

Caraka Tani: Journal of Sustainable Agriculture, 41(1), 17-31, 2026

URL: https://jurnal.uns.ac.id/carakatani/article/view/107896

DOI: http://dx.doi.org/10.20961/carakatani.v41i1.107896



Associations and Multi-Traits Selection for Identifying Superior and Stable Maize Hybrids (Zea mays L.) Under Tropical Regions

Dedy Supriadi¹, Yusuf Mufti Bimantara², Yuniel Melvanolo Zendrato³, Eko Widaryanto⁴, Kuswanto⁴ and Budi Waluyo^{4*}

¹Program Study of Agricultural Science, Graduate School, Brawijaya University, Malang, Indonesia; ²Plant Breeding and Biotechnology, Graduate School, IPB University, Bogor, Indonesia; ³Department of Agrotechnology, Faculty of Agriculture and Business, Satya Wacana Christian University, Salatiga, Indonesia; ⁴Department of Agronomy, Faculty of Agriculture, Brawijaya University, Malang, Indonesia

*Corresponding author: budiwaluyo@ub.ac.id

Abstract

The development of maize hybrids that combine desirable agronomic traits and grain yield could enhance the likelihood of adopting new superior cultivars. Breeding programs that use specific selection criteria aim to produce high-yielding and stable hybrids with good agronomic performance. The study aimed to determine the superior and stable tropical maize hybrids using simultaneous selection based on trait associations. Ten maize hybrids were evaluated across 10 different environments in tropical regions using a randomized complete block design with 3 replications. Genotype, environment, and genotype-by-environment interactions exhibited statistically significant effects on all observed traits, indicating the differential genetic responses among hybrids across environments. Grain yield is significantly associated with agronomic traits and yield components, thus rendering it a suitable selection criterion for identifying superior genotypes. The heritability of each trait was high, along with selection gains, indicating good prospects for selection. Identifying genotypes using multiple traits can be effective for selecting the best genotype based on the selection criteria under multiple environments. H07, H04, and H05 were identified as superior and stable hybrids based on the multi-trait genotype-ideotype distance index (MGIDI) and multi-trait stability index (MTSI), as well as the factor analytic best linear unbiased prediction (FAI-BLUP) and Smith-Hazel. These hybrids can be used in future breeding programs and as candidates for superior tropical maize hybrids.

Keywords: maize breeding; MGIDI; MTSI; selection criteria; simultaneous selection

Cite this as: Supriadi, D., Bimantara, Y. M., Zendrato, Y. M., Widaryanto, E., Kuswanto, & Waluyo, B. (2026). Associations and Multi-Traits Selection for Identifying Superior and Stable Maize Hybrids (*Zea mays* L.) Under Tropical Regions. *Caraka Tani: Journal of Sustainable Agriculture*, *41*(1), 17-31. doi: http://dx.doi.org/10.20961/carakatani.v41i1.107896

INTRODUCTION

Maize (*Zea mays* L.) is a major cereal in tropical regions and an important carbohydrate source in Indonesia, where its role as a strategic food reserve is continually expanding (Rozi et al., 2023). As an alternative food source, maize is expected to significantly contribute to future demand for cereals, including rice, wheat, sorghum, and other grains. Demand for maize is

increasing not only for human consumption but also for feed and industrial uses, creating a pressing need for genetic and agronomic innovations to enhance productivity (FAO, 2017; Grote et al., 2021; Albahri et al., 2023).

Productivity improvement is heavily dependent on the development of high-yielding, well-adapted, and stress-tolerant hybrids

^{*} Received for publication August 11, 2025 Accepted after corrections November 21, 2025

(Ruswandi et al., 2022; Konate et al., 2023). However, genotype \times environment (G \times E) interactions complicate the identification of superior genotypes, and yield alone does not always reflect desirable agronomic performance (Shojaei et al., 2022; Engida et al., 2024). An effective strategy for improving superior varieties is to develop an ideotype by considering preferences and selection criteria. Incorporating secondary traits aligned with stakeholder and producer needs can strengthen selection decisions and improve estimates of genotype performance and selection gain (Dermail et al., 2022; Singamsetti et al., 2023; Zendrato et al., 2024a).

The simultaneous analysis of multiple traits is a common practice in plant breeding, with tools such as genotype-by-trait (GT) biplots proving effective for visualizing trait associations and identifying superior genotypes (Yan and Rajcan, 2002), particularly concerning selection traits (Shojaei et al., 2020; Stansluos et al., 2023). However, the ideals of both morphological and physiological traits in selection ideotypes are frequently complex because of the quantitative inheritance of economically significant agronomic traits (Wicaksana et al., 2022). Classical selection indices such as Smith-Hazel (Smith, 1936; Hazel, 1943) are widely used; however, they are less suitable for multienvironment trials due to multicollinearity (Woyann et al., 2020; Olivoto and Nardino, 2021). Other methods, including the factor analytic best linear unbiased prediction (FAI-BLUP) (Rocha et al., 2018) and genotype × yield × trait (GYT) biplots (Yan and Frégeau-Reid, 2018), provide alternative frameworks but still lack the ability to integrate subjective weights and threshold values (Singamsetti et al., 2022).

The multi-trait genotype-ideotype distance index (MGIDI) addresses these limitations by integrating multiple traits into a single index and ranking genotypes based on their proximity to an ideotype. This method employs principal component analysis (PCA) to group traits, which effectively supports the visual interpretation of the strengths and weaknesses of each genotype (Olivoto and Nardino, 2021; Olivoto et al., 2022). Several genotype selection methods have been applied to crops such as barley, rice, maize, soybean, wheat, and other commodities, across various environmental conditions, both optimum and sub-optimum (Nardino et al., 2022; Habtegebriel and Abebe, 2023; Klein et al., 2023; Singamsetti et al., 2023; Debnath et al., 2024; Sholehah et al., 2024).

Understanding $G \times E$ is particularly critical in multi-environment trials (MET), where stability statistics-such as regression analyses and parametric or non-parametric indices-are commonly used to evaluate yield stability (Shojaei et al., 2021; Liu et al., 2022; Uberti et al., 2023; Daemo et al., 2024; Supriadi et al., 2024). However, yield-stable genotypes may still lack desirable agronomic attributes that farmers and breeders need. The multi-trait stability index (MTSI) enables simultaneous selection for stability and multi-trait performance (Olivoto et al., 2019), improving genetic gain relative to traditional methods (Zuffo et al., 2020; Benakanahalli et al., 2021; Aruna et al., 2024; Subramani et al., 2024). The above selection indices have been applied; however, few studies have simultaneously compared MGIDI, MTSI, FAI-BLUP, and Smith-Hazel within tropical maize breeding contexts. Therefore, this study aimed to identify superior and stable tropical maize hybrids using multi-trait and multienvironment selection indices to guide future maize breeding under tropical conditions.

MATERIALS AND METHOD

Genetic materials

Ten maize hybrids were used in this study, consisting of 8 test hybrids and 2 hybrids as a check. The test hybrids were developed by Restu Agropro Jayamas (RAJA) Ltd. from single maize crosses and served as candidates for new superior varieties, namely R0211 (H01), R0J020 (H02), R0654 (H03), R0105 (H04), R0118 (H05), R0498 (H06), R0641 (H07), and R0J016 (H08). The 2 checks were commercial hybrid varieties released in Indonesia, namely RSA002 (H09) from RAJA Ltd. and NK7328 or NK SUMO (H10) from Syngenta Indonesia.

Experimental sites and management

The field trials were conducted between February and October 2023 across 10 maizegrowing locations in Indonesia: Wonosari-Klaten and Teras-Boyolali in Central Java: Banguntapan-Bantul, Yogyakarta; Jenu-Tuban, Ngronggot-Nganjuk, Wonodadi-Blitar, Plosoklaten–Kediri, Bandar Kedungmulyo-Jombang, and Tumpang-Malang in East Java; and South Galesong-Takalar in South Sulawesi. The trial utilized an experimental station owned by RAJA Ltd. and was conducted under official permission for multi-location testing. Each field trial has different agro-ecology and agro-climate. The soil types encountered included Grumosols,

Ultisols, Alluvial, Andosols, and Inceptisols. The altitude of the field trials ranged from 55 to 658 m above sea level (m asl), while the average annual rainfall ranged from 1,275 to 2,030 mm in tropical regions. The specific conditions of each field trial are outlined in Table 1.

The field experimental design at each site was laid out using a randomized complete block design (RCBD) with 3 replications. The planting distance was 70 cm between rows and 30 cm within a row. Each experiment site consisted of plots with a harvested size of 4 rows by 5 m (14 m²) per hybrid. Border rows were used for each replication and field to minimize edge effects. Fertilization was conducted twice using NPK (400 kg ha⁻¹) and urea (350 kg ha⁻¹), at 10 days after planting (DAP) and 30 to 35 DAP. Additional farming practices, including weed removal, mound formation, water management, and pest and disease control, were implemented in accordance with the technical guidelines provided by the Indonesian Ministry of Agriculture. Harvesting was undertaken when the plants had reached physiological maturity, characterized by the appearance of a black layer at the base of the kernels.

Phenotypical data collection

Ten agronomic traits, including yield and yield components, were observed at both the vegetative and generative stages for phenotypic data collection. After the maximum vegetative stage, plant height (cm) was measured from the distance of ground level to the node containing the flag leaf. The anthesis-silking interval was

calculated as the difference between days to silking and days to anthesis. The plant aspect was observed when the genotype was still green and scored on a scale of 1 (good) to 5 (poor). The yield component traits included ear aspect, scored on a scale of 1 (good) to 5 (poor); husk cover, scored on a scale of 1 (good) to 5 (poor); ear diameter (mm); number of ear rows; number of kernels per row; weight of 1,000 kernels; shelling percentage (%); and grain yield (ton ha⁻¹), calculated using the Equation 1.

Statistical analysis

The statistical analyses of all observed traits included a combined analysis of variance (ANOVA) and employed the F-test to examine the effects of environment, genotype, and genotype-by-environment interactions. Trait associations were analyzed to determine the relationship between observed characters using the Pearson correlation and GT biplot method. Pearson correlation analysis was employed to examine and investigate the relationship between agronomic traits, yield, and yield components. The GT biplot approach used Equation 2 (Yan and Rajcan, 2002).

The simultaneous selection was used for identifying the most superior maize hybrids under all locations using MGIDI as developed by Olivoto and Nardino (2021). The selection traits used all the observed traits, including agronomic, yield, and yield components traits, with grain yield being weighted as 2, while the other traits were weighted as 1. Grain yield was assigned double weight because it is the primary economic

Table 1. Description of 10 environments used for maize hybrid evaluation under tropical regions in Indonesia

Env.	Landing	Coil true	Altitude	Rainfall	Temperature (°C)		
code	Location	Soil type	(m asl)	(mm)	Minimum	Maximum	
KLN	Wonosari, Klaten, Central	Grumosols	217	1,279	22.58	31.67	
	Java						
BTL	Banguntapan, Bantul,	Grumosols	80	1,275	22.41	31.17	
	Yogyakarta						
TBN	Jenu, Tuban, East Java	Grumosols	116	1,731	22.24	31.37	
BYL	Teras, Boyolali, Central Java	Ultisols	106	1,832	19.97	29.42	
NGJ	Ngronggot, Nganjuk, East	Alluvial	55	1,828	20.20	29.65	
	Java						
BTR	Wonodadi, Blitar, East Java	Alluvial	97	1,742	19.62	30.14	
KDR	Plosoklaten, Kediri, East Java	Andosols	70	1,330	22.16	32.81	
JBG	Bandar Kedungmulyo,	Alluvial	148	1,390	23.48	31.23	
	Jombang, East Java						
MLG	Tumpang, Malang, East Java	Inceptisols	658	1,697	21.70	31.56	
TKR	South Galesong, Takalar,	Alluvial	56	2,030	19.17	29.51	
	South Sulawesi						

and breeding target in maize improvement, directly determining hybrid adoption and productivity. All datasets were checked for missing or inconsistent values to enhance reproducibility. These preprocessing steps ensured that all genotypes were evaluated using complete and harmonized trait information. MGIDI was estimated based on the calculation steps and two-way best linear unbiased predictions (BLUPs) for each hybrid (row) and trait (column), followed by Equation 3.

The genotypes with the lowest MGIDI values were closer to the ideotype and exhibited the desired values for all studied traits. The strengths and weaknesses of each genotype were assessed based on the proportion of the MGIDI values of the *i*th genotype explained by the *j*th factor (ω_{ij}) calculated using Equation 4.

The maize hybrids were selected with an intensity of selection of approximately 40%, and the selection differential within the population mean (ΔS %) for each trait was calculated using Equation 5.

For the comparison, the FAI-BLUP index, the multi-trait index based on factor analysis and ideotype design recently proposed by Rocha et al. (2018), and the Smith-Hazel index (Smith, 1936; Hazel, 1943) were used to select the ideal hybrids and compared to selected hybrids, estimated by using the same selection traits and criteria as MGIDI.

The stable maize hybrids were identified using MTSI, which is rooted in factor analysis. The MTSI employs the weighted average of absolute scores (WAASB) index for rescaled values, whereas the MGIDI is predicated on BLUP values. The WAASB index integrates both stability—as evaluated by the WAASB index—and the mean performance of traits. The WAASB is derived from the singular value decomposition of the BLUP matrix for genotype-by-environment interaction (GEI) effects. Genotypes with lower WAASB scores were considered more stable. MTSI was estimated using Equation 6.

All analyses (ANOVA, GT biplot, MGIDI, FAI-BLUP, Smith-Hazel index, and MSTI) were

Yield (ton ha⁻¹) =
$$\frac{10,000}{\text{Plot size}} \times \frac{100\text{-MC}}{100\text{-}15} \times \frac{\text{EW}}{1,000} \times \text{SP}$$
 (1)

Where, plot size in m², MC is the actual kernel moisture content during harvesting (%), EW is the ear weight per plot (kg), SP is the shelling percentage (%), and yield is the grain yield.

$$\frac{\alpha_{ij} - \beta_{j}}{\sigma_{i}} = \sum_{n=1}^{2} \lambda_{n} \xi_{in} \eta_{jn} + \varepsilon_{ij} = \sum_{n=1}^{2} \xi_{in}^{*} \eta_{jn}^{*} + \varepsilon_{ij}$$
 (2)

Where, α_{ij} is the average amount of genotype i for every trait j; β_j is the average amount of all the genotypes for the traits; σ_j is the standard deviation of traits j in the average genotypes; ε_{ij} is the amount of genotype i that remained in the traits j; λ_n is a certain amount for the main element (PC_n); ξ_{in} is the amount of PC_n for genotype i; and η_{in} is the amount of PC_n for the genotype j.

$$MGIDI_{i} = \left[\sum_{i=1}^{f} (\gamma_{ij} - \gamma_{j})^{2}\right]^{0.5}$$
(3)

Where, MGIDI_i is the multi-trait genotype-ideotype distance index for the *i*th genotype; γ_{ij} is the score of the *i*th genotype for the *j*th factor (i = 1, 2, ..., g; j = 1, 2, ..., f), and γ_j is the score of the ideotype.

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^f \sqrt{D_{ij}^2}} \tag{4}$$

Where, D_{ij} is the distance between the *i*th genotype and the ideotype for the *j*th factor. The smallest contribution to a factor indicated that the corresponding trait was close to the ideotype.

$$\Delta S\% = \frac{(X_s - X_0)}{X_0} \times 100 \tag{5}$$

Where, X_s is the mean value of the selected genotype's performance and X_0 is the mean value of the population used.

$$MTSI_{i} = \left[\sum_{i=1}^{f} (F_{ij} - F_{j})^{2}\right]^{0.5}$$
 (6)

Where, MTSI_i is the multi-trait stability index for the *i*th genotype; F_{ij} is the score of the *i*th genotype for the *j*th factor (i = 1, 2, ..., g; j = 1, 2, ..., f), and F_i is the score of the ideotype.

performed using RStudio (R version 4.5.1) using "metan" package (Olivoto and Lúcio, 2020).

RESULTS AND DISCUSSION

Combined analysis and hybrid performance

The combined analysis in this experiment showed that the mean square for the environment (E) and genotype (G) had a significant effect on all observed traits, including agronomic and yield components. At the probability level of 0.01 (Table 2), indicating that differences between the environment and genotype used influenced the performance of maize hybrids. The effect of GEI also showed a significant difference in terms of grain yield and hybrid performance. Because environmental conditions affect genotype performance, a hybrid that exhibits superior yields in one environment may not necessarily maintain that advantage in other environments.

Significant variability performance of hybrids was observed for yield and agronomic traits in this study, indicating the existence of different genetic responses of hybrids for observed traits across all environments. In general, the performance of cereal crops, including maize, in tropical regions was influenced by multiple vagaries of abiotic effects, i.e., agro-ecologies, agro-climates, and high moisture conditions (Supriadi et al., 2024). GEI in plant breeding is a phenomenon of unstable genotype performance under different environmental conditions (Falcon et al., 2019). The coefficient of variation value ranged from 1.40 for the shelling percentage to 30.86 for the anthesis-silking interval.

In combined environments, the grain yield varies from 10.95 tons ha⁻¹ for H08 to 13.19 tons ha⁻¹ for H01 (Table 3). Based on this analysis, some test hybrids performed better than the

Table 2. Mean square for agronomic traits, yield, and yield components of 10 hybrids across different environments

E(E)	D1': 4':/E	C(C)	C. F	E	CV
Environment (E)	Replication/E	Genotype (G)			CV
9	20	9	81	180	(%)
8311.07**	85.45 ^{ns}	482.26**	99.67**	60.95	3.35
1.19**	$0.09^{\rm ns}$	15.94**	0.89**	0.25	30.86
5.72**	0.71**	0.80**	0.41**	0.15	25.56
0.77**	$0.05^{\rm ns}$	2.09**	0.27**	0.10	24.40
4.31**	$0.04^{\rm ns}$	31.73**	0.38**	0.05	8.08
94.34**	$0.70^{\rm ns}$	79.73**	2.10**	1.34	2.29
9.43**	0.28^{ns}	25.86**	0.81**	0.43	4.20
262.97**	4.60**	74.56**	3.82**	1.66	3.50
25.28**	$1.05^{\rm ns}$	104.44**	4.15**	1.26	1.40
17.91**	2.17**	15.92**	1.79**	0.50	5.81
	8311.07** 1.19** 5.72** 0.77** 4.31** 94.34** 9.43** 262.97**	9 20 8311.07** 85.45 ^{ns} 1.19** 0.09 ^{ns} 5.72** 0.71** 0.77** 0.05 ^{ns} 4.31** 0.04 ^{ns} 94.34** 0.70 ^{ns} 9.43** 0.28 ^{ns} 262.97** 4.60** 25.28** 1.05 ^{ns}	9 20 9 8311.07** 85.45 ^{ns} 482.26** 1.19** 0.09 ^{ns} 15.94** 5.72** 0.71** 0.80** 0.77** 0.05 ^{ns} 2.09** 4.31** 0.04 ^{ns} 31.73** 94.34** 0.70 ^{ns} 79.73** 9.43** 0.28 ^{ns} 25.86** 262.97** 4.60** 74.56** 25.28** 1.05 ^{ns} 104.44**	9 20 9 81 8311.07** 85.45 ^{ns} 482.26** 99.67** 1.19** 0.09 ^{ns} 15.94** 0.89** 5.72** 0.71** 0.80** 0.41** 0.77** 0.05 ^{ns} 2.09** 0.27** 4.31** 0.04 ^{ns} 31.73** 0.38** 94.34** 0.70 ^{ns} 79.73** 2.10** 9.43** 0.28 ^{ns} 25.86** 0.81** 262.97** 4.60** 74.56** 3.82** 25.28** 1.05 ^{ns} 104.44** 4.15**	9 20 9 81 180 8311.07** 85.45ns 482.26** 99.67** 60.95 1.19** 0.09ns 15.94** 0.89** 0.25 5.72** 0.71** 0.80** 0.41** 0.15 0.77** 0.05ns 2.09** 0.27** 0.10 4.31** 0.04ns 31.73** 0.38** 0.05 94.34** 0.70ns 79.73** 2.10** 1.34 9.43** 0.28ns 25.86** 0.81** 0.43 262.97** 4.60** 74.56** 3.82** 1.66 25.28** 1.05ns 104.44** 4.15** 1.26

Note: df = Degree of freedom; ** = Significant at p-value 0.01; ns = Not significant; CV = Coefficient of variation

Table 3. The mean performance of traits in 10 hybrids in the troplear region										
Hybrid	PH	ASI	PA	EA	HC	ED	ER	KR	SP	Y
H01	242.58	0.40	1.23	1.03	1.02	48.94	15.52	37.03	77.49	13.19
H02	233.06	1.17	1.45	1.00	2.85	51.18	16.70	38.69	82.22	12.51
H03	235.92	2.50	1.62	1.28	2.85	52.42	16.15	37.89	80.07	12.68
H04	228.95	0.97	1.30	1.15	2.65	50.43	15.77	38.09	78.56	12.48
H05	230.94	1.13	1.55	1.03	2.88	50.97	16.93	36.15	80.96	12.53
H06	230.48	1.87	1.63	1.35	2.92	51.52	15.27	35.51	80.78	11.40
H07	234.01	1.27	1.30	1.08	1.05	52.27	16.36	36.08	82.90	12.49
H08	233.22	2.20	1.63	1.57	4.65	51.17	15.69	39.37	79.20	10.95
H09	232.21	2.10	1.68	1.77	2.85	47.16	14.75	35.11	81.38	11.70
H10	229.04	2.57	1.53	1.50	2.87	49.33	13.83	34.83	77.61	11.30
Mean	233.04	1.62	1.49	1.28	2.66	50.54	15.70	36.88	80.12	12.12
SE	1.06	0.06	0.04	0.03	0.06	0.15	0.07	0.20	0.14	0.08
LSD	3.98	0.25	0.19	0.16	0.11	0.59	0.34	0.66	0.57	0.36

Table 3. The mean performance of traits in 10 hybrids in the tropical region

Note: PH = Plant height; ASI = Anthesis-silking interval; PA = Plant aspect; EA = Ear aspect; HC = Husk cover; ED = Ear diameter; ER = Number of ear rows; KR = Number of kernels per row; SP = Shelling percentage; Y = Grain yield; SE = Standard error; LSD = Least significant difference

checks (H01, H02, H04, H05, H07) in terms of anthesis-silking interval, plant and ear aspects, husk cover, yield, and yield components. These results indicate that some of the tested hybrids showed promising results as superior hybrid candidates. However, determining the superior hybrids across multiple locations poses complex challenges, particularly when considering the desired and emphasized traits (Singamsetti et al., 2021).

Trait associations and correlation analysis

A multi-trait selection approach in hybrid development requires breeders to prioritize traits that not only correlate with grain yield but also contribute to improved plant architecture, stress resilience, and harvestability. This is essential because many secondary traits are genetically interrelated and may generate multicollinearity (Dermail et al., 2022; Ambrósio et al., 2024). As shown in Figure 1a, grain yield exhibited significant correlations (p < 0.001) with all agronomic and yield components, indicating that improvements in these traits can indirectly enhance yield potential. The husk cover, ear and plant aspects, as well as the anthesis-silking interval had a negative correlation with grain yield, suggesting a lower direction for simultaneous selection using these traits. These traits are strong indicators of stress tolerance and reproductive efficiency. For example, a shorter anthesis-silking interval reflects better synchrony between anthesis and silking, which is crucial for maintaining kernel set under drought or heat stress. Therefore, selecting for lower values of these traits will

enhance both yield potential and stability across environments.

The strong positive association between the number of kernels per row and plant height suggests that more vigorous vegetative growth may support a larger reproductive sink. Likewise, correlations among ear diameter and kernel row traits emphasize the importance of ear architecture as a driver of yield formation. These relationships confirm findings from previous studies (Aman et al., 2020; Shrestha et al., 2023; Zendrato et al., 2024b) and reinforce the relevance of yield components as reliable selection indicators in maize breeding programs.

Evaluating genetic phenotypic and correlations is essential for guiding selection, as positive correlations indicate that increasing a trait will enhance grain yield, while negative correlations indicate that yield improves when the trait is reduced (Azrai et al., 2023; Korsa et al., 2024). Thus, traits such as anthesis-silking interval, plant/ear aspect, and husk cover-traits associated with stress susceptibility-are expected to have low values in selected genotypes to ensure synchronized flowering and robust plant and ear development (Zendrato et al., 2024a). Meanwhile, moderate plant height is preferred to reduce lodging risk and improve harvestability (Dermail et al., 2022).

The GT biplot (Figure 1b) further illustrates relationships, providing these a visual interpretation of how hybrids interact with key traits. The first two principal components captured 67.83% of the total variability, indicating good representativeness. Hybrids positioned closer to specific trait vectors-such as H01 for grain yield and plant height, or H02 to H05 for yield components-demonstrate superior performance for those traits. In contrast, hybrids like H06 and H08 aligned with anthesis-silking plant interval. aspect. and husk highlighting their relative weakness for yield but potential utility in stress-expression studies. Although GT biplots are informative for exploring trait associations and identifying broadly or specifically adapted genotypes, they are not sufficient as a stand-alone basis for recommending cultivars because they do not quantify selection accuracy or stability across environments (Kendal, 2019).

Simultaneous selection for identifying superior hybrids

All traits were used in the MGIDI-based simultaneous selection (Table 4), with plant height, anthesis-silking interval, plant and ear aspects, and husk cover targeted for reduction, as well as yield components targeted for improvement. The high heritability values for nearly all traits (0.49 to 0.99) indicate that genetic effects dominate over environmental noise, suggesting strong potential for effective genetic gains. Notably, the largest negative gains for anthesis-silking interval, ear aspect, and husk cover (-27.00%, -12.40%, and -11.00%), reflect improvements in reproductive synchrony, canopy structure, and ear protection—traits strongly linked to stress tolerance and yield stability. Conversely,

increased numbers of ear rows and higher grain yield (4.44% and 2.47%) confirm progress toward enhanced sink capacity and yield potential.

Figure 2a presents the rankings of hybrids by MGIDI values, using a 40% selection intensity, denoted by a red circle. H07, H02, H05, and H04 were selected hybrids based on the ideotype of selection traits across all the environments, indicating that these hybrids had significant performance. These hybrids combined favorable values for key yield components with improved agronomic traits, implying strong adaptability across the tested environments. Although the environment can limit the expression of high trait scores, the multiple-trait framework allows breeders to distinguish whether a hybrid's performance advantage derives from architecture. reproductive efficiency, or yield components. In this case, understanding the strengths and weaknesses of each genotype enables the easy identification of hybrids based on the multipletrait framework (Olivoto et al., 2022; Azrai et al., 2023).

The strengths and weaknesses of hybrids were categorized through factor analysis (Figure 2b). There were 3 factor analyses: FA1, including plant height, anthesis-silking interval, plant and ear aspects, husk cover, and grain yield; FA2, associated with ear diameter, the number of ear rows, and shelling percentage; and FA3, representing the number of kernels per row. H01 performed well, indicating that this hybrid

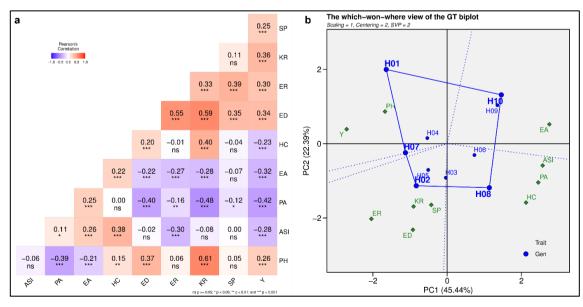


Figure 1. (a) Correlation among observed traits; (b) The which-won-where view of the GT biplot Note: PH = Plant height; ASI = Anthesis-silking interval; PA = Plant aspect; EA = Ear aspect; HC = Husk cover; ED = Ear diameter; ER = Number of ear rows; KR = Number of kernels per row; SP = Shelling percentage; Y = Grain yield

Tuble 4: Selection gains for the selection dates using the WODF									
Trait	Factor	Sense	X_{o}	X_{s}	SD	SD (%)	h^2	SG	SG (%)
PH	FA1	Decrease	233.00	232.00	-1.03	-0.44	0.79	-0.82	-0.35
ASI	FA1	Decrease	1.63	1.16	-0.47	-28.70	0.94	-0.44	-27.00
PA	FA1	Decrease	1.49	1.45	-0.05	-3.03	0.49	-0.02	-1.47
EA	FA1	Decrease	1.28	1.09	-0.18	-14.30	0.87	-0.16	-12.40
HC	FA1	Decrease	2.66	2.36	-0.30	-11.20	0.99	-0.29	-11.00
Y	FA1	Increase	12.10	12.50	0.34	2.79	0.89	0.30	2.47
ED	FA2	Increase	50.50	51.20	0.66	1.30	0.97	0.64	1.26
ER	FA2	Increase	15.70	16.40	0.72	4.58	0.97	0.70	4.44
SP	FA2	Increase	80.10	81.10	1.00	1.25	0.96	0.96	1.20
KR	FA3	Increase	36 90	37.20	0.36	0.97	0.95	0.34	0.92

Table 4. Selection gains for the selection traits using the MGIDI

Note: $PH = Plant height; ASI = Anthesis-silking interval; PA = Plant aspect; EA = Ear aspect; HC = Husk cover; ED = Ear diameter; ER = Number of ear rows; KR = Number of kernels per row; SP = Shelling percentage; Y = Grain yield; FA = Factor analysis; <math>X_o$ = Mean of original population; X_s = Mean od the selected hybrids; SD = Selection differential; h^2 = Heritability; SG = Selection gain

was associated with the traits in this factor analysis; however, this hybrid had a weakness in FA2. FA2 and FA3 demonstrated strong performance in most of the hybrids, indicating that the hybrids had the desired traits based on this factor analysis. The selected hybrids demonstrated strong performance in FA2 and FA3, indicating that improvements in ear morphology and kernel set were major contributors to their superiority. These insights help breeders target specific parents—e.g., hybrids strong in FA2 for enhancing ear architecture or those strong in FA1 for improving the anthesis-silking interval and plant type. Researchers

employed the multiple trait combination index as an analytical tool to evaluate hybrid performance, enabling the identification of genotypes that closely approximate the ideotype (Debnath et al., 2024).

This study presents the selected hybrids using the FAI-BLUP method (Figure 3a) and the Smith-Hazel index (Figure 3b), both of which utilize the same adapted ideotype as MGIDI. H02, H05, H03, and H04 were the selected hybrids based on the FAI-BLUP, while the Smith-Hazel index selected H03, H02, H07, and H01 as the superior hybrids using the simultaneous selection. Comparisons with FAI-BLUP and Smith-Hazel

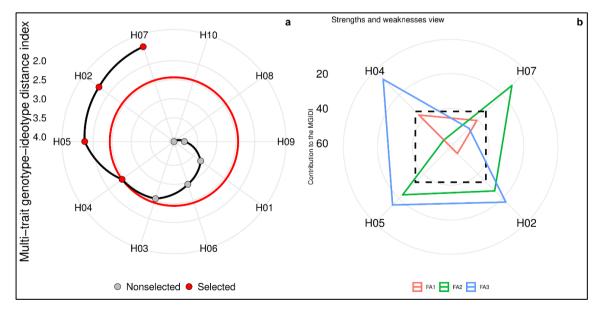


Figure 2. (a) The ranking of hybrids in ascending order based on MGIDI; (b) The strengths and weaknesses view of all hybrids based on MGIDI

Note: FA = Factor analysis; FA1 = Plant height, anthesis-silking interval, plant aspect, ear aspect, husk cover, grain yield; FA2 = Ear diameter, number of ear rows, shelling percentage; FA3 = Number of kernels per row

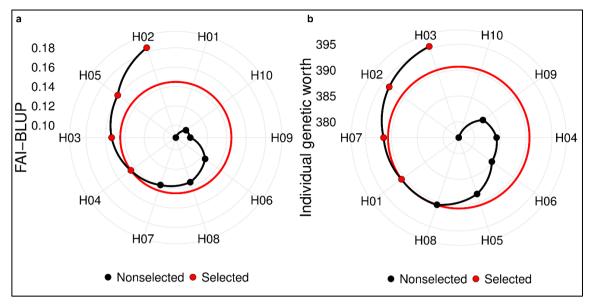


Figure 3. The hybrid ranking based on simultaneous selection using: (a) FAI-BLUP; (b) Smith-Hazel Index

showed overlap but also differences in selected hybrids, reflecting each method's sensitivity to trait weighting and correlation structure. MGIDI highlighted hybrids with more balanced performance across trait groups, which is valuable for developing widely adapted hybrids rather than those excelling in one trait at the expense of others.

Olivoto et al. (2022) stated that MGIDI has many advantages over other selection methods, such as PCA and linear indices, including good graphic interpretation, free and open software implementation, powerful data computing, solutions to collinearity issues, easy genotype ranking, strength mapping, identification of trait weaknesses in each genotype, and character weighting in ranking genotypes. Overall, this method is recommended for analyzing multi-character plant data and developing genotype selection strategies, as it facilitates the visualization of good genotype selection and positively divergent selection of characters that correlate with the selected genotype, which is useful for future breeding methods (Debnath et al., 2024).

The stable hybrids based on the MTSI method

The highly varied environmental conditions in tropical regions significantly affect the growth and yield of maize (Zendrato et al., 2025), which presents the GEI phenomenon with a complex challenge in selecting the best genotypes. Traditionally, stable genotypes focused on a single trait, namely grain yield, which is the primary desired trait, using several stability

statistical methods (Gela et al., 2023; Supriadi et al., 2024). However, these univariate approaches fail to capture genotype stability across multiple traits, as they concentrate solely on grain yield, potentially resulting in suboptimal selections (Olivoto et al., 2019). Genotype stability testing using selection traits serves as a model for identifying desirable genotypes for farmers and breeders. In comparison to other stability statistics, the MTSI addresses this need by selecting genotypes that combine high mean performance with multi-trait stability (Olivoto et al., 2021). Hybrids exhibiting performance closer to the ideal, as determined by their position in the factor analysis results, received higher MTSI scores (Benakanahalli et al., 2021).

Table 5 shows that factor analysis grouped traits into 4 biologically meaningful clusters, enabling clearer interpretation of stability patterns: FA1 included anthesis-silking interval and ear diameter; FA2 included plant aspect, husk cover, shelling percentage, and grain yield; FA3 included ear aspect; and FA4 included plant height, number of ear rows, and number of kernels per row. Hybrids H07, H04, H05, and H08 showed the most desirable stability profiles (Figure 4a). H07 and H04 excelled in FA2 and FA4, indicating consistent performance in traits related to ear development (number of ear rows and number of kernels per row) and plant structure (plant height) while maintaining high shelling percentage. H08 showed stability across FA2 to FA4, suggesting robust ear architecture and kernel traits, while H05 displayed balanced

Table 5. Defection gains for the selection traits using the WITSI									
Trait	Factor	Sense	X_{o}	X_{s}	SD	SD (%)	h^2	SG	SG (%)
ASI	FA1	Decrease	1.62	1.39	-0.23	-13.90	0.94	-0.21	-13.10
ED	FA1	Increase	50.50	51.20	0.67	1.33	0.97	0.65	1.29
PA	FA2	Decrease	1.49	1.45	-0.05	-3.18	0.49	-0.02	-1.54
HC	FA2	Decrease	2.66	2.81	0.15	5.64	0.99	0.15	5.58
SP	FA2	Increase	80.10	80.40	0.29	0.36	0.96	0.27	0.34
Y	FA2	Increase	12.10	12.10	0.01	0.08	0.89	0.01	0.07
EA	FA3	Decrease	1.28	1.21	-0.07	-5.35	0.87	-0.06	-4.65
PH	FA4	Decrease	233.00	232.00	-1.26	-0.54	0.79	-1.00	-0.43
ER	FA4	Increase	15.70	16.20	0.49	3.13	0.97	0.48	3.04
KR	FA4	Increase	36 90	37 40	0.55	1 49	0.95	0.52	1 41

Table 5. Selection gains for the selection traits using the MTSI

Note: $PH = Plant height; ASI = Anthesis-silking interval; PA = Plant aspect; EA = Ear aspect; HC = Husk cover; ED = Ear diameter; ER = Number of ear rows; KR = Number of kernels per row; SP = Shelling percentage; Y = Grain yield; FA = Factor analysis; <math>X_o$ = Mean of original population; X_s = Mean od the selected hybrids; SD = Selection differential; h^2 = Heritability; SG = Selection gain

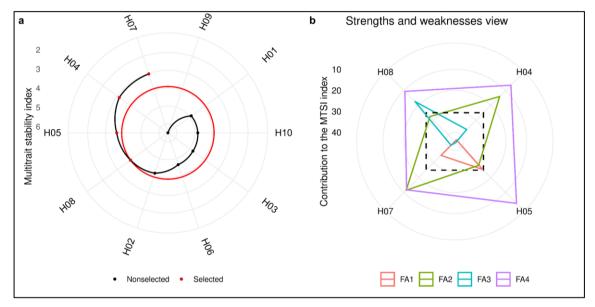


Figure 4. (a) The ranking of hybrids in ascending order based on MTSI; (b) The strengths and weaknesses view of all hybrids based on MTSI

Note: FA = Factor analysis; FA1 = Anthesis-silking interval, ear diameter; FA2 = Plant aspect, husk cover, shelling percentage, grain yield; FA3 = Ear aspect; FA4 = Plant height, number of ear rows, number of kernels per row

stability, including traits related to reproductive timing (FA1). These results highlight that the stable hybrids performed well not only in grain yield but also in trait groups essential for resilience—such as anthesis-silking interval, husk cover, and ear morphology—making them strong candidates for regions with fluctuating climatic stresses.

From a breeding perspective, these hybrids represent valuable parental candidates for advancing both productivity and environmental adaptability. By prioritizing genotypes with favorable MTSI scores, researchers can more effectively select candidates for breeding programs that aim to enhance agricultural productivity and sustainability. The MTSI method has also been widely cited as an ideal method for genotype selection in several commodities, including sugar beet (Taleghani et al., 2023), green gram (Aruna et al., 2024), barley (Pour-Aboughadareh et al., 2025), and several other agricultural commodities.

A Venn diagram (Figure 5) illustrates the consistency of hybrid selection across 4 multi-trait methods. Differences in overlap primarily reflect each method's emphasis—performance, ideotype proximity, or stability—yet several hybrids emerged as consistently superior. Hybrids H02

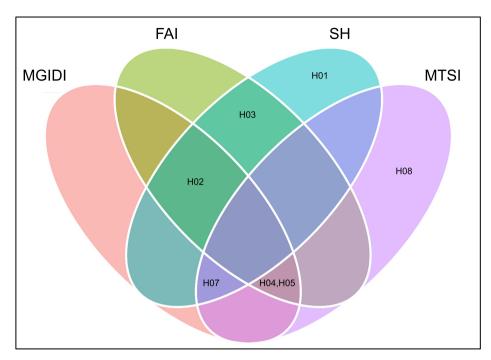


Figure 5. The comparison of the superior and stable hybrids selected from simultaneous selection in the Venn chart

and H03 were selected using 2 methods, indicating good performance for specific trait groups; however, their exclusion by MTSI suggests sensitivity to environmental variation. H08, selected solely by MTSI, showed strong stability across environments but did not meet all performance-based criteria. These differences highlight biological trade-offs often encountered in multi-trait selection—some genotypes excel in stress resilience, while others express high yield potential but with lower stability.

H04, H05, and H07 were selected by at least 3 methods and represent the strongest candidates for broad adaptation. Their consistent selection suggests that these hybrids combine high grain vield with favorable agronomic traits such as shorter anthesis-silking interval, improved ear architecture, and better husk characteristics, all of which are essential for performance under tropical conditions. Crucially, H04, H05, and H07 outperformed the commercial checks in both yield and multi-trait stability. These hybrids produced 8.5 to 9.0% higher grain yield, while also expressing substantially improved stabilityrelated traits compared to checks (Table 3). Their anthesis-silking interval values were 42 to 54% lower than the checks, indicating superior reproductive synchrony and greater tolerance to environmental stress. Notably, H07 also exhibited a 63% improvement in husk cover, suggesting enhanced protection against pests and ear rot.

Overall, integrating multi-trait and stability-based selection allows breeders to identify hybrids with real-world advantages—higher yield, stronger stress tolerance, and more predictable performance—beyond what can be captured through yield-focused selection alone. The selected hybrids, especially H07, H04, and H05, represent promising candidates for release in tropical production zones and thus provide a strong foundation for further maize breeding efforts in tropical environments.

CONCLUSIONS

Genotype, environment, and GEI significantly (p < 0.01) affected all agronomic traits, yield, and yield components evaluated. Grain yield had significantly correlated with other traits, indicating a strong association. High heritability (≥ 0.50) and substantial selection gains (-27%) for anthesis-silking interval; +4.4% for ear row number) confirm a strong potential for genetic improvement. Across 10 tropical environments, hybrids H07, H04, and H05 consistently outperformed commercial checks by 8.5 to 9.0% in grain yield (12.48 to 12.53 tons ha⁻¹). These hybrids also showed markedly improved multitrait stability, including lower anthesis-silking interval and superior ear and plant attributes. These hybrids are therefore recommended for further multi-location validation and potential varietal release in tropical regions.

ACKNOWLEDGEMENT

The authors thank the research and development team of Restu Agropro Jayamas Ltd. for funding and providing plant material, as well as the technicians' stations for helping with the experiments.

REFERENCES

- Albahri, G., Alyamani, A. A., Badran, A., Hijazi, A., Nasser, M., Maresca, M., & Baydoun, E. (2023). Enhancing essential grains yield for sustainable food security and bio-safe agriculture through latest innovative approaches. *Agronomy*, *13*(7), 1709. https://doi.org/10.3390/agronomy13071709
- Aman, J., Bantte, K., Alamerew, S., & Sbhatu, D. B. (2020). Correlation and path coefficient analysis of yield and yield components of quality protein maize (*Zea mays* L.) hybrids at Jimma, western Ethiopia. *International Journal of Agronomy*, 2020(1), 9651537. https://doi.org/10.1155/2020/9651537
- Ambrósio, M., Daher, R. F., Santos, R. M., Santana, J. G. S., Vidal, A. K. F., Nascimento, M. R., ... & Dos Santos, P. R. (2024). Multitrait index: Selection and recommendation of superior black bean genotypes as new improved varieties. *BMC Plant Biology*, 24(1), 525. https://doi.org/10.1186/s12870-024-05248-5
- Aruna, K., Kumar, B. M. D., Sridhara, S., Sowjanya, B. A., Kumar, K. L. N., Moussa, I. M., ... & Olivoto, T. (2024). Multi-trait stability index for identification of stable green gram (*Vigna radiata* (L.) Wilczek) genotypes with MYMV resistance. *Heliyon*, *10*(12), e32763. https://doi.org/10.1016/j.heliyon. 2024.e32763
- Azrai, M., Aqil, M., Efendi, R., Andayani, N. N., Makkulawu, A. T., Iriany, R. N., ... & Suwarno, W. B. (2023). A comparative study on single and multiple trait selections of equatorial grown maize hybrids. *Frontiers in Sustainable Food Systems*, 7, 1185102. https://doi.org/10.3389/fsufs.2023.1185102
- Benakanahalli, N. K., Sridhara, S., Ramesh, N., Olivoto, T., Sreekantappa, G., Tamam, N., ... & Abdelmohsen, S. A. (2021). A framework for identification of stable genotypes basedon MTSI and MGDII indexes: An example in guar (*Cymopsis tetragonoloba* L.). *Agronomy*,

- 11(6), 1221. https://doi.org/10.3390/agronomy 11061221
- Daemo, B. B., Wolancho, G. B., Arke, Z. A., Wakalto, D. D., & Onu, M. H. (2024). Performance evaluation and stability of maize (*Zea mays* L.) genotypes for grain yield using AMMI and GGE biplot. *International Journal of Agronomy*, 2024(1), 8801999. https://doi.org/10.1155/2024/8801999
- Debnath, P., Chakma, K., Bhuiyan, M. S. U., Thapa, R., Pan, R., & Akhter, D. (2024). A novel multi trait genotype ideotype distance index (MGIDI) for genotype selection in plant breeding: Application, prospects, and limitations. *Crop Design*, *3*(4), 100074. https://doi.org/10.1016/j.cropd.2024. 100074
- Dermail, A., Fuengtee, A., Lertrat, K., Suwarno, W. B., Lübberstedt, T., & Suriharn, K. (2022). Simultaneous selection of sweet-waxy corn ideotypes appealing to hybrid seed producers, growers, and consumers in Thailand. *Agronomy*, *12*(1), 87. https://doi.org/10.3390/agronomy12010087
- Engida, B. T., Tarekegne, A., Wegary, D., Van Biljon, A., & Labuschagne, M. T. (2024). Genotype × environment interaction and grain yield stability of quality protein maize hybrids under stress and non-stress environments. *Cogent Food & Agriculture*, *10*(1), 2324537. https://doi.org/10.1080/23311932.2024.2324537
- Falcon, C. M., Kaeppler, S. M., Spalding, E. P., Miller, N. D., Haase, N., AlKhalifah, N., ... & de Leon, N. (2019). Relative utility of agronomic, phenological, and morphological traits for assessing genotype-by-environment interaction in maize inbreds. *Crop Science*, 60(1), 62–81. https://doi.org/10.1002/csc 2.20035
- FAO. (2017). The future of food and agriculture Trends and challenges. Rome: Food and Agriculture Organization of the United Nations. Retrieved from https://open knowledge.fao.org/server/api/core/bitstreams/2e90c833-8e84-46f2-a675-ea2d7afa4e24/content
- Gela, T. S., Khazaei, H., Podder, R., & Vandenberg, A. (2023). Dissection of genotype-by-environment interaction and simultaneous selection for grain yield and

- stability in faba bean (*Vicia faba* L.). *Agronomy Journal*, 115(2), 474–488. https://doi.org/10.1002/agj2.21268
- Grote, U., Fasse, A., Nguyen, T. T., & Erenstein, O. (2021). Food security and the dynamics of wheat and maize value chains in Africa and Asia. *Frontiers in Sustainable Food Systems*, 4, 617009. https://doi.org/10.3389/fsufs. 2020.617009
- Habtegebriel, M. H., & Abebe, A. T. (2023). Grain yield stability of soybean (*Glycine max* (L.) Merrill) for different stability models across diverse environments of Ethiopia. *Agrosystems, Geosciences & Environment*, 6(3), e20396. https://doi.org/10.1002/agg2. 20396
- Hazel, L. N. (1943). The genetic basis for constructing selection indexes. *Genetics*, 28(6), 476–490. https://doi.org/10.1093/genetics/28.6.476
- Kendal, E. (2019). Comparing durum wheat cultivars by genotype× yield× trait and genotype× trait biplot method. *Chilean Journal of Agricultural Research*, 79(4), 512–522. http://dx.doi.org/10.4067/S0718-583920 19000400512
- Klein, L. A., Marchioro, V. S., Toebe, M., Olivoto, T., Meira, D., Meier, C., ... & Finatto, J. L. B. (2023). Selection of superior black oat lines using the MGIDI index. *Crop Breeding and Applied Biotechnology*, 23(3), e45112332. https://doi.org/10.1590/1984-70332023v23 n3a25
- Konate, L., Badu-Apraku, B., Coulibaly, M., Menkir, A., Laouali, M. N., Meseka, S., & Mengesha, W. (2023). Agronomic performance and yield stability of extra-early maturing maize hybrids in multiple environments in the Sahel. *Heliyon*, *9*(11), e21659. https://doi.org/10.1016/j.heliyon. 2023.e21659
- Korsa, F., Dessalegn, O., Zeleke, H., & Petros, Y. (2024). Genetic variability for the yield and yield-related traits in some maize (*Zea mays* L.) inbred lines in the central highland of Ethiopia. *International Journal of Agronomy*, 2024(1), 9721304. https://doi.org/10.1155/2024/9721304
- Liu, C., Ma, C., Lü, J., & Ye, Z. (2022). Yield stability analysis in maize hybrids of Southwest China under genotype by

- environment interaction using GGE biplot. *Agronomy*, *12*(5), 1189. https://doi.org/10.3390/agronomy12051189
- Nardino, M., Perin, E. C., Aranha, B. C., Carpes, S. T., Fontoura, B. H., de Sousa, D. J. P., & Freitas, D. S. D. (2022). Understanding drought response mechanisms in wheat and multi-trait selection. *PLoS ONE*, *17*(4), e0266368. https://doi.org/10.1371/journal.pone.0266368
- Olivoto, T., & Lúcio, A. D. (2020). Metan: An R package for multi-environment trial analysis. *Methods in Ecology and Evolution*, 11(6), 783–789. https://doi.org/10.1111/2041-210x. 13384
- Olivoto, T., & Nardino, M. (2021). MGIDI: Toward an effective multivariate selection in biological experiments. *Bioinformatics*, *37*(10), 1383–1389. https://doi.org/10.1093/bioinformatics/btaa981
- Olivoto, T., Diel, M. I., Schmidt, D., & Lúcio, A. D. (2022). MGIDI: A powerful tool to analyze plant multivariate data. *Plant Methods*, *18*(1), 121. https://doi.org/10.1186/s13007-022-00952-5
- Olivoto, T., Lúcio, A. D., da Silva, J. A., Marchioro, V. S., de Souza, V. Q., & Jost, E. (2019). Mean performance and stability in multi-environment trials I: Combining features of AMMI and BLUP techniques. *Agronomy Journal*, *111*(6), 2949–2960. https://doi.org/10.2134/agronj2019.03.0220
- Olivoto, T., Nardino, M., Meira, D., Meier, C., Follmann, D. N., de Souza, V. Q., ... & Baretta, D. (2021). Multi-trait selection for mean performance and stability in maize. *Agronomy Journal*, *113*(5), 3968–3974. https://doi.org/10.1002/agj2.20741
- Pour-Aboughadareh, A., Jamshidi, B., Jadidi, O., Bocianowski, J., & Niemann, J. (2025). Multitrait stability index in the selection of high-yielding and stable barley genotypes. *Journal of Applied Genetics*, 1–7. https://doi.org/10.1007/s13353-025-00998-w
- Rocha, J. R. D. A. S. D. C., Machado, J. C., & Carneiro, P. C. S. (2018). Multitrait index based on factor analysis and ideotype-design: Proposal and application on elephant grass breeding for bioenergy. *GCB Bioenergy*, *10*(1), 52–60. https://doi.org/10.1111/gcbb. 12443

- Rozi, F., Santoso, A. B., Mahendri, I. G. A. P., Hutapea, R. T. P., Wamaer, D., Siagian, V., ... & Syam, A. (2023). Indonesian market demand patterns for food commodity sources of carbohydrates in facing the global food crisis. *Heliyon*, *9*(6), e16809. https://doi.org/10.1016/j.heliyon.2023.e16809
- Ruswandi, D., Syafii, M., Wicaksana, N., Maulana, H., Ariyanti, M., Indriani, N. P., ... & Yuwariah, Y. (2022). Evaluation of high yielding maize hybrids based on combined stability analysis, sustainability index, and GGE biplot. *BioMed Research International*, 2022(1), 3963850. https://doi.org/10.1155/2022/3963850
- Shojaei, S. H., Mostafavi, K., Khosroshahli, M., Reza Bihamta, M., & Ramshini, H. (2020). Assessment of genotype-trait interaction in maize (*Zea mays* L.) hybrids using GGT biplot analysis. *Food Science & Nutrition*, 8(10), 5340–5351. https://doi.org/10.1002/fsn3.1826
- Shojaei, S. H., Mostafavi, K., Omrani, A., Illés, Á., Bojtor, C., Omrani, S., ... & Nagy, J. (2022). Comparison of maize genotypes using drought-tolerance indices and graphical analysis under normal and humidity stress conditions. *Plants*, *11*(7), 942. https://doi.org/10.3390/plants11070942
- Shojaei, S. H., Mostafavi, K., Omrani, A., Omrani, S., Nasir Mousavi, S. M., Illés, Á., ... & Nagy, J. (2021). Yield stability analysis of maize (*Zea mays* L.) hybrids using parametric and AMMI methods. *Scientifica*, 2021(1), 5576691. https://doi.org/10.1155/2021/5576691
- Sholehah, M. R., Suwarno, W. B., Hapsari, V. P., Sulistyo, N. N., Marwiyah, S., & Aswidinnoor, H. (2024). Rice breeding for multi-canopy system: Estimations of genetic parameters and response to selection. *Agronomy Journal*, *116*(5), 2129–2140. https://doi.org/10.1002/agj2.21629
- Shrestha, S., Niraula, D., Regmi, S., Basnet, S., Chhetri, S. T., & Kandel, B. P. (2023). Performance evaluation and genetic parameters estimation of multi-companies maize hybrids in Lamahi Dang, Nepal. *Heliyon*, 9(3), e14552. https://doi.org/10.1016/j.heliyon.2023.e14552
- Singamsetti, A., Shahi, J. P., Zaidi, P. H., & Seetharam, K. (2022). Study on applicability

- of genotype x yield x trait (GYT) biplots over genotype x trait (GT) biplots in selection of maize hybrids across soil moisture regimes. *Indian Journal of Agricultural Research*, 58(6), 1145–1151. https://doi.org/10.18805/IJARE.A-5850
- Singamsetti, A., Shahi, J. P., Zaidi, P. H., Seetharam, K., Vinayan, M. T., Kumar, M., ... & Madankar, K. (2021). Genotype× environment interaction and selection of maize (*Zea mays* L.) hybrids across moisture regimes. *Field Crops Research*, 270, 108224. https://doi.org/10.1016/j.fcr.2021.108224
- Singamsetti, A., Zaidi, P. H., Seetharam, K., Vinayan, M. T., Olivoto, T., Mahato, A., ... & Shikha, K. (2023). Genetic gains in tropical maize hybrids across moisture regimes with multi-trait-based index selection. *Frontiers in Plant Science*, 14, 1147424. https://doi.org/10.3389/fpls.2023.1147424
- Smith, H. A. (1936). A discriminant function for plant selection. *Annals of Eugenics*, 7(3), 240–250. https://doi.org/10.1111/j.1469-1809. 1936.tb02143.x
- Stansluos, A. A. L., Öztürk, A., Niedbała, G., Türkoğlu, A., Haliloğlu, K., Szulc, P., ... & Piekutowska, M. (2023). Genotype–trait (GT) biplot analysis for yield and quality stability in some sweet corn (*Zea mays* L. Saccharata sturt.) genotypes. *Agronomy*, *13*(6), 1538. https://doi.org/10.3390/agronomy13061538
- Subramani, P., Nalliappan, G. K., Narayana, M., Veerasamy, R., & Natesan, S. (2024). Selection of superior and stable fodder maize hybrids using MGIDI and MTSI indices. *Crop Breeding and Applied Biotechnology*, 24(4), e498624418. https://doi.org/10.1590/1984-70332024v24n4a55
- Supriadi, D., Bimantara, Y. M., Zendrato, Y. M., Widaryanto, E., Kuswanto, K., & Waluyo, B. (2024). Assessment of genotype by environment and yield performance of tropical maize hybrids using stability statistics and graphical biplots. *PeerJ*, *12*, e18624. https://doi.org/10.7717/peerj.18624
- Taleghani, D., Rajabi, A., Saremirad, A., & Fasahat, P. (2023). Stability analysis and selection of sugar beet (*Beta vulgaris* L.) genotypes using AMMI, BLUP, GGE biplot and MTSI. *Scientific Reports*, *13*(1), 10019. https://doi.org/10.1038/s41598-023-37217-7

- Uberti, A., Rezende, W. M., Caixeta, D. G., Reis, H. M., Resende, N. C. V., Destro, V., & DeLima, R. O. (2023). Assessment of yield performance and stability of hybrids and populations of tropical maize across multiple environments in Southeastern Brazil. *Crop Science*, 63(4), 2012–2032. https://doi.org/10.1002/csc2.20964
- Wicaksana, N., Maulana, H., Yuwariah, Y., Ismail, A., Ruswandi, Y. A. R., & Ruswandi, D. (2022). Selection of high yield and stable maize hybrids in mega-environments of Java Island, Indonesia. *Agronomy*, *12*(12), 2923. https://doi.org/10.3390/agronomy12122923
- Woyann, L. G., Meira, D., Matei, G., Zdziarski, A. D., Dallacorte, L. V., Madella, L. A., & Benin, G. (2020). Selection indexes based on linear-bilinear models applied to soybean breeding. *Agronomy Journal*, *112*(1), 175–182. https://doi.org/10.1002/agj2.20044
- Yan, W., & Frégeau-Reid, J. (2018). Genotype by yield* trait (GYT) biplot: A novel approach for genotype selection based on multiple traits. *Scientific Reports*, 8(1), 8242. https://doi.org/10.1038/s41598-018-26688-8
- Yan, W., & Rajcan, I. (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Science*, 42(1), 11–20. https://doi.org/10.2135/cropsci2002.1100

- Zendrato, Y. M., Azizah, Y. A., Humam, B. K., Marwiyah, S., Ritonga, A. W., Azrai, M., ... & Suwarno, W. B. (2025). Maize hybrids' response to optimum and suboptimum abiotic environmental conditions using genotype by environment interaction analysis. *Sabrao Journal of Breeding and Genetics*, *57*(2), 447–458. http://doi.org/10.54910/sabrao2025.57. 2.5
- Zendrato, Y. M., Suwarno, W. B., & Marwiyah, S. (2024a). Multi-trait selection of tropical maize genotypes under optimum and acidic soil conditions. *Sabrao Journal of Breeding and Genetics*, 56(1), 142–155. http://doi.org/10.54910/sabrao2024.56.1.13
- Zendrato, Y. M., Suwarno, W. B., & Marwiyah, S. (2024b). Simultaneous selection of several tropical maize hybrids under acidic soil conditions. *IOP Conference Series: Earth and Environmental Science*, 1377(1), 012096. http://doi.org/10.1088/1755-1315/1377/1/012096
- Zuffo, A. M., Steiner, F., Aguilera, J. G., Teodoro,
 P. E., Teodoro, L. P. R., & Busch, A. (2020).
 Multi-trait stability index: A tool for simultaneous selection of soya bean genotypes in drought and saline stress. *Journal of Agronomy and Crop Science*, 206(6), 815–822. https://doi.org/10.1111/jac.12409