



Research article

Yield stability evaluation in melon (*Cucumis melo* L.) hybrid based on additive main effects and multiplicative interaction, GGEbiplot software and multi-trait stability index in Malang, Indonesia

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Abstract

Importance of the work: The increasing demand for melon in Malang City, Indonesia, coupled with agro-climatic challenges, necessitates the development of stable and high-yielding varieties.

Objectives: To evaluate stable and high-yielding hybrid melon genotypes by integrating multiple methods, namely additive main effects and multiplicative interaction (AMMI), GGEbiplot software and the multi-trait stability index (MTSI).

Materials and Methods: In total, 20 low-temperature-resistant hybrid melon genotypes were evaluated (selected for their resilience across four locations in Malang), using a randomized complete block design with three replications. AMMI and GGEbiplot analyses were conducted on fruit weight and fruit sweetness, while the MTSI was used to assess multiple traits, including size and quality.

Results: The AMMI analysis identified G4 and G13 as genotypes with high fruit weight and stable performance across the various environments. G10, G14 and G16 had high sweetness and stable performance across these environments. The GGEbiplot analysis, using the means versus stability model, identified G4, G11 and G13 as the best genotypes for fruit weight and G9 and G4 as the best for sweetness. Furthermore, the “Which-Won-Where” model revealed that, for fruit weight, G3 was the best genotype in locations L1, L2, L4, while G10 was the best in L3. However, for fruit sweetness, no specific environmental preferences were observed. The MTSI analysis identified G9 as the best genotype, demonstrating promising trait stability.

Main finding: High-yielding and stable hybrid melon genotypes were identified. These could serve as a basis for melon breeding programs in Malang City.

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Introduction

Melon (*Cucumis melo* L.) is one of the horticultural crops that has high economic value due to increasing consumer demand, both in domestic and international markets (Kesh and Kaushik, 2021). In Indonesia, Malang City is known as one of the centers of horticultural crop production because it has a diverse agroclimate, making it a strategic area for the expansion of melon cultivation centers (Adrianto and Ravetz, 2020). Adding this center is an urgent priority because melon production has fluctuated and even decreased from year to year (Adiredjo et al., 2024).

However, there are considerable challenges in achieving stable production yields, primarily due to agroclimatic variability in the region. Specifically, environmental factors, such as differences in rainfall, temperature and humidity limit melon production because these conditions influence cultivation timing and site feasibility, causing yield instability (Huda and Bayuardi Suwarno, 2023). Often, the complex genotype $\times$ environment ($G \times E$) interaction affects the stability and adaptability of melon genotypes, thus hindering efforts to increase consistent production. For example, several studies have shown that the stability of crop productivity, including melon yield, can be affected by environmental factors such as temperature, rainfall and water availability (Walters et al., 2021; Shayanmehr et al., 2022; Lyon et al., 2022). The $G \times E$ interaction underscores the importance of testing multiple genotypes across various growing environments (Adiredjo et al., 2024), supported by appropriate statistical approaches.

The current study aimed to explain $G \times E$ interactions through multi-site or multi-season analyses based on statistical methods. For example, additive main effects and multiplicative interaction (AMMI), Gauch and Zobel (1996) effectively captures the complexity of $G \times E$ interactions, revealing major differences in genotype performance under diverse environmental conditions (Zewdu et al., 2020). In addition, the GGEbiplot software (genotype main effect and genotype $\times$ environment interaction), developed by Gabriel (1971), provides a graphical representation that helps breeders visualize which genotypes are best suited for particular environments, exhibit stability and perform well across various conditions (Dogan et al., 2016; Chaudhary et al., 2024). Furthermore, the multi-trait stability index (MTSI) method (Sellami et al., 2021) ranks genotypes based on overall performance and stability across multiple traits, indicating superior adaptability of specific genotypes (Yue et al., 2021).

The objective of the current study was to evaluate the $G \times E$ interaction and its effect on the stability of yield and agronomic traits of melons in Malang City's agroclimate environment using AMMI, GGEbiplot and MTSI approaches. Furthermore, this study aimed to identify melon genotypes with high stability that could adapt across various environments and in specific environments. By integrating the MTSI with AMMI and GGEbiplot analyses, the results should provide a more comprehensive understanding and improve accuracy regarding genotype stability across different traits and environments (Olivoto et al., 2019; Saxena et al., 2024).

Previous $G \times E$ studies in melon have primarily applied AMMI or GGEbiplot analyses to assess yield stability across temporal or broad environmental variations (Feyzian et al., 2009; Dia et al., 2016). However, the current study proposed an innovative approach by combining AMMI, GGEbiplot and the MTSI to evaluate stability for single traits, such as fruit weight and sweetness, as well as multi-trait stability in low-temperature-tolerant hybrids under the specific rainy season conditions in Malang, Indonesia. The uniqueness of this research lies in identifying specific genotypes that are adaptive to highly variable environmental conditions, particularly resistance to high rainfall (1,500–1,900 mm/yr). These genotypes demonstrate better yield stability even under extreme climate conditions, which has not been extensively discussed. This combined approach offers a more holistic analysis of yield stability in highly specific environments, a topic that has received limited attention in the context of melons.

The current study offers novelty by integrating three analytical approaches AMMI, GGEbiplot and the MTSI to evaluate $G \times E$ interactions in melon hybrids in Malang City. The combination of these methods not only assesses yield stability across different environments but also analyzes important agronomic traits holistically. Thus, this research aimed to make a substantial scientific contribution by supporting the development of stable, adaptive and high-quality melon varieties, especially in Malang City. The hypotheses of this study were: 1) the $G \times E$ interaction greatly influences yield stability; 2) an integrated approach using AMMI, GGEbiplot and the MTSI can identify melon genotypes that are stable and high-performing across various environments, as well as location-specific genotypes; and (3) melon genotypes with high multi-trait stability will demonstrate consistent agronomic performance.

Materials and Methods

The research was carried out during the rainy season, from March to June 2024, at four locations in Malang Regency, Indonesia, representing contrasting growing conditions based on rainfall intensity. The selected sites were Dau District (Jetis Village) with an average annual rainfall of 1,849 mm, Dau District (Kucur Village) with 1,900 mm, Lawang District (Lawang Village) with 1,723 mm, and Lowokwaru District (Ketawanggede Village) with 1,500 mm. These locations were chosen to represent environmental variability relevant to melon cultivation. The plant materials consisted of 20 low-temperature-resistant melon hybrids along with three commercial comparison varieties (Leorentina et al., 2023; Mubarak et al., 2024). The experiment was arranged in a randomized complete block design across environments with three replications.

Yield performance and stability were evaluated using the AMMI and GGEbiplot methods, with a particular focus on fruit weight and fruit sweetness. The GGEbiplot analysis was further used to identify genotypes with specific adaptability to particular environments. In addition, the multi-trait stability index (MTSI) was applied to evaluate multiple agronomic traits, including fruit length, fruit diameter, fruit flesh thickness, seed cavity width, fruit weight, and sweetness level.

Statistical analysis

Additive main effects and multiplicative interaction analysis

Combined analysis of variance across locations, as well as AMMI analysis of variance, was performed using the PKBT STAT statistical software package (<https://pbstat.com/pkbt-stat/>). In the AMMI model, the GEI was further partitioned into interaction principal component analysis (PCA). The AMMI model (Gauch and Zobel, 1988) used is shown in Equation 1:

$$Y_{ij} = \mu + G_i + E_j + (\sum_{n=1}^n k_n U_{ni} S_{nj}) + Q_{ij} + \varepsilon_{ij} \quad (1)$$

where Y_{ij} is the average yield of a particular variety in an environment, μ is the grand mean, G_i is the additional effect of a particular variety or strain, E_j is the additional effect of a particular environment, k_n is the singular value for the n^{th} PC axis, U_{ni} and S_{nj} are the scores for varieties/strains and environments on the n^{th} PC axis, respectively, the residuals (Q_{ij}) reflect the variation not explained by the 1st– n^{th} multiplicative

components and the residual errors (ε_{ij}) are assumed to be normally distributed and independent.

GGEbiplot analysis

GGEbiplot analysis is used to study $G \times E$ interactions in genotypes with specific environments and genotypes with stable and high yields to determine ideal genotypes. The GGEbiplot equation (Yan et al., 2000) is described by Equation 2:

$$Y_{ij} - Y_j = \lambda_1 \varepsilon_{i1} \eta_{j1} + \lambda_2 \varepsilon_{i2} \eta_{j2} + \varepsilon_{ij} \quad (2)$$

where Y_{ij} is the average yield of the i^{th} genotype in the j^{th} environment, Y_j is the average yield of all genotypes in the j^{th} environment, λ_1 and λ_2 are the singular values for the first and second principal components (PC1 and PC2), respectively, ε_{i1} and ε_{i2} are the PC1 and PC2 scores of the i^{th} genotype, η_{j1} and η_{j2} are the PC1 and PC2 scores of the j^{th} environment, and ε_{ij} is the residual not explained by PC1 and PC2.

Multi-trait stability index analysis

The $MTSI_i$ was calculated using the formula developed by Olivoto et al. (2019) to identify stable and superior accessions based on the evaluated traits. Accessions with the lowest MTSI values were considered superior, as shown in Equation 3:

$$MTSI_i = [\sum_{j=1}^f (F_{ij} - F_j)^2]^{0.5} \quad (3)$$

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, and F_j is the score of the ideal genotype for the j^{th} factor.

Statistical analyses were conducted using PKBT-STAT (version 3.2), R (version 4.4.2), and RStudio IDE (<https://rstudio.com/products/rstudio/download/>). R is a language and environment for statistical computing and graphics (R Core Team, 2024).

Results

The AMMI and GGEbiplot methods were used to evaluate stability and yield performance in fruit weight and fruit sweetness. Specifically, the GGEbiplot was used to assess genotypes with site-specific potential. In addition, the MTSI approach evaluated multiple traits, consisting of fruit length, fruit diameter, fruit flesh thickness, seed cavity width, fruit weight and sweetness level.

Additive main effects and multiplicative interaction analysis modeling

The AMMI model was used to assess the effects of genotype, location (environment) and genotype-by-environment interaction. This model is a powerful analytical tool for genotype $\times$ environment studies, allowing for the identification of adaptation targets, adaptive traits and test sites (Sharma et al., 2020). The results of the AMMI analysis on fruit weight and sweetness level are shown in Figs. 1–2.

The AMMI biplot for fruit weight (Fig. 1) reveals the interaction between genotype (G) and environment (L) based on two principal components (PC1=65.9%, PC2=21.2%), which together explain 87.1% of the total variance. Genotypes close to the center, such as G4 and G13, demonstrated stability across the various environments. Conversely, genotypes at the edges, such as G3 in L1, G23 in L2, G5 in L3 and G17 in L4, exhibited specific interactions with their environments and were classified as site-specific adaptable genotypes. Environments L1 and L2 contributed the most to the variation in fruit weight among the four test sites. The negative direction observed in L3 indicated a unique response in that environment, meaning genotypes performing well in L1, L2 and L4 did not necessarily perform best in L3.

The AMMI biplot for sweetness level (Fig. 2) shows the interaction between genotype and environment based on two PC (PC1=41.6%, PC2=34.3%), together explaining 75.9%

of the total variance. Genotypes close to the center, such as G10, G14 and G16, demonstrated stability across various environments. In contrast, genotypes at the edges, such as G12 in L4, showed specific interactions and were classified as environment specific. For the traits of fruit sweetness, no genotypes showed specific adaptation to L1, L2, or L3. However, environment L2 was less favorable for optimizing sweetness levels.

GGEbiplot software modeling

The GGEbiplot interpretation allows for in-depth exploration of genotype-by-environment interactions and helps to identify genotypes that perform best under various conditions. These plots facilitated the location of genotypes that were not only high yielding but also stable across different environments. Figs. 3–4 display stability for fruit weight and sweetness, respectively.

Based on Fig. 3 (fruit weight), the most stable genotypes were G4, G11 and G13, although G3 had the highest fruit weight but was less stable. Conversely, the lowest fruit weights were observed in genotypes G14 and G20. Fig. 4 (fruit sweetness/Brix level) shows that G9 and G4 had the most stable fruit sweetness levels, while G14 had the highest but less stable fruit sweetness. G7 had the lowest fruit sweetness level and was unstable. Figs. 5–6 illustrate location-specific genotypes.

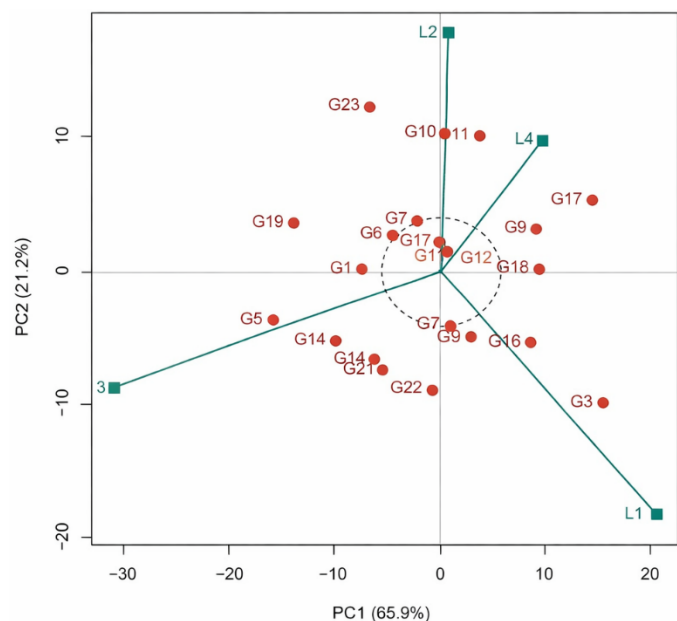


Fig. 1 Additive main effects and multiplicative interaction analysis biplot of principal component (PC1 versus PC2) for fruit weight character, where G1–G23 = different genotypes and L1–L4 = various environments.

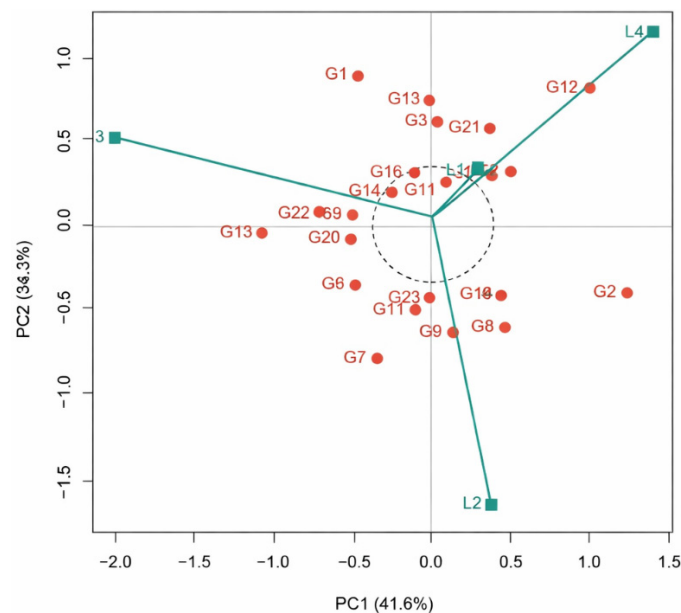


Fig. 2 Additive main effects and multiplicative interaction analysis biplot of principal component (PC1 versus PC2) for sweetness level character, where G1–G23 = different genotypes and L1–L4 = various environments.

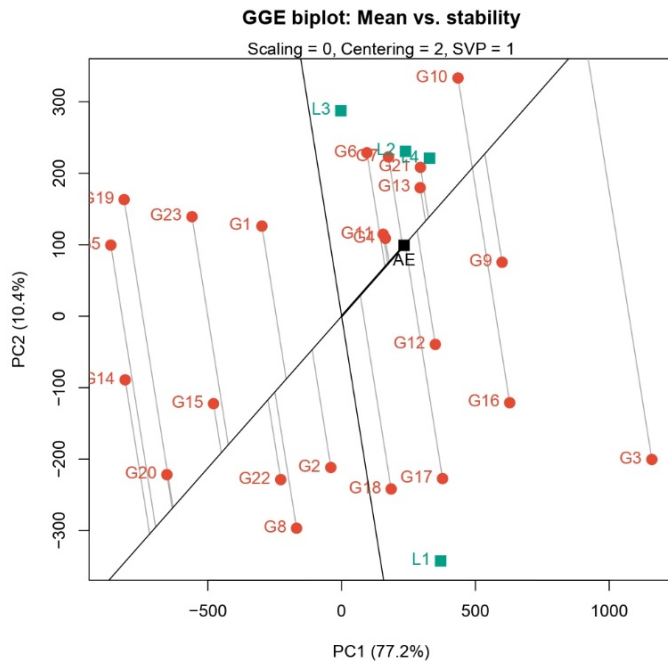


Fig. 3 GGEbiplot software output of principal component (PC1 versus PC2) for mean versus stability of fruit weight character, where G1–G23 = different genotypes and L1–L4 = various environments. The analysis was conducted with scaling = 0 (no scaling), centering = 2 (environment-centered), and singular value partitioning (SVP) = 1 (genotype-focused).

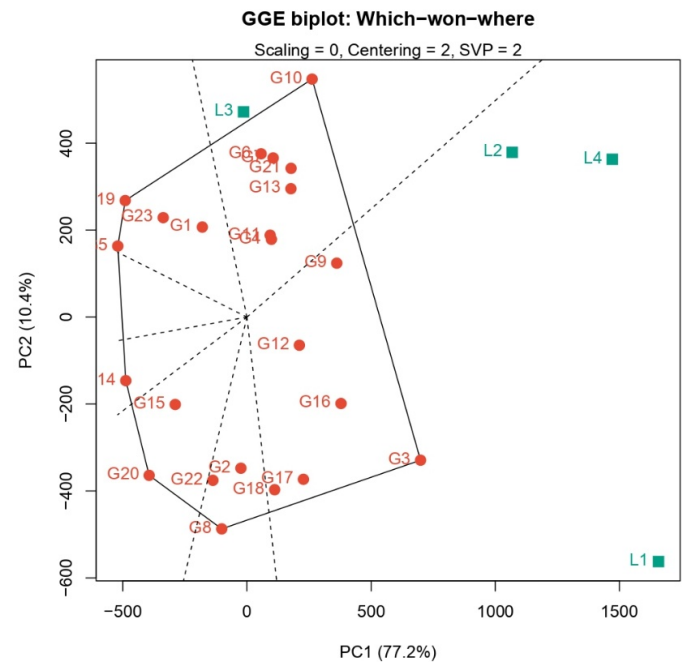


Fig. 5 GGEbiplot software output of “Which-Won-Where” analysis of fruit weight, where G1–G23 = different genotypes and L1–L4 = various environments. The analysis was conducted with scaling = 0 (no scaling), centering = 2 (environment-centered), and singular value partitioning (SVP) = 1 (genotype-focused)

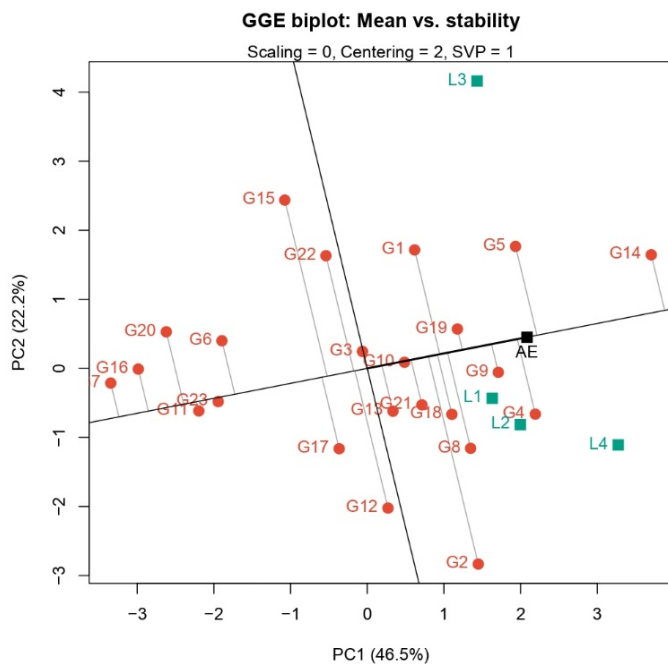


Fig. 4 GGEbiplot software output of principal component (PC1 versus PC2) for mean versus stability for fruit sweetness level character, where G1–G23 = different genotypes and L1–L4 = various environments. The analysis was conducted with scaling = 0 (no scaling), centering = 2 (environment-centered), and singular value partitioning (SVP) = 1 (genotype-focused).

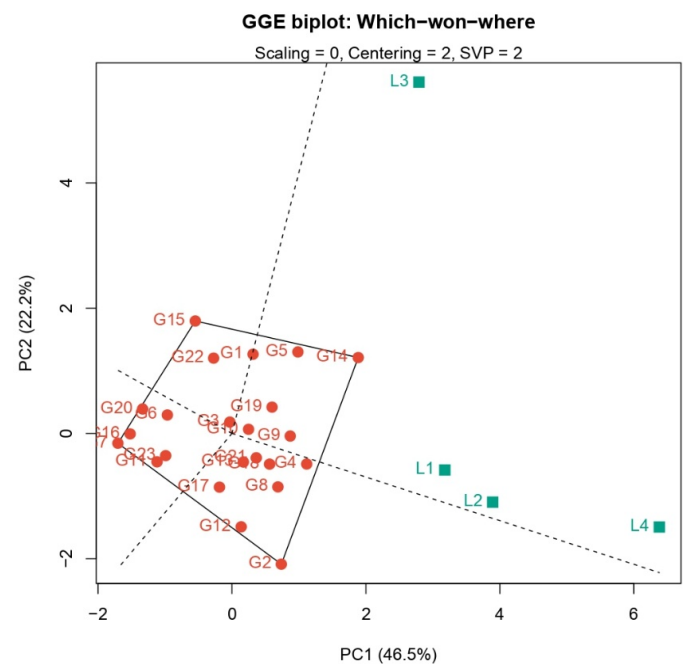


Fig. 6 GGEbiplot software output of “Which-Won-Where” analysis of fruit sweetness level, where G1–G23 = different genotypes and L1–L4 = various environments. The analysis was conducted with scaling = 0 (no scaling), centering = 2 (environment-centered), and singular value partitioning (SVP) = 1 (genotype-focused)

In Fig. 5 (fruit weight), genotype G3 performed best in environments 1 (Lawang), 2 (Jetis) and 4 (Lowokwaru), while G10 had the highest fruit weight in environment 3 (Kucur). Fig. 6 (fruit sweetness level) indicates that G14 and G5 performed best in sweetness across all four environments.

Multi-trait stability index modeling

The MTSI is a comprehensive method used to evaluate genotypes based on multiple yield traits while considering their stability across different environments. The results of the MTSI analysis for melon yield traits are shown in Fig. 7, indicating that genotypes G12, G17 and G9 were identified as ideal accessions based on their combined traits. Among these, G9 exhibited the best overall performance due to its stability and ideal trait values across multiple traits, including fruit weight, fruit sweetness level, fruit flesh thickness, fruit length, fruit diameter and seed cavity width. Consequently, G9 could be recommended for broader adaptation.

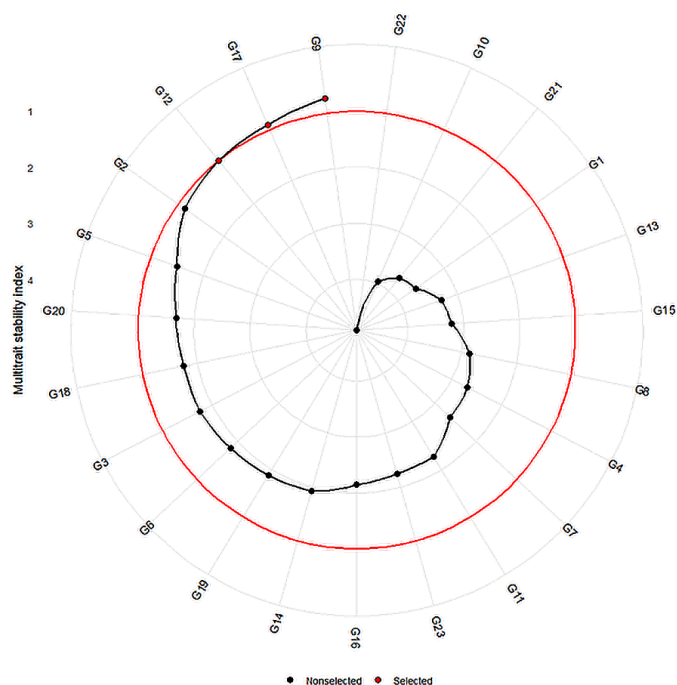


Fig. 7 Results of multi-trait stability index analysis.

Discussion

The multiple approaches used in this research enhanced the robustness of the results. The use of AMMI and GGEbiplot analysis focused on identifying stable and high-yielding genotypes, as well as site-specific genotypes. Based on the analysis, there was clustering of hybrid melon genotypes, effectively explained based on PC1 and PC2. The MTSI approach facilitated multi-trait analysis to identify ideal genotypes with stable traits, marked as the selected genotypes in Fig. 7. The apparent inconsistency in the selection of the most stable genotypes by the AMMI, GGEbiplot and MTSI models is a direct reflection of their distinct statistical objectives and foci, rather than a weakness in the analysis. Each model addresses a different breeding question. This multi-model approach provides a more nuanced and comprehensive understanding of genotype performance than any single method could offer. The following sections detail the outcomes of each model and a dedicated synthesis explains the differences, including the notable case of the high-sweetness genotypes G14 and G5.

Additive main effects and multiplicative interaction analysis

Based on the current results, the AMMI analysis was effective in evaluating $G \times E$ interactions for melon traits stability. Fruit weight and sweetness level contributed greatly to PC1 and PC2, accounting for 87.1% and 75.9% of the variation, respectively. These findings supported Gauch et al. (2008), who stated that AMMI could effectively separate genotype and environmental effects from $G \times E$ interactions. Furthermore, the greater magnitude of variation in fruit weight compared to the Brix values for sweetness indicated that fruit weight had a stronger $G \times E$ interaction, suggesting environmental factors played a more dominant role in determining fruit weight (Roohanitaziani et al., 2020; Sellami et al., 2021). This was evidenced by the position of the lines in environments 1 (Lawang) and 2 (Jetis), showing high environmental variation, as well as in environment 3 (Kucur), displaying negative values. The AMMI biplot revealed substantial agro-climatic differences between environments 1 and 2, as well as a different pattern in environment 3. Genotypes G4 and G13 were identified as superior for fruit weight, while G10, G14 and G16 excelled in fruit sweetness. Stable genotypes were those located near the center of the biplot, whereas some genotypes presented with negative directions, indicating complex $G \times E$ interactions that should be considered in selection (Crossa et al., 1990).

GGEbiplot analysis

The ‘Mean versus Stability’ GGEbiplots (Fig. 3 and Fig. 4) provided additional insights into genotype performance, emphasizing both stability and average performance. This approach is particularly relevant for traits such as fruit weight and Brix level (sweetness), where growers aim to balance yield and quality. GGEbiplots visually depict genotype performance under various environmental conditions, enabling the identification of superior genotypes with high yields and stability across environments (Fana et al., 2018; Gonçalves et al., 2020). For fruit weight, genotypes G4, G11 and G13 had the highest stability, maintaining consistent performance across environments. For fruit sweetness, G9 and G4 showed the most stability, delivering reliable results. However notably, genotypes G14 and G5, despite being categorized as unstable in the ‘Mean versus Stability’ view, had the highest mean fruit sweetness across all environments. This discrepancy suggested that these genotypes possess “dynamic stability” rather than “static stability”. While they may be sensitive to environmental changes, performing exceptionally well in favorable environments but fluctuating in marginal ones, they represent valuable genetic resources for specific high-input environments, indicating specific adaptation or as parental lines for improving sweetness traits in breeding programs. These findings highlight the utility of GGEbiplots in selecting genotypes that balance quantity and quality essential goal in plant breeding (Olaniyi et al., 2013; Fana et al., 2018).

The ‘Which-Won-Where’ analysis using the GGEbiplots (Figs. 5–6) revealed site-specific genotypes, which is a valuable point for breeders and farmers. Understanding the unique performance of genotypes in different locations allows for more targeted variety selection and optimizing melon production. For example, as shown in Fig. 5, genotype G3 performed best in terms of fruit weight in environments 1 (Lawang), 2 (Jetis) and 4 (Lowokwaru), while G10 excelled in environment 3 (Kucur). This underscores the importance of $G \times E$ interactions and the ability of GGEbiplots to detect crossover patterns. Similar patterns have been observed in durum wheat studies, where mega-environments and winning genotypes were identified clearly (Solonechnyi et al., 2018). Recognizing location-specific superiority aids in making informed decisions to improve production efficiency and genotype adaptation (Haile et al., 2022).

Multi-trait stability index analysis

The MTSI offers a comprehensive evaluation of genotypes by considering multiple traits and their stability across environments. In the current study, genotype G9 was identified as superior due to its high stability across parameters such as fruit weight, fruit sweetness level, fruit length, fruit flesh thickness and seed cavity width. Genotypes with low MTSI values are considered more stable and superior, as they consistently perform well across environments (Yue et al., 2022; Azam et al., 2023). Other research supported the effectiveness of the MTSI in identifying superior genotypes in crops, including sugar beet and soybean, even under stress conditions such as drought and salinity (Padmaja et al., 2022; Taleghani et al., 2023). Integrating the MTSI with other models, such as AMMI, can further enhance the accuracy and robustness of stability assessments (Durai et al., 2025). Overall, MTSI is a holistic approach that covers a wide range of important agronomic traits, supporting its utility in genotype selection (Olivoto et al., 2019).

Model comparisons and the identified differences in genotype selection outcomes across AMMI, GGEbiplot and the MTSI stem from their distinct methodological emphases and breeding objectives. AMMI partitions variance into additive (genotype, environment) and multiplicative (interaction) components, excelling in identifying stable performers for individual traits, such as fruit weight (G4, G13) and sweetness (G10, G14, G16), by minimizing noise in PC axes (Gauch et al., 2008). In contrast, the GGEbiplot analysis merges genotype effects with $G \times E$ for a holistic visual interpretation, simultaneously highlighting mean performance, stability and mega-environments (Yan et al., 2000). This explains why G4 and G13 remained stable for fruit weight, but G9 and G4 emerged stable for sweetness in the “Mean versus Stability” views (Fig. 3 and Fig. 4, respectively).

A critical case is that of genotypes G14 and G5 for fruit sweetness. In the GGE “Which-Won-Where” view (Fig. 6), they were identified as winners across environments due to their superior mean performance. However, their longer vector projections in the “Mean vs Stability” view (Fig. 4) indicated high environmental sensitivity, a form of “dynamic stability” where they excelled in favorable conditions but fluctuated in suboptimal ones. This discrepancy between high mean performance and low stability is not contradictory but informative; these genotypes are ideal for specific adaptation to optimal environments or as parental donors for sweetness trait introgression, rather than as broadly stable varieties (Fana et al., 2018).

The MTSI operates on a fundamentally different principle of a multi-trait selection index. It aggregates stability based on the Weighted Average of Absolute Scores from the BLUP (WAASB) based stability across multiple traits (weight, sweetness, length), favoring genotypes such as G9 that best approximate an ideal 'ideotype' by balancing overall performance and stability, inevitably penalizing genotypes that excel in one trait but are mediocre or unstable in others (Olivoto et al., 2019). Therefore, the apparent inconsistency in genotype selection was methodological and expected: AMMI and single-trait GGE identify trait-specific performers, while the MTSI identifies multi-trait ideotypes. The overlap of some genotypes (such as G4) across models strengthens the confidence in their general merit. Such variations are common when combining single-trait versus multi-trait models, as demonstrated in crops such as maize (Yue et al., 2022) and sugar beet (Taleghani et al., 2023).

For breeding and practical applications, the identified genotypes provide actionable insights for melon improvement in Malang. Broadly stable G9 (based on the MTSI) and G4 (consistent in AMMI and GGE) could be prioritized as parents in hybrid breeding programs to enhance resilience against rainfall fluctuations, potentially accelerating cultivar release for commercial use. Site-specific genotypes, such as G3 (superior in three locations via GGE), enable targeted deployment, optimizing yields in high-rainfall areas (Jetis) while minimizing $G \times E$ risks. Future strategies could involve crossing stable lines with high performers (G14 for fruit sweetness) to pyramid traits, supported by marker-assisted selection for low-temperature tolerance. These findings should guide sustainable production amid climate variability, aligning with regional goals for a consistent supply (Walters et al., 2021).

Conflict of Interest

The authors declare that there are no conflicts of interest.

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