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ORIGINAL PAPER

Genetic variation of sugar beet genotypes based on root yield and sugar-related characteristics through the GT biplot model

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Abstract

In the present research, 20 sugar beet genotypes were examined in a randomized block design for sugar content (SC), white sugar content (WSC), potassium amount (K), sodium content (Na), alpha-amino nitrogen (AN), alkalinity coefficient (ALC), extraction coefficient of sugar (ECS), molasses sugar (MS), plant number at harvesting (PNH) and storage root yield (RY) using standard protocols. The genotype × trait (GT) method was used to investigate the interaction patterns, revealing that the mentioned interaction accounted for 66% of the total observed variability. The biplot is categorized into four sections, and the traits RY, PNH, AN and Na were located in the section of genotype G3, meaning that G3 had the highest potential for developing these traits, while traits SC, WSC, ECS were located in the section of genotype G19. Genotype G16 was the best with respect to MS and K, while G9 was the best in terms of ALC. Thus, G3, followed by genotypes G4 and G5, was the most favorable one regarding root yield, while G19, followed by genotypes G11 and G13, was identified as the best for sugar-related traits. The other biplot demonstrated that SC, WSC, and ECS were positively correlated, while there was a negative correlation between these traits versus K, MS, AN and Na. Also, RY and PNH were positively correlated, while there was a negative correlation between these traits versus ALC. According to ideal genotype properties, G3 was the best, followed by G4, G1 and G12, and among the tested properties, RY and PNH scored the highest, followed by AN and Na. This study offers a new perspective on the varying performance of genotypes across attributes, and emphasizes the effectiveness of the GT biplot model in discovering superior genotypes. The selected genotypes – G3 and G4 for root yield, and G19 and G11 for sugar-related trait – present viable possibilities for commercial endorsement to farmers. These findings highlight the necessity of incorporating sophisticated multivariate techniques, such as the GT biplot, into breeding initiatives to improve sugar beet yield and quality.

Keywords: *Beta vulgaris* L., biplot, genotype by trait (GT) interaction, sugar-related traits

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INTRODUCTION

Sugar beet (*Beta vulgaris* L.) is the second source for sugar production following sugar cane, with an annual output of 281 million tons cultivated over approximately 4.5 million hectares, yielding an average of 62 tons per hectare (FAOSTAT 2023). Iran, ranked tenth worldwide and second in Asia following China, produces roughly 5.1 million tons yearly from 90,000 hectares, with an average yield of about 56.7 tons per hectare (FAOSTAT 2023). Despite Iran's notable standing as a major sugar beet producer, genetic improvement of this crop has proven to be a considerable challenge. The dry matter of sugar beet contains about 20% sugar and 5% pulp, while the exact amounts of sugar can vary between 12 and 21% according to the variety and growing conditions (Rana et al. 2022). Over the past two centuries of sugar beet breeding, there has been a notable increase in the sugar content from 8% to 20% in contemporary cultivars. Genetic improvement has played a pivotal role in this enhancement and has been actively employed to develop traits such as resistance to viral and fungal diseases, improved root performance, seed monogermy, and resistance to bolting. This utilization of genetic diversity in sugar beet has proven beneficial for breeding programs aimed at achieving desired characteristics. Therefore, it is evident that genetic diversity is crucial, highlighting the necessity for genetic assessments to pinpoint the diversity within sugar beet plants.

Genetic diversity is vital for plant survival and biodiversity, providing raw material for evolution through natural selection. It enables breeders to develop improved cultivars with desirable traits, benefiting farmers and breeders alike (Yağmur, Yaşar 2023). This diversity, found in wild species, mutants, and improved resources, serves as a source of valuable genes. Incorporating novel traits, such as pest resistance and resilience to environmental stresses like salinity and high temperatures, is essential for targeted breeding (Mahmoud et al. 2018). Maintaining diverse genes in germplasm resources allows breeders to identify superior genotypes for direct use or crossbreeding. Genetic diversity also facilitates transgressive segregation, helping breeders create cultivars with specific traits, such as stress tolerance (Azizi et al. 2021).

Examining phenotypic variation is strongly advised as an initial step before delving into biochemical or molecular studies. Therefore, a thorough morphological description stands out as a crucial aspect in the exploration and conservation of plant genetic diversity. Utilizing various traits to investigate phenotypic variation unveils the genetic structure and the extent of variability within the studied population. This serves as the foundation for genetic improvement efforts (Abu-Ellail, Sasy 2021). However, it is thought that the phenotypic variation is the result of selection and reflects the adaptation to environmental changes as well as genetic diversity, trait mutations and genetic drift phenomena. Several investigations have demonstrated that phenotypic flexibility is the main mechanism which allows plants to cope with variability in environmental factors and how their resilience can be improved when there is enough genetic diversity. A phenotype result from a genotype, the environment and their interaction, which reflects the adaptation of a genotype to environmental changes. Thus, a phenotype emerges as a consequence of prolonged stress selection and embodies irreversible processes that can be reliably passed on to the offspring through inheritance (Abu-Ellail et al. 2023). Phenotypes reflect the environmental adaptation of plants and therefore genetic variation in morphological traits is of immense importance in adaptation.

In breeding programs, selection is carried out based on several characteristics that may have a positive or negative relationship among them; therefore, statistical methods that reveal the traits' structure and their effect on yield performance without the elimination of a large amount of useful information are very important. Therefore, multivariate statistics have been used to determine the data pattern among different traits. In Azizi et al. (2021) study, the relationship between different traits was investigated and according to the results obtained, yield performance demonstrated a positive and significant correlation with root yield, sugar percentage, and sugar extraction percentage. Conversely, there was a negative and significant correlation with sodium, potassium, and molasses sugar percentage. The results of Mahmoud et al. (2018) confirmed the significant effect of sugar percentage, relative leaf water content and chlorophyll index on pure sugar yield. Firouzabadi et al. (2011) showed that root yield had a positive correlation with root dry matter percentage and, based on the regression and path analysis, root dry matter percentage as well as petiole dry weight explained the most variation in root yield. Multivariate methods serve as highly effective tools for offering reliable information about the genetic distances between genotypes. As a result, they can be utilized to assess genetic diversity accurately.

The GGE biplot technique, as described by Yan (2001), offers a straightforward means to pinpoint stable genotypes through visual representation. Yan and Rajcan (2002) pioneered the exploration of genotype by trait interaction, a fundamental aspect encapsulated within GGE biplots. Furthermore, Akinwale et al. (2014) demonstrated the usefulness of genotype by trait (GT) biplots in discerning dependable traits for indirect selection of primary parameters. Additionally, Akcura and Kokten (2017) utilized the GGE biplot methodology to assess the correlation between characteristics via genotype-trait biplot graphics. Genotype-by-trait (GT) interactions are critical in sugar beet breeding, influencing the selection of genotypes with superior agronomic and quality traits. Hassani et al. (2018) emphasized that sugar yield depends on multiple interacting traits, including sugar content, extraction efficiency, and impurity levels, making multivariate statistical tools like AMMI and GGE biplots essential for identifying favorable genotypes. Hassani et al. (2023) further highlighted that unfavorable correlations, such as between root yield and sugar purity, complicate genetic improvement, underscoring the need for selection strategies that consider GT interactions to develop high-performing sugar beet varieties.

This study aims to assess the genetic variation among 20 sugar beet genotypes using the genotype × trait (GT) biplot approach, with a particular focus on identifying genotypes with high root yield and superior sugar-related traits. The novelty of this research lies in the evaluation of newly developed genotypes and their potential for commercial use. Additionally, the study seeks to understand the stability of key agronomic traits under the environmental conditions of Miandoab, Iran.

MATERIALS AND METHODS

In this research, 20 sugar beet genotypes (Table 1) were studied as a one-year field trial at Miandoab Agricultural Research Station (36°57′ N, 46°06′ E, altitude = 1314 m) located in West Azarbaijan Province, Iran. The genotypes tested in this study were developed by the Sugar Beet Research Institute (SBRI), Iran, through breeding programs aimed at improving root yield and sugar-related traits. The long-term climatic data of Miandoab Agricultural Research Station in 2023 were shown in Figure 1. Climatic data during the experiment period at Miandoab Agricultural Research Station in 2023 were shown in Figure 2.

Table 1

Code and pedigree of twenty sugar beet genotypes

Code	Pedigree		Code	Pedigree
G1	(7112 × SB36) × SB34 - P.1		G11	(7112 × SB36) × 31285 - P1
G2	(7112 × SB36) × SB34 - P.6		G12	(7112 × SB36) × 31285 - P5
G3	(7112 × SB36) × 89003 - P.5		G13	(7112 × SB36) × 31285 - P6
G4	(7112 × SB36) × 89016 - P.2		G14	(7112 × SB36) × 31285 - P10
G5	(7112 × SB36) × 89016 - P.3		G15	(7112 × SB36) × 31285 - P11
G6	(7112 × SB36) × 89016 - P.4		G16	SBSI - 1
G7	(7112 × SB36) × 89029 - P.1		G17	SBSI - 19
G8	(7112 × SB36) × 89053 - P.2		G18	F - 20704
G9	(7112 × SB36) × 31283 - P.6		G19	F - 20707
G10	(7112 × SB36) × 31283 - P.9		G20	SBSI - 4

The soil of this region is of silty loam type, with a pH of 7.3. Other chemical, physical, and nutrient characteristics of the soil are presented in Table 2. Soil organic carbon, phosphorus, and potassium levels were assessed according to Iranian soil quality standards.

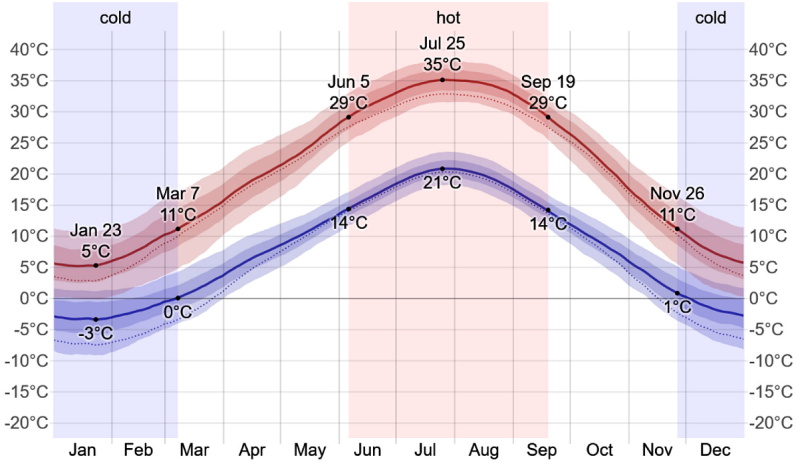

Fig. 1. Long-term climatic data for Miandoab, Iran. The daily average high (red line) and low (blue line) temperatures are shown, with 25th to 75th and 10th to 90th percentile bands. The thin dotted lines represent the corresponding average perceived temperatures (Anonymous 2025)

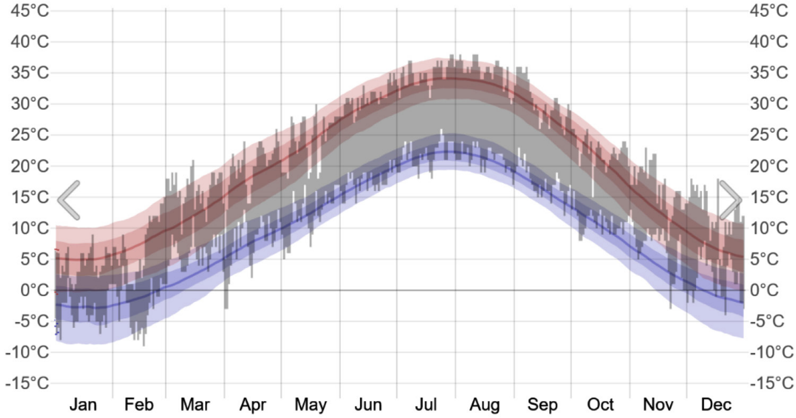

Fig. 2. Climatic data of 2023 year for Miandoab, Iran. The daily range of reported temperatures (gray bars) and 24-hour highs (red ticks) and lows (blue ticks), placed over the daily average high (faint red line) and low (faint blue line) temperature, with 25th to 75th and 10th to 90th percentile bands (Anonymous 2025)

Table 2

Soil characteristics of the experimental field

Soil Depth (cm)	Salinity EC (mmol cm^{-1}) ×10	pH	Clay (%)	Silt (%)	Sand (%)	Soil texture	Organic carbon (%)	Available P (ppm)	Available K (ppm)
0-30	0.84	7.3	22	60	18	Silty Loam	0.72	12	390
30-60	0.59	7.3	25	53	22	Silty Loam	0.66	6.1	250

After routine tillage operations, the beets were sown in a randomized complete block design on eight-meter-long rows, with a distance of 60 cm between rows in six blocks. The seeds were planted in a row at a distance of 17 cm and at a depth of 3 to 4 cm. More seeds were placed in the rows and then the emergent plants were thinned at the stage of 2-4 leaves. The chemical fertilizers consisted of 200 kg ha^{-1} of $(NH_4)_3PO_4$ and 250 kg ha^{-1} of nitrogen as urea (half in the planting time + half as top-dressing in the 4-6 leaf stage). Irrigation of the plants was managed according to the water requirement, with the use of a volumetric meter and pipes leading to all the plots. The irrigation regime was was adjusted to the real-time soil moisture conditions, following regional agronomic recommendations. Grass and broadleaf weeds in the field were controlled by manual weeding during several plant growth stages and by applying herbicides. In late October, the beet plants were harvested, and the roots in the plots were counted and weighed. Then, the roots were transported to the laboratory, where sugar content (SC), white sugar content (WSC), potassium amount (K), sodium content (Na), alpha-amino nitrogen (AN), alkalinity coefficient (ALC), extraction coefficient of sugar (ECS), molasses sugar (MS), plant number at harvesting (PNH) and storage root yield (RY) were measured according to standard protocols suggested by (Liu et al. 2022).

Before data analysis, normal distribution of the data was examined using the Ryan-Joiner test with the Minitab v. 21 software. Then, the data were subjected to a genotype by trait (GT) biplot via the GGEbiplot software (Yan 2001). This model graphically represents the pattern of the GT interaction using the following formula:

$$\frac{X_{ij}-\mu_j}{S_j} = \sum_{n=1}^{2} \alpha_n \beta_{in} \gamma_{jn} + E_{ij},$$

where: X_{ij} represents the genotype i for character j, μ_j is the mean of genotypes for character j, S_j is the root square of variance in character j across genotypes, α_n is the singular value, β_{in} and η_{jn} are PC-values of genotypes and characters, and E_{ij} is the residual magnitude of the model. To achieve symmetric scaling in the values of both genotypes and traits, the singular value α_n needs to be adjusted via absorption of their vectors (β_{in} and γ_{jn}). This adjustment helps in obtaining a balanced representation of treatments and traits in the analysis; $\beta_{in}^{*} = \sqrt{\lambda_n}\xi_{in}$ and $\gamma_{jn}^{*} = \sqrt{\alpha_n}\gamma$. The GT interaction biplot graphs are created by plotting the symmetrical values of the genotypes and traits. In these graphs, genotypes and traits are shown by a unique marker, allowing for a graphical indication of the associations between traits as well as genotypes. This comprehensive approach allowed for a detailed exploration of the relationships between treatments and traits.

RESULTS AND DISCUSSION

The analysis of the mean values and descriptive statistics for the 20 sugar beet genotypes across the studied traits, as presented in Table 3, revealed significant variability in trait expression. The first two principal components (PC1 and PC2) accounted for 66% of the total observed variability (47% and 19%, respectively) (Figure 1). According to the Kaiser criterion (Kaiser 1960), components with eigenvalues greater than one should be retained. Additional components explained smaller proportions of variability (<15% each); therefore, the remaining components collectively explain 34% of the variability, but their individual contributions are small and do not significantly enhance the interpretation of genotype-trait relationships. The noteworthy amount of GT interaction observed implies both additive and crossover interactions in our dataset, indicating differential rankings of measured traits across genotypes. This finding aligns with similar observations in other crops (Dehghani et al. 2008, El-Nenny et al. 2022) in canola, Sabaghnia et al. (2015) in spinach, Zeinalzadeh-Tabrizi and Mansouri (2021) in sesame, Shojaei et al. (2023) in sunflower, highlighting the challenge of achieving an indirect response to selection overall genotypes without considering the GT interaction. Taking into account the importance of the GT interaction, this research employed a site regression model, similar to the recommendation of Yan and Frégeau-Reid (2018), as a suitable model through biplot presentation, which is used to identify the GT interaction and can provide valuable information (Song et al. 2019), thus Figure. 3 indicates which genotypes excelled in which traits. Some measured characteristics, comprising Na, AN, RY and PNH, were categorized in section G3, while SC, WSC and ECS were situated in a distinct section of G19. In the study of Kiymaz and Ertek (2015), the associations among Na, alpha-amino nitrogen and root dry matter of sugar beet were significant. Conversely, the sector for ALC featured G9 as the top-performing genotype and G16 was the best genotype for K and MS. Thus, to achieve optimal performance across sugar traits, it appears that the cultivation of G19, followed by G11, G13, G8 and G6, would be beneficial for high SC, WSC and ECS. Although G3, followed by G4, G5, G2, G1 and G12, had the highest root yield and plant number at harvesting, the same genotypes had high values of harmful factors like sodium content (Na) and alpha-amino nitrogen (AN). A finding of this research was the relation between SC and WSC, which supports the report of Tsialtas and Maslaris (2013), who found similar results in sugar beet.

Figure 3 illustrates the associations of sugar beet traits via lines that connect each character to the plot origin, whereas the size of vectors estimates the mean squares of error of the corresponding character, and the cosine of vectors estimates the magnitude of the association. The biplot also indicates interrelationships among traits of sugar beet. The circles represent confidence regions for the genotypes and traits, with their size reflecting the

Table 3

Mean values and descriptive statistics of the genotypes and studied traits

Genotype	Sc (%)	WSC (%)	K (mEq 100 g^{-1})	Na (mEq 100 g^{-1})	AN (mEq 100 g^{-1})	Alc (%)	ECS (%)	Ms (%)	PNH	RY (t ha^{-1})
1	18.83	16.30	4.95	1.25	1.28	4.94	86.46	1.94	25.83	24.05
2	18.61	16.01	5.07	1.32	1.29	5.04	85.99	2.00	29.00	21.18
3	18.38	15.79	5.10	1.23	1.32	4.91	85.90	1.99	35.83	30.56
4	18.49	15.88	5.18	1.20	1.37	4.72	85.88	2.01	27.33	24.91
5	18.56	15.96	5.13	1.26	1.29	5.03	85.96	2.00	27.17	25.95
6	18.60	16.11	4.97	1.12	1.22	5.06	86.59	1.89	25.83	27.34
7	18.37	15.76	5.23	1.17	1.30	5.06	85.76	2.01	24.00	22.66
8	18.90	16.37	5.07	1.12	1.23	5.08	86.57	1.93	28.17	25.95
9	18.78	16.24	5.24	1.03	1.15	5.49	86.42	1.95	25.83	20.85
10	18.23	15.62	5.12	1.30	1.26	5.15	85.66	2.01	27.17	23.26
11	19.26	16.69	5.22	1.06	1.29	4.95	86.63	1.97	26.33	22.05
12	18.88	16.35	5.07	1.10	1.28	4.96	86.56	1.92	30.67	24.48
13	18.73	16.22	4.97	1.14	1.24	5.04	86.58	1.90	27.83	21.88
14	18.38	15.80	5.12	1.21	1.28	5.00	85.89	1.98	20.67	21.44
15	18.53	15.92	5.31	1.11	1.32	4.97	85.85	2.02	25.33	23.78
16	18.33	15.69	5.31	1.22	1.27	5.23	85.52	2.05	25.00	25.61
17	18.38	15.80	5.17	1.16	1.28	5.04	85.91	1.98	23.83	20.66
18	18.73	16.03	5.34	1.33	1.26	5.38	85.57	2.10	29.17	25.61
19	19.03	16.59	4.97	1.01	1.13	5.33	87.11	1.85	28.50	24.39
20	18.61	15.96	5.25	1.27	1.29	5.16	85.73	2.05	23.50	24.31
Mean	18.63	16.05	5.14	1.18	1.27	5.08	86.13	1.98	26.85	24.05
StDev	0.78	0.89	0.32	0.30	0.20	0.63	1.34	0.17	9.18	10.48
Median	18.60	15.94	5.19	1.19	1.25	5.01	85.92	2.00	27.00	23.44
Minimum	16.85	14.08	4.24	0.68	0.94	3.80	83.55	1.56	7.00	3.65
Maximum	20.95	18.24	5.98	2.05	1.75	6.40	88.95	2.40	50.00	59.38
CV (%)	4.20	5.56	6.15	25.45	15.61	12.32	1.56	8.72	34.18	43.59

variability explained by the principal components. Overlapping circles indicate similarities in trait profiles or genotype performance (Yan 2001). As seen in Figure 3, traits SC, WSC and ECS exhibit a high positive correlation, indicating that they provide the same information about the variation of the genotypes and such findings align with those reported by Azizi et al. (2021), who studied the associations among 20 sugar beet varieties to identify the important traits for root yield performance. Also, RY with PNH, AN with Na, and MS with K exhibit a positive correlation with each other due to the relatively close angles of their vectors (Figure 2). Abbasi et al. (2015) evaluated 13 morphological characteristics of sugar beet 168 genotypes and found similar associations for RY, PNH, AN, Na, MS and K. Furthermore, there seems to be a nearly nonexistent correlation between ALC and SC, WSC, and ECS, as well as between ALC and MS and K, as indicated by the consistently stable trend lines. Similarly, a relatively near-zero correlation was seen between RY and PNH with SC, WSC and ECS as well as between RY and PNH with AN and Na, as demonstrated by the relatively vertical lines in Figure 4. Regarding the obtuse angle between ALC with RY and PNH as well as between Na and NS with SC, WSC and ECS, they had strong negative associations and most of these findings align with those reported by Azizi et al. (2021). In both investigations, the inverse effect of low K on SC was ascribed to a dilution of sucrose due to the high-water content of roots, which resulted from the osmotic reaction of Na (Ghaffari et al. 2021). Some of these observations can be confirmed via the correlation values (Table 4), whereas it is noted that certain discrepancies between the predic-

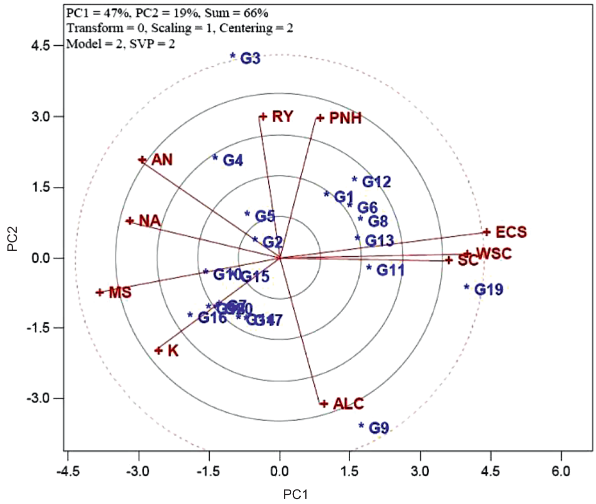

Fig. 3. A biplot indicating interrelationships among traits of sugar beet. The traits are: sugar content (SC), sodium content (Na), potassium amount (K), alpha-amino nitrogen (AN), alkalinity coefficient (ALC), white sugar content (WSC), extraction coefficient of sugar (ECS), molasses sugar (MS), plant number at harvesting (PNH) and root yield (RY)

Table 4

Simple correlation coefficients of traits in twenty genotypes of sugar beet

Specification	Na†	K	AN	ALC	WSC	ECS	MS	PNH	RY
SC	-0.540*	-0.249	-0.411	0.133	0.984**	0.785**	-0.487*	0.189	-0.100
Na		0.168	0.514*	-0.121	-0.622**	-0.736**	0.691**	0.055	0.169
K			0.313	0.252	-0.383	-0.685**	0.824**	-0.248	-0.095
AN				-0.780**	-0.488*	-0.603**	0.580**	0.024	0.156
ALC					0.116	0.039	0.045	-0.101	-0.161
WSC						0.882**	-0.633**	0.190	-0.098
ECS							-0.922**	0.190	-0.060
MS								-0.136	0.048
PNH									0.596**

† Traits are: sugar content (SC), sodium content (Na), potassium amount (K), alpha-amino nitrogen (AN), alkalinity coefficient (ALC), white sugar content (WSC), extraction coefficient of sugar (ECS), molasses sugar (MS), plant number at harvesting (PNH) and root yield (RY), * and ** correlation coefficients significant at 0.05 and 0.01 statistical level with degrees of freedom equals to 18.

tions of the graphic model and the numerical data were expected. This is because the GT biplot model only accounts for less than 100% of the total observed variation (in this case, approximately 66%) and not exactly the total variation. Nitrogenous substances, especially alpha-amino nitrogen (AN), play a major role in creating molasses, so they are called harmful nitrogen and are not separated in the purification steps and enter the molasses. The AN in this study showed a moderately positive correlation with RY and MS, while a negative correlation with sugar-related traits (SC, WSC and ECS) is indicated. Previously, the low level of harmful nitrogen, which is considered a non-sugar substance in sugar beet, was proven by Varga et al. (2022). High levels of nitrogen caused a decrease in quality traits such as sugar content, total soluble solids and purity percentage (Gobarah et al. 2019).

The arrow in the circles shown in Figure 4 determines the location of an ideal genotype as the largest vector of the genotypes with the highest performance and by a low projection onto the other axis, hence a genotype is more favorable if it is closer to the ideal genotype. An ideal genotype is defined as the hypothetical genotype that exhibits both high performance and stability across multiple traits, making it the most desirable candidate for breeding or commercial use (Yan, Kang 2002). In the context of this study, the ideal genotype was identified using the GT biplot model, where it is represented by the largest vector of genotypes with the highest performance and minimal deviation from the desired trait profile (Figure 4). Specifically, the ideal genotype is positioned closest to the origin of the biplot, reflecting a balance between high performance and favorable trait combinations.

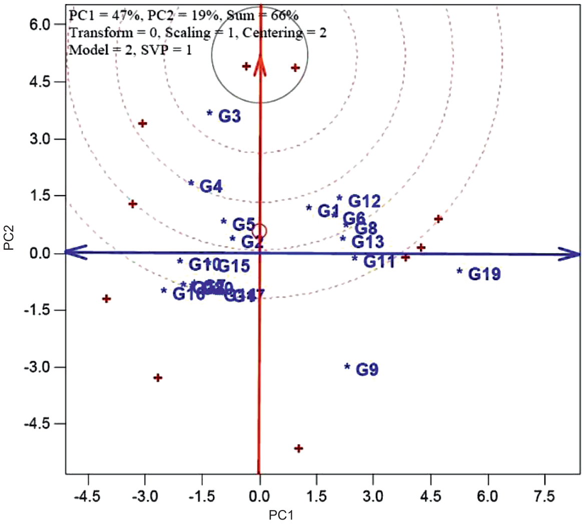

Fig. 4. A biplot indicating the position of an ideal genotype and the tested sugar beet genotypes

Hence, among sugar beet genotypes, G3, G4, G1, and G12 exhibited greater favorability compared to others, with G9, G19, and G16 being less desirable due to their significant deviation from the location of the ideal genotype (Figure 4). It is obvious that the genotype G3 [(7112 × SB36) × 89003 - P.5] with the highest root yield can be considered one of the candidates for sugar beet production; however, its sugar-related traits were not the best. For the studied traits, an ideal trait should be able to differentiate the genotypes according to the representativeness of the target trait (ideal) and considering the traits that have the representativeness ability of the special trait (Figure 5). The arrow in the middle of the circles in Figure 4 has the largest vector of the traits with positive projections onto the average of the coordinate axis of the traits. A trait is more favorable if it is closer to the location of the special trait; therefore, RY and PNH were favorable ones following AN and Na. In the next step, MS, SC, WSC and ECS were favorable traits, whereas ALC following K, were relatively undesirable ones (Figure 5).

The performance of genotypes in terms of the root yield (RY) obtained, being the final economic trait, is evaluated in Figure 6, where a lateral line passes via the plot origin reaching the final trait, and the genotypes are ranked as follows: G3 followed by G4, G12 and G1 were the most desirable genotypes considering RY, while G9 followed by G19 were the least desirable ones in terms of RY (Figure 6). The lateral axis categorizes genotypes that yielded below and above the average achieved by RY, hence nine genotypes (G3, G4, G12, G1, G5, G6, G8, G2 and G13) performed above the average, while the other ones performed below it (Figure 6). Similar to RY, white sugar content (WSC) was tested across the genotypes in Figure 6, proving that G19 followed by G11, G13, G8, G6, G9, G12 and G1 were the most desirable

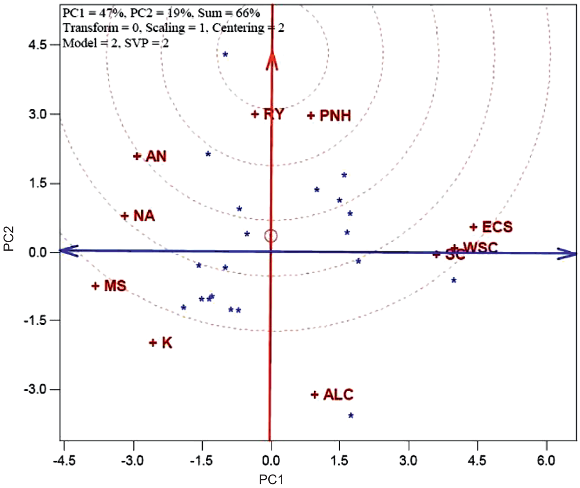

Fig. 5. A biplot indicating the position of an ideal trait regarding traits of sugar beet. The traits are: sugar content (SC), sodium content (Na), potassium amount (K), alpha-amino nitrogen (AN), alkalinity coefficient (ALC), white sugar content (WSC), extraction coefficient of sugar (ECS), molasses sugar (MS), plant number at harvesting (PNH) and root yield (RY)

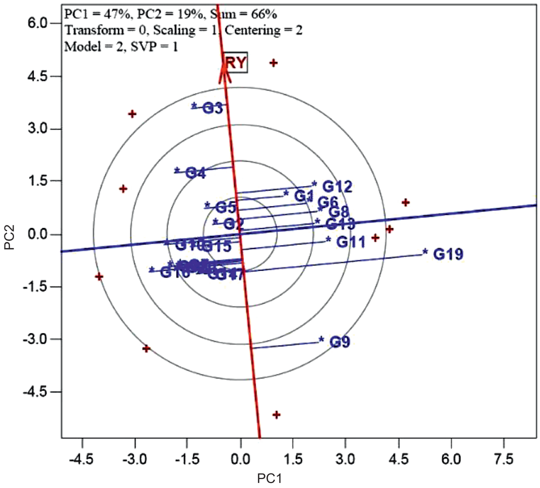

Fig. 6. A biplot indicating ranks of sugar beet genotypes regarding the position of the target trait as root yield (RY)

genotypes with regard to WSC, while G16 followed by the remaining genotypes were the most undesirable in terms of WSC (Figure 7). Thus, the lateral axis categorized the genotypes related to G19 as the ones yielding above the average, while the twelve remining genotypes related to G16 were identified as the ones yielding below it with respect to WSC (Figure 7).

The concept of an ideal genotype is inherently flexible and depends on the specific objectives of the end-user. For instance, farmers prioritize traits such as taproot biomass (root yield) and plant number at harvesting (PNH),

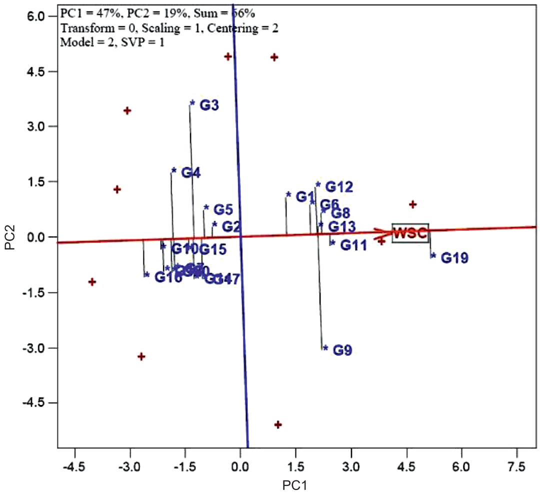

Fig. 7. A biplot indicating ranks of sugar beet genotypes regarding the position of the target trait as white sugar content (WSC)

which directly impact their income. In Fig. 6, genotypes such as G3, G4, G12, and G1 were identified as the most favorable for root yield (RY), making them ideal candidates for farmers focused on maximizing biomass production. Technologists (sugar producers) are more interested in the traits related to sucrose concentration (SC, WSC), extraction efficiency (ECS), and low concentrations of impurities such as alpha-amino nitrogen (AN), potassium (K), and sodium (Na). In Figure 7, genotypes such as G19, G11, G13, and G8 were identified as the most favorable for white sugar content (WSC) and related traits, making them ideal candidates for technologists aiming to optimize sucrose extraction and minimize impurities.

The GT biplot analysis provides a visual representation of the relationships between genotypes and traits, enabling the identification of genotypes that best meet the criteria for an ideal genotype. For example, G3 is highlighted as the most stable and high-yielding genotype for root yield, while G19 stands out as the most stable and high-performing genotype for sugar-related traits. These findings underscore the importance of both stability and performance when defining an ideal genotype.

Successful cultivars of sugar beets need to be generated with the use ofeffective tools for selecting the most favorable genotypes in order to ensure their efficient performance and economic gain. The graphical model employed here enables visual analysis of the GT interaction and comparison with conventional models. This approach, as outlined by Yan and Frégeau-Reid (2018), offers several advantages, including graphic representation, which enhances our ability to comprehend and interpret the data. Additionally, it simplifies the understanding of genotypes and traits, facilitates the categorization of genotypes based on specific traits, and enables the identification of clusters of similar genotypes or traits.

The analysis of variance and multivariate statistical methods applied in this study revealed significant interactions between sugar beet genotypes and key traits such as root yield (RY), sugar content (SC), white sugar content (WSC), sodium (Na+), and alpha-amino nitrogen (AN). By utilizing GT biplot model, a comprehensive understanding of genotype performance in relation to multiple traits was achieved. Findings from Hassani et al. (2018) demonstrated that sugar beet genotypes exhibited significant variability in trait expression across different environments. The GT interaction analysis indicated that sugar yield and extractable sugar content were influenced by unfavorable correlations with impurities such as Na+ and AN. Despite these negative correlations, certain genotypes, including G21, G28, and G29, maintained superior performance across diverse conditions, showcasing their stability and adaptability. The study further emphasized that selection based solely on root yield without considering sugar-related traits could lead to suboptimal outcomes. Similarly, Hassani et al. (2023) highlighted the importance of integrating GT interaction analysis with genotype selection. The application of BLUP and AMMI models revealed that stable genotypes, such as G19 and G11, excelled in sugar-related traits, whereas G3 and G4 were more favorable for root yield. The genotype by yield-trait (GYT) biplot analysis further confirmed that an ideal genotype balances high yield with superior sugar extraction efficiency, while minimizing impurity traits.

This study is based on a one-year experiment; however, the long-term climatic data demonstrates a remarkable stability in weather conditions over the years (Figures 1 and 2). This stability suggests that the environmental conditions in 2023 were representative of the long-term climatic trends in the region. It is reasonable to infer that the observed genotype-utility traits, such as the high root yield of the G3 variety, are likely to remain consistent in subsequent years. The stable climatic conditions over the past decade indicate that the environmental factors influencing these traits have not varied significantly. Therefore, the results obtained in 2023 are likely to be reproducible under similar conditions in future years.

CONCLUSIONS

The findings of this study highlight the significant impact of GT interactions on sugar beet breeding, emphasizing the necessity of selecting genotypes that balance high root yield with superior sugar-related traits. The GT biplot analysis effectively identified genotypes such as G3 and G4 as ideal candidates for root yield improvement, while G19 and G11 emerged as superior for sugar extraction efficiency. Future breeding efforts should prioritize multi-trait selection strategies to optimize both productivity and sugar quality, ensuring the development of commercially viable sugar beet cultivars.

Author contributions

H.H.M and K.F. – Conceptualization, N.S. – methodology and data collection, H.H.M., N.S. and H.Z.T. – data validation, N.S. – data analysis and original draft preparation, N.S. and H.Z.T. – writing, review and editing.

Conflicts of interest

The authors ensure that they have neither professional nor financial connections related to the manuscript sent to the Editorial Board.

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REFERENCES

Abbasi, Z., Majidi, M. M., Arzani, A., Rajabi, A., Mashayekhi, P., Bocianowski, J. (2015) 'Association of SSR markers and morpho-physiological traits associated with salinity tolerance in sugar beet (*Beta vulgaris* L.)', *Euphytica*, 205, 785-797, available: DOI:https://doi.org/10.1007/s10681-015-1408-1

Abu-Ellail, F., Sasy, A. (2021) 'GT biplot analysis for yield and related traits in some sugar beet varieties as affected by compost under saline soil', *Egyptian Journal of Applied Science*, 36(3), 66-83, available: DOI:https://dx.doi.org/10.21608/ejas.2021.163587

Abu-Ellail, F. F., Sadek, K., Abd El-Azez, Y., Fares, W. (2023) 'Simultaneous evaluation of yield and stability of sugar beet (*Beta vulgaris L.*) *varieties under Egyptian conditions using AMMI and GGE biplot approaches*', *Indian Journal of Genetics and Plant Breeding*, 83(04), 587-601, available: DOI:https://doi.org/10.31742/ISGPB.83.4.15

Akcura, M., Kokten, K. (2017) 'Variations in grain mineral concentrations of Turkish wheat landraces germplasm', *Quality Assurance and Safety of Crops and Foods*, 9(2), 153-159, available: DOI:https://doi.org/10.3920/QAS2016.0886

Akinwale, R., Fakorede, M., Badu-Apraku, B., Oluwaranti, A. (2014) 'Assessing the usefulness of GGE biplot as a statistical tool for plant breeders and agronomists', *Cereal Research Communications*, 42(3), 534-546, available: DOI:https://doi.org/10.1556/crc.42.2014.3.16

Anonymous. (2025) Weatherspark climatic data. https://weatherspark.com/y/148822/Average-Weather-at-Sahand-Airport-Iran-Year-Round#Figures-Summary.

Azizi, H., Pedram, A., Fasahat, P. (2021) 'Identification of effective traits on sugar beet (*Beta vulgaris* L.) root yield under natural infection conditions to rhizomania virus disease', *Journal of Crop Breeding*, 13(37), 197-204, available: DOI:http://dx.doi.org/10.52547/jcb.13.37.197

Dehghani, H., Omidi, H., Sabaghnia, N. (2008) 'Graphic analysis of trait relations of rapeseed using the biplot method', *Agronomy Journal*, 100(5), 1443-1449, available: DOI:https://doi.org/10.2134/agronj2007.0275

El-Nenny, E., Ibrahim, H. E., Shawky, A., Abd El-Rahman, R. H. (2022) 'Graphic analysis of trait relations of canola genotypes using the biplot method', *Egypt Journal of Applied Science*, 37(9-10), 17-29, available: DOI:https://doi.org/10.21608/ejas.2022.275071

FAOSTAT. (2023) Agriculture Organization of the United Nations Statistics Division (2022). Available online at: http://www.fao.org/faostat/en/#data. Accessed Jenuary 2024.

Firouzabadi, M.B., Farrokhi, N., Parsaeyan, M. (2011) 'Sequential path analysis of some yield and quality components in sugar beet grown in normal and drought conditions', *Italian Journal of Agronomy*, 6(4), e39-e39, available: DOI:https://doi.org/10.4081/ija.2011.e39

Ghaffari, H., Tadayon, M. R., Bahador, M., Razmjoo, J. (2021) ‘Investigation of the proline role in controlling traits related to sugar and root yield of sugar beet under water deficit conditions’, *Agricultural Water Management*, 243, 106448, available: DOI:https://doi.org/10.1016/j.agwat.2020.106448

Gobarah, M., Hussein, M.M., Tawfik, M., Ahmed, A.G., Mohamed, M.F. (2019) ‘Effect of different sowing dates on quantity and quality of some promising sugar beet *(Beta vulgaris* L.) varieties under North Delta condition’, *Egyptian Journal of Agronomy*, 41(3), 343-354, available: DOI:https://doi.org/10.21608/agro.2019.20126.1197

Hassani, M., Heidari, B., Dadkhodaie, A., Stevanato, P. (2018) ‘Genotype by environment interaction components underlying variations in root, sugar and white sugar yield in sugar beet (*Beta vulgaris* L.)’, *Euphytica*, 214, 1-21, available: DOI:https://doi.org/10.1007/s10681-018-2160-0

Hassani, M., Mahmoudi, S.B., Saremirad, A., Taleghani, D. (2023) ‘Genotype by environment and genotype by yield* trait interactions in sugar beet: analyzing yield stability and determining key traits association’, *Scientific Reports*, 13(1), 23111, available: DOI:https://doi.org/10.1038/s41598-023-51061-9

Kaiser, H.F. (1960) ‘The application of electronic computers to factor analysis’, *Educational and Psychological Measurement*, 20(1), 141-151.

Kiymaz, S., Ertek, A. (2015) ‘Yield and quality of sugar beet (*Beta vulgaris* L.) at different water and nitrogen levels under the climatic conditions of Kırsehir, Turkey’, *Agricultural Water Management*, 158, 156-165, available: DOI:https://doi.org/10.1016/j.agwat.2015.05.004

Liu, D., Wang, X., Li, W., Li, J., Tan, W., Xing, W. (2022) ‘Genetic diversity analysis of the phenotypic traits of 215 sugar beet germplasm resources’, *Sugar Tech*, 24(6), 1790-1800, available: DOI:https://doi.org/10.1007/s12355-022-01120-8

Mahmoud, E.-S.A., Hassanin, M.A., Borham, T.I., Emara, E.I. (2018) ‘Tolerance of some sugar beet varieties to water stress’, *Agricultural Water Management*, 201, 144-151, available: DOI:https://doi.org/10.1016/j.agwat.2018.01.024

Rana, A.K., Gupta, V.K., Newbold, J., Roberts, D., Rees, R.M., Krishnamurthy, S., Thakur, V.K. (2022) ‘Sugar beet pulp: Resurgence and trailblazing journey towards a circular bioeconomy’, *Fuel*, 312, 122953, available: DOI:https://doi.org/10.1016/j.fuel.2021.122953

Sabaghnia, N., Behtash, F., Janmohammadi, M. (2015) ‘Graphic analysis of trait relations of spinach (*Spinacia oleracea* L.) landraces using the biplot method’, *Acta Univers Agric Silv Mendel Brun*, 63(4), 1187-1194, available: DOI:https://doi.org/10.11118/actaun201563041187

Shojaei, S., Mostafavi, K., Ansarifad, I., Bihamta, M., Zeinalzadeh-Tabrizi, H., Omrani, A., Gore, M., Mousavi, S.M.N. (2023) ‘Comparison of genotype×trait and genotype×yield-trait biplots in sunflower cultivars’, *International Journal of Agriculture Environment and Food Sciences*, 7(1), 136-147, available: DOI:https://doi.org/10.31015/jaefs.2023.1.17

Song, X., Zhou, G., Ma, B.-L., Wu, W., Ahmad, I., Zhu, G., Yan, W., Jiao, X. (2019) ‘Nitrogen application improved photosynthetic productivity, chlorophyll fluorescence, yield and yield components of two oat genotypes under saline conditions’, *Agronomy*, 9(3), 115, available: DOI:https://doi.org/10.3390/agronomy9030115

Tsialtas, J., Maslaris, N. (2013) ‘Nitrogen effects on yield, quality and K/Na selectivity of sugar beets grown on clays under semi-arid, irrigated conditions’, *International Journal of Plant Production*, 7(3), 355-372, available: DOI:https://doi.org/10.22069/ijpp.2013.1109

Varga, I., Jović, J., Rastija, M., Markulj Kulundžić, A., Zebec, V., Lončarić, Z., Iljkić, D., Antunović, M. (2022) ‘Efficiency and management of nitrogen fertilization in sugar beet as spring crop: A review’, *Nitrogen*, 3(2), 170-185, available: DOI:https://doi.org/10.3390/nitrogen3020013

Yağmur, H., Yaşar, M. (2023) ‘Investigation of yield and quality parameters of some sugar beet varieties in Muş ecological conditions’, *International Journal of Agriculture Environment and Food Sciences,* 7(2), 436-447, available: DOI:https://doi.org/10.31015/jaefs.2023.2.22

Yan, W. (2001) ‘GGEbiplot – A Windows application for graphical analysis of multienvironment trial data and other types of two-way data’, *Agronomy Journal*, 93(5), 1111-1118. DOI:https://doi.org/10.2134/agronj2001.9351111x

Yan, W., Frégeau-Reid, J. (2018) ‘Genotype by yield* trait (GYT) biplot: a novel approach for genotype selection based on multiple traits’, *Scientific Reports*, 8(1), 8242, available: DOI:https://doi.org/10.1038/s41598-018-26688-8

Yan, W., Kang, M.S. (2002) GGE Biplot Analysis: A Graphical Tool For Breeders, Geneticists, And Agronomists. CRC Press.

Yan, W., Rajcan, I. (2002) ‘Biplot analysis of test sites and trait relations of soybean in Ontario’, *Crop Science*, 42(1), 11-20, available: DOI:https://doi.org/10.2135/cropsci2002.1100

Zeinalzadeh-Tabrizi, H., Mansouri, S. (2021) ‘Identification of adapted genotypes in sesame lines based on multi-trait selection’, *Isfahan University of Technology - Journal of Crop Production and Processing*, 11(1), 17-37, available: DOI:http://dx.doi.org/10.47176/jcpp.11.1.35431