BIODIVERSITAS
Volume 26, Number 12, December 2025
Pages: 6427-6436

ISSN: 1412-033X
E-ISSN: 2085-4722
DOI: 10.13057/biodiv/d261240

In-situ screening of high-yielding maize (*Zea mays*) for climate resilience in the semi-arid tropics of East Nusa Tenggara, Indonesia

ERLANGGA DWI ATMOJO[1], SHANASYA NAJWA DEVYA ASYARI[1], AZERI GAUTAMA ARIFIN[2], ARIFIN NOOR SUGIHARTO[2,♥]

[1]Department of Agronomy, Faculty of Agriculture, Universitas Brawijaya. Jl. Veteran, Malang 65145, East Java, Indonesia
[2]Laboratory of Plant Breeding, Department of Agronomy, Faculty of Agriculture, Universitas Brawijaya. Jl. Veteran, Malang 65145, East Java, Indonesia. Tel.: +62-341-575826, Fax.: +62-341-559701, ♥email: sugiharto.noor@gmail.com

Manuscript received: 11 September 2025. Revision accepted: 23 December 2025.

Abstract. *Atmojo ED, Asyari SND, Arifin AG, Sugiharto AN. 2025. In-situ screening of high-yielding maize* (Zea mays) *for climate resilience in the semi-arid tropics of East Nusa Tenggara, Indonesia. Biodiversitas 26: 6427-6436.* Developing climate-resilient maize (*Zea mays*) is crucial for ensuring food security in Indonesia's semi-arid regions, particularly in East Nusa Tenggara, where recurring droughts severely impact maize productivity. Maize farming in these areas faces extreme environmental challenges, highlighting the need for varieties capable of thriving under water-limited conditions. This study evaluated the performance of ten top-cross maize hybrids (UB 21-UB 30), derived from elite S_3 inbred lines, under semi-arid conditions, comparing them to two commercially available varieties as controls. Genetic parameters were calculated from variance components, phenotypic variation was assessed using analysis of variance, and superior hybrids were identified through hierarchical clustering and Genotype × Trait (GT) analysis. The studied traits showed medium to high heritability, with low to moderate genotypic and phenotypic coefficients of variation. UB 25 emerged as the top performer, with a potential yield of 6.39 t ha^{-1}, surpassing the best commercial variety. This hybrid also demonstrated significant drought resilience, characterized by a shorter anthesis-silking interval and fewer unfilled tips, both of which are essential for maintaining yield stability under drought stress. Additionally, UB 28 was identified as another promising hybrid, exhibiting high yield potential and favorable stress-adaptive traits. These results underscore the importance of in-situ screening to identify maize varieties tailored to the specific challenges of semi-arid environments. The hybrids identified in this study provide a strong foundation for developing drought-resilient maize in Indonesia's semi-arid tropics.

Keywords: Drought stress, genotype × trait analysis, hybrid, in-situ screening, semi-arid

INTRODUCTION

Maize (*Zea mays* L.) is a crucial crop in Indonesia and plays a significant role in food security, livestock feed, and local economies, particularly in East Nusa Tenggara. In this region, maize provides essential calories for local populations and serves as a primary feed source for livestock farming. It also yields various traditional maize-based products that are deeply ingrained in the culture and traditions of the East Nusa Tenggara people. There are 16 distinct traditional maize-based products are produced locally, each with its unique name (Naisali et al. 2023). These products are not only consumed daily but also hold cultural significance during ceremonies and community events, underlining maize's importance as a staple food in East Nusa Tenggara. However, maize productivity in the region in 2024 was notably lower than the national average, at just 2.69 tons ha^{-1} (BPS 2025).

East Nusa Tenggara is a climatically marginal area that has a semi-arid tropical climate, while a suite of abiotic stresses limits agricultural production. The province is characterized by recurrent droughts, often coinciding with the critical growth stages of maize (Kuswanto et al. 2021). The physiological effects of drought stress on maize are complex, as they impact the maize plant at all stages of its life cycle. Specifically, drought stress during the vegetative phase can inhibit cell division, restrict photosynthesis, and diminish chlorophyll synthesis (Deribe 2024). However, drought stress encountered during the reproductive stage typically imposes the most severe reductions in grain yields (Pongtip et al. 2023). The consequences of this stress are far-reaching, affecting both the livelihoods of farmers and regional food security.

As climate change intensifies these challenges, the need for climate-resilient crops in East Nusa Tenggara is increasingly urgent. However, the majority of maize varieties currently grown in the region are poorly adapted to its semi-arid conditions. This highlights the need for breeding programs tailored to local environmental constraints. Several methods, such as controlled-environment and in-situ screenings, are commonly used to evaluate maize genotypes. One promising approach is in-situ screening, a method that evaluates maize genotypes directly under natural field stress, rather than in controlled or simulated environments. This approach facilitates the identification of genotypes that are truly resilient and productive under the region's climatic conditions. In-situ screening has been successfully applied in sub-Saharan Africa and parts of Asia, where it has led to the development of high-yielding, climate-resilient maize hybrids (Meseka et al. 2018). A similar study demonstrated the success of in-situ screening for identifying climate-resilient maize genotypes in the dry region of Punjab, Pakistan (Ahmad et al. 2024).

Despite its proven benefits, in-situ screening remains underutilized in Indonesia's semi-arid regions, particularly in East Nusa Tenggara. Aji and Sugiharto (2024) initiated early in-situ screening of S_2 inbred lines through top-cross progeny evaluation, offering preliminary insights into local adaptation in the semi-arid tropics of East Nusa Tenggara. However, for enhanced genetic stability and selection accuracy in maize, in-situ evaluations should be extended to later generations of inbred lines. The S_3 generation, with its higher homozygosity, allows for more reliable assessments of genetic potential and environmental interaction. By screening each generation under real field conditions, it is possible to select genotypes that consistently exhibit adaptability to local climatic stress across breeding cycles, avoiding the risk of selecting genotypes that perform well in one generation but regress in subsequent cycles. This study aimed to fill this gap by conducting in-situ evaluations of ten top-cross maize hybrids derived from elite S_3 inbred lines, under semi-arid conditions in East Nusa Tenggara. The findings from this study are expected to significantly contribute to the development of locally adapted, climate-resilient maize hybrids and reinforce the importance of in-situ screening as a core strategy in breeding programs aimed at improving maize performance in drought-prone areas.

MATERIALS AND METHODS

Study area

The research was conducted from July to December 2024 at the experimental field of Universitas Brawijaya, located in Oesao Village, Kupang District, East Nusa Tenggara, Indonesia (Figure 1). This site was selected for its strategic relevance in evaluating maize genotypes under natural semi-arid conditions. The area experiences low annual rainfall (<1,000 mm), typical of the drought-prone environment of East Nusa Tenggara (Suriadi et al. 2021). Additionally, daily temperatures ranged from 27.20 to 37.10°C (Putri and Sofro 2025). The soil, classified as sandy clay, is characterized by low water retention, further intensifying the stress conditions for maize cultivation.

Genetic materials

A total of 12 maize genotypes were evaluated, including ten top-cross hybrids and two commercial comparison varieties. The 10 top-cross hybrids (UB 21, UB 22, UB 23, UB 24, UB 25, UB 26, UB 27, UB 28, UB 29, and UB 30) were developed from crosses between S_3 inbred lines and a non-inbred tester. All inbred lines utilized as top-cross parents originated from the CV. Blue Akari line collection, having been selected in a prior S_2 cycle as part of a selection program focused on general combining ability under the semi-arid conditions prevalent in East Nusa Tenggara. Two commercial maize varieties (AR 21 and NS 01) were included as checks to compare the yield and climate-resilience performance of the top-cross hybrids. These varieties were selected because they are the most commonly grown hybrids by farmers in East Nusa Tenggara.

Procedures

The experiment was conducted using a Randomized Complete Block Design (RCBD) with three replications, resulting in 36 experimental plots. All genotypes were randomly assigned to each replication to minimize field variability (error). Each plot covered an area of 15 m² and was planted with a spacing of 100 × 15 cm. Standard local agronomic practices, including fertilization (60 kg N ha^{-1}, 45 kg P_2O_5 ha^{-1}, and 45 kg K_2O ha^{-1}), weed management, and pest control, were uniformly applied across all plots. Weed management was performed manually, while pest control was implemented using insecticides to manage *Spodoptera frugiperda*, and fungicides were applied to control rust disease.

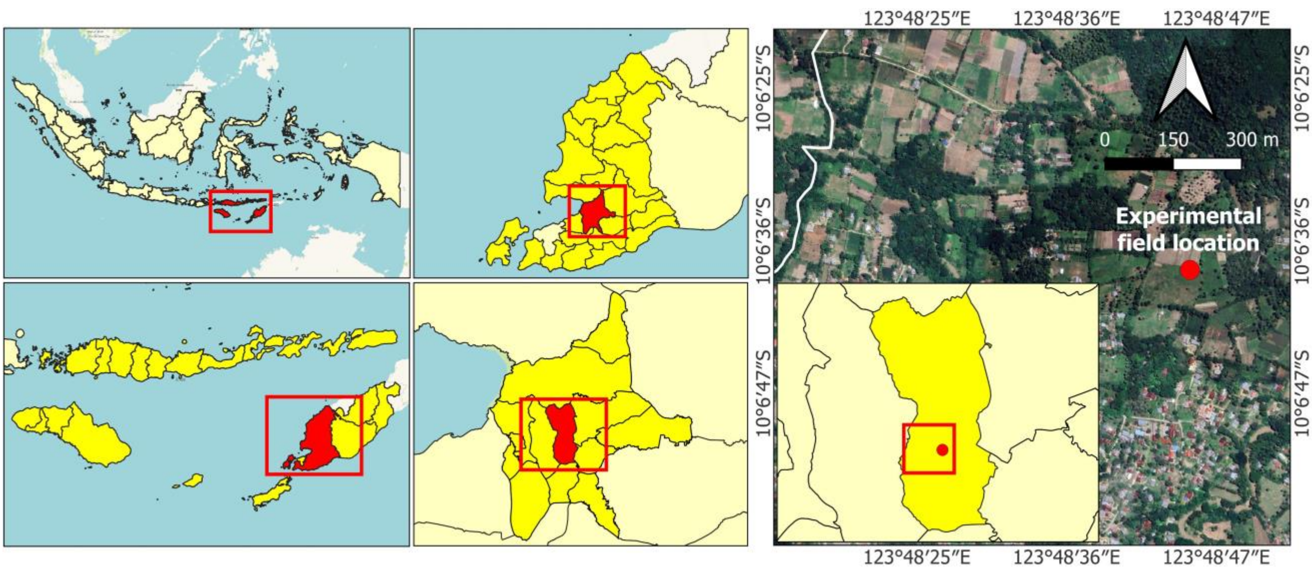

Figure 1. Location of experimental field in Oesao Village, East Kupang Sub-district, Kupang District, East Nusa Tenggara, Indonesia (coordinate point: 10°06'38.0"S 123°48'44.9"E)

Drought stress was induced through natural rainfall variation during the maize growing season, with irrigation only provided before planting. Phenotypic data were collected from 20 representative plants, selected using restricted random sampling from non-border rows and columns to minimize edge effects. Nine quantitative traits were measured: anthesis-silking interval (days), unfilled tips (cm), ear length (cm), ear diameter (mm), number of kernel rows (rows), 1,000-kernel weight (g), dehusked ear weight (g), kernel percentage (%), and potential yield (t ha^{-1}). All ear-related traits were assessed at physiological maturity and adjusted to a standard grain moisture content of 11%. Meanwhile, anthesis-silking interval is calculated as the date when 50% of plants are silking minus the date when 50% of plants begin tasseling. These traits provided direct, quantitative evaluations of F_1 top-cross hybrid performance under the semi-arid conditions of East Nusa Tenggara. Trait measurements adhered to the official guidelines for testing distinctness, uniqueness, uniformity, and stability in maize No. PVT/PPU/17/4 2014, as established by the Ministry of Agriculture of the Republic of Indonesia.

Data analysis

Analysis of Variance (ANOVA) was performed under the RCBD model after testing the assumptions of normality (Shapiro-Wilk test) and homogeneity of variances (Levene's test). Mean separation was conducted using the Scott-Knott test ($\alpha = 0.05$), which allows for clearer genotype grouping (Scott and Knott 1974), making it easier to identify variations in genotype performance under drought stress based on non-overlapping groups. Analysis of Variance, Shapiro-Wilk test, Levene's test, and Scott-Knott test were performed using RStudio version 2023.09.1+394.

Phenotypic and genotypic coefficients of variation (PCV and GCV), along with broad-sense heritability (H), were estimated from variance components to assess selection potential. PCV and GCV values were categorized as low (<10%), moderate (10-20%), or high (>20%), as defined by Sivasubramanian and Madhavamenon (1973). Heritability was classified as low (<0.30), moderate (0.30-0.60), or high (>0.60), as defined by Johnson et al. (1955). Estimation for PCV, GCV, and H was performed using Microsoft Excel 2021.

Hierarchical Cluster Analysis (HCA) was performed using Pearson's distance, with a heatmap generated to visualize patterns of similarity or dissimilarity among the objects. Genotype × Trait (GT) analysis was applied for comprehensive multi-trait evaluation. For traits with desirable smaller values (anthesis-silking interval and unfilled tip), the data were transformed using the inverse function (1/x) (Osborne 2002), where x represents the observed data. This transformation ensured that higher scores in the biplot consistently indicated superior performance. All data in the GT biplot were standardized as z-scores to place traits on a comparable scale and prevent variables with larger numerical ranges from disproportionately influencing the results. HCA and GT biplot were performed using RStudio version 2023.09.1+394.

RESULTS AND DISCUSSION

Variation in phenotypic performance

Significant variation was observed in the nine phenotypic traits across the ten top-cross hybrids and two commercial checks, as indicated by the Analysis of Variance. The Scott-Knott test successfully grouped the genotypes, revealing distinct performance levels under the semi-arid conditions of East Nusa Tenggara (Table 1).

A short anthesis-silking interval is a key indicator of reproductive success under drought stress. Hybrids UB 21 and UB 28 displayed synchronized flowering and high yield performance under drought conditions. Despite the small difference of 1-2 days, a shorter anthesis-silking interval improves pollination and kernel set under stress, reinforcing its role as a drought resilience trait. The results show that even minor reductions in this interval can enhance assimilate flow and increase kernel development when water is limited. Drought stress around flowering disrupts the source-sink process, impeding silk growth and assimilate delivery to developing ovaries, which explains why even slight reductions in the anthesis-silking interval result in significant improvements in kernel set (Li et al. 2023). Our study consistently highlights the association between a shorter anthesis-silking interval and higher kernel set under water deficit, making it an essential trait for selection in drought breeding (Li et al. 2018).

Unfilled tips provide additional insights into drought adaptation. Hybrids UB 25 and UB 28 consistently showed fewer unfilled tips while maintaining high yields under drought stress. Unfilled tips, which are linked to ovary abortion during drought, indicate improved reproductive partitioning in these genotypes, enhancing yield stability under environmental stress. Drought stress during flowering and early grain filling accelerates ovary abortion at the apical part of the ear, reducing kernel number and yield potential (Wang et al. 2025). The timing and intensity of stress during the reproductive stage are key factors in determining the extent of unfilled tips. Genotypes with fewer unfilled tips not only maintain kernel set under stress, but also exhibit better assimilate partitioning to reproductive organs, which is crucial for stabilizing yield under drought (Song et al. 2023). This trait contributes to higher yield potential and improves productivity, benefiting farmers' income.

Hybrids UB 25 and UB 28 also demonstrated superior yield traits, such as ear length, dehusked ear weight, and potential yield, likely due to their stable physiological responses under stress. These include better stomatal control, photosynthetic maintenance, and improved water-use efficiency, which support sustained growth and yield in water-limited conditions. Cai et al. (2020) highlighted the importance of maintaining chlorophyll fluorescence and stomatal conductance to support yield under drought in maize. However, the 1,000-kernel weight in UB 25 and kernel percentage in UB 28 were lower than expected, potentially due to limited sink strength or impaired assimilate partitioning during grain filling. Drought stress alters the kernel proteome and reduces starch accumulation, limiting final grain weight (Guo et al. 2021). These findings underscore the need for enhanced source-sink dynamics and grain-filling efficiency in future breeding efforts. Extending grain-filling duration and optimizing assimilate supply could significantly enhance kernel weight (Pico and Vyn 2021).

Traits such as the number of kernel rows and ear diameter in all tested hybrids were generally lower than those in the commercial variety NS 01. These traits showed limited performance under drought and should be prioritized in future breeding programs. Both traits directly affect sink capacity, and enhancing them could significantly increase productivity in water-limited environments. Drought stress reduces photosynthetic rates, weakening source strength, and lowers phloem cell turgor, which increases sucrose viscosity and impairs flow to sink tissues (Sevanto 2014). Yao et al. (2024) also demonstrated that drought stress impairs sugar translocation within the maize ear, further limiting grain weight, especially in apical and basal kernels. Additionally, ear architectural traits, such as the number of kernel rows and kernel number per row, influence drought response, with variations in ear shape affecting resilience under water deficit (Chen et al. 2022).

Genetic parameters and potential for selection

Genetic parameters are crucial for assessing genetic variation and guiding selection decisions in plant breeding programs. This study estimated key parameters, including the Phenotypic Coefficient of Variation (PCV), Genetic Coefficient of Variation (GCV), and Heritability (H). The PCV reflects total variation in a trait, encompassing both genetic and environmental factors, while the GCV focuses solely on genetic variation (Tareque et al. 2025). Heritability indicates the proportion of phenotypic variation attributed to genetic factors (Limbongan et al. 2024). A summary of the estimated GCV and PCV values for the studied traits is provided in Table 2.

A key component of any successful breeding program is the presence of usable genetic variation within the germplasm pool. In this study, most traits exhibited a low Genetic Coefficient of Variation (GCV), indicating limited genetic variability available for improvement. As expected, the Phenotypic Coefficient of Variation (PCV) values generally exceeded the GCV values, highlighting the environmental influence on trait expression and suggesting that phenotypic observations may obscure underlying genetic signals (Magar et al. 2021). This low genetic variability indicates that conventional selection methods may not lead to substantial genetic progress (Lal et al. 2020). However, the presence of high-performing genotypes under drought stress provides an opportunity for targeted improvement. Breeders can still achieve progress by focusing on traits that play key roles in stress adaptation and exhibit favorable selection efficiency. Specifically, secondary traits with moderate GCV and strong correlations to yield can be useful as indirect selection criteria in drought-prone environments, as shown in previous maize studies under stress (Magar et al. 2021).

Table 1. Comparison of genotypic and phenotypic coefficient of variation

Character	GCV (%)	Category	PCV (%)	Category
Anthesis-silking interval	15.69	Low	20.79	Low
Unfilled tips	40.57	High	46.85	High
Ear length	5.29	Low	6.31	Low
Ear diameter	4.81	Low	5.70	Low
Number of kernel rows	7.36	Low	8.23	Low
1,000-kernel weight	4.96	Low	6.18	Low
Dehusked ear wight	8.80	Low	10.17	Moderate
Kernel percentage	2.44	Low	2.66	Low
Potential yield	12.06	Moderate	14.56	Moderate

Note: GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation. Low: GCV or PCV<10%, Moderately Low: 10%≤GCV or PCV≤20%, High: GCV or PCV>20%

Table 2. Comparison of mean quantitative traits in 12 genotypes

Genotype	ASI	UT	NR	EL	ED	KW	EW	KP	PK
UB 21	3.00 b	0.35 a	14.53 b	15.43 b	42.08 d	245.83 b	162.98 b	87.37 b	5.24 a
UB 22	3.00 b	0.18 b	13.20 d	15.93 b	43.77 c	266.60 a	166.10 b	89.93 a	5.72 a
UB 23	3.00 b	0.23 b	14.67 b	15.49 b	45.08 c	266.86 a	168.88 b	86.36 b	5.79 a
UB 24	2.67 b	0.18 b	14.10 c	16.68 a	46.56 b	276.31 a	178.99 a	86.57 b	5.91 a
UB 25	2.00 b	0.14 b	15.27 b	17.51 a	45.25 c	241.63 b	183.57 a	87.87 b	6.39 a
UB 26	3.00 b	0.22 b	14.13 c	17.49 a	43.08 d	242.73 b	166.24 b	89.81 a	5.67 a
UB 27	2.67 b	0.17 b	13.53 c	16.11 b	44.71 c	262.82 a	162.68 b	86.79 b	5.31 a
UB 28	2.67 b	0.16 b	15.20 b	17.65 a	45.04 c	252.96 b	188.76 a	82.69 d	6.11 a
UB 29	3.67 a	0.41 a	13.03 d	15.31 b	43.59 c	288.47 a	151.15 c	85.23 c	4.45 c
UB 30	3.33 a	0.42 a	12.80 d	15.24 b	40.96 d	270.94 a	137.20 c	84.52 c	4.01 c
AR 21	4.00 a	0.37 a	12.80 d	15.81 b	44.18 c	268.31 a	147.17 c	84.39 c	5.03 b
NS 01	2.67 b	0.42 a	16.13 a	15.52 b	49.97 a	264.93 a	179.53 a	85.07 c	6.13 a

Note: ASI: Anthesis-Silking Interval (day), UT: Unfilled Tips (cm), NR: Number of kernel Rows, EL: Ear Length (cm), ED: Ear Diameter (mm), KW: 1,000-Kernel Weight (g), EW: Dehusked Ear Weight (g), KP: Kernel Percentage (%), PK: Potential yield (t ha^{-1}). Values followed by the same letter in the same column are not significantly different based on the Scott-Knott test at a 5% significance level

A notable trait is unfilled tips, which exhibited a high GCV. This trait is directly linked to kernel number per ear, making it highly relevant for yield potential under stress. In breeding programs, unfilled tips can serve as a surrogate indicator of hybrid performance in early selection stages. Their variability across genotypes provides a basis for identifying lines with improved stress resilience. Integrating unfilled tips into multi-trait selection indices can enhance drought-tolerant breeding programs (Shahzad et al. 2023). This approach is supported by Badu-Apraku et al. (2018), who emphasized the importance of selecting traits with sufficient genetic variability for drought adaptation. Similarly, Gazal et al. (2017) highlighted the value of traits with higher variability in assessing genotype adaptability under drought conditions.

In contrast, ear diameter and number of kernel rows exhibited low GCV and PCV values, and the average performance of all tested genotypes was below that of the NS 01 check variety. These results suggest limited potential for significant genetic progress through selection on these traits. The low variability may indicate a genetic bottleneck or selection plateau, particularly in traits that are structurally conserved. Inbreeding depression, which increases homozygosity and exposes deleterious alleles that were previously hidden in the heterozygous state, could be contributing to this low variability (Achrem et al. 2023). This issue is especially pronounced in traits controlled by multiple genes. To address this, the selection program for the next population should incorporate the inbreds from the current program as testers in a recurrent selection scheme focused on specific combining ability. This strategy will help identify favorable non-additive genetic interactions and expand the genetic base, particularly for traits with limited variation.

Heritability estimates provide insight into the effectiveness of selection for each trait (Table 3). Encouragingly, most yield-associated traits showed relatively high heritability. This suggests that observed genotype differences for these traits are primarily genetic and can be reliably passed on to the next generation, which is advantageous for breeders. Notably, traits such as ear length, dehusked ear weight, and kernel percentage exhibited high mean values and heritability, making them valuable for early selection in the breeding cycle. Other traits, including ear diameter, number of kernel rows, 1,000-kernel weight, and potential yield, also demonstrated promising heritability, increasing confidence in phenotype-based selection. Dawaki et al. (2023) reported that targeting highly heritable yield components accelerates genetic gains, particularly in stress-prone environments. The heritability values observed in this study align with or exceed those found in maize drought stress studies in Africa (Badu-Apraku et al. 2018).

The medium heritability of the anthesis-silking interval points to the potential genetic cost of selecting for this trait. While anthesis-silking interval is a useful indicator of drought tolerance, its lower heritability suggests a stronger environmental influence, requiring careful management to avoid trade-offs with other high-yielding traits. This result supports the use of anthesis-silking interval primarily as a supplementary criterion rather than a main selection target. Mechanistically, drought stress around flowering can alter silk growth and pollination dynamics, leading to a prolonged anthesis-silking interval and limited kernel set, which may explain why its heritability is lower than that of some sink traits (Liu et al. 2021). While anthesis-silking interval remains important for drought tolerance, breeding programs should prioritize traits with higher heritability to ensure consistent genetic gains without compromising other agronomic traits. Combining anthesis-silking interval with yield-related traits can also improve selection reliability under stress, as demonstrated in multi-trait models in tropical maize breeding (Azrai et al. 2025).

A key finding in this study was the unfilled tips trait, which is strongly linked to genotype performance under drought stress. Unlike anthesis-silking interval, which can be influenced by environmental fluctuations, unfilled tips exhibited both agronomic relevance and higher heritability, making it a more reliable trait for phenotypic selection. Unfilled tips show greater consistency across drought-prone environments, enabling breeders to distinguish genotypes more effectively. Recent studies support the use of unfilled tip-related traits as robust indicators in drought breeding programs. For example, Cagnola et al. (2018) highlighted that unfilled tips are one of the most responsive traits under water stress, allowing for effective genotype screening in early selection cycles. Similarly, Yue et al. (2018) demonstrated that unfilled tips and related ear traits could serve as reliable criteria for improving yield stability in moisture-limited conditions. These findings underscore the value of unfilled tips as a primary selection trait for drought tolerance, especially when combined with other moderately heritable traits.

Identification of superior hybrids under semi-arid conditions

Hierarchical clustering analysis proved effective in identifying performance patterns among the maize genotypes by grouping them based on similarities in trait expression. The accompanying heatmap enhanced interpretation, where darker shades indicated higher trait values within genotype groups. The analysis grouped the twelve genotypes into two major performance clusters (Figure 2), allowing for clear differentiation between superior and lower-performing entries under drought stress. Notably, genotypes within the high-performance cluster generally exhibited favorable values for key yield-related and adaptability traits. This clustering provides useful framework for selecting promising genotypes in early-stage drought tolerance breeding programs.

Table 3. Comparison of heritability

Character	σ^2_g	σ^2_P	H	Category
Anthesis-silking interval	0.217	0.381	0.57	Medium
Unfilled tips	0.012	0.016	0.75	High
Ear length	0.733	1.043	0.70	High
Ear diameter	4.580	6.440	0.71	High
Number of kernel rows	1.080	1.350	0.80	High
1,000-kernel weight	169.563	262.683	0.65	High
Dehusked ear weight	213.417	285.457	0.75	High
Kernel percentage	4.437	5.277	0.84	High
Potential yield	0.437	0.637	0.69	High

Note: σ^2_g: Genotypic variance, σ^2_p: Phenotypic variance, H: heritability (%). Low: Heritability<0.30, Medium: 0.30≤Heritability≤0.60, High: Heritability>0.60

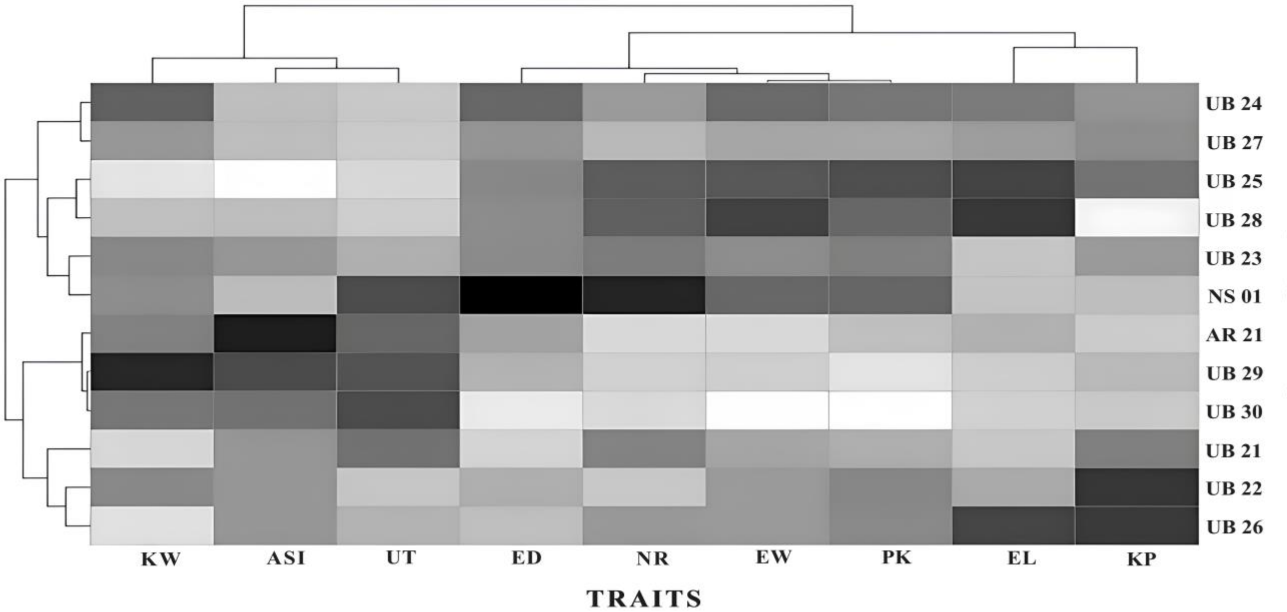

Figure 2. Hierarchical Clustering Analysis (HCA) of maize genotypes and observed traits. Note: ASI: Anthesis-Silking Interval, UT: Unfilled Tips, NR: Number of kernel Rows, EL: Ear Length, ED: Ear Diameter, KW: 1,000-Kernel Weight, EW: Dehusked Ear Weight, KP: Kernel Percentage, PK: Potential yield. Darker colors represent a higher mean value of a trait in the genotype group

Cluster 1, which included UB 23, UB 24, UB 25, UB 27, UB 28, and the elite check NS 01, emerged as the top-performing group. These genotypes displayed favorable trait combinations for drought-prone environments, such as consistently shorter anthesis-silking intervals, fewer unfilled tips, and higher values for key yield traits, including ear length, ear diameter, kernel row number, and dehusked ear weight. These traits demonstrate the genotypes' ability to maintain productivity under water stress, making them well-suited for semi-arid regions like East Nusa Tenggara. According to Musvosvi et al. (2018), optimizing these traits together contributes to yield stability under moisture-deficient conditions. In contrast, Cluster 2, which included the remaining hybrids, including AR 21, exhibited poorer trait expression, making these genotypes less suitable for advancement. Selecting genotypes from Cluster 1 holds potential for not only improving yield under drought conditions, but also for reducing input costs, such as water use, thus increasing crop stability in marginal environments.

Trait-based clustering divided the traits into two distinct groups. Cluster 1 included traits directly related to grain yield, such as kernel percentage, potential yield, ear length, and dehusked ear weight, emphasizing their interconnected role in driving productivity. Cluster 2, on the other hand, grouped traits like unfilled tips, anthesis-silking interval, and 1,000-kernel weight, which could limit yield potential under drought stress. This pattern suggests that traits in Cluster 1 are more reliable selection targets, while those in Cluster 2 may indicate underlying vulnerabilities to stress. According to Ortez et al. (2022), kernel development under stress is constrained by physiological factors and weak sink strength, where traits such as unfilled tips and extended anthesis-silking interval highlight reproductive inefficiencies. Genotypes like UB 25 and UB 28, which consistently perform well for Cluster 1 traits, can be prioritized in breeding programs targeting both yield potential and stress resilience.

The heatmap analysis further confirms the superior performance of UB 25, with darker shades indicating higher yield traits and lighter shades for drought-related traits, such as unfilled tips and anthesis-silking interval. Its phenotypic profile closely mirrors that of UB 28. In hierarchical cluster analysis, the closer the phenotypic performance between genotypes, the smaller the distance between them (López-Cortés et al. 2020). This consistency across multiple selection indices confirms that both UB 25 and UB 28 combine strong yield potential with desirable drought-response characteristics. Drought-tolerant genotypes, such as UB 25 and UB 28, typically exhibit lower lipid peroxidation, maintaining cell membrane integrity, and accumulate higher levels of osmolytes to help maintain cellular turgor and water balance under drought stress (Gelaw and Sanan-Mishra 2024). Their shared clustering and balanced trait profiles suggest they are promising candidates for developing high-performing, drought-resilient hybrids suited to semi-arid environments like East Nusa Tenggara.

Genotype × Trait (GT) analysis further clarifies the relationship between genotypes and key yield and drought-resilience traits, helping identify elite genotypes adaptable across multiple traits (Figures 3 and 4). The correlation value of anthesis-silking interval and unfilled tips on yield characters means that the higher the inverse yield value (the smaller actual value of anthesis-silking interval and unfilled tips) positively impacts maize yields. This suggests that reducing either of these traits may simultaneously enhance yield performance. The GT biplot also revealed positive correlations among key yield traits, such as ear length, ear diameter, number of kernel rows, dehusked ear weight, and potential yield (Figure 3.A), implying that improving one of these traits could simultaneously enhance others. These findings align with Dolatabad et al. (2010), which reported positive correlations between grain yield and ear-related traits, such as kernel rows, ear weight, and kernel depth. Additionally, these results emphasize the importance of multi-trait selection strategies in improving overall maize performance under stress conditions.

The "which-won-where" polygon effectively highlights the genotypes that excel in specific trait sectors, allowing for targeted selection based on performance in particular trait groups. The "which-won-where" view (Figure 3.B) identifies the strengths of the vertex genotypes: UB 25 excelled in yield-related traits (ear length, ear weight, and kernel number) and stress-adaptation traits (unfilled tips and anthesis-silking interval); NS 01 was superior in ear structure, particularly ear diameter and kernel row number; UB 26 performed best for kernel percentage; and UB 29 showed the highest 1,000-kernel weight. This visualization method has been shown to effectively identify superior genotypes for specific traits, as demonstrated in recent GT biplot studies where hybrids were selected based on their strong performance in yield-related traits (Singamsetti et al. 2024). Based on these results, UB 25 stands out for its overall superiority across most traits. However, UB 25's ear diameter and kernel row number are not as strong as UB 28's, and both genotypes require improvement in kernel percentage and 1,000-kernel weight.

The genotypes were ranked based on their mean performance across all traits (Figure 4.A) and their distance from the "ideal genotype" (Figure 4.B). Genotypes closer to the center of the Average Tester Axis (ATA) typically exhibit higher mean performance and a more balanced trait profile (Yan and Frégeau-Reid 2018). Both analyses consistently identified UB 25 and UB 28 as the top-performing hybrids, surpassing all other experimental lines and both commercially available check varieties. Based on mean performance, UB 25 was recognized as the superior hybrid. However, in terms of proximity to the ideal genotype, UB 28 displayed a more balanced trait profile compared to UB 25. These hybrids represent a near-optimal combination of high yield potential and drought tolerance. Drought-tolerant maize genotypes are known to produce higher levels of antioxidant enzymes, which help mitigate oxidative stress by neutralizing reactive oxygen species formed under drought conditions (Yang et al. 2015). As such, the parental inbred lines of these top-cross hybrids are strong candidates for future breeding cycles focused on enhancing resilience to semi-arid climates.

Implications for maize breeding in Indonesia and future directions

This study emphasizes the need to prioritize in-situ screening as a key strategy in maize breeding programs in Indonesia, especially in drought-prone areas like East Nusa Tenggara. Evaluating genotypes under local environmental conditions allows breeding programs to gather more accurate data on performance under real-world stress. Screening genetic materials within target production zones further accelerates breeding progress, enhancing varietal adaptability and encouraging farmer adoption through locally validated performance data (de Sousa et al. 2021). Ahmad et al. (2024) show that screening genetic materials in target production zones accelerates breeding progress. This approach is especially relevant in Indonesia, given its diverse climates and soils that require region-specific solutions. Incorporating in-situ screening into national breeding programs will enhance varietal adaptability and encourage farmer adoption by providing locally validated performance data.

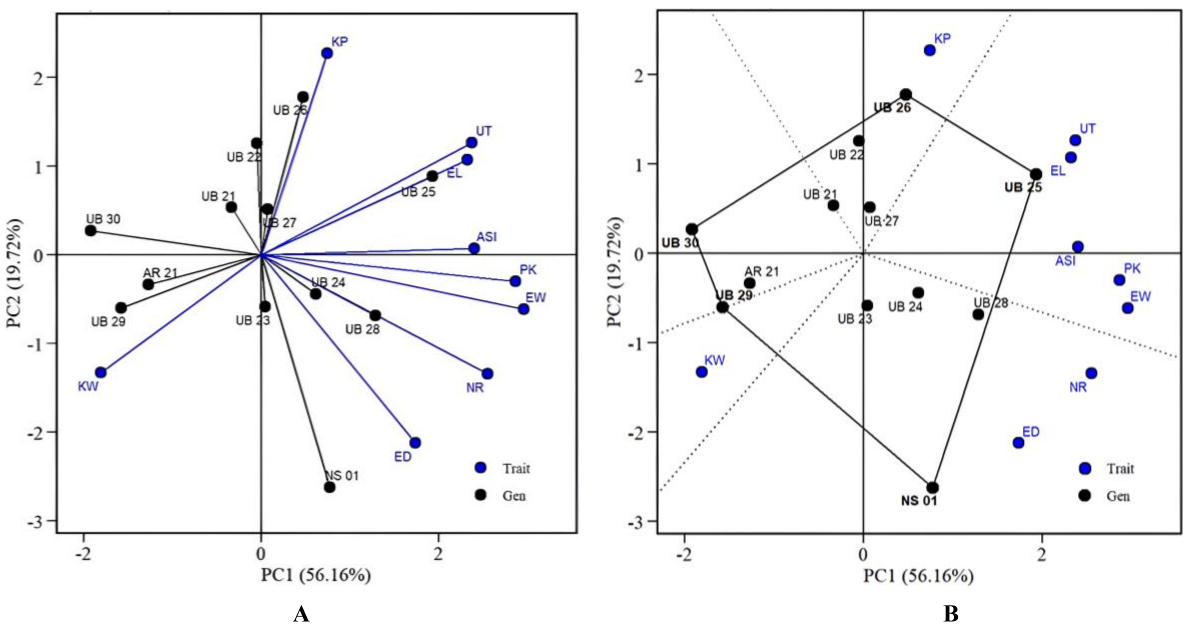

Figure 3. Genotype × Trait (GT) biplot analysis: A. Relationships among traits, B. Which-won-where polygon view. PC1: Principal Component 1, PC2: Principal Component 2, ASI: Anthesis-Silking Interval, UT: Unfilled Tips, NR: Number of kernel Rows, EL: Ear Length, ED: Ear Diameter, KW: 1,000-Kernel Weight, EW: Dehusked Ear Weight, KP: Kernel Percentage, PK: Potential yield

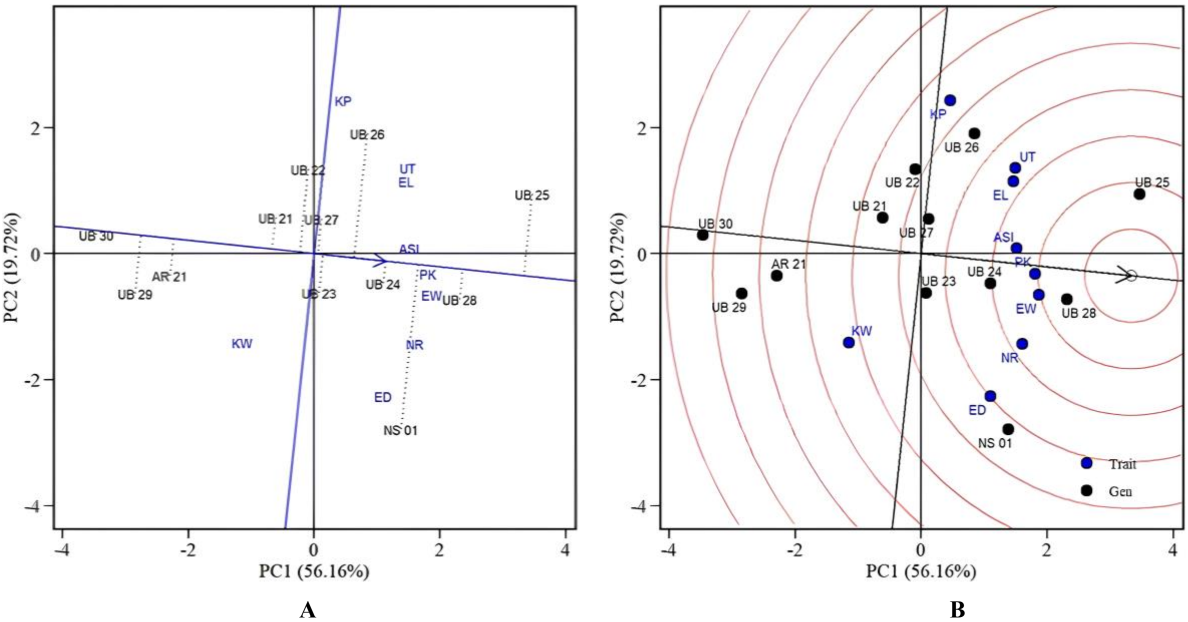

Figure 4. Genotype × Trait (GT) biplot analysis: A. Ranking by mean performance, B. Ranking by proximity to the ideal genotype. Note: PC1: Principal Component 1, PC2: Principal Component 2, ASI: Anthesis-Silking Interval, UT: Unfilled Tips, NR: Number of kernel Rows, EL: Ear Length, ED: Ear Diameter, KW: 1,000-Kernel Weight, EW: Dehusked Ear Weight, KP: Kernel Percentage, PK: Potential yield

Given the challenges posed by climate change and recurring drought, in-situ screening can be an important strategy to advance national agricultural goals. This strategy supports national goals aimed at boosting maize production in drought-prone, marginal areas by developing drought-tolerant varieties and expanding cultivation into less fertile lands (Syahruddin et al. 2020). Ensuring that selected genotypes are high-yielding and well-suited to local conditions is crucial for strengthening food security. Additionally, incorporating drought-tolerant traits will help mitigate the risks associated with climatic variability, benefiting both farmers and consumers by improving production sustainability.

Although the findings of this study offer valuable insights, they are based on a single season and location, limiting their broader applicability. To better assess the stability and adaptability of the identified genotypes, future research should include multi-location and multi-season trials that cover a wider range of agroecological conditions (Yue et al. 2022). Expanding testing across diverse environments is essential to ensure that the genotypes perform consistently under various conditions. This will strengthen national strategies for sustainable agricultural intensification and improved food security. Broader trials will provide more reliable data, ensuring that the identified genotypes are truly resilient to different environmental stresses.

The integration of molecular techniques, such as Marker-Assisted Selection (MAS), alongside in-situ screening, will improve the precision of genotype evaluations. Molecular markers help identify Quantitative Trait Loci (QTL) associated with key traits like drought tolerance and yield, improving the accuracy and efficiency of selection, particularly for complex traits (Zhang et al. 2017). Future breeding efforts should focus on combining elite lines with disease resistance and nutrient-use efficiency to develop more robust hybrids. By combining conventional breeding methods, molecular tools, and location-specific screening, Indonesia's maize breeding programs can achieve faster genetic progress, ensuring that the selected varieties meet both environmental and socio-economic needs.

In conclusion, UB 25 and UB 28 emerged as high-yielding maize hybrids under the semi-arid conditions of East Nusa Tenggara, Indonesia. These hybrids should be prioritized for multi-location trials to assess yield stability and environmental adaptability. Breeders are encouraged to integrate their inbred parents into drought-tolerance breeding pipelines, while policymakers should support their rapid evaluation and potential scale-up. Future molecular characterization will also enhance the precision of selecting drought-resilient traits for national maize improvement programs.

ACKNOWLEDGEMENTS

This research was funded by Professor Grant 2024 under contract number 03641.11/UN10.F0401/B/KS/2024. The authors extend their gratitude to CV. Blue Akari for their support, especially in providing genetic materials. The authors also appreciate the collaboration, knowledge, and support of the partner farmers in East Nusa Tenggara, Indonesia, whose contributions were essential to the success of the study.

REFERENCES

Achrem M, Stępień E, Kalinka A. 2023. Epigenetic changes occurring in plant inbreeding. Intl J Mol Sci 24 (6): 5407. DOI: 10.3390/ijms24065407.

Ahmad K, Ullah A, Islam B, Khan MA, Qadir MS, Saleem S, Ahmad I, Rehman ZU, Aslam M, Hussain S. 2024. Identification of climate resilient genotypes on base of physio-morphic and yield related traits in maize (*Zea mays* L.). Biol Clin Sci Res J 2024 (1): 1267. DOI: 10.54112/bcsrj.v2024i1.1267.

Aji AP, Sugiharto AN. 2024. Yield trials on 10 lines of yellow corn (*Zea mays* L.) resulted top cross S_2 generation. Jurnal Produksi Tanaman 12: 150-159. DOI: 10.21776/ub.protan.2024.012.03.02. [Indonesian]

Azrai M, Aqil M, Efendi R, Andayani NN, Suwardi, Zainuddin B, Pabendon MB, Sitaresmi T, Anshori MF, Riadi M, Yasin M, Laurenze R, Bahtiar, Suwarti, Syam A. 2025. Integrating multi-trait and multi-index approaches for identifying drought tolerant tropical maize genotypes. Front Sustain Food Syst 9: 1608307. DOI: 10.3389/fsufs.2025.1608307.

Badu-Apraku B, Ifie BE, Talabi AO, Obeng-Bio E, Asiedu R. 2018. Genetic variances and heritabilities of traits of an early yellow maize population after cycles of improvement for *Striga* resistance and drought tolerance. Crop Sci 58 (6): 2261-2273. DOI: 10.2135/cropsci2017.10.0628.

BPS-Statistics of Indonesia. 2025. Maize harvest area, production, and productivity by province, 2024. https://www.bps.go.id/id/statistics-table/2/MjIwNCMy/luas-panen--produksi--dan-produktivitas-jagung-menurut-provinsi.html. Downloaded June 9, 2025. [Indonesian]

Cagnola JI, De Chassart GJD, Ibarra SE, Chimenti C, Ricardi MM, Delzer B, Ghiglione H, Zhu T, Otegui ME, Estevez JM, Casal JJ. 2018. Reduced expression of selected fasciclin-like arabinogalactan protein genes associates with the abortion of kernels in field crops of *Zea mays* (maize) and of *Arabidopsis* seeds. Plant Cell Environ 41 (3): 661-674. DOI: 10.1111/pce.13136.

Cai F, Zhang Y, Mi N, Ming H, Zhang S, Zhang H, Zhao X. 2020. Maize (*Zea mays* L.) physiological responses to drought and rewatering, and the associations with water stress degree. Agric Water Manag 241: 106379. DOI: 10.1016/j.agwat.2020.106379.

Chen X-M, Li F-Y, Dong S, Liu X-F, Li B-B, Xiao Z-D, Deng T, Wang Y-B, Shen S, Zhou S-L. 2022. Stubby or slender? Ear architecture is related to drought resistance in maize. Front Plant Sci 13: 901186. DOI: 10.3389/fpls.2022.901186.

Dawaki KD, Magashi AI, Daraja YB, Yawale MA, Garko MS, Fulani MS, Saad AM, Abdussalam SS. 2023. Genetic variability, heritability and genetic advance for yield and its related traits in maize (*Zea mays* L.) inbred lines as influenced by drought and heat stress conditions in Sudan Savannah of Nigeria. Eur Mod Stud J 7 (3): 467-474. DOI: 10.59573/emsj.7(3).2023.44.

De Sousa K, van Etten J, Poland J, Fadda C, Jannink J-L, Kidane YG, Lakew BF, Mengistu DK, Pè ME, Solberg SØ, Dell'Acqua M. 2021. Data-driven decentralized breeding increases prediction accuracy in a challenging crop production environment. Commun Biol 4 (1): 944. DOI: 10.1038/s42003-021-02463-w.

Deribe H. 2024. Review on effects of drought stress on maize growth, yield and its management strategies. Commun Soil Sci Plant Anal 56 (1): 123-143. DOI: 10.1080/00103624.2024.2404663.

Dolatabad SS, Choukan R, Hervan EM, Dehghani H. 2010. Multienvironment analysis of traits relation and hybrids comparison of maize based on the genotype by trait biplot. Am J Agric Biol Sci 5 (1): 107-113. DOI: 10.3844/ajabssp.2010.107.113.

Gazal A, Nehvi FA, Lone AA, Dar ZA. 2017. Assessment of genetic variability of a set of maize inbred lines for drought tolerance under temperate conditions. Intl J Curr Microbiol Appl Sci 6 (12): 2380-2389. DOI: 10.20546/ijcmas.2017.612.275.

Gelaw TA, Sanan-Mishra N. 2024. Molecular priming with H_2O_2 and proline triggers antioxidant enzyme signals in maize seedlings during drought stress. Biochim Biophys Acta Gen Subj 1868 (7): 130633. DOI: 10.1016/j.bbagen.2024.130633.

Guo J, Qu L, Hu Y, Lu W, Lu D. 2021. Proteomics reveals the effects of drought stress on the kernel development and starch formation of waxy maize. BMC Plant Biol 21 (1): 434. DOI: 10.1186/s12870-021-03214-z.

Johnson HW, Robinson HF, Comstock RE. 1955. Estimates of genetic and environmental variability in soybeans. Agron J 47 (7): 314-318. DOI: 10.2134/agronj1955.00021962004700070009x.

Kuswanto H, Puspa AW, Ahmad IS, Hibatullah F. 2021. Drought analysis in East Nusa Tenggara (Indonesia) using regional frequency analysis. Sci World J 2021: 6626102. DOI: 10.1155/2021/6626102.

Lal K, Kumar S, Singh L, Singh HC, Singh M, Kumar A. 2020. Genetic analysis of yield and its component traits in maize (*Zea mays* L.). Intl J Chem Stud 8: 2684-2687. DOI: 10.22271/chemi.2020.v8.i6al.11190.

Li Y, Tao H, Zhang B, Huang S, Wang P. 2018. Timing of water deficit limits maize kernel setting in association with changes in the source-flow-sink relationship. Front Plant Sci 9: 1326. DOI: 10.3389/fpls.2018.01326.

Li Y, Zhang P, Sheng W, Zhang Z, Rose RJ, Song Y. 2023. Securing maize reproductive success under drought stress by harnessing CO_2 fertilization for greater productivity. Front Plant Sci 14: 1221095. DOI: 10.3389/fpls.2023.1221095.

Limbongan Y, Sjahril R, Pata'dungan AM, Parari TY. 2024. Genetic performance, heritability, and correlation of traits in new plant type of rice lines for highland ecosystem. Reprod Breed 4 (4): 203-211. DOI: 10.1016/j.repbre.2024.08.002.

Liu B, Zhang B, Yang Z, Liu Y, Yang S, Shi Y, Jiang C, Qin F. 2021. Manipulating ZmEXPA4 expression ameliorates the drought-induced prolonged anthesis and silking interval in maize. Plant Cell 33 (6): 2058-2071. DOI: 10.1093/plcell/koab083.

López-Cortés XA, Matamala F, Maldonado C, Mora-Poblete F, Scapim CA. 2020. A deep learning approach to population structure inference in inbred lines of maize. Front Genet 11: 543459. DOI: 10.3389/fgene.2020.543459.

Magar BT, Acharya S, Gyawali B, Timilsena K, Upadhayaya J, Shrestha J. 2021. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. Heliyon 7 (9): e07939. DOI: 10.1016/j.heliyon.2021.e07939.

Meseka S, Menkir A, Bossey B, Mengesha W. 2018. Performance assessment of drought tolerant maize hybrids under combined drought and heat stress. Agronomy 8 (12): 274. DOI: 10.3390/agronomy8120274.

Musvosvi C, Setimela PS, Wali MC, Gasura E, Channappagoudar BB, Patil SS. 2018. Contribution of secondary traits for high grain yield and stability of tropical maize germplasm across drought stress and non-stress conditions. Agron J 110 (3): 819-832. DOI: 10.2134/agronj2017.04.0199.

Naisali H, Witoyo JE, Utoro PAR, Permatasari ND. 2023. Literature review of the physico-chemical characteristics of corn from East Nusa Tenggara, and its traditional derived products. Agrica: J Sustain Dryland Agric 16 (2): 151-163. DOI: 10.37478/agr.v16i2.3006. [Indonesian]

Ortez OA, McMechan AJ, Hoegemeyer T, Ciampitti IA, Nielsen R, Thomison PR, Elmore RW. 2022. Abnormal ear development in corn: A review. Agron J 114 (2): 1168-1183. DOI: 10.1002/agj2.20986.

Osborne J. 2002. Notes on the use of data transformations. Pract Assess Res Eval 8 (1): 6. DOI: 10.7275/4vng-5608.

Pico LBO, Vyn TJ. 2021. Dry matter gains in maize kernels are dependent on their nitrogen accumulation rates and duration during grain filling. Plants 10 (6): 1222. DOI: 10.3390/plants10061222.

Pongtip A, Thobunluepop P, Nakasathien S, Kongsil P, Sarobol E, Chitbanchong W, Pawelzik E. 2023. Growth and physiological responses of maize (*Zea mays* L.) under drought stress at different development stages. J Curr Sci Technol 14 (1): 15. DOI: 10.59796/jcst.v14n1.2024.15.

Putri SN, Sofro A. 2025. Prediction of air temperature in East Nusa Tenggara using extreme value theory. J Gaussian 14 (1): 149-156. DOI: 10.14710/j.gauss.14.1.149-156. [Indonesian]

Scott AJ, Knott M. 1974. A cluster analysis method for grouping means in the analysis of variance. Biometrics 30 (3): 507-512. DOI: 10.2307/2529204.

Sevanto S. 2014. Phloem transport and drought. J Exp Bot 65 (7): 1751-1759. DOI: 10.1093/jxb/ert467.

Shahzad A, Gul H, Ahsan M, Wang D, Fahad S. 2023. Comparative genetic evaluation of maize inbred lines at seedling and maturity stages under drought stress. J Plant Growth Regul 42 (2): 1-17. DOI: 10.1007/s00344-022-10608-2.

Singamsetti A, Shahi JP, Zaidi PH, Seetharam K. 2024. Study on applicability of Genotype × Yield × Trait (GYT) biplots over Genotype × Trait (GT) biplots in selection of maize hybrids across soil moisture regimes. Indian J Agric Res 58 (6): 1145-1151. DOI: 10.18805/ijare.a-5850.

Sivasubramanian V, Madhavamenon P. 1973. Path analysis for yield and yield components of rice. Madras Agric J 60: 1217-1221.

Song X, Zhou G, Zhang Z, Zhang H, Xue L, Wang H, Shi M, Lu H, Mao Y, Chen G, Huang X, Zheng H, Hao D. 2023. Genome-wide association study of ear tip barrenness in waxy maize. Breed Sci 73 (3): 261-268. DOI: 10.1270/jsbbs.22056.

Suriadi A, Mulyani A, Hadiawati L, Suratman. 2021. Biophysical characteristics of dry-climate upland and agriculture development challenges in West Nusa Tenggara and East Nusa Tenggara Provinces. IOP Conf Ser: Earth Environ Sci 648: 012014. DOI: 10.1088/1755-1315/648/1/012014.

Syahruddin K, Azrai M, Nur A, Abid M, Wu WZ. 2020. A review of maize production and breeding in Indonesia. IOP Conf Ser: Earth Environ Sci 484: 012040. DOI: 10.1088/1755-1315/484/1/012040.

Tareque AMMMU, Hassan L, Habib MA, Nayak S, Robin AHK. 2025. Estimation of genetic parameters in hybrid and F_2 generations of aromatic fine rice for breeding improvement. BMC Plant Biol 25 (1): 1080. DOI: 10.1186/s12870-025-07155-9.

Wang Z, Yu Y, Chen X, Li Y, Jones A, Rose RJ, Ruan Y-L, Song Y. 2025. Mitigating drought-associated reproductive failure in maize: From physiological mechanisms to practical solutions. Crop J 13 (4): 1022-1031. DOI: 10.1016/j.cj.2025.05.004.

Yan W, Frégeau-Reid J. 2018. Genotype by Yield*Trait (GYT) biplot: A novel approach for genotype selection based on multiple traits. Sci Rep 8 (1): 8242. DOI: 10.1038/s41598-018-26688-8.

Yang L, Fountain JC, Wang H, Ni X, Ji P, Lee RD, Kemerait RC, Scully BT, Guo B. 2015. Stress sensitivity is associated with differential accumulation of reactive oxygen and nitrogen species in maize genotypes with contrasting levels of drought tolerance. Intl J Mol Sci 16 (10): 24791-24819. DOI: 10.3390/ijms161024791.

Yao X-Y, Wei C-H, Yang L, Zhou Y-N, Chen Z-Y, Zhou S-L, Chen X-M, Shen S. 2024. Hindered translocation of sugars within maize ear reduces grain weight under drought stress. Environ Exp Bot 226: 105900. DOI: 10.1016/j.envexpbot.2024.105900.

Yue H, Chen S, Bu J, Wei J, Peng H, Li Y, Li C, Xie J. 2018. Response of main maize varieties to water stress and comprehensive evaluation in hebei province. IOP Conf Ser: Earth Environ Sci 108: 042002. DOI: 10.1088/1755-1315/108/4/042002.

Yue H, Olivoto T, Bu J, Li J, Wei J, Xie J, Chen S, Peng H, Nardino M, Jiang X. 2022. Multi-trait selection for mean performance and stability of maize hybrids in mega-environments delineated using envirotyping techniques. Front Plant Sci 13: 1030521. DOI: 10.3389/fpls.2022.1030521.

Zhang A, Wang H, Beyene Y, Semagn K, Liu Y, Cao S, Cui Z, Ruan Y, Burgueño J, Vicente FS, Olsen M, Prasanna BM, Crossa J, Yu H, Zhang X. 2017. Effect of trait heritability, training population size and marker density on genomic prediction accuracy estimation in 22 bi-parental tropical maize populations. Front Plant Sci 8: 1916. DOI: 10.3389/fpls.2017.01916.