Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Genotype × environment interaction, yield stability, and adaptability of sugar beet genotypes revealed by AMMI and GGE Biplot Analyses

Ghasem Parmoon

Ghasem.parmoon@gmail.com

Sugar Beet Research Department, Kermanshah Agricultural and Natural Resources Research and Education Center, Education and Extension Organization (AREEO)

Farhnaz Hamdi

Sugar Beet Seed Institute, Agricultural Research Education and Extension Organization (AREEO)

Dariush Taleghani

Sugar Beet Seed Institute, Agricultural Research Education and Extension Organization (AREEO)

Parviz Fasahat

Sugar Beet Seed Institute, Agricultural Research Education and Extension Organization (AREEO)

Hasan Hamidi

Razavi Khorasan Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO)

Mohsen Bazrafshan

Fars Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO)

Saeed Darabi

Fars Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO)

Article

Keywords: AMMI, GGE, Root yield, Sugar beet, Sugar yield

Posted Date: November 13th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-10966396/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Genotype × environment interaction, yield stability, and adaptability of sugar beet genotypes revealed by AMMI and GGE Biplot Analyses

Ghasem Parmoon. Farhnaz Hamdi. Dariush Taleghani. Parviz Fasahat. Hasan Hamidi. Mohsen Bazrafshan. Saeed Darabi.

Abstract

This study evaluated twelve sugar beet genotypes across five contrasting environments to identify high-yielding and relatively stable genotypes for root yield (RY) and sugar yield (SY). AMMI analysis revealed significant ($p \leq 0.001$) effects of environment, genotype, and genotype × environment interaction (GEI) for both traits. GEI accounted for the largest proportion of variation in RY (32.7%), whereas environment contributed the largest proportion of variation in SY (29.4%). The first two interaction principal component axes explained 77.8% and 76.7% of the GEI variation for RY and SY, respectively. Root and sugar yields ranged from 56.7–79.9 and 9.3–13.5 t ha^{-1}, respectively. The stability indices consistently ranked G2 (Arta) among the genotypes with the highest yield and favorable stability, followed by G10 (Shokofa) and G12 (Tara). AMMI and GGE biplot analyses showed substantial agreement, identifying G2, G3, and G9 as genotypes with favorable yield performance and relatively broad adaptation across the tested environments, while G3 and G9 also showed evidence of specific adaptation. One mega-environment was identified for RY and two for SY. E4 (Mahidasht) showed high representativeness, whereas E3 (Zarghan) provided strong discrimination among genotypes. Overall, G2 (Arta) showed a favorable combination of high productivity and stability across the environments evaluated in this study. Further multi-year and multi-environment testing is needed to confirm the consistency of these responses and their applicability to broader production environments.

Keywords: AMMI, GGE, Root yield, Sugar beet, Sugar yield

Introduction

Sugar beet (*Beta vulgaris* L.) is an important industrial crop that provides a large part of human sugar consumption [1]. Besides its vital role in sugar production, it sustains the agricultural economy by providing income to farmers and supporting rural employment. Its sugar content can reach more than 20% and is converted into several products, such as molasses and animal feed [2]. As the world's sugar requirements are on the rise, more and more efforts are being made in breeding and agricultural technology to improve the production efficiency and sustainability of the sugar beet crop [3].

Increasing root yield and sugar content remains a major target in sugar beet breeding programs [4]. However, environmental conditions strongly influence genotype performance, and the selection of stable and high-yielding cultivars is complicated by genotype × environment interaction [5]. The key environmental parameters, such as soil type, moisture, and temperature, greatly influence yield and sugar accumulation [6]. Therefore, successful breeding programs should adopt a holistic approach that integrates both genetic and environmental data. Advanced techniques like marker-assisted selection contribute to the breeding process by identifying desirable traits at the molecular level and selecting genotypes with desirable responses to different environments before field trials. The integration of genomic information with phenotypic data results in more accurate predictions of cultivar performance [7,8].

In countries like Iran, where a wide range of climatic conditions exist, multi-environment trials (METs) are required to evaluate yield stability and genotypic adaptation [9]. Among the statistical methods employed for GEI analysis, the Additive Main Effects and Multiplicative Interaction (AMMI) model and the GGE biplot approach have gained popularity due to their capacity to visualize interaction patterns and identify mega-environments [10,11]. AMMI combines analysis of variance (ANOVA) with principal component analysis (PCA) to

differentiate main effects from interaction effects[12]. The GGE biplot, based on PCA of environment-centered data allows for the simultaneous identification of superior genotypes and ideal test environments [13]. When used in conjunction, these methods empower scientists to unravel complex interactions, identify high-performing cultivars, and define homogeneous environments. This will support breeders in decision making, better allocation of resources, and breeding for varieties specific to climatic and soil conditions, thereby improving the crop yield, stability, and food security under climate variability [14,15].

While several studies have been conducted on the yield stability in sugar beet all over the world, little information is available on the mega-environment identification for sugar beet production under the climatic conditions of Iran using both AMMI and GGE biplot methods simultaneously. The combined use of AMMI and GGE is a powerful tool for GEI analysis, identification of major environmental factors, and selection of genotypes with high yield potential and stability under diverse climatic conditions. Localized understanding of genotype adaptation in such regions as western Iran can greatly enhance varietal selection and agronomic practices. Therefore, the objectives of this study are to: (1) evaluate genotype × environment interaction for root yield and sugar content in a set of sugar beet genotypes; (2) identify mega environments existing in the tested locations using AMMI and GGE biplot analyses; and (3) identify high-yielding and stable genotypes (or specifically adapted genotypes) for recommendation under different growing conditions.

Material and method

Description of Study Area

The field experiment was conducted during the primary growing season (2022–2023) across five distinct environments. These locations differed substantially in key edaphic and climatic attributes, including soil type, altitude, and mean annual rainfall. A detailed description of these environmental parameters is provided in Figure 1. Given the significant heterogeneity in these

factors, each site was considered a unique ecosystem and consequently treated as an individual environment for the purpose of this study (Fig 1).

Experimental material

Twelve sugar beet genotypes used in the study are displayed in Table 1. From the total genotypes, Agatella and Shokofa were controls.

Experimental Design and Management

The experiment was arranged in a randomized complete block design (RCBD) with six replications (i.e., six blocks). Each block contained 12 plots, resulting in a total of 72 plots. Individual plot dimensions were 3 m × 6 m, providing a gross plot area of 18 m^2. The spacing between rows within a plot was 50 cm, between plots within a block was 50 cm, and between blocks was 150 cm. Each plot consisted of six rows.

Seeds of the experimental beet variety were sown via direct drilling into the soil. The seeding rate was calculated as 1.5 units ha^{-1} per plot. Fertilizers were applied uniformly at a rate of 100 kg ha^{-1} each for NPS and urea (46% N). For yield assessment, the three central rows of each plot (excluding the two outer rows to minimize border effects) were harvested. Fresh beet root weight was recorded using a calibrated scale and subsequently converted to yield expressed in tons per hectare (t ha^{-1}).

Data Analysis

All statistical analyses were performed using R statistical software, version 4.2.1. Before analysis, the beet yield and sugar yield were tested for normality [16]. Because some variables deviated from normality, a log transformation was applied to satisfy the assumptions of analysis of variance (ANOVA). To evaluate the presence and magnitude of genotype-by-environment interaction, a combined ANOVA was conducted across environments. In this combined analysis, each combination of year and location was treated as

a distinct and autonomous environment. The combined ANOVA was based on the additive main effects and multiplicative interaction (AMMI) model, in which genotypes were treated as fixed factors and environments as random variables [17]. The AMMI model integrates the main (additive) effects of genotypes and environments with multiplicative interaction terms derived from principal component analysis (PCA), thereby providing a robust framework for interpreting GEI. The AMMI analysis was implemented using the Agricolae package in R. For graphical visualization of genotype and environment relationships, a GGE biplot (genotype + genotype-by-environment biplot) was constructed using the GGEBiplotGUI package. In the GGE biplot, the term G+GE*G*+*GE* (i.e., genotype main effect plus interaction) was subjected to singular value decomposition, and the first two principal components were retained for biplot generation.

AMMI Analysis

The AMMI model's RY and SY were examined. AMMI stands for additive main effect and multiplicative interaction. Because in the validity test, the MS component of the RCBD design for the block within replication is less than the residual error across all sites, the analysis of variance was a combined analysis based on the RCBD. The main effects and AMMI model were applied to analyze both RY (t ha^{-1}) and SY (t ha^{-1}). The AMMI model combines a standard two-way analysis of variance (ANOVA) for the main (additive) effects of genotypes (G) and environments (E) with a principal component analysis (PCA) of the genotype-by-environment (GE) interaction residuals, thereby partitioning the multiplicative interaction into a series of orthogonal axes (interaction principal components, IPCs)[18]:

$$Yij=\mu+Gi+Ej+\sum k=1n\lambda k\alpha ik\gamma jk+\varepsilon ij \quad (1)$$

$$Yij=\mu+Gi+Ej+\lambda 1\alpha i1\gamma j1+\lambda 2\alpha i2\gamma j2+\varepsilon ij \quad (2)$$

where: *Yij* = mean yield of the *i*th genotype in the *j*th environment, μ = grand mean over all

genotypes and environments, Gi = deviation of the ith genotype from the grand mean (main additive effect of genotype), Ej = deviation of the jth environment from the grand mean (main additive effect of environment), $\lambda 1$ and $\lambda 2$ = singular values for the first and second interaction principal component axes (square roots of the corresponding eigenvalues of the interaction matrix), $\alpha i1$,$\alpha i2$= genotype principal component scores for IPC1 and IPC2, respectively, $\gamma j1$, $\gamma j2$= environment principal component scores for IPC1 and IPC2, respectively, εij = residual error term, assumed to be independently and normally distributed with mean zero and constant variance.

AMMI stability value (ASV) for genotype ranking

The standard AMMI analysis, while effective at partitioning GE interaction into interpretable principal components, does not provide a single quantitative measure for directly ranking genotypes by their stability across environments. To address this limitation, [19] proposed the AMMI stability value (ASV), which integrates the weighted scores of the first two interaction principal components (IPC1 and IPC2) into a single scalar index. The ASV quantifies the relative stability of each genotype: lower ASV values indicate greater stability, whereas higher ASV values indicate lower stability (i.e., stronger sensitivity to environmental changes).

The ASV is calculated as the distance from the origin in a two-dimensional scatter plot of IPC1 versus IPC2 scores, with weighting applied to account for the proportion of the GE interaction sum of squares explained by each IPC axis. The formula, as described by [19] is:

$$\text{ASVi}=\sqrt{\left(\frac{\text{SSIPC1}}{\text{SSIPC2}}\times \text{IPC1i}\right)^2+(\text{IPC2}i)^2} \quad (3)$$

where: ASVi= AMMI stability value for the ii-the genotype, *SSIPC1 and SSIPC2* = the sum of squares explained by the first and second interaction principal components, respectively (obtained from the AMMI analysis output), IPC1i and IPC2i = the genotype scores (principal

component scores) on the first and second IPC axes, respectively, The ratio $\frac{SSIPC2}{SSIPC1}$ serves as a weight, giving greater importance to IPC1 because it typically explains a larger proportion of the GE interaction variance.

Genotype Selection Index (GSI) Analysis

To simultaneously select genotypes based on both mean yield performance and stability across environments, the genotype selection index (GSI) was calculated following the method proposed by Farshadfar [20] The GSI combines two independent rankings into a single composite criterion, allowing for the identification of genotypes that exhibit both high yield and high stability. The GSI is computed as:

$$GSI_i = R(ASV)_i + R(Y)_i \quad (4)$$

where: GSI*i* = genotype selection index for the i*i*-the genotype, *R*(ASV)*i* = rank of the i*i*-the genotype based on its AMMI stability value (ASV), with genotypes ranked in ascending order (lowest ASV = rank 1), *R*(Y)*i* = rank of the i*i*-the genotype based on its mean yield (t ha^{-1}) across all environments, with genotypes ranked in descending order (highest yield = rank 1).

Gene Environment Biplot

Based on the singular value decomposition (SVD) of the first two principal components, the model for a GGE biplot is expressed as Yan et al., [21].

$$Yij - \mu - Ej = \lambda 1 \varepsilon i1 \eta j1 + \lambda 2 \varepsilon i2 \eta j2 + \varepsilon ij \quad (5)$$

where: Yij = mean yield of the ith genotype in the jth environment; μ = grand mean; Ej = main effect of the jth environment (deviation from μ), λ1 and λ2 = singular values for PC1 and PC2; Ɛi1, Ɛi2 = genotype scores for PC1 and PC2, respectively; ηj1,ηj2 = environment scores for PC1 and PC2, respectively; εij = residual error term.

Results

1. AMMI

1.1. AMMI ANOVA

Application of the AMMI model to twelve sugar beet genotypes cultivated across five locations revealed that RY and SY (t ha^{-1}) were significantly influenced ($p < 0.001$) by the main effects of environment (E) and genotype (G), as well as their interaction.

The AMMI-based analysis of variance (Table 2) revealed that the first interaction principal component (IPCA1) was highly significant ($p < 0.001$), confirming a pronounced GE interaction that substantially differentiated yield performance among the studied sugar beet genotypes. This significant interaction, in turn, suggests the feasibility of selecting either broadly stable genotypes or those specifically adapted to particular target environments. These findings are consistent with prior reports that have similarly emphasized the significant role of GE interactions in sugar beet.

Based on the sum-of-squares partitioning (Table 2), the variance in RY was primarily attributed to the GE interaction (32.7%), followed by genotype (22.6%) and environment (12.0%). Conversely, for SY, the environment accounted for the largest proportion (29.4%), while the GE interaction and genotype contributed 25.6% and 19.3%, respectively. The substantially larger sum of squares for GEI relative to the genotype effect indicates marked differential genotypic responses across environments. Consequently, the prominent role of GE interaction in the total variance supports the targeted development of cultivars adapted to specific environments. The combined contributions of IPCA1 (57.0% and 44.7%) and IPCA2 (20.8% and 32.0%) accounted for 77.8% and 76.7% of the total GEI sum of squares, with IPCA1 alone exceeding the genotype sum of squares.

Average RY across genotypes ranged from 56.7 t ha^{-1} (Homa, G6) to 79.8–79.9 t ha^{-1} (Arta,

G2, and Arya, G3), whereas mean RY across environments varied from 62.9 t ha^{-1} at E2(Torogh) to 81.3 t ha^{-1} at E1 (Table 3). Genotype ranking orders differed among environments, indicating crossover-type GEI for several genotypes, except for G2 (Arta) and G3 (Arya), which maintained consistently higher yields across all conditions (Table 3). Specifically, G2 (Arta) ranked top at E2(Torogh) and E4 (Mahidasht), G3 (Arya) ranked top at E1(Kamal-Abad) and E5(Miandoab), and G9 (Nika) ranked top at E3(Zarghan) (Table 3).

For SY, genotypic means ranged from 9.3 t ha^{-1} (Homa, G6) to 13.5 t ha^{-1} (Arta, G2), while environmental means ranged from 10.9 t ha^{-1} at E4 (Mahidasht) to 13.4 t ha^{-1} at E3(Zarghan) (Table 3). Crossover GEI was observed for several genotypes, except for G2(Arta) and G9 (Nika), which exhibited the highest SY across environments and maintained stable rankings (Table 4). The top-ranking genotypes were G1(Agatella) at E1(Kamal-Abad), G9(Nika) at E2(Torogh) and E3(Zarghan), G12(Tara) at E4(Mahidasht), and G2(Arta) at E5(Miandoab) (Table 3).

1.2. AMMI Biplot

The AMMI1 biplot (Fig. 2) is divided into four quadrants, with high-yielding environments located in quadrants 2 and 3, and low-yielding ones in quadrants 1 and 4. The greater dispersion of genotype points relative to environment points indicates higher genotypic variability, corroborating the ANOVA results (Table 2).

Genotypes with general adaptation are positioned near the IPCA = 0 axis (indicating negligible GE interaction) and to the right of the grand mean (indicating high mean performance). Accordingly, for RY, genotypes G12(Tara), G9(Nika), and G2(Arta), along with environments E3(Zarghan), E1(Kamal-Abad), and E5(Miandoab), were located to the right of the vertical axis (Fig. 2A).

For SY, genotype G9 (Nika) and environment E3 occupied this region (Fig. 2B). Genotypes

G10(Shokofa) and G11(Sina) exhibited weak environmental sensitivity (lower interaction effects) for both traits. Conversely, genotypes G6(Homa), G1(Agatella), and G4(Asia) demonstrated strong environmental influence (higher interaction effects, Fig. 2). However, lower environmental sensitivity did not necessarily correspond to higher RY or SY. Genotypes G10(Shokofa) and G11(Sina), positioned closest to the IPCA = 0 axis, were identified as adaptable, high-yielding, and stable across the tested environments, making them favorable candidates. Similarly, G2(Arta), G3(Arya), and G9(Nika) achieved high RY and SY with broad adaptability across all environments. In contrast, G6(Homa), G1(Agatella), and G4(Asia), which were located farther from the IPCA = 0 axis, produced low RY and SY (Fig. 2).

The contribution of individual environments to the GE interaction varied: E4 (Mahidasht) showed a modest contribution, E3(Zarghan) and E1(Kamal-Abad) a moderate contribution, and E2(Torogh) and E5(Miandoab) a significant contribution (Fig. 2). Environments E3(Zarghan), E1(Kamal-Abad) and E5(Miandoab) yielded mean RY and SY exceeding the overall means (75.7–81.3 t ha^{-1} for RY and 11.9–13.4 t ha^{-1} for SY), indicating that they were the most suitable locations for identifying high-yielding genotypes. The highest-potential environments (E1(Kamal-Abad) and E3(Zarghan)) exhibited differential genotypic responses for both traits and were characterized by strongly positive IPCA1 scores (Fig. 2).

The AMMI2 biplot analysis of RY and SY accounted for 77.8% and 76.9% of the total GE interaction sum of squares, respectively, with the IPCA1 and IPCA2 explaining 44.7–57.0% and 20.8–32.0% of the variation. This model effectively delineated the specific adaptation patterns of the genotypes across the test environments. The AMMI 1 biplot links the variance of genotypes with the environmental effects, aiding in setting apart stable genotypes and selecting the best environment. AMMI 1 depicts the IPCA1score against the mean of RY and SY for both environments and the genotypes. The IPCA1 score for RY and SY was observed to be 57% and 44.7%, respectively (Fig. 2A, B). Genotypes G2 (Arta), G10 (Shokofa), G5

(Dena), and G7 (Hosna) for root yield and genotypes G11 (Sina), G10 (Shokofa), G5 (Dena), and G3 (Arya) for sugar yield were closer to the origin (zero IPC1 score), indicating that they recorded almost zero scores on the first IPC1. In contrast, genotypes such as G1 (Agatella), G6 (Homa), and G8 (Kimya) were far from the origin. Furthermore, the mean performance of environments or genotypes in AMMI 1 falling on the same parallel line about the ordinate was similar. The genotypes placed on the right side (first and fourth coordinates) of the biplot exhibited higher yield, among which the highest ones were G3 (Arya) and G2 (Arta), for RY and SY, respectively. However, the genotypes placed on the left side of the center of the axis exhibited poor yield, among which the poorest ones were G6 (Homa) and G8 (Kimya).

AMMI 2 biplot of pigeon pea genotypes is illustrated in Figure 2B. AMMI 2 denotes the genotype × environment interaction to understand the response of genotypes in each test environment. The first two IPCs (IPC1 and IPC2) explained 77.8% (57% and 20.8%, respectively) and 76.7% (44.7% and 32%, respectively) of the total variation for RY and SY, respectively. Genotypes G1 (Agatella), G7 (Hosna), G4 (Asia), G9 (Nika), and G6 (Homa), in plot RY, and genotypes G5 (Dena), G2 (Arta), G1 (Agatella), G6 (Homa), and G8 (Kimya), in plot of SY were placed more distant from the origin and occupied the vertices of the polygon. Environment E2(Torogh) in root yield had the highest score on the IPC1, followed by E3(Zarghan), but the highest score on the IPC1 of RY was recorded by E3(Zarghan). However, the relatively lowest environmental score was observed for E4(Mahidasht). For the RY, it was observed that genotypes G3 (Arya), G7 (Hosna), and G1 (Agatella), specifically adapted to E1(Kamal-Abad), whereas G11 (Sina), G2 (Arta), G6(Homa) to E2 (Torogh), and G8(Kimya), G10(Shokofa) specifically adapted to E3(Zarghan) and G4 (Asia) specifically adapted to E5(Miandoab). For the SY, it was observed that genotypes G5 (Dena), and G2 (Arta), specifically adapted to E5(Miandoab), whereas G9 (Nika), G8 (Kimya), to E2 (Torogh) and G6 (Homa), G12(Tara) specifically adapted to E3(Zarghan) and E4(Mahidasht) and

G1(Agatella), G4(Asia) specifically adapted to E1(Kamal-Abad). It was determined using AMMI 2 that genotypes G12 (Tara), G5 (Dena), G10 (Shokofa), and G3(Arya) were grouped in proximity to the origin.

The principal outcome derived from the WAAS index is illustrated in a two-way biplot, which incorporates both the index and yield, categorizing the examined genotypes and test conditions into four distinct sections. The first section (I) includes genotypes that have lower yield than average and contribute significantly to GEI. This quadrant also includes environments with high discriminatory ability. The second section (II) includes unstable, highly productive genotypes and environments that effectively discriminate between genotypes. The third section (III) includes low-yielding genotypes with broad adaptation; environments here have low discriminatory ability. The fourth section (IV) has the highest significance and features genotypes that have above-average productivity along with high stability. Nevertheless, the environments within this section are productive but possess low discriminatory power.

The result RY showed that genotype G6(Homa) and environments E2 (Torogh) were classified in the first quadrant. The second portion included genotypes G4(Asia), and G1(Agatella) in conjunction with environments E5(Miandoab), E3(Zarghan), and E1(Kamal-Abad). Genotypes G6(Homa), G8(Kimya), and G11(Sina) were located in the third segment. The fourth segment included genotypes G2(Arta), G7(Hosna), G9(Nika), and G10(Shokofa). Genotype G3(Arya) was situated near the demarcation between the second and fourth portions (Fig. 3A). Also, the result SY showed that genotypes G6(Homa), G8(Kimya), and environments E2(Torogh), E1(Kamal-Abad), and E5(Miandoab) were classified in the first quadrant. The second portion included genotype G1(Agatella). Genotypes G5(Dena) and G12(Tara) were located in the third segment. The fourth segment included genotypes G2(Arta), G3(Arya), G7(Hosna), G9(Nika), and G10(Shokofa). Genotypes G4(Asia) and G12(Tara)

were situated near the demarcation between the second and fourth portions (Fig. 3B).

For the simultaneous selection of genotypes with MPS, we used a unique integrated stability parameter based on WAASB that combines the features of both AMMI and BLUP models. Genotypes G2 (Arta), G10 (Shokofa), G12(Tara), G9 (Nika), G3(Arya), G7(Hosna), and G5 (Dena) showcased the highest WAASBY values for RY (Fig. 3) and ranked as the most stable genotypes in the described order. Consequently, two of these G10(Shokofa), G3(Arya), G2(Arta), G7(Hosna), G9(Nika) and G11(Sina) also exhibited highest WAASB values for SY. This parameter is effective in identifying stable genotypes in METs.

Ranged genotypes by IPAs heatmap in Fig 4. For RY, genotypes G2(Arta), G10(Shokofa), G12(Tara), and G5(Dena) had the lowest 1PCA scores, while genotypes G6(Homa), G1(Agatella), and G3(Arya) had the highest scores, and the remaining genotypes were in an intermediate category. In terms of SY, genotypes G11(Sina), G10(Shokofa), and G3(Arya) showed the lowest PCA scores, whereas, based on their heights, PCA scores of genotypes G6(Homa) and G9(Nika) were found to be the least performing (Fig. 4A, B).

The WAASY index evaluated the genotypes according to their performance and stability. This technique assigns each genotype a yield performance ratio and a stability ratio, allowing for the selection of genotypes that score highest in both performance and stability as high-yielding and stable genotypes. Figure 3 presents the ranking pattern for the examined genotypes. Accordingly, genotypes G2(Arta), G10(Shokofa), G12(Tara), G9(Nika), G3(Arya), and G7(Hosna) with a performance: stability ratio of 50:50 was identified as the best for RY. genotypes G3(Arya), G10(Shokofa), G2(Arta), G7(Hosna), and G12(Tara) with a performance: stability ratio of 50:50 was identified as the best for SY. Genotypes G2(Arta), G3(Arya), and G9(Nika) had higher values for some stability: performance ratios, indicating they may be more adapted to specific environments (Fig. 4, B, D).

AMMI nominal yield plots presented in Figure 5 show the stability of the 12 genotypes in five different environments (E1-E5). The nominal yield plots have a complementary advantage over AMMI stability indexes because they integrate and visualize information on productivity and stability. Genotypes G3(Arya) and G4(Asia) were the most productive as RY genotypes across environment E5. However, in terms of stability alone (without considering RY), G2(Arta) had a gentle slope and was observed to be the most stable across genotypes. When the environments E2(Torogh), E3(Zarghan), and E4(Mahidasht) were evaluated, we still observed that G9(Nika) and G2(Arta) had the highest RY and gentle slopes showing higher stability (Fig. 5, A). Foremove G2(Arta) and G1 (Agatella) were the most productive as SY genotypes across environment E5. However, G11(Sina) and G4(Asia) had a gentle slope and were observed to be the most stable across genotypes. Under the environments E2(Torogh), E3(Zarghan), and E4(Mahidasht), G9(Nika) and G11(Sina) had the highest SY and gentle slopes showing higher stability (Fig. 5, B).

1.3. AMMI Stability Value (ASV)

An AMMI stability value was computed to determine the stability of the genotypes (Tables 4 and 5). ASV is the distance from zero in a two-dimensional scatter graph comparing IPCA1 scores to IPCA2 scores. The difference in stability measurements between the two primary components can be made up for using the proportional difference between the IPCAs (1:2), which can then be calculated using the Pythagorean theorem to account for the AMMI stability value. The AMMI stability value (ASV) quantifies and ranks genotypes based on their yield stability rather than providing a quantitative stability indicator.

In this respect, greater ASV values are associated with unstable genotypes, whereas genotypes with lower ASV values are associated with more stable genotypes. The genotypes G1(Agatella), G4(Asia), and G6(Homa) were the most unstable in terms of RY, with ASV values of 8.05, 8.14, and 8.65, respectively (Table 3). Genotype G2 (Arta) was the most stable,

with an ASV value of 1.41, followed by genotype G10 (Shokofa), with an ASV value of 1.96, in RY. The genotypes G1(Agatella) and G6 (Homa) were the most unstable in terms of SY, with ASV values of 1.65 and 2.19, respectively (Table 4). Genotype G10 (Shokofa) was the most stable, with an ASV value of 0.29, followed by genotype G3 (Arya), with an ASV value of 0.61, in SY.

Furthermore, the SI estimated for test genotypes across environments for RY ranged from very low (3%) for G2 (Arta) to high (24%) for G6 (Homa), and for SY ranged from very low (6%) for G2 (Arta) to high (24%) for G6 (Homa). Among all the best three genotypes with the lowest SI values, G2 (3% and 6%) had the lowest ASVs as well and performed higher than the trial means for RY and SY (Table 4, 5).

The YSI was determined based on the rank of the mean yield of genotypes and the rank of the AMMI stability value (RASV) for test genotypes, and it was observed that the lowest YSI was observed for G2 (Arta) of approximately 3 and 6 for root and SY, respectively, and the highest for G6 (Homa) of approximately 24. The best genotypes identified based on the mean RY and SY, ASVs, and YSI are presented in Table 5.

1.4. Genotype Selection Index Analysis

Genotype Selection Index (GSI), as a single selection index, combines the rank of ASV and the rank of mean yield. The lowest GSI value, with a high mean yield, is regarded as the most stable. The smallest GSI is considered the most stable (Table 4, 5); in that regard, the most stable genotypes with the highest RY and SY were G2(Arta), which had the lowest GSI values of 3. These genotypes were followed by G10(Shokofa) and G12(Tara), which had GSI values of 8 and 7, respectively, suggesting that they were stable and high-yielding.

2. GGE Biplot

2.1. Mean performance vs. stability

The average environment (tester) coordinate (AEC) methods were used in the GGE biplot to determine mean RY and genotype stability (Fig. 6). The average PC1 and PC2 scores across all environments are used to define the average environmental (tester) coordinate (AEC). The mean root yield performance axis of genotypes is indicated by the AEC X axis (PC1) line that goes through the biplot's origin and has an arrow pointing in the direction of the positive end. The stability of genotypes (PC2) is measured using the line that runs through the origin and is perpendicular to the average environmental axis. Stable genotypes had PC2 scores that were practically zero, were close to AEC (PC1), and had the lowest number of perpendicular lines. Away from the biplot origin, however, any direction on the axis denotes a greater GE interaction and a lower level of stability. The best genotypes for selection criteria are those with both high mean yield and high stability. In this regard, in the present study, the single arrowed line pointed to a higher yield across environments. Therefore, genotype G2(Arta) had the highest mean root yield, followed by G3(Arya). They were the most stable, while G1(Agatella), G4(Asia), and G6(Homa) were highly unstable, and among them, G6(Homa) performed poorly. Genotypes G2(Arta) and G7(Hosna) had the highest mean sugar yield and were the most stable (Fig. 6).

2.2. Which-won-Where

Use of a polygon view of "which-won-where" biplot is a key component of the GGE, which helps to visualize the interaction patterns between genotypes and environments, to show the presence of crossover GEI, mega environment differentiation, and specific adaptation. Figure 6 illustrates the polygon view of the GGE biplot pattern of RY and SY. The IPCA1 and PCA2 of G + GE biplot accounted for 76.6% and 78.6% of the total variation for RY and SY, respectively.

The test environments fell into one of the five sectors and two of the six sectors, outlined on the polygon view for RY and SY, respectively. The RY has one mega environment including E5(Miandoab), E1(Kamal-Abad), and E4(Mahidasht), two mega-environments for SY with E1(Kamal-Abad), E4(Mahidasht) grouped together in a mega-environment, while E5(Miandoab) and E3(Zarghan) are in the second mega-environment. G9(Nika), G2(Arta), G3(Arya), and G1(Agatella) are the vertex genotypes identified for RY, and they are the most responsive to environmental interaction. The most responsive genotypes forming the vertices of SY were G1(Agatella), for the first mega environment, with one mega environment G2(Arta) and G9(Nika), for the second mega-environment. Some vertex genotypes fell into sectors having no test environment, for instance, G6(Homa), G8(Kimya), G11(Sina), G5(Dena), and G10(Shokofa).

2.3. Discriminativeness vs. representativeness

Selection of an optimal test environment is of utmost importance in the implementation of a successful breeding strategy that results in the identification and cultivation of superior genotypes. Figure 7 depicts the 'Discriminativeness vs. representativeness' view of GGE biplots for four traits being investigated, denoted as patterns A and B. The vector length associated with each environment provided insight into the discriminatory capacity of the environment, while the angle produced by each vector with the abscissa indicated the level of representativeness. Environments characterized by longer vectors demonstrate a greater propensity for classifying genotypes in comparison to environments characterized by shorter vectors.

The vector with the smallest magnitude among the patterns was E4(Mahidasht) and E3(Zarghan) for RY and SY, respectively, whereas the vector with the largest magnitude was seen for E5(Miandoab). The measurements of angles formed by the environment in relation to the abscissa line were also documented. In the context of RY and SY, it was observed that the

angle formed by E4(Mahidasht) and E3(Zarghan) was the shortest, while the angles formed by E2 (Torogh) were found to be the longest. Nevertheless, an environment characterized by a longer vector that creates a smaller angle with the AEC abscissa line is considered optimal for the identification and selection of superior genotypes. Among the various patterns, it was observed that E4 (Mahidasht) and E3 (Zarghan) exhibited a tiny angle in conjunction with a lengthy vector, where the AEC abscissa indicated that the test environment was both representative and capable of distinguishing itself from other settings. The biplot analysis revealed that the E1(Kamal-Abad) environment exhibited the highest proximity to the AEC across all the attributes examined (Fig. 7).

2.4. Ranking genotypes

The application of a biplot enabled the determination of the optimal and most desirable genotype from a set of 12 genotypes that were assessed. The ideal genotype is consistently located within the middle region and in close proximity to the peak of the arrow within the circular band, as illustrated in Figure 7. In the instance of RY, it was noted that genotype G2(Arta) was located within the inner circle and considered to be optimal. The genotypes that exhibited close spatial closeness to the inner circle were G8(Kimya) and G1(Agatella). In contrast, it was seen that G6(Homa) exhibited the greatest distance from the arrowhead in the plot, whereas G7(Hosna) followed suit in terms of their proximity to the arrowhead. In the specific instance of SY (Fig. 7 B), it was observed that the genotype G7(Hosna) demonstrated the closest proximity to the ideal genotype, followed by G3(Arya) and G2(Arta). Conversely, genotypes G10(Shokofa) and G9(Nika) were situated further away from the innermost circle.

Discussion

Genotype × environment interaction can substantially affect sugar beet yield and complicate the identification and recommendation of consistently performing genotypes [3,22]. Although

agronomic practices such as irrigation scheduling and nitrogen management can alleviate some environmental stresses [23], the evaluation of genotypes across multiple environments remains important for identifying materials with stable and/or specifically adapted performance [24].

The considerable variation observed among the 12 genotypes for RY (56.7–79.9 t ha^{-1}) and SY (9.3–13.5 t ha^{-1}) indicates substantial differences in yield performance among the evaluated genotypes and is consistent with previous reports of genetic variation in commercial and pre-breeding sugar beet germplasm [25,26]. The AMMI-based ANOVA indicated that GEI accounted for a greater proportion of the total variation in RY than the genotypic main effect (32.7% vs. 22.6%). This finding highlights the importance of environmental conditions in determining the expression of genetic differences for root yield. Such responses are expected in root crops because biomass accumulation can be influenced by temperature, soil moisture, and other environmental factors [23]. For SY, environment accounted for the largest proportion of the total variation (29.4%), indicating a substantial environmental influence on sucrose accumulation. This result is consistent with previous reports indicating that sugar accumulation in sugar beet can be affected by temperature and other environmental conditions during the later stages of crop development [27]. The significance of IPCA1 indicated a significant component of GEI and was reflected in changes in genotype rankings across environments. For example, G9 (Nika) ranked highly at E3 (Zarghan) but did not show the same relative performance at E2 (Torogh). Such crossover interactions indicate that the relative performance of genotypes can change according to environmental conditions. Similar GEI patterns have been reported in sugar beet and other crops [28,29]. Consequently, both broadly adapted genotypes and genotypes with specific adaptation may be useful depending on the objectives of cultivar selection and the target environments.

The AMMI1 biplot provided a useful visualization of genotype performance and interaction patterns. For RY, G2 (Arta), G9 (Nika), and G12 (Tara) were positioned to the right of the

grand mean and relatively close to the IPCA = 0 axis, indicating above-average yield with comparatively small interaction effects. Such a position is generally associated with relatively broad adaptation and stable performance across the environments evaluated [30]. The genotypes G2 (Arta), G9 (Nika), and G12 (Tara) were placed to the right of the grand mean and near the IPCA = 0 axis, indicating high RY and low interaction, a feature of wide adaptability. G9 (Nika) did well in this region for SY as well. These findings are in line with previous findings in sugar beet (Pandey et al., 2016) and other root crops [31], where genotypes closer to the origin of AMMI1 are desirable for commercial deployment. However, G10 (Shokofa) and G11 (Sina) had very low IPCA values but moderate yields, which implies they could be used as stable donors in breeding programs even if they were not the highest-yielding varieties. Importantly, the AMMI2 biplot further analysis of specific adaptation patterns showed that G3 (Arya), G7 (Hosna), and G1 (Agatella) were specifically adapted to E1 (Kamal-Abad) for RY, while G9 (Nika) and G8 (Kimya) performed best at E2 (Torogh) for SY. Such environment-specific superiority is often attributed to local edaphic or climatic factors, as shown by Cattivelli et al [32] in cereal systems, and indicates the need for decentralized selection.

The WAASBY index, which integrates the WAASB stability parameter with yield performance [33], provided an additional criterion for simultaneous assessment of productivity and stability. For RY, G2 (Arta), G7 (Hosna), G9 (Nika), and G10 (Shokofa) were located in the desirable quadrant characterized by relatively high yield and stability. For SY, G2 (Arta), G3 (Arya), G7 (Hosna), and G9 (Nika) also showed favorable combinations of yield and stability. The WAASBY results were generally consistent with the ASV results, with G2 (Arta) showing low ASV values for both RY (1.41) and SY (0.29), as well as favorable YSI and GSI rankings. The agreement among several stability measures increases confidence that G2 performed favorably across the environments evaluated. However, these results should be

interpreted as evidence of favorable performance within the tested environments rather than as proof that G2 is universally superior or an intrinsically ideal genotype. Similar studies have emphasized the value of combining multiple stability measures to obtain a more comprehensive assessment of genotype performance [34,35].

The GGE biplot "which-won-where" polygon revealed the existence of distinct mega-environments. For RY, a single mega-environment comprising E5 (Miandoab), E1 (Kamal-Abad), and E4 (Mahidasht) was identified, with G3 (Arya) and G9 (Nika) as winning genotypes. For SY, however, two mega-environments emerged: the first (E1 and E4) won by G1 (Agatella), and the second (E5 and E3) won by G2 (Arta) and G9 (Nika). Such differentiation is common in crops with a broad geographic distribution [36] and underscores the importance of environment-specific breeding. Notably, vertex genotypes that fell into sectors devoid of test environments (e.g., G6/Homa, G8/Kimya) indicate unpredictable responses and should be viewed cautiously, as they may possess undesirable instability traits. The identification of mega-environments enables breeders to streamline testing networks and allocate resources more efficiently; a strategy successfully applied in sorghum [37] and chickpea [38].

The discriminativeness versus representativeness view of the GGE biplot identified E4 (Mahidasht) as a highly representative environment for RY and E3 (Zarghan) as a strongly discriminating environment for SY. These characteristics suggest that E4 may provide useful information about genotype performance under the set of environments evaluated for RY, whereas E3 may be particularly useful for differentiating genotypes for SY. E1 (Kamal-Abad) showed relatively high representativeness but moderate discrimination, indicating that it may provide useful information for assessing genotype performance while offering less differentiation among genotypes than the more discriminating environments. Nevertheless, the usefulness of these environments as representative or discriminating testing sites should be

confirmed through additional years and environments. The ranking biplot further confirmed G2 (Arta) as the genotype closest to the ideal genotype for RY, while G7 (Hosna) took that position for SY, echoing earlier findings that different traits may be governed by distinct genetic architectures [39].

The physiological and genetic mechanisms underlying the observed stability patterns were not directly investigated in the present study and therefore remain hypothetical. The favorable performance of G2 (Arta) across the tested environments could potentially be associated with physiological or morphological characteristics such as root architecture, assimilate partitioning, sucrose transport, or osmotic adjustment; however, these mechanisms require direct physiological and genetic investigation before causal relationships can be established. Similarly, the relatively favorable performance of G9 (Nika) in particular environments may reflect responses to local climatic or edaphic conditions, but the specific mechanisms responsible cannot be determined from the present dataset. Therefore, these possible explanations should be considered hypotheses for future research rather than direct conclusions from this study.

The integration of AMMI, GGE biplot, and WAASB-based approaches provided complementary information on genotype performance and GEI. AMMI was useful for quantifying GEI and visualizing interaction patterns, GGE biplot analysis facilitated the assessment of genotype-environment associations and environmental differentiation, and WAASB-based measures enabled simultaneous consideration of stability and yield performance [30,33]. The general agreement among these approaches, particularly regarding the favorable performance of G2 (Arta), provides convergent evidence that G2 performed well across the environments included in this study. However, the results should not be interpreted as demonstrating that G2 is unequivocally superior under all environments or production

conditions. Differences among methods and traits also indicate that genotype selection may depend on the specific breeding objective and target environment.

The observed differences between yield potential and stability among some genotypes may also have practical implications for breeding. For example, a genotype showing high performance in a particular environment but greater GEI may still be useful as breeding material if its specific adaptation or other desirable traits are of interest. However, the value of such genotypes as parents cannot be determined from yield and stability data alone and would require additional information on combining ability, disease resistance, quality traits, and other agronomic characteristics [40,41].

A number of limitations should be considered when interpreting these findings. First, the study included 12 genotypes and five environments, and therefore the identified patterns of adaptation and mega-environment differentiation represent the environmental conditions sampled in this experiment and should not be generalized directly to all sugar beet production environments in Iran. Second, additional years and environments would be useful for determining whether the observed genotype rankings and stability patterns remain consistent under different climatic conditions. Third, the present study focused primarily on yield-related traits and stability parameters; physiological, disease-resistance, quality, and other agronomic characteristics were not incorporated into the selection criteria. Finally, although the agreement among AMMI, GGE, and stability-based methods provides useful evidence, validation through independent multi-year and multi-environment trials is necessary before making broad recommendations for cultivar deployment. Within these limitations, G2 (Arta) can be considered a promising genotype for further evaluation because it combined high yield with favorable stability across the environments tested in this study.

Conclusions

In conclusion, the combined AMMI and GGE biplot analyses demonstrated that genotype × environment interaction (GEI) substantially influenced sugar beet performance across the tested environments, highlighting the importance of considering both yield potential and stability when evaluating genotypes. Among the evaluated genotypes, G2 (Arta) showed the highest mean performance and favorable stability based on the combined results of ASV, WAASB, GSI, and GGE biplot analyses. These results indicate that G2 (Arta) has promising performance and relatively broad adaptation across the environments evaluated in this study. Genotypes G10 (Shokofa), G9 (Nika), and G3 (Arya) also showed favorable combinations of yield performance and stability, while G9 and G1 exhibited adaptation to specific environments or mega-environments. Among the test environments, E4 (Mahidasht) showed high representativeness, whereas E1 (Kamal-Abad), E3 (Zarghan), and E5 (Miandoab) provided useful discrimination among genotypes and may therefore be valuable for genotype evaluation. Overall, the findings suggest that G2 (Arta), together with genotypes showing specific adaptation to target environments, could be considered promising material for sugar beet production and breeding programs under environments similar to those evaluated in this study. However, further multi-year and multi-environment testing is required to confirm the stability, adaptability, and consistency of these genotypic responses before making broader recommendations for commercial cultivation across Iran.

Acknowledgments The authors thank the Sugar Beet Seed Institute (SBSI), Karaj, Iran, for helping to conduct the experiments.

Author contributions Conceptualization, G.P., P.F., H.H, and M.B; methodology, F.H. and D.T.; software, G.P.; validation, G.P.; formal analysis, G.P.; investigation, F.H.; resources, P.F.; data curation, G.P., P.F., H.H, and M.B, S.D.; writing-original draft preparation, G.P.;

writing-review and editing, P.F. All authors have read and agreed to the published version of the manuscript

Data availability: The datasets used and/or analyzed during the current study available from the corresponding author on reasonable request.

Declaration of competing: the authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Research funding: This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

References

1. Ćirić, M. *et al.* Sugar beet: perspectives for the future. *Sugar Tech* **26**, 1208–1219 (2024).
2. De Lucchi, C. *et al.* Sugar beet (Beta vulgaris Ssp. Vulgaris L.) improvement with next-generation breeding technology. in *Advances in Plant Breeding Strategies: Vegetable Crops: Volume 8: Bulbs, Roots and Tubers* 305–343 (Springer, 2021).
3. Stevanato, P. *et al.* Sustainability of the sugar beet crop. *Sugar Tech* **21**, 703–716 (2019).
4. McGrath, J. M. & Panella, L. Sugar beet breeding. *Plant Breed. Rev.* **42**, 167–218 (2018).
5. Pour-Aboughadareh, A., Khalili, M., Poczai, P. & Olivoto, T. Stability indices to deciphering the genotype-by-environment interaction (GEI) effect: An applicable review for use in plant breeding programs. *Plants* **11**, 414 (2022).
6. Srivastava, A. K. & Rai, M. K. Sugarcane production: Impact of climate change and its mitigation. *Biodiversitas* **13**, 214–227 (2012).
7. Xu, Y. *et al.* Smart breeding driven by big data, artificial intelligence, and integrated genomic-enviromic prediction. *Mol. Plant* **15**, 1664–1695 (2022).

8. Aono, A. H., Ortiz, R. & Chawade, A. Integrating Genomic and Phenomic Data Improves Prediction of Key Traits in Potato Breeding. *Hortic. Res.* uhag175 (2026).

9. Bocianowski, J., Niemann, J. & Nowosad, K. Genotype-by-environment interaction for seed quality traits in interspecific cross-derived Brassica lines using additive main effects and multiplicative interaction model. *Euphytica* **215**, 7 (2019).

10. Wodebo, K. Y. *et al.* AMMI and GGE biplot analyses for mega-environment identification and selection of some high-yielding oat (Avena sativa L.) genotypes for multiple environments. *Plants* **12**, 3064 (2023).

11. Mortazavian, S. M. M. *et al.* GGE biplot and AMMI analysis of yield performance of barley genotypes across different environments in Iran. (2014).

12. Ghaffari, M. *et al.* Stability and genotype× environment analysis of oil yield of sunflower single cross hybrids in diverse environments of Iran. *Euphytica* **217**, 187 (2021).

13. Sadeghi, S. M., Samizadeh, H., Amiri, E. & Ashouri, M. Additive main effects and multiplicative interactions (AMMI) analysis of dry leaf yield in tobacco hybrids across environments. *Afr. J. Biotechnol.* **10**, 4358 (2011).

14. Olanrewaju, O. S., Oyatomi, O., Babalola, O. O. & Abberton, M. GGE biplot analysis of genotype× environment interaction and yield stability in Bambara groundnut. *Agronomy* **11**, 1839 (2021).

15. Islam, S. S., Anothai, J., Nualsri, C. & Soonsuwon, W. Analysis of genotype-environment interaction and yield stability of Thai upland rice ('Oryza sativa'L.) genotypes using AMMI model. *Aust. J. Crop Sci.* **14**, 362–370 (2020).

16. Ahmad, W. M. A. W., Ghazali, F. M. M. & Yaqoob, M. A. *Basic Statistical Analysis Using RStudio Software*. (Penerbit USM, 2023).

17. Bomma, N. *et al.* Multi-environment testing for G× E interactions and identification of high-yielding, stable, medium-duration pigeonpea genotypes employing AMMI, GGE biplot, and YREM analyses. *Front. Plant Sci.* **15**, 1396826 (2024).

18. Gauch Jr, H. G. Model selection and validation for yield trials with interaction. *Biometrics* 705–715 (1988).

19. Purchase, J. L., Hatting, H. & Van Deventer, C. S. Genotype× environment interaction of winter wheat (Triticum aestivum L.) in South Africa: II. Stability analysis of yield performance. *South African Journal of Plant and Soil* **17**, 101–107 (2000).

20. Farshadfar, E. Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. *Pakistan Journal of biological sciences* **11**, 1791 (2008).

21. Yan, W., Hunt, L. A., Sheng, Q. & Szlavnics, Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.* **40**, 597–605 (2000).

22. Ober, E. S. *et al.* Evaluation of physiological traits as indirect selection criteria for drought tolerance in sugar beet. *Field Crops Res.* **91**, 231–249 (2005).

23. Hoffmann, C. M. & Kluge-Severin, S. Growth analysis of autumn and spring sown sugar beet. *European journal of agronomy* **34**, 1–9 (2011).

24. Poggio, S. L., Chaneton, E. J. & Ghersa, C. M. Landscape complexity differentially affects alpha, beta, and gamma diversities of plants occurring in fencerows and crop fields. *Biol. Conserv.* **143**, 2477–2486 (2010).

25. Tshikunde, N. M., Mashilo, J., Shimelis, H. & Odindo, A. Agronomic and physiological traits, and associated quantitative trait loci (QTL) affecting yield response in wheat (Triticum aestivum L.): a review. *Front. Plant Sci.* **10**, 1428 (2019).

26. Hosseinzadeh, A., Zhou, J. L., Altaee, A., Baziar, M. & Li, D. Effective modelling of hydrogen and energy recovery in microbial electrolysis cell by artificial neural network and adaptive network-based fuzzy inference system. *Bioresour. Technol.* **316**, 123967 (2020).

27. Bloch, D., Hoffmann, C. M. & Märländer, B. Impact of water supply on photosynthesis, water use and carbon isotope discrimination of sugar beet genotypes. *European Journal of Agronomy* **24**, 218–225 (2006).

28. Draycott, A. P. *Sugar Beet*. vol. 474 (Wiley Online Library, 2006).

29. Yan, W. & Kang, M. S. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. (CRC press, 2002).

30. Gauch Jr, H. G. Statistical analysis of yield trials by AMMI and GGE. *Crop Sci.* **46**, 1488–1500 (2006).

31. Adugna, A. Analysis of in situ diversity and population structure in Ethiopian cultivated Sorghum bicolor (L.) landraces using phenotypic traits and SSR markers. *Springerplus* **3**, 212 (2014).

32. Cattivelli, L. *et al.* Drought tolerance improvement in crop plants: an integrated view from breeding to genomics. *Field Crops Res.* **105**, 1–14 (2008).

33. Olivoto, T., Lúcio, A. D. C., da Silva, J. A. G., Sari, B. G. & Diel, M. I. Mean performance and stability in multi-environment trials II: Selection based on multiple traits. *Agron. J.* **111**, 2961–2969 (2019).

34. Singamsetti, A. *et al.* Genetic gains in tropical maize hybrids across moisture regimes with multi-trait-based index selection. *Front. Plant Sci.* **14**, 1147424 (2023).

35. Abdelghany, A. M., Lamlom, S. F. & Naser, M. Dissecting the resilience of barley genotypes under multiple adverse environmental conditions. *BMC Plant Biol.* **24**, 16 (2024).

36. Yan WeiKai, Y. W. & Kang, M. S. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. (2003).

37. Rakshit, S. *et al.* GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica* **185**, 465–479 (2012).

38. Farayedi, Y., Abdi, H., Ahakpaz, F., Kanouni, H. & Mahmoodi, A. A. Genotype and environment interaction analysis for grain yield of chickpea genotypes using AMMI and GGE biplot models. *Iranian Journal of Field Crop Science* **52**, 155–166 (2021).

39. Baldin, R. C. *et al.* Yield stability of common bean genotypes in the state of Santa Catarina, Brazil. *Pesqui. Agropecu. Bras.* **56**, e02302 (2021).

40. Ceccarelli, S. & Grando, S. Participatory plant breeding: who did it, who does it and where? *Exp. Agric.* **56**, 1–11 (2020).

41. Dia, M. *et al.* Genotype× environment interaction and stability analysis for watermelon fruit yield in the United States. *Crop Sci.* **56**, 1645–1661 (2016).

Figure legends

Fig. 1 Test environments, geographical location, and description in this study in Iran.

Fig.2 AMMI1 and AMMI2 biplots for root and sugar yield of sugar beet genotypes evaluated across environments. A: AMMI1 for RY, B: AMMI1 for SY; C: AMMI2 for RY; D: AMMI2 for SY.

Fig. 3 Plot view of GY x WAAS and WAASBY biplots of test genotypes of Sugar beet. A: GY x WAAS for RY, B: AMMI1 GY x WAAS for SY, C: WAASBY for RY, D: WAASBY for SY.

Fig. 4. Plot the heat map graphics of Ranks of Sugar beet genotypes depending on the number of PCAs used to estimate the WAAS and the WAAS/GY ratio. A: PCA used to estimate the WAAS for RY, B: WAAS/GY ratio for RY, C: PCA used to estimate the WAAS for SY, D: WAAS/GY ratio for SY.

Fig. 5 Plot view of nominal yield and environment biplots of test genotypes for RY and SY of Sugar beet. A: RY, B: SY.

Fig. 6 Plot view of ranking genotypes by means. stability (A, B) and ranking genotypes based on which-won-where (C, D) of sugar beet based on PC1 and PC2, showing G × E interactions of the 12 groundnut accessions under five locations. A: RY means. stability, B: SY means. stability, C: RY which-won-where, D: SY which-won-where.

Fig. 7 Plot view of ranking genotypes by Discriminativeness vs. representativeness (A, B) and ranking genotypes based on optimal genotype (C, D) of sugar beet based on PC1 and PC2, showing G × E interactions of the 12 groundnut accessions under five locations. A: RY discriminativeness vs. representativeness, B: SY discriminativeness vs. representativeness, C: RY ranking genotypes, D: SY ranking genotypes.

Authors and Affiliations

Ghasem Parmoon*[1]. Farhnaz Hamdi[2]. Dariush Taleghani[2]. Parviz Fasahat[2]. Hasan Hamidi[3]. Mohsen Bazrafshan[4]. Saeed Darabi[4].

Ghasem Parmoon
E-mail: Ghasem.parmoon@gmail.com

1. Sugar Beet Research Department, Kermanshah Agricultural and Natural Resources Research and Education Center, Education and Extension Organization (AREEO), Kermanshah, Iran.
2. Sugar Beet Seed Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
3. Razavi Khorasan Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO), Mashhad, Iran.
4. Fars Agricultural and Natural Resources Research and Education Center, Agricultural Research, Education and Extension Organization (AREEO), Shiraz, Iran.

751
752 **Table 1** Description of Sugar beet (*Beta vulgaris*) genotypes used for the study

No	Genotype name	Genotype code	Status	Company
1	Agatella	G1	Hs	KWS
2	Arta	G2	Rh+ Hs	SBSI
3	Arya	G3	Rh+ Hs	SBSI
4	Asia	G4	Rh+ Hs	SBSI
5	Dena	G5	Rh+Rs	SBSI
6	Homa	G6	B +Cb	SBSI
7	Hosna	G7	Rh+ Hs	SBSI
8	Kimya	G8	Rh	SBSI
9	Nika	G9	Rh+ Hs	SBSI
10	Shokofa	G10	Rh+ Hs	SBSI
11	Sina	G11	Rh+Rs	SBSI
12	Tara	G12	Rh+ Hs	SBSI

753 Rh: Rhizomania, Hs; Heterodera schachii, Rs; Rhizoctonia solani, B; Bolting, Cb; Cercospora beticola

754

755

756

757

758

759

760

761

762

763

764

765

766

767

768

769

Table 2 Combined analysis of variance from the AMMI model for Root yield and Sugar yield of Sugar beet genotypes.

Source	Df	RY			SY		
		S. S	M.S.	(%) SS Explained	S. S	M.S.	(%) SS Explained
Environments	4	21421.5	5355.4**	12.0	239.79	59.95**	29.4
Block	25	2929.5	117.2**	-	107.70	4.31	-
Genotypes	11	14084.6	1280.4**	22.6	452.02	41.09**	19.3
Interactions	44	18646.1	423.8**	32.7	656.23	14.91**	25.6
IPCA 1	14	10627.6	759.1**	57	293.64	20.97**	44.7
IPCA 2	12	3882.7	323.6**	20.8	209.73	17.48**	32.0
IPCA 3	10	2579.1	257.9**	13.8	111.01	11.10**	16.9
IPCA 4	8	1556.7	194.6**	8.3	41.86	5.23**	6.4
Residuals	275	17570.9	63.9	-	557.86	2.03	-
Total	403	93298.7	231.5	-	2669.84	6.62	-

Key: *** $p \leq 0.001$ and ** $p \leq 0.05$.

788

789 **Table 3 Combined** analysis of variance for root yield and sugar yield across testing locations.

Genotypes		RY (t/ha)						
		Environments					Genotypic Means	Rank
Code	Name	E_1	E_2	E_3	E_4	E_5		
G1	Agatella	87.8	53.3	65.4	66.2	90.1	72.6	7
G2	Arta	86.0	75.1	75.2	76.9	86.0	79.8	2
G3	Arya	99.3	64.1	74.9	69.3	91.8	79.9	1
G4	Asia	82.8	46.1	82.0	62.1	92.7	73.1	5
G5	Dena	71.0	58.9	70.1	58.7	83.9	68.5	9
G6	Homa	64.6	55.2	63.8	57.0	42.9	56.7	10
G7	Hosna	91.2	64.9	68.8	59.0	81.0	73.0	6
G8	Kimya	68.0	61.1	77.2	55.1	62.2	64.7	11
G9	Nika	77.9	73.2	91.4	63.8	82.9	77.8	3
G10	Shokofa	84.1	64.5	83.0	59.0	75.0	73.1	5
G11	Sina	81.2	75.4	74.4	54.8	72.1	71.6	8
G12	Tara	81.2	63.2	82.3	74.0	74.4	75.0	4
Environmental Mean		81.3(1)	62.9(4)	75.7(3)	63.0(4)	77.9(2)	72.2	
LSD (5%)		10.1	7.6	6.9	8.5	11.5		
CV (%)		11.0	10.7	8.0	11.9	13.0		
F value		**	**	**	**	**		
Genotypes		SY (t/ha)						
		Environments					Genotypic Means	Rank
Code	Name	E_1	E_2	E_3	E_4	E_5		
G1	Agatella	15.1	10.2	13.7	12.4	13.2	12.9	3
G2	Arta	13.6	13.8	12.5	12.6	15.1	13.5	1
G3	Arya	13.5	11.7	13.4	12.0	12.6	12.6	5
G4	Asia	12.3	8.7	14.5	10.8	14.0	12.1	6
G5	Dena	9.4	11.9	12.8	9.6	13.9	11.5	9
G6	Homa	8.8	9.8	12.3	9.9	5.8	9.3	11
G7	Hosna	14.6	12.7	12.3	10.9	13.2	12.7	4
G8	Kimya	8.5	11.8	13.6	9.3	9.2	10.5	10
G9	Nika	11.7	14.5	15.6	10.9	12.9	13.1	2
G10	Shokofa	11.6	11.4	14.1	10.1	11.3	11.7	8
G11	Sina	12.3	13.4	12.7	9.1	12.6	12.0	7
G12	Tara	11.8	11.5	13.5	13.0	10.1	12.0	7
Environmental Mean		11.9(3)	11.8(4)	13.4(1)	10.9(5)	12.0(2)	12.0	
LSD (5%)		1.58	1.65	1.44	1.39	1.97		
CV (%)		11.7	12.3	9.5	11.2	14.4		
F value		**	**	*	**	**		

790

791

792

Table 4 Grand mean root yield, RY, ASV, RASV, GSI, YSI, SI, IPCA1, and IPCA2 of 12 Sugar beet genotypes across environments.

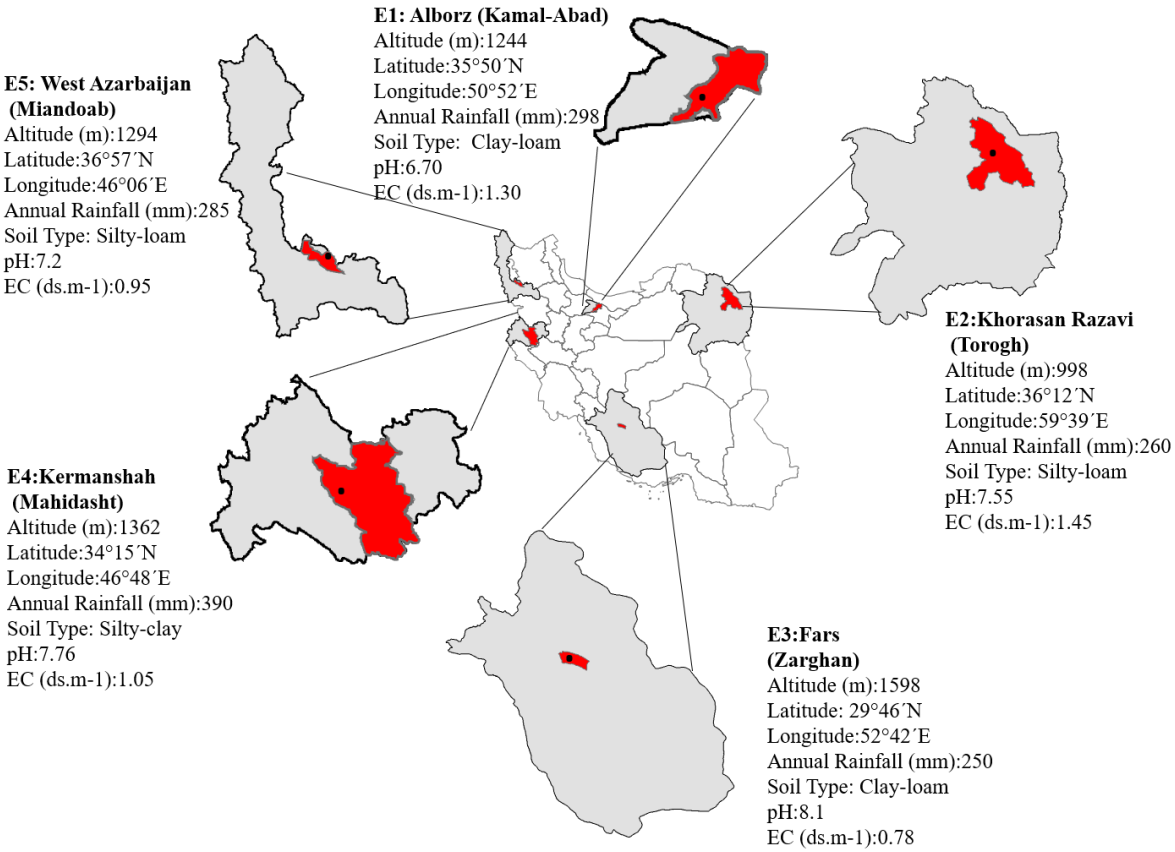
Genotype		Mean	RY	ASV	RASV	GSI	YSI	SI %	IPCA1	IPCA2
code	name									
G1	Agatella	73	8	8.05	10	18	18	18	-2.92	0.99
G2	Arta	80	2	1.41	1	3	3	3	0.11	1.38
G3	Arya	80	1	5.96	9	10	10	10	-2.11	1.46
G4	Asia	73	5	8.14	11	16	16	16	-2.81	-2.69
G5	Dena	69	10	2.65	4	14	14	14	-0.91	-0.88
G6	Homa	57	12	8.65	12	24	24	24	3.13	1.13
G7	Hosna	73	7	3.25	5	12	12	12	-0.97	1.87
G8	Kimya	65	11	5.78	8	19	19	19	2.07	-1.10
G9	Nika	78	3	4.17	6	9	9	9	1.31	-2.14
G10	Shokofa	73	6	1.96	2	8	8	8	0.67	-0.66
G11	Sina	72	9	4.36	7	16	16	16	1.54	1.10
G12	Tara	75	4	2.47	3	7	7	7	0.89	-0.47

RY: rank of yield; ASV: AMMI stability value; RASV: rank of AMMI stability value, SI: stability index; GSI: Genotype Selection Index, YSI: yield stability index.

Table 5 Grand mean sugar yield, RY, ASV, RASV, GSI, YSI, SI, IPCA1, and IPCA2 of 12 Sugar beet genotypes across environments.

Genotype		Mean	RY	ASV	RASV	GSI	YSI	SI %	IPCA1	IPCA2
Code	name									
G1	Agatella	12.9	3	1.65	11	14	14	14	-0.90	-1.07
G2	Arta	13.5	1	1.10	5	6	6	6	-0.74	0.40
G3	Arya	12.6	5	0.61	2	7	7	7	-0.32	-0.42
G4	Asia	12.0	6	1.29	9	15	15	15	-0.87	-0.41
G5	Dena	11.5	10	1.22	8	18	18	18	-0.28	1.15
G6	Homa	9.3	12	2.19	12	24	24	24	1.45	-0.83
G7	Hosna	12.7	4	1.02	4	8	8	8	-0.73	-0.04
G8	Kimya	10.4	11	1.64	10	21	21	21	1.13	0.45
G9	Nika	13.1	2	1.17	6	8	8	8	0.61	0.80
G10	Shokofa	11.7	9	0.29	1	10	10	10	0.21	-0.02
G11	Sina	12.0	7	0.86	3	10	10	10	-0.17	0.82
G12	Tara	11.9	8	1.20	7	15	15	15	0.60	-0.85

RY: rank of yield; ASV: AMMI stability value; RASV: rank of AMMI stability value, SI: stability index; GSI: Genotype Selection Index, YSI: yield stability index.



828

829 **Fig. 1** Test environments, geographical location, and description in this study in Iran.

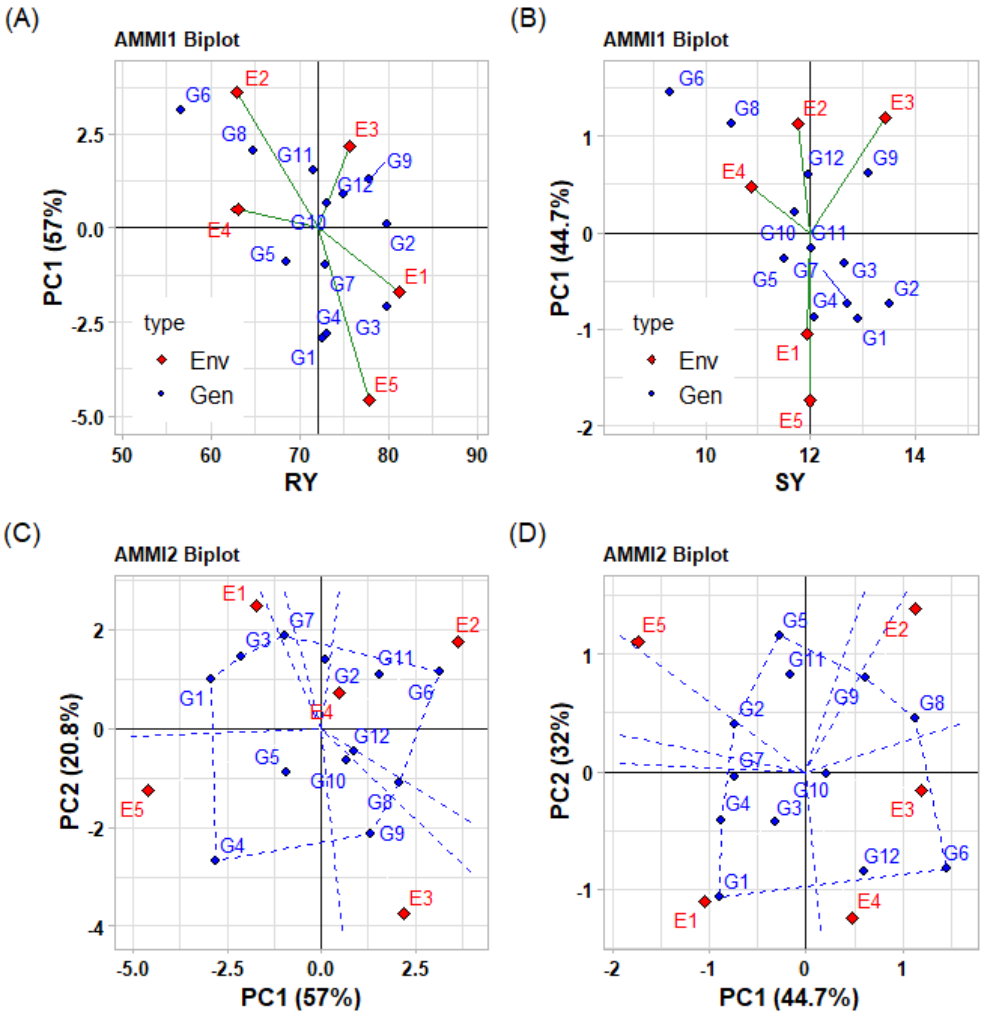
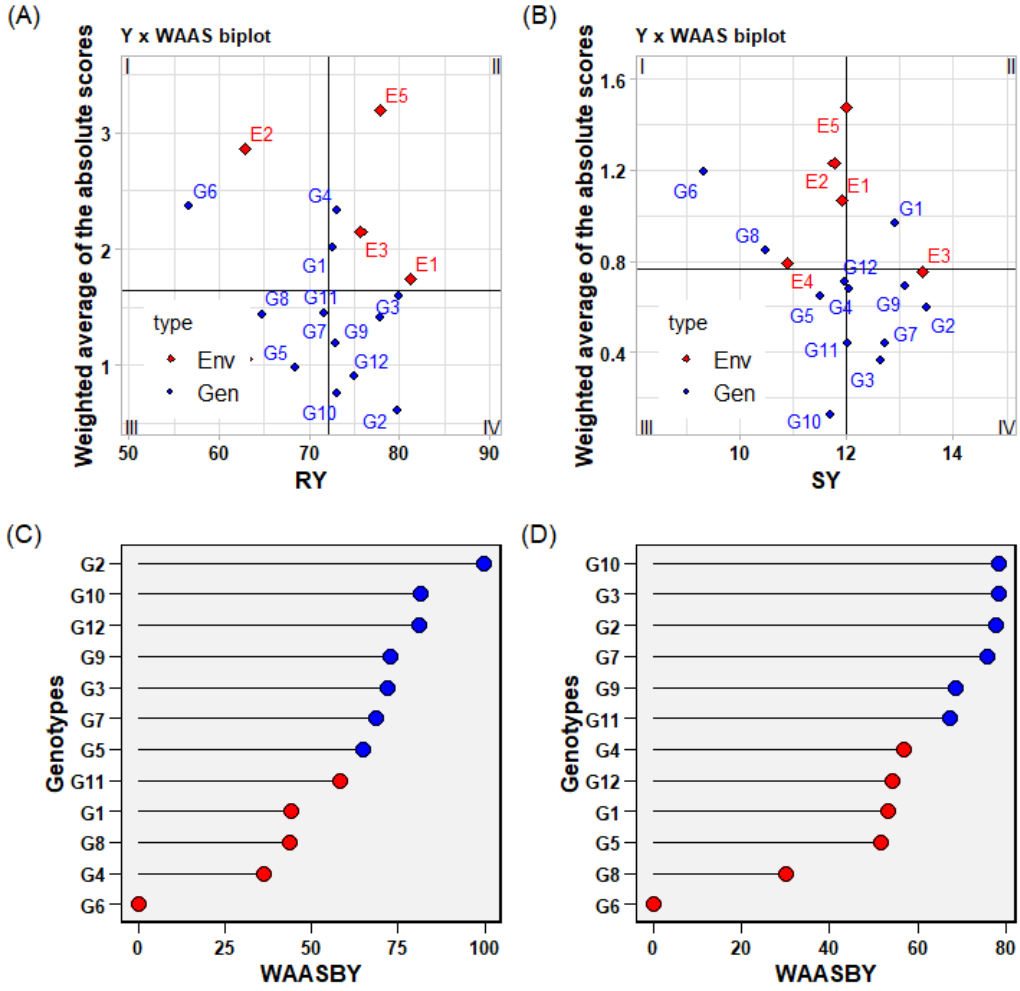


Fig.2 AMMI1 and AMMI2 biplots for root and sugar yield of sugar beet genotypes evaluated across environments. A: AMMI1 for RY, B: AMMI1 for SY; C: AMMI2 for RY; D: AMMI2 for SY.



833
834 **Fig. 3** Plot view of GY x WAAS and WAASBY biplots of test genotypes of Sugar beet. A: GY x
835 WAAS for RY, B: AMMI1 GY x WAAS for SY, C: WAASBY for RY, D: WAASBY for SY.

836

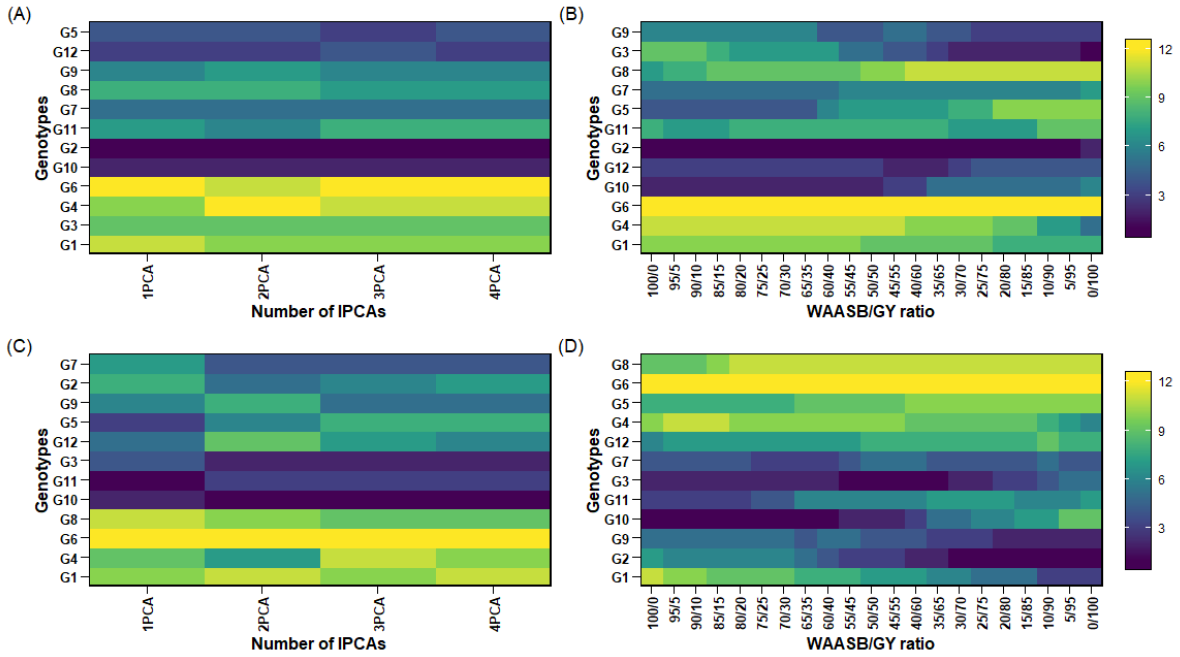


Fig. 4. Plot the heat map graphics of Ranks of Sugar beet genotypes depending on the number of PCAs used to estimate the WAAS and the WAAS/GY ratio. A: PCA used to estimate the WAAS for RY, B: WAAS/GY ratio for RY, C: PCA used to estimate the WAAS for SY, D: WAAS/GY ratio for SY.

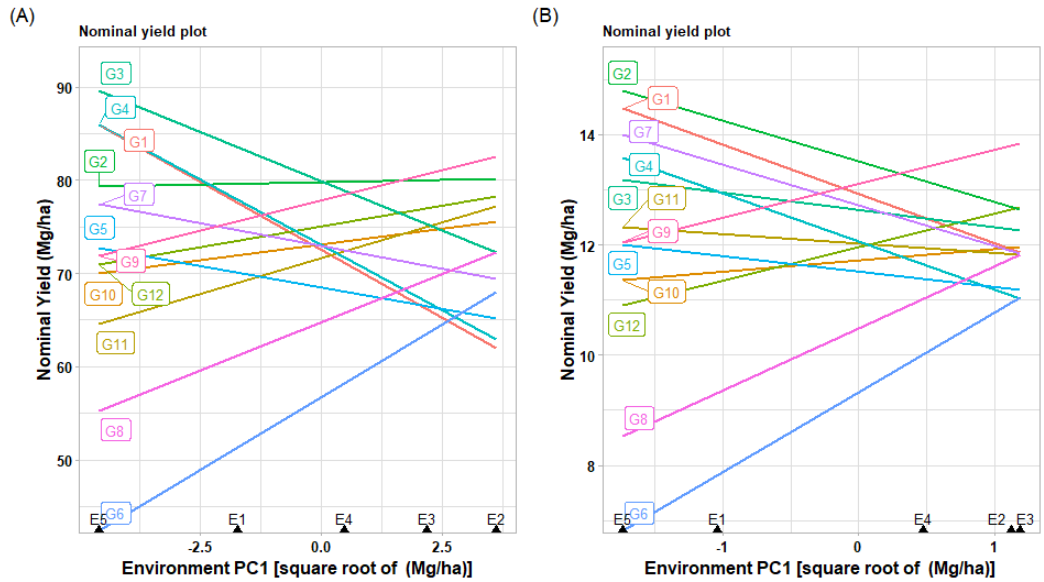


Fig. 5 Plot view of nominal yield and environment biplots of test genotypes for RY and SY of Sugar beet. A: RY, B: SY.

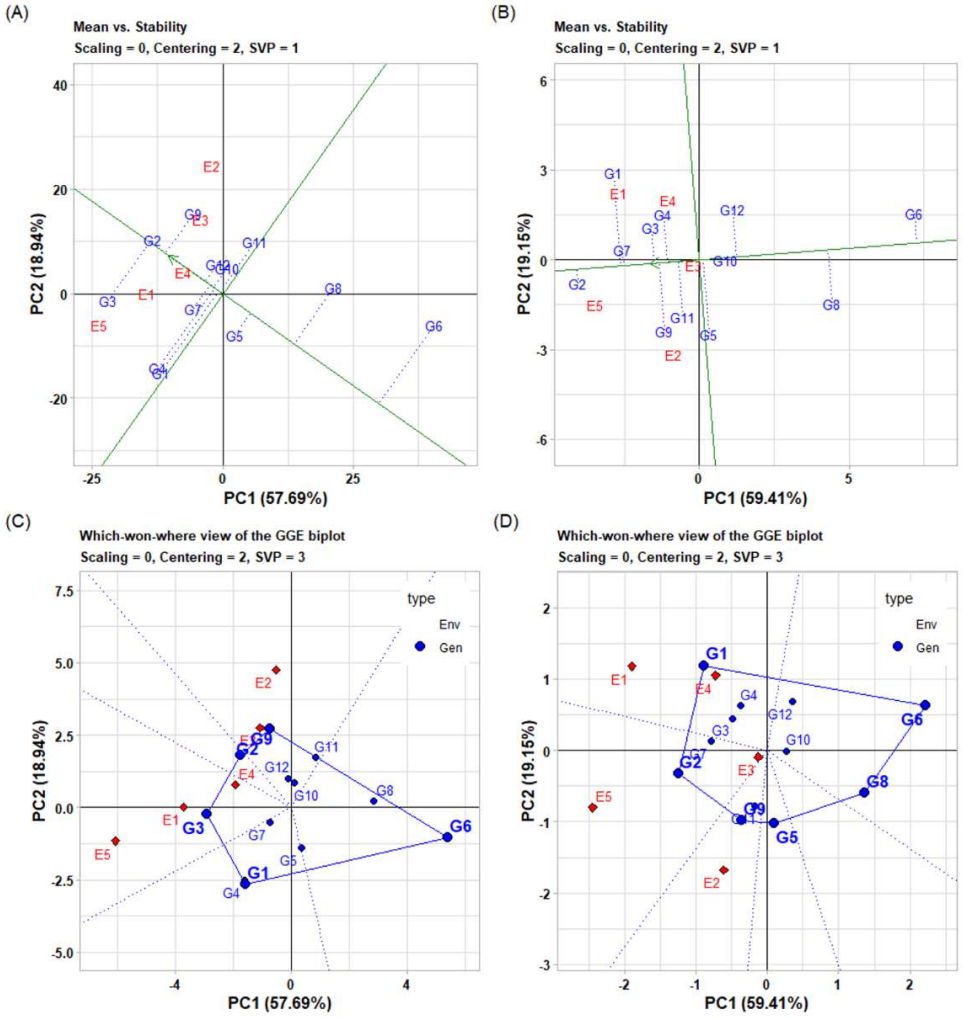


Fig. 6 Plot view of ranking genotypes by means. stability (A, B) and ranking genotypes based on which-won-where (C, D) of sugar beet based on PC1 and PC2, showing G × E interactions of the 12 groundnut accessions under five locations. A: RY means. stability, B: SY means. stability, C: RY which-won-where, D: SY which-won-where.

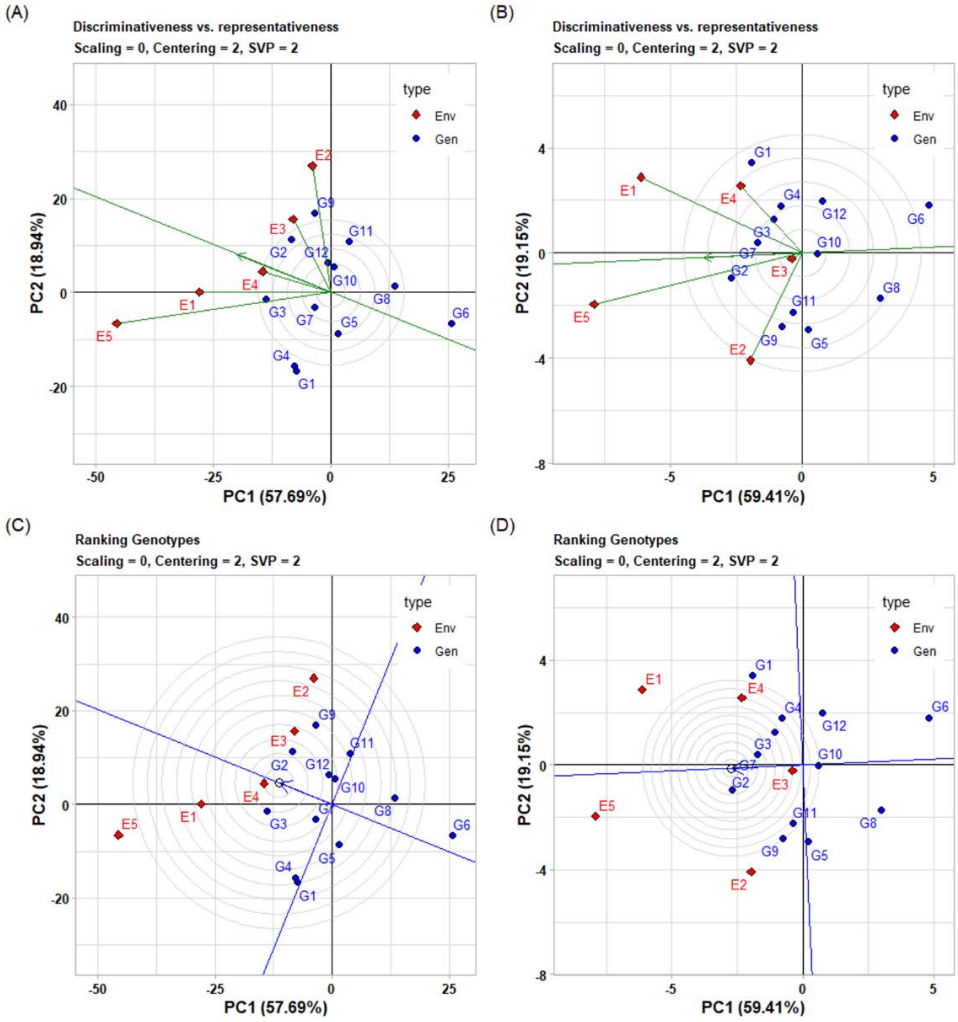


Fig. 7 Plot view of ranking genotypes by Discriminativeness vs. representativeness (A, B) and ranking genotypes based on optimal genotype (C, D) of sugar beet based on PC1 and PC2, showing G × E interactions of the 12 groundnut accessions under five locations. A: RY discriminativeness vs. representativeness, B: SY discriminativeness vs. representativeness, C: RY ranking genotypes, D: SY ranking genotypes.