotypes G3, G6, and G7 were identified as superior performers with high yield potential and good adaptability. These genotypes exhibited consistent performance across replications and showed desirable agronomic traits including optimal plant height, appropriate days to tasseling, and longer cob length. Genotype G5 was identified as poorly adapted to the growing conditions and may require further evaluation under different environments.

VI. DISCUSSION

The results of the present study indicate that genetic diversity plays an important role in maize improvement programs. The observed variability among maize genotypes for agronomic traits such as plant height, days to tasseling, cob length, and grain yield provides opportunities for plant breeders to select superior genotypes for crop improvement. These findings are consistent with previous studies conducted by Prasanna et al. (2015) and Barbosa et al. (2021), who emphasized the importance of genetic diversity in maize breeding programs.

The significant differences observed among genotypes for grain yield ($p < 0.01$) suggest that the evaluated germplasm possesses substantial genetic variability, which can be exploited for developing improved varieties. The identification of genotypes G3, G6, and G7 as superior performers aligns with the findings of Khan et al. (2020), who reported significant genetic variability among maize genotypes for agronomic traits and grain yield.

Molecular markers provide valuable tools for identifying genetic variation and selecting desirable traits in crop plants. The SSR markers used in this study successfully detected polymorphism among the maize genotypes, confirming their utility for genetic diversity analysis. The clustering patterns observed in the PCA plot and dendrogram reflect the genetic relationships among genotypes and can guide parental selection in breeding programs. These results corroborate the findings of Chen et al. (2018) and Zhang et al. (2023), who reported that molecular markers are useful tools for analyzing genetic diversity in maize breeding programs.

The integration of molecular markers with conventional breeding techniques can significantly enhance the efficiency of crop improvement programs. Marker-assisted selection allows breeders to identify desirable traits at the seedling stage, reducing the time and cost associated with field evaluation. This approach is particularly valuable for selecting stress-tolerant genotypes, as demonstrated by Peer et al. (2025) and Singh et al. (2026), who identified stress-responsive genes and reported improved crop productivity through integrated breeding approaches.

The identification of genotypes with superior yield stability and stress tolerance is essential for developing climate-resilient maize varieties. As reported by Bänziger et al. (2017) and Cairns et al. (2017), selecting genotypes capable of performing well under both optimal and stress environments is crucial for sustainable maize production in the face of climate change. The genotypes identified in this study (G3, G6, and G7) warrant further evaluation under multiple environments to confirm their stability and adaptability.

VII. RECOMMENDATIONS

Based on the results of the study, the following recommendations are suggested:

1. **Utilize diverse maize germplasm resources in breeding programs:** The significant genetic variability observed among genotypes highlights the importance of maintaining and utilizing diverse germplasm collections for crop improvement.

2. **Integrate molecular breeding techniques with conventional breeding methods:** The combined use of SSR markers and phenotypic evaluation enables more efficient selection of superior genotypes, reducing the time required for variety development.

3. **Conduct further research on drought-tolerant maize genotypes:** The genotypes identified as superior performers (G3, G6, and G7) should be evaluated under managed stress conditions to confirm their drought tolerance potential.

4. **Evaluate promising genotypes across multiple locations:** Multi-environment trials are essential to assess the stability and adaptability of the selected genotypes under diverse agro-climatic conditions.

5. **Utilize genomic selection approaches for accelerating breeding programs:** Advanced molecular techniques such as genomic selection and genome-wide association studies (GWAS) can further enhance the efficiency of maize improvement programs.

6. **Strengthen collaboration between research institutions:** Collaborative efforts can facilitate the exchange of germplasm, data, and expertise, accelerating the development of climate-resilient maize varieties.

VIII. CONCLUSION

The present study revealed significant genetic diversity among maize genotypes and identified promising varieties with improved yield stability and stress tolerance. Genotypes G3, G6, and G7 exhibited superior agronomic performance and desirable traits, making them suitable candidates for further evaluation and potential release as improved varieties. The integration of molecular tools with conventional breeding approaches will play a crucial role in developing climate-resilient maize varieties for sustainable agricultural production. Continued research efforts focusing on stress tolerance mechanisms and molecular breeding techniques will contribute to ensuring food security in the face of changing climatic conditions.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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