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Abstract

The methods utilized to analyze genotype-by-environment interaction (GEI) and assess the yield stability of crop varieties are constantly evolving, favoring integrated multi-method analytical frameworks. In this study, an integrated BLUP-AMMI-WAASB-MTSI framework was deployed to evaluate kernel yield (KY) stability and multi-trait performance in maize. Ten genotypes (nine elite experimental hybrids and one commercial check, CHK) were evaluated in a randomized complete block design across 18 environments (nine locations over two cropping seasons). Combined analysis of variance revealed significant effects for location, genotype, and spatio-temporal interactions (LG and YLG) on KY. AMMI analysis decomposed the multiplicative interaction into four significant interaction principal components (IPCs), explaining 81.70% of the total GEI variation. Under the mixed-model (REML/BLUP) framework, high genotypic mean heritability (0.69) and selective accuracy (0.83) were achieved. According to the WAASB quadrant biplot and WAASBY superiority index (50:50 yield: stability weighting), hybrids H2, H3, and H1 combined top-tier predicted BLUP yields (13.35, 12.95, and 12.80 t ha^{-1}) with broad environmental stability, outperforming the check cultivar (CHK: 12.65 t ha^{-1}). For multi-trait selection across 10 traits, exploratory factor analysis (FA) partitioned the traits into four dimensions. Based on the multi-trait stability index (MTSI) at a 30% selection intensity, hybrids H2, H6, and H3 were selected as ideal ideotypes, achieving positive genetic gains for KY (+3.91%) and grain-filling duration (+2.20%), alongside desirable reductions in plant height (-1.55%) and ear height (-0.47%) for lodging resistance. Overall, hybrids H2 and H3 were identified as consensus elite germplasm for commercial deployment.

Keywords: Best linear unbiased prediction, Genotype × environment interaction, Multi-trait stability index.

1| Introduction

Ensuring global food security under the constraints of demographic growth, climate change, and resource degradation represents one of the most pressing scientific challenges of the twenty-first century (Cassman, 2012; Ehrlich and Harte, 2015; Shirzad *et al*., 2025). The global human population, currently exceeding eight billion, is projected to reach nearly ten billion by 2050, driving an estimated 60% to 70% increase in global agricultural demand (Foley, 2013; Ma *et al*., 2024; UN, 2024). Meeting this heightened demand is severely complicated by the acceleration of climate variability, extreme weather events, declining soil fertility, and water scarcity (Tardieu, 2013; Ureta *et al*., 2020; Chen *et al*., 2024). Consequently, narrowing the yield gap—the disparity between potential yield achieved under non-limiting experimental conditions and actual yield obtained in farmers' fields—has become a central imperative for crop scientists (Jaggard *et al*., 2012; Agus *et al*., 2019). Yield gap losses, which frequently exceed 30% to 40% across diverse cropping regions, are largely driven by the instability of high-yielding crop cultivars when exposed to fluctuating environmental conditions (Fischer *et al*., 2014; Taleghani *et al*., 2023). Among major agricultural staples, maize (*Zea mays* L.) occupies a paramount position in global food security, serving as a vital source of calories and protein for billions of people, a primary feedstock for livestock industries, and a major industrial raw material (Shiferaw *et al*., 2011; Haarhoff and Swanepoel, 2018; Zhang *et al*., 2021). Given its physiological efficiency as a C_4 cereal, enhancing maize productivity through genetic improvement and multi-environment evaluation is essential for sustaining global food supplies (Duvick, 2005; Swarup *et al*., 2021).

Grain yield in maize is a complex, polygenically inherited quantitative trait governed by numerous genes interacting with environmental factors (Boote *et al*., 2001; Singamsetti *et al*., 2021). When elite genotypes are evaluated across contrasting locations and seasons, their relative performance often changes, a phenomenon known as GEI (Becker and Léon, 1988; Annicchiarico, 2002; de Leon *et al*., 2016). Phenotypic variation observed in multi-environment trials (METs) is a function of main genotypic effects, main environmental effects, and multiplicative GEI effects (Gauch, 1992; Bocianowski *et al*., 2024). A pronounced GEI complicates the selection of superior cultivars by masking genetic potential, reducing the correlation between phenotype and genotype, and impeding selection progress in plant breeding programs (Falconer and Mackay, 1996; Ebdon and Gauch, 2002). GEI can manifest as non-crossover interactions, where differences in yield magnitude occur without rank changes, or as crossover interactions, where relative genotypic ranks shift across environments (Baker, 1988; Signor *et al*., 2001). While crossover GEI presents a major hurdle for introducing widely adapted cultivars, it offers valuable opportunities to identify genotypes tailored to specific agro-climatic niches (Atlin *et al*., 2017; Engida *et al*., 2024). Therefore, conducting rigorous METs across representative geographic locations over multiple cropping years is indispensable for evaluating genotypic yield potential, environmental sensitivity, and phenotypic stability (Crossa, 1990; Yan and Kang, 2002; Smith *et al*., 2005).

Historically, the analysis of MET data relied heavily on fixed-effects linear models and univariate analysis of variance (Aastveit and Martens, 1986; Vlachostergios and Roupakias, 2008). However, classical analysis of variance assumes error variance homogeneity and treats environmental effects as fixed, which limits its statistical power when dealing with heterogeneous environmental variances, missing data, or complex covariance structures typical of multi-location field trials (Bartlett, 1937; Piepho *et al*., 2008). To address these constraints, linear mixed-effects models (LMMs) utilizing restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP) have gained widespread adoption in plant breeding (Henderson, 1953; Piepho, 1994; Bernardo, 2002). By treating genotypic effects or GEI as random variables, BLUP minimizes mean

squared error, accounts for spatial heterogeneity, and shrinks unreliable estimates toward the grand mean (Robinson, 1991; Smith *et al*., 2005). Consequently, BLUP yields highly accurate predictions of true genetic merit and provides a robust framework for multi-environment genetic evaluation (Resende and Duarte, 2007; Olivoto *et al*., 2019a).

Complementing mixed-model approaches, multivariate statistical techniques have been developed to dissect the multiplicative components of GEI (Gauch and Zobel, 1988; Crossa, 1990). The additive main effects and multiplicative interaction (AMMI) model combine standard analysis of variance for additive main effects with principal component analysis (PCA) for multiplicative interaction terms (Zobel *et al*., 1988; Gauch, 2013). AMMI effectively partitions interaction variance into IPCAs, offering high diagnostic precision for visual interpretation and stability quantification (Purchase *et al*., 2000; Sabaghnia *et al*., 2008). Despite its utility, conventional AMMI methods frequently truncate the analysis after the first one or two IPCAs, discarding higher-order interaction axes that may retain statistically significant and biologically meaningful interaction variation (Rodrigues *et al*., 2014; Zhang *et al*., 2026). To overcome this limitation, Olivoto *et al*. (2019a) integrated the advantages of mixed models and AMMI by introducing the weighted average of absolute scores from BLUPs (WAASB) index. The WAASB index utilizes singular value decomposition of the BLUP-derived GEI matrix and incorporates all IPCA axes, thereby capturing the complete interaction variance (Olivoto *et al*., 2019a). Recognizing that breeders must balance yield potential with environmental consistency, the WAASBY index was subsequently formulated to allow flexible weighting between productivity (Y) and stability (WAASB), enabling simultaneous selection for high performance and stability (Olivoto *et al*., 2019a; Nataraj *et al*., 2021; Taleghani *et al*., 2023).

Although grain yield remains the primary focus of crop improvement programs, selecting genotypes based solely on yield is often inefficient and can lead to undesirable shifts in correlated agronomic traits (Yan and Frégeau-Reid, 2018; Falcon *et al*., 2019). Maize yield is fundamentally determined by a network of phenological, morphological, and yield-component traits (Alvarez *et al*., 2014; Hosseini *et al*., 2025). Traditional multi-trait selection methods, such as the Smith-Hazel index or desirable index techniques, face severe practical constraints due to multicollinearity among traits and the subjective difficulty of assigning accurate economic weights (Smith, 1936; Rocha *et al*., 2018). To circumvent these challenges, the MTSI was developed based on factor analysis and BLUP theory (Olivoto *et al*., 2019b). The MTSI removes multicollinearity by grouping traits into uncorrelated factors, calculates the Euclidean distance between each genotype and an ideotype possessing optimal BLUP values for all evaluated traits, and provides positive or negative selection differentials tailored to trait-specific breeding objectives (Olivoto *et al*., 2019b; Zuffo *et al*., 2020; Koundinya *et al*., 2021; Shirzad *et al*., 2025).

Despite the theoretical strengths of combining REML/BLUP, AMMI, WAASB/WAASBY, and MTSI approaches, empirical applications integrating these advanced analytical frameworks across multi-environment trials in maize remain limited (Yue *et al*., 2022; Shirzad *et al*., 2025; Zhang *et al*., 2026). In regions with highly heterogeneous climate regimes, maize cultivation spans diverse agro-ecological zones characterized by substantial variations in temperature, soil properties, thermal unit accumulation, and water availability (Akbari *et al*., 2018; Mostafavi and Saremirad, 2021). Evaluating elite maize hybrids across contrasting environmental conditions provides a robust platform to dissect complex GEI structures and trait associations. Therefore, the objectives of this study were to: (i) analyze grain yield performance and GEI patterns in a set of maize hybrids using an integrated AMMI, BLUP, and WAASB/WAASBY framework to evaluate yield stability and identify high-yielding, stable genotypes; and (ii) employ the MTSI incorporating phenological,

morphological, and yield-component traits to perform multi-trait selection and identify superior hybrids matching an ideal agronomic ideotype for target production environments.

2| Materials and methods

2.1| Plant materials

Ten maize genotypes, comprising nine elite experimental hybrids (designated as H1 through H9) and one widely grown commercial check cultivar (KSC704; designated as CHK), were evaluated in this study (Table 1). These experimental hybrids were developed at the Seed and Plant Improvement Institute (SPII), Karaj, Alborz, Iran, through targeted pedigree breeding programs aimed at optimizing physiological maturity (developing earlier-maturing germplasm) while enhancing grain yield potential, yield stability, and agronomic performance. The genetic pedigrees and code designations of the tested genotypes are summarized in Table 1.

Table 1. Code numbers, pedigrees, and descriptions of the maize genotypes evaluated in the study

2.2| Research sites and experimental design

Field trials were conducted across two consecutive cropping seasons (2024 and 2025) at nine agricultural research stations belonging to the Agricultural Research, Education and Extension Organization (AREEO), Iran. The experimental sites included Karaj (KRJ), Kermanshah (KSH), Kerman (KER), Moghan (MGN), Mashhad (MHD), Miandoab (MDB), Dezful (DZF), Jiroft (JRF), and Mazandaran (MZN). These nine locations represent highly contrasting agro-climatic zones, ranging from warm arid/semi-arid regions to temperate and humid coastal plains, providing a total of 18 distinct testing environments (9 locations × 2 years). Detailed geographical and climatic characteristics of the experimental sites are presented in Table 2.

At each testing location, the trial was established using a randomized complete block design (RCBD) with three replications. Each experimental plot consisted of four planting rows, 3.25 m in length, with an inter-row spacing of 0.75 m and an intra-row plant distance of 0.19 m, resulting in a target plant density of approximately 70,000 plants ha^{-1}. Depending on regional thermal regimes, sowing was performed between early May and mid-June, with harvesting occurring between September and November. Fertilizer applications were guided by soil analysis results for each location; baseline applications comprised 150 kg N ha^{-1} (split into three applications: pre-planting, V6 stage, and pre-tasseling), 80 kg P_2O_5 ha^{-1}, and 60 kg K_2O ha^{-1}. Weed control was achieved through a pre-emergence application of S-metolachlor combined with selective hand weeding during early vegetative stages. Plots were routinely scouted for insect pests, particularly the European corn borer (*Ostrinia nubilalis*), and control measures were applied according to integrated pest management (IPM) thresholds.

Table 2. Description of the environments with their respective latitudes, longitudes, altitudes (m), soil group, mean temperature, rainfall, and climate condition in regard to the maize trial

2.3| Phenotypic measurements and data collection

To avoid border effects, all phenotypic observations were performed on the two central rows of each experimental plot. Phenological parameters were monitored on a plot-wide basis throughout the cropping season. Days to silking (DTS) was determined as the number of days elapsed from sowing until 50% of the plants within a plot exhibited visible silk emergence. Similarly, days to maturity (DTM) was recorded when 50% of the plants reached physiological maturity, identified by black layer formation at the basal membrane of the kernels. The silking-maturity interval (SMI),

which reflects the effective duration of the grain-filling phase, was calculated as the difference between DTM and DTS. Plant architectural traits were measured at physiological maturity from 10 randomly selected plants per plot. Plant height (PH) was measured in centimeters from the soil surface to the base of the main tassel, while ear height (EH) was recorded as the distance from the soil surface to the primary ear-bearing node.

Yield components and harvest attributes were evaluated upon physiological maturity to dissect the structural determinants of grain yield. Ear morphological traits, including kernel row number (KRN) and kernels per row (KPR), were counted on ten representative ears harvested from each plot. To determine thousand-kernel weight (KW), a random sample of 1,000 sound kernels was drawn from the bulked grain harvest of each plot and weighed in grams using a precision digital balance. Grain moisture content at harvest (KM) was measured immediately after shelling using a calibrated portable electronic grain moisture meter. Finally, total kernel yield (KY) was determined by harvesting all ears from the two central rows of each plot. The harvested ears were shelled, weighed, and converted to grain yield in metric t ha^{-1}, with final yield values adjusted to a standardized grain moisture content of 14%.

2.4| Statistical analysis

Prior to combined analysis, the homogeneity of residual error variances across all 18 experimental environments (9 locations × 2 crop seasons) was evaluated using Bartlett's test (Bartlett, 1937). Once homogeneity of error variances was confirmed, a combined LMM was fitted to the multi-environment data using REML to estimate variance components and BLUPs for each evaluated trait (Henderson, 1953; Smith *et al*., 2005; Piepho *et al*., 2008). The statistical model for the multi-environment evaluation is expressed as equation 1:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{k(j)} + \varepsilon_{ijk} \quad (1)$$

where Y_{ijk} is the observed phenotypic value of the i^{th} genotype in the j^{th} environment and k^{th} block; μ is the overall grand mean; G_i is the main effect of the i^{th} genotype; E_j is the main effect of the j^{th} environment; GE_{ij} is the interaction effect between the i^{th} genotype and j^{th} environment; $B_{k(j)}$ is the effect of the k^{th} block nested within the j^{th} environment; and ε_{ijk} is the random residual error term assumed to be independently and identically distributed with zero mean and variance σ_ε^2. In the mixed model framework, genotypic effects (G_i) and interaction effects (GE_{ij}) were treated as random effects to derive BLUP estimates ($\hat{g}_i$), whereas environmental and block effects were considered fixed factors (Piepho *et al*., 2008). The significance of random variance components was evaluated using the LRT with a chi-square distribution (Piepho, 1994).

To dissect the main and multiplicative interaction effects for KY, the AMMI model was fitted according to the equation 2 (Gauch and Zobel, 1988; Gauch 1992):

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{k=1}^{n} \lambda_k \gamma_{gk} \delta_{ek} + \rho_{ge} \quad (2)$$

where Y_{ge} is the grain yield of genotype *g* in environment *e*; μ is the grand mean; α_g is the genotype deviation from the grand mean; β_e is the environment deviation; λ_k is the singular value for the k^{th} *IPCA*; γ_{gk} is the eigenvector value for genotype *g* and component *k*; δ_{en} is the eigenvector scores for environment *e* and component *k*, with both eigenvectors scaled as unit vectors; and ρ_{ge} is the residual.

To combine the precision of mixed-model BLUP estimates with the exploratory power of singular value decomposition interaction components, the WAASB index was computed for each genotype across all retained IPCA axes as proposed by Olivoto *et al*. (2019a) based on equation 3:

$$WAASB_{i} = \frac{\sum_{k=1}^{P} |IPCA_{ik} \times EP_{k}|}{\sum_{k=1}^{P} EP_{k}} \quad (3)$$

where $WAASB_i$ is the weighted average of absolute scores of the i^{th} genotype; $IPCA_{ik}$ is the absolute eigenvector score of the i^{th} genotype in the k^{th} interaction principal component axis derived from the singular value decomposition of the BLUP-derived GEI matrix; and EP_k is the proportion of GEI variance explained by the k^{th} IPCA (Olivoto *et al*., 2019a). Lower WAASB values designate genotypes with high stability across environments.

To facilitate simultaneous selection for both high (KY) and yield stability (WAASB), the superior performance-stability index (WAASBY) was calculated according to the following weighting equation 4 (Olivoto *et al*., 2019a):

$$WAASBY_{i} = \frac{(rY_i \times \theta_Y) + (rW_i \times \theta_S)}{\theta_Y + \theta_S} \quad (4)$$

Where $WAASBY_i$ is the superiority index score for the i^{th} genotype; rY_i and rW_i are the rescaled values (ranging from 0 to 100) for grain yield performance (KY) and stability ($WAASB_i$), respectively; and θ_Y and θ_S represent the relative weights assigned to grain yield performance and stability, respectively. In this study, equal weights ($\theta_Y = 50$ and $\theta_S = 50$) were assigned to balance productivity and environmental stability (Olivoto *et al*., 2019a).

To enable simultaneous selection across all ten evaluated agronomic, phenological, morphological, and yield-component traits (KY, KRN, KPR, KW, KM, PH, EH, DTS, SMI, and DTM), the MTSI was calculated based on factor analysis of the BLUP matrix (Olivoto *et al*., 2019b). The underlying factor analytic model is expressed as equation 5 (Rocha *et al*., 2018):

$$F = ZL(L^T L)^{-1} \quad (5)$$

where F is a matrix of factor scores; Z is the matrix of standardized BLUP values for the traits; and L is the factor loading matrix derived from principal component factor analysis. Factors with eigenvalues greater than 1.0 were retained. The MTSI score for each genotype was calculated as the Euclidean distance between the genotype's factor scores and those of an ideal ideotype using equation 6 (Olivoto *et al*., 2019b):

$$MTSI_i = \left[\sum_{j=1}^{f} \left(\gamma_{ij} - \gamma_j\right)^2\right]^{0.5} \quad (6)$$

where $MTSI_i$ is the multi-trait selection index value for the i^{th} genotype; γ_{ij} is the score of the i^{th} genotype in the j^{th} factor; γ_j is the score of the ideal ideotype in the j^{th} factor; and f is the total number of retained factors. Desired selection directions were specified to maximize grain yield (KY) and yield components (KRN, KPR, KW, SMI), while minimizing phenological duration (DTS, DTM), harvest kernel moisture (KM), and plant architectural traits (PH, EH) to select for early-maturing, lodging-resistant, and high-yielding hybrids (Shirzad *et al*., 2025; Zhang *et al*., 2026). Genotypes with lower MTSI scores reflect closer proximity to the ideotype and were selected as superior hybrids.

All statistical analyses, including combined mixed-model (REML/BLUP) estimation, AMMI decomposition, WAASB/WAASBY index calculation, and MTSI computation, were executed in the R statistical environment (R Core Team, 2024) using the specialized metan package (Olivoto and Lúcio, 2020).

3| Results and discussion

3.1| Combined analysis of variance

The assumption of normality for the experimental KY data across all 18 environments (nine locations over two cropping seasons) was confirmed. Furthermore, the non-significant chi-square values obtained from Bartlett's test for homogeneity of variance confirmed the uniformity of experimental error variances across the test environments, establishing the validity of conducting a combined analysis of variance. A multi-environment combined analysis of variance was performed to describe the main effects of year, location, genotype, and their two-way and three-way interaction effects on maize KY (Table 3).

The combined ANOVA revealed that the main effect of location and the year-location interaction were highly significant ($p < 0.01$), whereas the main effect of year was statistically non-significant (Table 3). The genotypic main effect showed a significant difference ($p < 0.05$), indicating inherent genetic diversity among the evaluated maize hybrids. Regarding interaction effects, the two-way location-genotype interaction was highly significant ($p < 0.01$), whereas the year-genotype interaction was non-significant. Furthermore, the three-way year-location-genotype interaction exhibited statistical significance ($p < 0.05$).

The predominant contribution of environmental variation—specifically driven by location and macro-environmental fluctuations across seasons year-location—highlights the substantial eco-geographic diversity among the nine testing locations in Iran, spanning temperate highland plateaus (Karaj and Mashhad) to warm, semi-arid, and subtropical agro-ecologies (Dezful, Jiroft, and Moghan) (Mostafavi and Saremirad, 2021; Shirzad *et al*., 2025). The non-significance of the year-genotype interaction alongside the highly significant location-genotype interaction and year-location-genotype interactions indicates that while the performance of maize hybrids remained relatively consistent across cropping seasons within a given site, their yield rankings altered substantially when evaluated across diverse geographical locations and specific year-by-location combinations (Baker, 1988; Signor *et al*., 2001; Engida *et al*., 2024). This complex spatio-temporal GEI reflects pronounced crossover-type yield responses, where relative genotype superiority is conditioned by local environmental determinants, thereby complicating direct phenotypic selection and broad varietal recommendations (Crossa, 1990; Yan and Tinker, 2006; Azrai *et al*., 2022).

These findings align closely with recent METs conducted in maize. Shirzad *et al*. (2025) reported that environmental heterogeneity and multi-way interaction structures heavily governed KY expression in elite maize hybrids developed at SPII. Similarly, Ma *et al*. (2024) and Zhang *et al*. (2026) demonstrated that environmental main effects and GEI accounted for the largest proportion of total variance in maize multi-location trials, frequently overshadowing true genotypic breeding values under unadjusted linear models (Singamsetti *et al*., 2021). Bocianowski *et al*. (2024) and Engida *et al*. (2024) likewise underscored that significant location-genotype and year-location-genotype interactions severely constrain the broad adaptability of maize hybrids, mandating regional stability evaluations. Furthermore, in multi-location trials across Iran, Hassani *et al*. (2023) and Taleghani *et al*. (2023) observed that the magnitude of three-way interactions underscores the volatile nature of field environments. Because standard analysis of variance provides limited resolution regarding the multiplicative nature and underlying patterns of GEI, the integrated deployment of LMMs (REML/BLUP), AMMI decomposition, WAASB/WAASBY superiority indices, and the MTSI framework becomes essential to dissect these complex interactions, filter out environmental noise, and identify superior maize hybrids combining high

yield potential with broad environmental resilience (Smith *et al*., 2005; Piepho *et al*., 2008; Olivoto *et al*., 2019a, 2019b).

Table 3. Combined analysis of variance of kernel yield in experimental maize hybrids

3.2| Integration of AMMI and BLUP models

To enhance the reliability of stability evaluation in METs and gain a comprehensive understanding of GEI, KY data of the studied maize hybrids were analyzed using an integrated AMMI and REML/BLUP framework. The AMMI analysis of variance revealed that KY was significantly influenced by the main effects of environment, genotype, and GEI ($p<0.01$, Table 4). The phenotypic expression of KY in maize is polygenic, regulated by quantitative trait loci (QTLs) and linked genomic regions that exhibit high sensitivity to environmental conditions. Consequently, environmental variability and its interplay with the genetic background can either facilitate or severely restrict selection response, underscoring the critical necessity of modeling these interaction components accurately in breeding programs (Engida *et al*., 2024; Shirzad *et al*., 2025). Further partitioning of the multiplicative interaction sums of squares through PCA indicated that the first four interaction principal component axes (PC1 to PC4) were statistically significant (Table 4). Specifically, PC1, PC2, and PC3 were highly significant ($p<0.01$), explaining 29.90%, 25.90%, and 16.20% of the GEI variation, respectively, while PC4 was significant at $p<0.05$, accounting for 9.70% of the interaction variance. Collectively, these four significant IPCs captured 81.70% of the total GEI sum of squares. The remaining component axes (PC5 to PC9) were non-significant and represented residual noise (18.30%). In complex MET datasets, relying solely on the first two principal components (which explained only 55.80% of the interaction variance in this study) is insufficient to capture the multidimensional nature of GEI. Similar requirements for multiple IPCs to explain complex GEI structures have been reported in maize by Bocianowski *et al*. (2024) and Shirzad *et al*. (2025), as well as in other crops by Hassani *et al*. (2023) and Taleghani *et al*. (2023). This limitation highlights the advantage of integrating AMMI with mixed models via the WAASB index, which accounts for all significant IPCs rather than restricting stability assessment to PC1 alone.

The LRT under the REML mixed model framework confirmed the significance of environmental, genotypic, and GEI variance components ($p<0.01$, Table 4). Environmental variance accounted for the largest proportion of total phenotypic variance ($\sigma p^2=4.39$), contributing 69.40, followed by GEI variance (24.74%), whereas the genotypic variance contributed the smallest share (5.86%). The predominance of environmental and interaction variances over genotypic variance indicates that environmental conditions exerted a substantially stronger influence on KY than the additive genetic background of the hybrids. Under such conditions, phenotypic selection based on unadjusted means becomes inefficient due to environmental masking effects (Falconer & Mackay, 1996; Shirzad *et al*., 2025). This finding is consistent with multi-environment maize studies by Ma *et al*. (2024) and Zhang *et al*. (2026), who reported that environmental factors and GEI accounted for the vast majority of yield variation.

Genetic parameter estimates derived from the REML/BLUP model provided deeper insights into the predictability of selection (Table 4). Although individual plot heritability was low ($h^2=0.06$), the genotypic mean heritability (h_{mg}^2) reached a high value of 0.69, accompanied by a high selective accuracy (0.83). High values for h^2_{mg} and selective accuracy demonstrate that the experimental design and statistical modeling were exceptionally robust, ensuring that the BLUP-predicted genotypic values reflect true genetic merit rather than environmental noise (Hassani *et al*., 2023; Taleghani *et al*., 2023). On the other hand, the genotypic correlation across environments

was low (r_{ge} = 0.26), confirming the presence of severe crossover-type GEI and indicating that hybrid rankings changed drastically across the 18 environments. Additionally, the genotypic coefficient of variation (CV_g = 4.02%) was lower than the residual coefficient of variation (CV_r = 13.84%), resulting in a CV ratio (CV_g/CV_r) of 0.29. The low r_{ge} and CV ratio reinforce that evaluating hybrids based on yield performance alone is inadequate, validating the implementation of BLUP-based stability indices (WAASB and WAASBY) for selecting high-yielding and stable maize hybrids.

Table 4. AMMI-based analysis of variance, REML/BLUP likelihood ratio test, and estimation of genetic variance components for kernel yield of 10 maize hybrids evaluated across 18 environments

To accurately evaluate the genotypic yield potential of the 10 maize hybrids while adjusting for environmental noise, genotypic values were predicted using the LMM framework (Figure 1). The predicted BLUP mean KY across the 18 environments ranged from 12.00 t ha^{-1} (H9) to 13.35 t ha^{-1} (H2), with an overall grand mean of 12.63 t ha^{-1} (represented by the dashed vertical reference line in Figure 1). Five genotypes—namely H2 (13.35 t ha^{-1}), H6 (13.03 t ha^{-1}), H3 (12.95 t ha^{-1}), H1 (12.80 t ha^{-1}), and the commercial check cultivar CHK (12.65 t ha^{-1})—exhibited predicted BLUP yields above the overall mean (blue circles, Figure 1). Among the newly developed experimental hybrids, H2, H6, H3, and H1 outperformed the commercial check (CHK), demonstrating superior genetic gain for KY potential. Conversely, hybrids H4, H7, H8, H5, and H9 produced mean yields below the grand mean (red circles, Figure 1). The narrow prediction confidence intervals for H2, H3, and H1 reflect high precision in genotypic value estimation, providing strong statistical confidence in their superior yield potential under multi-environment conditions (Shirzad *et al*., 2025).

Figure 1. Best linear unbiased prediction mean values of maize hybrids for kernel yield

3.3| Joint evaluation of grain yield and stability

Although a considerable portion of GEI variation can be modeled by the first two IPCAs in the AMMI framework, complex METs often generate higher-order interaction patterns that require additional axes for complete genetic interpretation (Rodrigues *et al*., 2014; Bocianowski *et al*., 2024). Consequently, the WAASB index, computed via SVD of the BLUP-derived GEI matrix, serves as a comprehensive quantitative stability statistic by integrating all retained, statistically significant IPCAs (Olivoto *et al*., 2019a).

Figure 2 illustrates the joint distribution of mean KY (horizontal axis) and environmental stability (WAASB, vertical axis) across the 18 test environments. The vertical reference line represents the grand mean KY (12.63 t ha^{-1}), separating high-yielding from low-yielding genotypes and environments. The horizontal reference line corresponds to the overall mean of the WAASB index (0.42), dividing the biplot into four distinct quadrants based on the joint interpretation of productivity and stability (Olivoto *et al*., 2019a; Taleghani *et al*., 2023). Quadrant I (KY < 12.63 t ha^{-1}, WAASB > 0.42) represents unstable, low-yielding entries. This quadrant comprised genotypes H4, H7, H8, and the CHK, along with environments MGN24, KER24, MHD24, and MHD25. These genotypes and environments displayed high WAASB values coupled with below-average yields, underscoring their pronounced sensitivity to environmental fluctuations and poor agronomic productivity. Consequently, these genotypes contribute substantially to crossover GEI noise and cannot be recommended for wide-scale cultivation (Hassani *et al*., 2023; Shirzad *et al*., 2025).

Quadrant II (KY > 12.63 t ha^{-1}, WAASB > 0.42) contains high-yielding yet environmentally responsive genotypes and mega-environments. Genotypes H2, H3, and H6, alongside environments KSH25 and MGN25, were positioned within this quadrant. Furthermore, genotype H1 (x ≈ 12.8 t ha^{-1}, y ≈ 0.44) mapped to the lower boundary of quadrant II, in close proximity to the horizontal stability threshold. Genotypes in quadrant II possess superior yield potential and high responsiveness to favorable agronomic inputs and climatic conditions, achieving optimal performance in high-input environments. However, their elevated WAASB scores reflect specific adaptation rather than broad stability, indicating that their cultivation should be targeted to non-stress, high-yielding macro-environments such as KSH25 and MGN25 (Yan and Kang, 2002; Engida *et al*., 2024).

Quadrant III (KY < 12.63 t ha^{-1}, WAASB < 0.42) encompasses stable genotypes with suboptimal yield expression. Genotypes H5 and H9, along with environments DZF24, DZF25, JRF24, MZN24, MZN25, and KER25, fell into this quadrant. While genotypes H5 and H9 exhibited remarkable phenotypic buffering and minimal GEI sensitivity (low WAASB), their genetic yield potential remained below the trial average, rendering them unsuited as commercial grain hybrids unless specific stress-tolerance traits are targeted (Nataraj *et al*., 2021; Azrai *et al*., 2022). Environments clustering in quadrant III represented low-yielding sites with restricted discriminative ability for KY potential.

Quadrant IV (KY > 12.63 t ha^{-1}, WAASB < 0.42) represents the ideal target quadrant in MET evaluations, signifying superior productivity combined with wide environmental stability (Olivoto *et al*., 2019a; Shirzad *et al*., 2025). Highly productive, low-interaction environments, including KRJ24, KRJ25, MDB24, MDB25, KSH24, and JRF25, were located in this quadrant, designating them as optimal selection environments capable of maximizing genotypic expression with minimal experimental noise (Yan and Tinker, 2006). Notably, while no single hybrid was positioned deeply inside quadrant IV, genotypes H1, H2, and H3 occupied borderline positions adjacent to the stability threshold, with H1 exhibiting the lowest WAASB score among all above-average yielding hybrids.

The scarcity of genotypes strictly embedded within quadrant IV is a well-recognized phenomenon in cereal breeding; genes conferring superior yield potential often display synergistic interactions with high-yielding environments, thereby inflating absolute IPCA scores (Falconer and Mackay, 1996; Zhang *et al*., 2026). This reality underscores the limitation of relying solely on categorical quadrant classifications. To overcome this constraint, the WAASBY superiority index provides a continuous, weighted integration of yield and stability (Nataraj *et al*., 2021; Taleghani *et al*., 2023). By incorporating all four significant IPCAs (explaining 81.70% of the GEI variance) instead of restricting stability to IPCA1 alone (29.90%), the WAASB-based biplot provides a comprehensive, noise-filtered evaluation that confirms hybrids H1, H2, and H3 as the most promising candidates for subsequent multi-trait selection and commercial deployment.

Figure 2. Biplot analysis of kernel yield of maize hybrids, evaluated by weighted average absolute scores of the best linear unbiased predictions (WAASB)

3.4| Evaluation of the WAASBY index and yield-stability weighting scenarios

To evaluate yield performance and stability with enhanced precision and operational flexibility, the experimental maize hybrids were appraised using the WAASBY superiority index, which dynamically weights the relative contributions of broad stability (WAASB) and productivity (KY) across varying selection intensities (Olivoto *et al*., 2019a). Figure 3 illustrates the rank dynamics of the 10 maize genotypes across 21 consecutive weighting scenarios, moving from 100/0 (100%

weight assigned to stability and 0% to yield) on the far left to 0/100 (0% weight to stability and 100% to yield) on the far right in 5% increments. Moving across this horizontal gradient progressively diminishes the environmental stability requirement while inflating the economic weight of KY, such that the 0/100 ratio evaluates genotypes purely on their mean yield capacity (Nataraj *et al*., 2021; Hassani *et al*., 2023).

The heatmap analysis identified four contrasting functional groups among the tested germplasm, visually demarcated by the genotype label colors (Figure 3). The first group (red labels: H1, H2, and H3) represents the most agronomically desirable germplasm. Hybrid H2 demonstrated exceptional overall superiority, securing the top rank across nearly all scenarios as the weight assigned to yield increased beyond 80/20. Similarly, hybrids H1 and H3 displayed remarkable buffering capacity coupled with high productivity, consistently maintaining top-tier ranks (ranks 2–3 and 3–4, respectively) across the entire spectrum. The second group (blue labels: H4 and H6) comprises responsive, intermediate-performing hybrids. While hybrid H6 achieved high yield-based ranks (ranks 3–4) under yield-driven scenarios (0/100 to 20/80), its ranking dropped to intermediate levels (rank 7) under stability-prioritizing scenarios (100/0), reflecting significant sensitivity to environmental perturbations. Conversely, the third group (black labels: H5 and H9) illustrates the classic archetype of static stability devoid of yield potential. Hybrid H5 attained rank 1 under strictly stability-driven scenarios (100/0 to 70/30) due to its exceptionally low WAASB score; however, its rank dropped precipitously to ranks 7–8 as the emphasis on KY increased toward 0/100. A similar decline was observed for H9 (shifting from rank 2 to ranks 9–10). Finally, the fourth group (green labels: H7, H8, and the commercial check CHK) represents inferior germplasm. Hybrid H8 remained trapped at the lowest rank (bright yellow, rank 10) across all 21 scenarios, exhibiting severe yield depression and high interaction noise. Hybrids H7 and CHK likewise exhibited consistently substandard performance, generally occupying ranks 7 through 9.

For commercial breeding pipelines where equal value is placed on maximizing harvestable yield and ensuring environmental resilience, the 50:50 weighting scenario (WAASB/KY = 50/50) establishes a balanced, decisive selection benchmark (Figure 4) (Olivoto *et al*., 2019a; Taleghani *et al*., 2023). Under this balanced scenario, six genotypes achieved WAASBY scores above the grand trial mean (blue circles): H2 (WAASBY = 76.8, rank 1), H3 (62.7, rank 2), H1 (60.2, rank 3), H5 (57.1, rank 4), H4 (47.2, rank 5), and H6 (45.3, rank 6). Conversely, four genotypes performed below the overall threshold (red circles): H9 (33.4, rank 7), CHK (29.5, rank 8), H7 (24.4, rank 9), and H8 (10.8, rank 10). Crucially, all six top-performing experimental hybrids generated higher WAASBY scores than the commercial check cultivar CHK, demonstrating substantial genetic progress in yield potential and environmental buffering achieved by the SPII maize breeding program (Shirzad *et al*., 2025).

Developing maize hybrids that combine superior productivity with yield stability across variable production environments is an essential safeguard against rising climate volatility and erratic seasonal weather (Engida *et al*., 2024; Ma *et al*., 2024). The WAASBY index provides a robust analytical solution to the perennial dilemma of crossover GEI by allowing breeders to select genotypes tailored either to marginal, stress-prone environments (by elevating stability weights) or to high-input, non-limiting conditions (by prioritizing yield weights) (Olivoto *et al*., 2019a; Zhang *et al*., 2026). In our investigation, the simultaneous superiority scores under the 50:50 ratio definitively confirmed hybrids H2, H3, and H1 as the most elite candidates. These hybrids circumvented the negative trade-off between productivity and stability that constrained entries like H5 (stable but low-yielding) and H6 (yielding but unstable). These findings corroborate previous investigations demonstrating the efficiency of WAASBY-based ranking in identifying consensus,

broadly adapted maize genotypes under multi-location testing (Taleghani *et al*., 2023; Shirzad *et al*., 2025). Consequently, hybrids H2, H3, and H1 constitute prime genetic resources for multi-location promotion, variety registration, and future breeding cycles.

Figure 3. Ranking of maize hybrids based on varying importance of stability and kernel yield

Figure 4. Calculation of WAASBY in maize hybrids, considering equal weights of 50 for kernel yield, and WAASB

3.5| Multi-trait stability index

To perform simultaneous multi-trait selection for KY potential, environmental stability, lodging resistance, and phenological efficiency, exploratory FA was conducted on the WAASBY values across all 10 evaluated traits using principal component extraction followed by Varimax rotation (Olivoto *et al*., 2019b; Hassani *et al*., 2023). The 10 traits were grouped into four independent factor dimensions (FA1 to FA4, Table 5) that accounted for a cumulative variance of 84.67%. Factor 1 grouped traits governing primary productivity and grain-filling duration, comprising KY, KM, and SMI. Factor 2 accounted for kernel structure and physiological maturity, encompassing KRN, KW, and DTM. Factor 3 captured flowering precocity and ear fertility, consisting of KPR and DTS. Finally, Factor 4 grouped structural plant architectural traits associated with lodging resistance, namely PH and EH.

The MTSI was computed using the factor scores of these four dimensions, measuring the Euclidean distance between each hybrid and an ideotype possessing optimal values for all 10 traits simultaneously (Olivoto *et al*., 2019b). Lower MTSI scores denote closer proximity to the stable breeding ideotype. Applying a selection intensity of 30%, hybrids H2, H6, and H3 were identified as the most ideal, broadly adapted, and stable candidates across the full suite of evaluated traits (red circles, Figure 5A). The remaining seven genotypes fell within the non-selected zone (black circles), with hybrid H7 positioned at the innermost core of the spiral, exhibiting the greatest distance from the ideotype.

The selection differentials and predicted selection gains achieved by the selected hybrids demonstrated substantial, multi-directional genetic progress aligned with the breeding objectives (Table 5) (Rocha *et al*., 2018; Shirzad *et al*., 2025). Highly favorable positive genetic gains were realized for primary yield and phenological duration: KY exhibited an SD of +5.69% and an SG of +3.91%, elevating the mean KY of the selected hybrids from 12.62 t ha^{-1} to 13.34 t ha^{-1}. Simultaneously, SMI achieved a desirable positive gain (SD = +2.51%, SG = +2.20%), extending the effective grain-filling period from 63.53 to 65.12 days. Furthermore, KRN showed a marked increase (SD = +4.02%, SG = +3.96%, rising from 16.49 to 17.15 rows). Crucially, favorable negative selection gains were successfully attained for plant architecture and phenological earliness, mitigating lodging susceptibility: PH was reduced from 225.17 to 221.02 cm (SD = −1.84%, SG = −1.55%) and EH was lowered from 116.10 to 115.44 cm (SD = −0.57%, SG = −0.47%). In addition, DTS showed a desirable negative shift (SD = −0.43%, SG = −0.38%), confirming earlier anthesis and escape from terminal heat. High broad-sense heritabilities on a genotype-mean basis ranging from 0.69 for KY to 0.99 for KRN) ensured that predicted selection gains closely mirrored selection differentials across all 10 traits (Table 5).

The radar biplot of factor contributions provided an intuitive visual dissection of the specific strengths and weaknesses of the selected hybrids (H2, H6, and H3) (Figure 5B) (Olivoto *et al*., 2019b; Hassani *et al*., 2023). In this graphical representation, the lower the percentage contribution of a factor to the MTSI distance (plotted closer to the outer periphery, below the 25% theoretical

equal-contribution dashed line), the closer the attributes within that factor are to the stable ideal state (strengths). Conversely, factors pulled toward the center (high contribution share, > 25%) represent the primary sources of deviation from the ideotype (weaknesses) (Hassani *et al*., 2023). For all three selected hybrids, FA1 (KY, KM, SMI), FA2 (KRN, KW, DTM), and FA4 (PH, EH) were plotted near the outer margin (20–30% contribution), demonstrating that their shared superiority is driven by high KY, prolonged grain filling, optimal yield components, and reduced plant stature. Notably, hybrid H3 exhibited the lowest contribution share for FA1 (~15%, extending furthest toward the outer margin), underscoring its exceptional genetic superiority in combining prolonged SMI with high KY. In contrast, FA3 (KPR and DTS) was pulled inward toward the center (60–80% contribution) across all three hybrids, indicating that slight delays in silking or variations in kernels per row represented the primary bottleneck preventing these hybrids from achieving absolute ideotype perfection (Figure 5B).

Simultaneous selection across multiple quantitative and architectural traits represents a longstanding challenge in maize improvement due to unfavorable genetic correlations, particularly the antagonistic trade-offs between high grain yield, early maturity, and reduced plant stature (Engida *et al*., 2024; Ma *et al*., 2024). Traditional selection indices frequently fail under such conditions due to severe multicollinearity among yield components and the arbitrary nature of economic weights (Smith, 1936; Rocha *et al*., 2018). The MTSI framework effectively overcomes these limitations by integrating FA with mixed-model BLUP theory, thereby orthogonalizing correlated trait networks into independent dimensions and delivering balanced selection differentials tailored to trait-specific breeding targets (Olivoto *et al*., 2019b; Zuffo *et al*., 2020). The high efficacy of the MTSI in identifying consensus ideotypes that harmonize superior yield potential, lodging tolerance, and phenological efficiency has been extensively validated in recent multi-environment evaluations across diverse crops (Koundinya *et al*., 2021; Taleghani *et al*., 2023; Zhang *et al*., 2026). In our investigation, the MTSI conclusively identified hybrids H2, H6, and H3 as elite candidates. Although hybrid H1 exhibited high yield stability in the single-trait WAASBY analysis, the multi-trait MTSI framework refined the final selection by favoring H6 over H1 due to H6's superior balance in architectural dwarfness and yield-component traits. Consequently, hybrids H2, H6, and H3 emerge as the ultimate, broadly adapted maize hybrids recommended for commercial production and future breeding cycles.

Table 5. Prediction of selection differential for studied traits based on MTSI index

Figure 5. Ranking of hybrids in ascending order based on the multitrait stability index (A), and evaluation of selected hybrids in terms of their strengths and weaknesses represented as the ratio of each factor in the calculated multi-trait stability index (B)

4| Conclusion

GEI and environmental variations played a significant role in influencing the phenotypic expression of KY and agronomic traits in the evaluated maize hybrids across 18 environments. Environmental variance and spatio-temporal interactions accounted for the largest proportion of phenotypic variance in KY, highlighting the necessity of multi-environment evaluation. Although environmental effects masked raw phenotypic means, high genotypic mean heritability (0.69) and high selective accuracy (0.83) under the mixed model (REML/BLUP) framework confirmed the high reliability of genetic predictions. According to the single-trait yield stability analyses (AMMI, WAASB, and WAASBY), hybrids H2, H3, and H1 were identified as stable genotypes with superior kernel yield performance, consistently outperforming the commercial check cultivar

(CHK) across varying stability-yield weighting scenarios. For multi-trait ideotype selection, exploratory factor analysis successfully grouped the 10 evaluated traits into four independent dimensions. Based on the MTSI at a 30% selection intensity, hybrids H2, H6, and H3 emerged as the most ideal, broadly adapted candidates across all traits. The MTSI selection delivered favorable genetic gains for KY (+3.91%), grain-filling duration (+2.20%), and KRN (+3.96%), while simultaneously achieving desirable reductions in PH (-1.55%), EH (-0.47%), and DTS (-0.38%) to enhance lodging resistance and phenological precocity. Overall, combining mixed linear models, multiplicative interactions, and multi-trait factor analysis provides a comprehensive and highly accurate framework for dissecting GEI. In this context, hybrids H2 and H3 represent the consensus elite germplasm recommended for commercial release and broad-scale promotion in maize production systems.

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Competing interests
The authors have stated that they do not have any conflicting interests.

Data availability
The data that support the findings of this study are available from the corresponding author upon reasonable request.

Ethics declarations
Not applicable.

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Table 1. Code numbers, pedigrees, and descriptions of the maize genotypes evaluated in the study

Row	Hybrid	Pedigree	Row	Hybrid	Pedigree
1	H1	K47/2-2-1-2-2-1-1-1× MO17	6	H6	KLM77021/4-1-2-1-2-4-1× K47/3
2	H2	K47/2-2-1-4-1-1-1× MO17	7	H7	K47/2-2-1-2-2-1-1-1×K18
3	H3	K47/2-2-1-4-1-1-1-1 × K3640/3	8	H8	B73× K1264/1
4	H4	KLM82010/4 × K3640/3	9	H9	KSC647× MO17
5	H5	KLM82010/5 × K3640/3	10	CHK	KSC704 (Check)

Table 2. Description of the environments with their respective latitudes, longitudes, altitudes (m), soil group, mean temperature, rainfall, and climate condition in regard to the maize trial

Environment	Latitude	Longitude	Altitude (m)	Soil group	Temperature (˚C)	Rainfall (mm)	Climate condition
Karaj	35.49N	51.00E	1321	Clay Loam	16.45	280.00	Temperate
Kerman	28.45N	56.36E	1200	Clay Loam	22.67	82.00	Tropical
Mashhad	32.59N	36.19E	995	Sandy Loam	14.37	173.00	Temperate
Kermanshah	34.80N	47.26E	1380	Silty Clay	16.90	221.80	Temperate
Jiroft	28.40N	57.44E	630	Sandy Loam	23.48	168.00	Tropical
Moghan	39.41N	47.32E	73	Clay Loam	16.86	354.00	Temperate
Miandoab	37.01N	46.09E	1314	Clay Loam	18.88	285.00	Temperate
Dezful	32.75N	48.20E	150	Silty Clay Loam	25.54	431.00	Subtropical
Mazandaran	36.42N	53.35E	54	Clay Loam	16.01	500.70	Tropical

Table 3. Combined analysis of variance of kernel yield in experimental maize hybrids

Source of variation	df	Sum of square	Mean of square
Year	1	457.97	457.97^{ns}
Location	8	5417.66	677.21**
Year × location	8	766.25	95.78**
Error 1	36	302.46	8.40
Genotype	9	181.79	20.20*
Location × genotype	72	590.54	8.20**
Year × genotype	9	48.84	5.43^{ns}
Year × location × genotype	72	325.82	4.53*
Error 2	324	987.68	3.05

ns, *, **: non-significant and significant at five and one percent probability levels, respectively.

Table 4. AMMI-based analysis of variance, REML/BLUP likelihood ratio test, and estimation of genetic variance components for kernel yield of 10 maize hybrids evaluated across 18 environments

Source of variation	df	Sum of square	Mean of square	Proportion	Accumulated
Environment	17	6641.89	390.70**	-	-
Error 1	36	302.46	8.40	-	-
Genotype	9	181.79	20.20**	-	-
Genotype × environment	153	965.20	6.31**	-	-
PC1	25	288.90	11.56**	29.90	29.90
PC2	23	250.03	10.87**	25.90	55.80
PC3	21	156.54	7.45**	16.20	72.10
PC4	19	93.57	4.93*	9.70	81.70
PC5	17	61.40	3.61^{ns}	6.40	88.10
PC6	15	50.62	3.37^{ns}	5.20	93.40
PC7	13	44.10	3.39^{ns}	4.60	97.90
PC8	11	14.48	1.32^{ns}	1.50	99.40
PC9	9	5.58	0.62^{ns}	0.60	100.00
Error 2	324	987.68	3.05	-	-
REML/BLUP variance components		Variance		Percent	
Environment		3.05**		69.40	
Genotype		0.26**		5.86	
Genotype × environment		1.09**		24.74	
Genetic variance component		Value			
Phenotypic variance		4.39		-	
Heritability		0.06		-	
Genotype-environment interaction r^2		0.25		-	
h^2_{mg}		0.69		-	
Accuracy		0.83		-	
r_{ge}		0.26		-	
CV_g		4.02		-	
CV_r		13.84		-	
CV ratio		0.29		-	

ns, *, **: non-significant and significant at five and one percent probability levels, respectively.
PC: principal component axis of interaction; h^2: individual plot broad-sense heritability; h^2_{mg}: genotypic mean heritability; r_{ge}: genotypic correlation across environments; CV_g: genotypic coefficient of variation; CV_r: residual coefficient of variation.

Table 5. Prediction of selection differential for studied traits based on MTSI index

Variable	Factor	Goal	Xo	Xs	h^2	SD (%)	SG (%)
KY	FA 1	increase	12.62	13.34	0.69	5.69	3.91
KM	FA 1	decrease	20.71	20.75	0.79	0.23	0.18
SMI	FA 1	increase	63.53	65.12	0.87	2.51	2.20
KRN	FA 2	increase	16.49	17.15	0.99	4.02	3.96
KW	FA 2	increase	312.90	309.65	0.97	-1.04	-1.01
DTM	FA 2	decrease	120.81	122.38	0.87	1.30	1.13
KPR	FA 3	increase	41.65	41.48	0.92	-0.42	-0.38
DTS	FA 3	decrease	56.98	56.73	0.88	-0.43	-0.38
PH	FA 4	decrease	225.17	221.02	0.84	-1.84	-1.55
EH	FA 4	decrease	116.10	115.44	0.83	-0.57	-0.47

Xo: Original value; Xs: Selected value; h^2: Broad sense heritability; SD: Selection differential; SG: Selection gain.

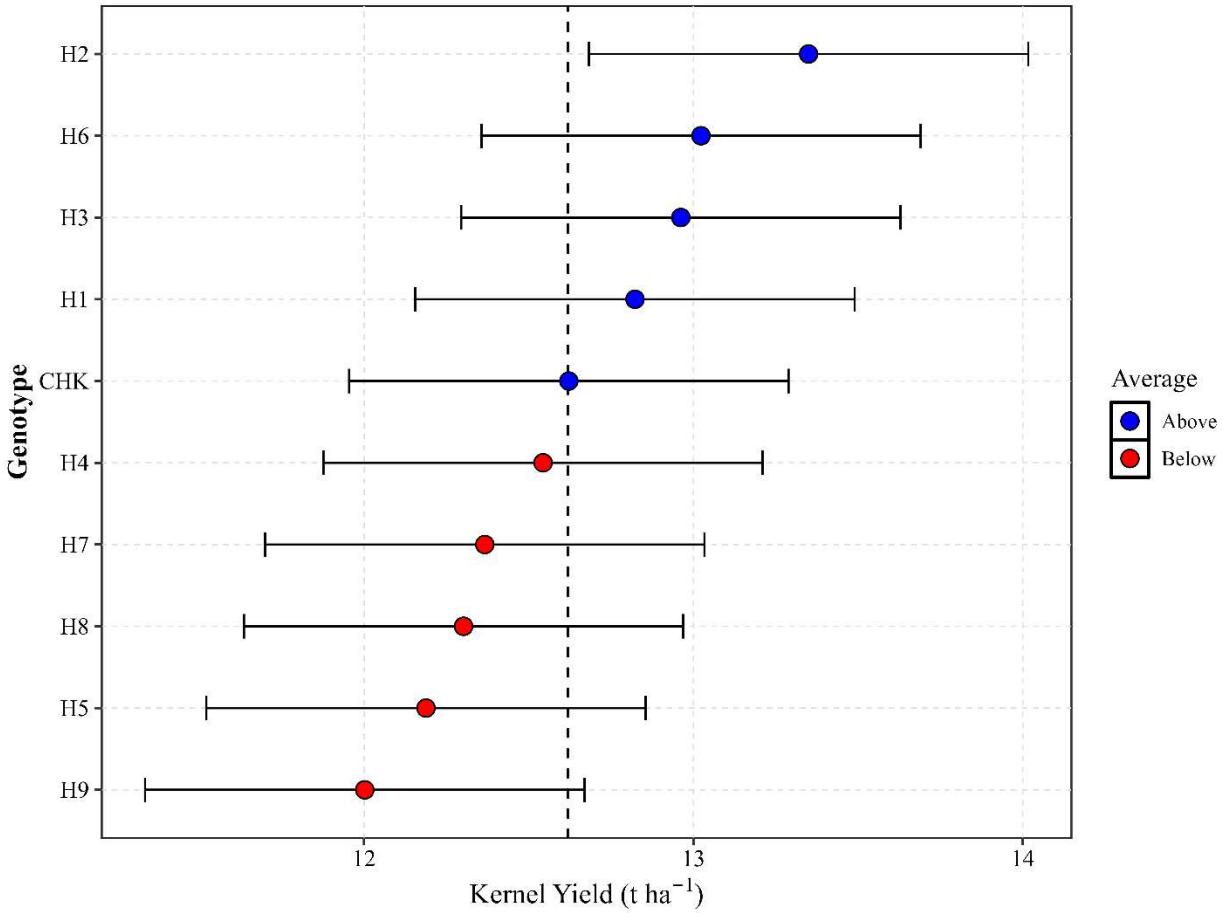


Figure 1. Best linear unbiased prediction mean values of maize hybrids for kernel yield

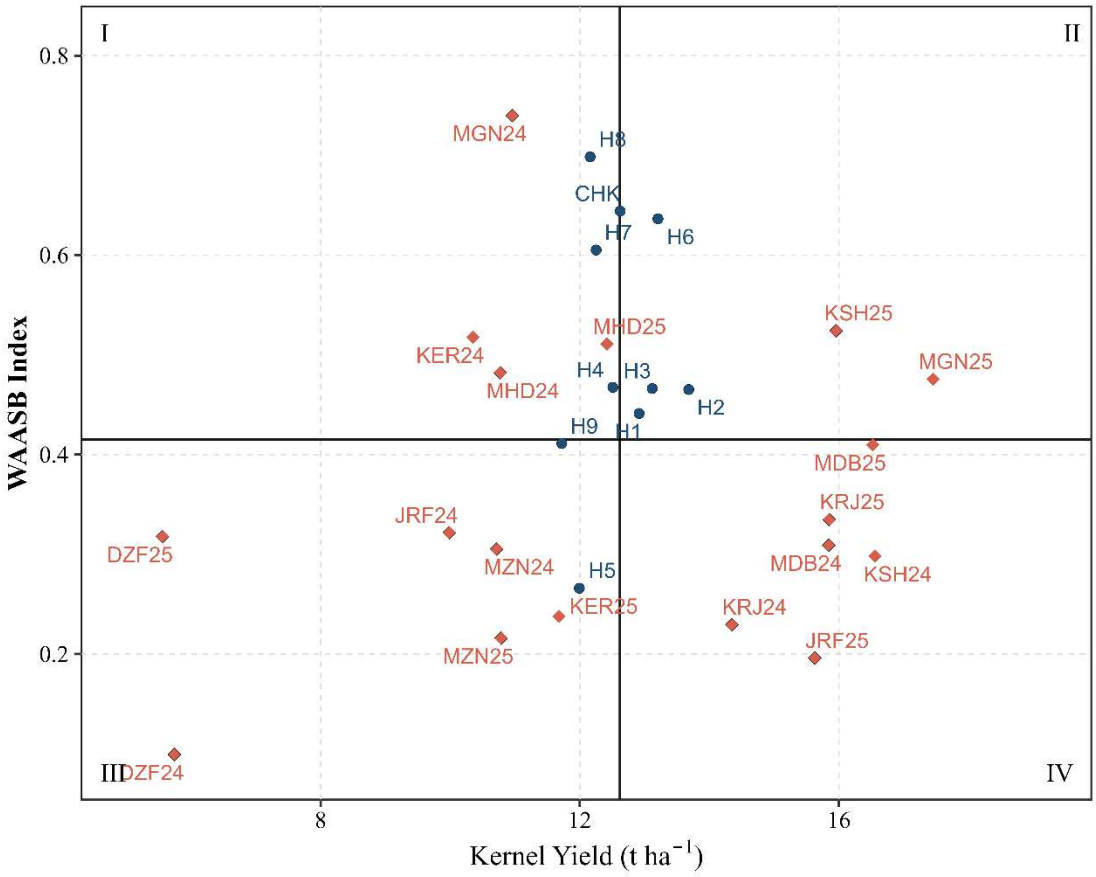


Figure 2. Biplot analysis of kernel yield of maize hybrids, evaluated by weighted average absolute scores of the best linear unbiased predictions (WAASB)

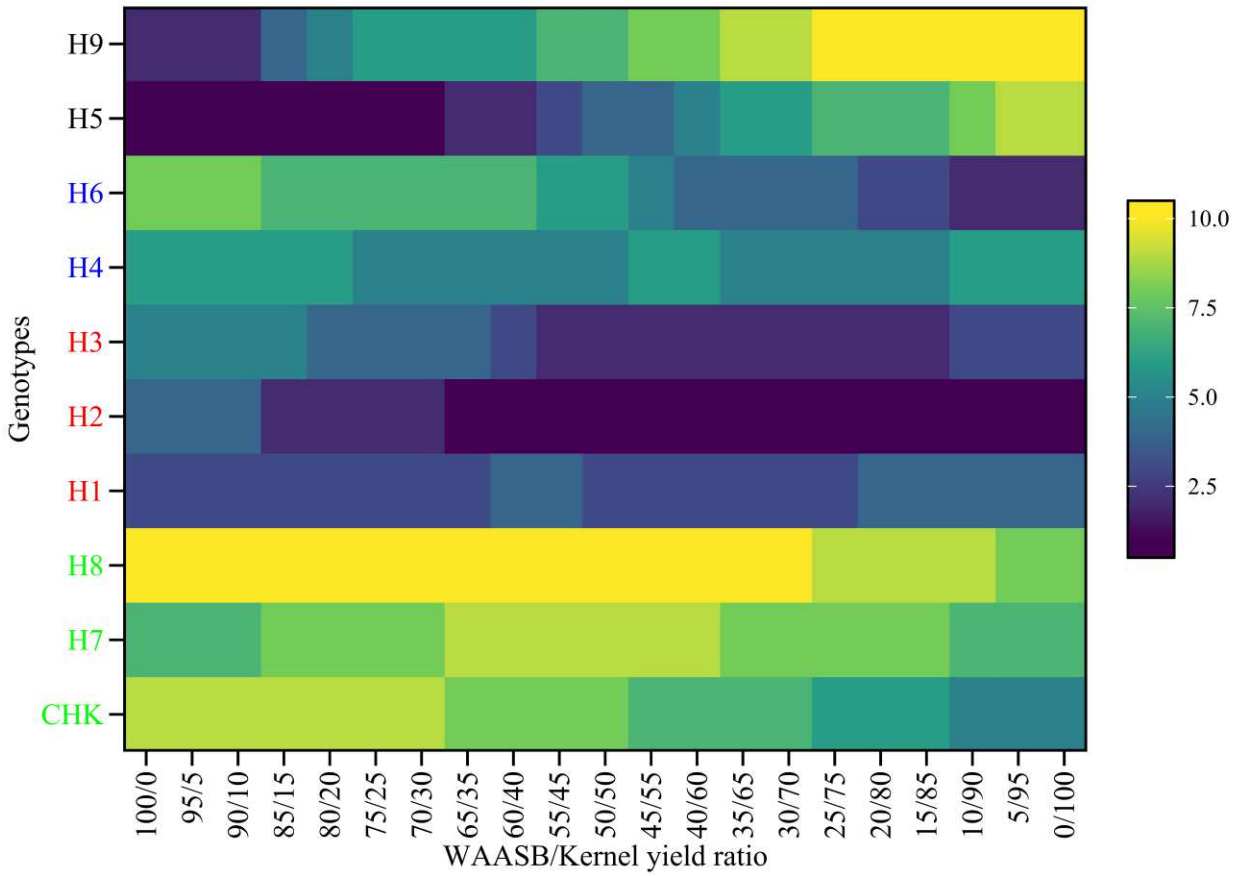


Figure 3. Ranking of maize hybrids based on varying importance of stability and kernel yield

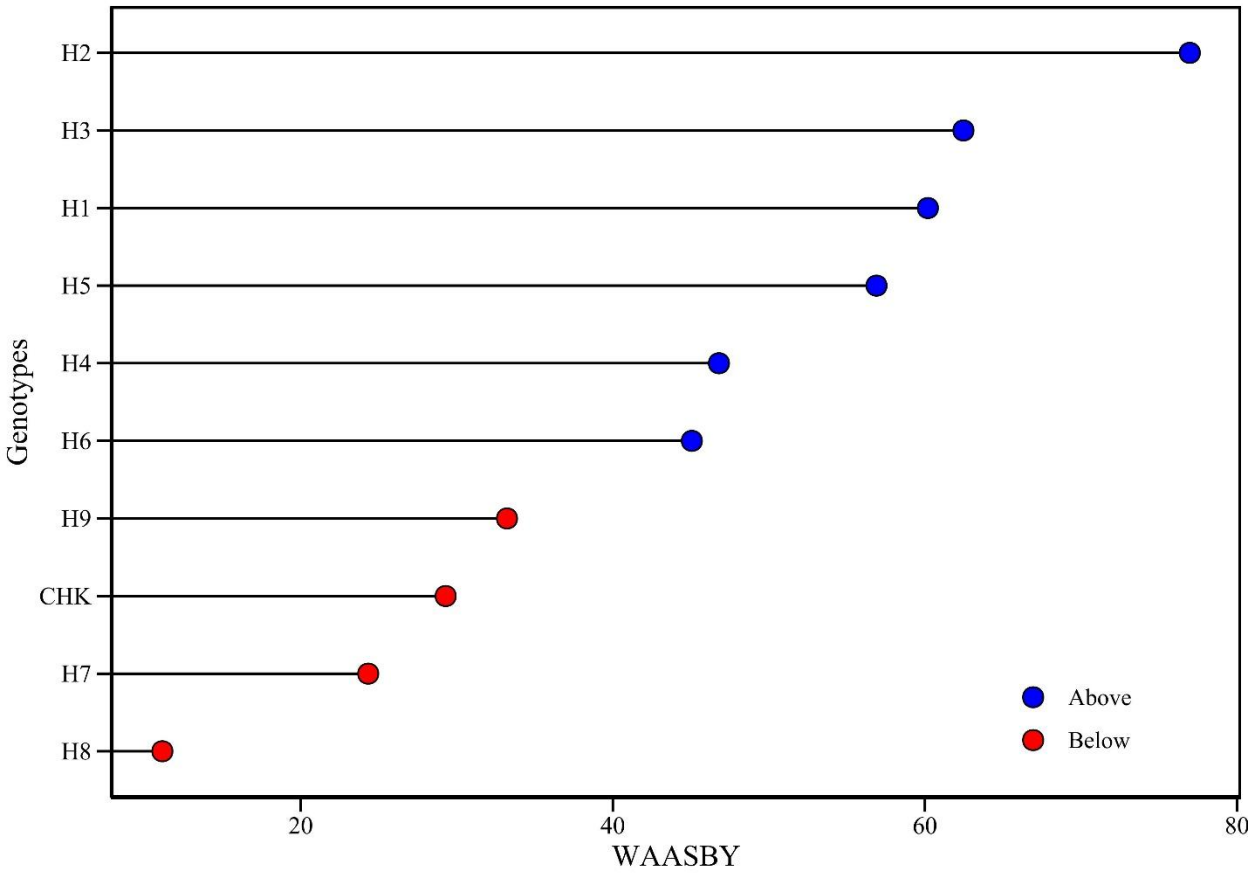
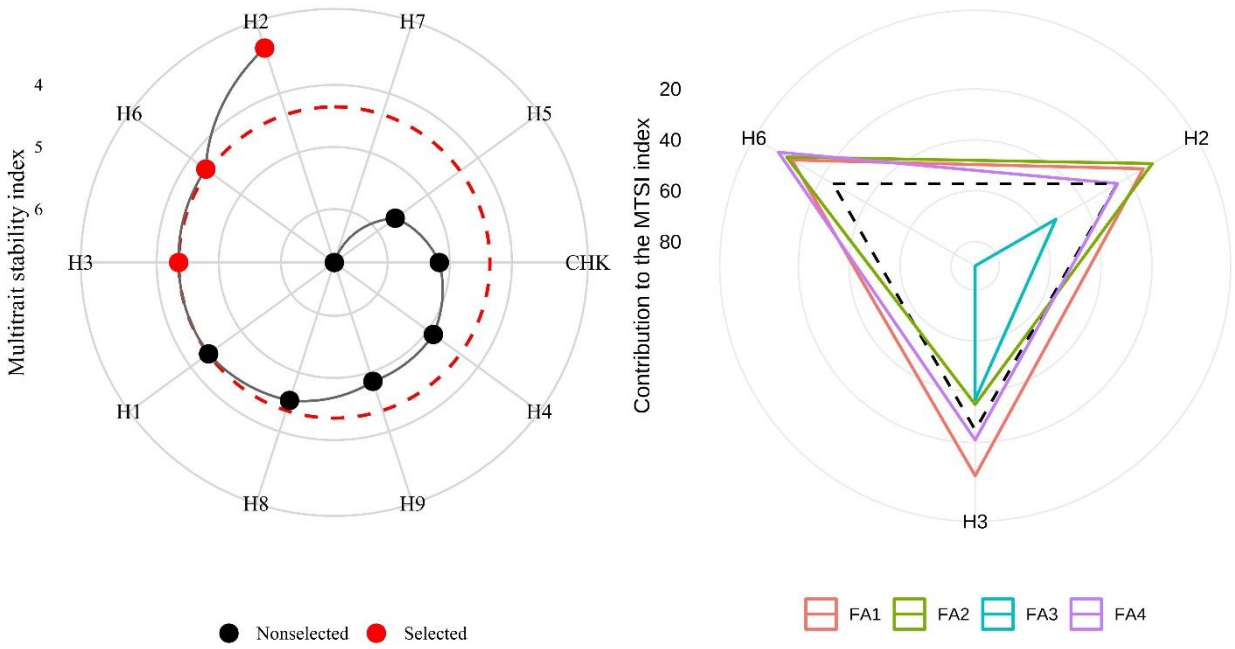


Figure 4. Calculation of WAASBY in maize hybrids, considering equal weights of 50 for kernel yield, and WAASB



A B

Figure 5. Ranking of hybrids in ascending order based on the multitrait stability index (A), and evaluation of selected hybrids in terms of their strengths and weaknesses represented as the ratio of each factor in the calculated multi-trait stability index (B)