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Evaluating the stability of modern sugar beet cultivars (*Beta vulgaris* L.) for introduction in rhizomania-contaminated areas

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ABSTRACT

Rhizomania destroys sugar beet globally, but breeding disease-resistant genotypes is crucial in fighting it. In this study, 13 modern genotypes were examined based on the list provided by the Iraniai Seed Registration and Certification Institute. Genotypes grown in a randomized complete block design, with four replications in Iran's Karaj, Mashhad, Miandoab, Shiraz, and Hamedan stations. Results revealed that F-21375 and F-21092 genotypes achieved the highest white sugar yield in all five investigated stations. The results of additive mean effect multiplicative interaction (AMMI) analysis based on white sugar yield showed that the additive effects of genotype and environment and the multiplicative effect of G×E accounted for 13.11, 51.29, and 10.60% of the total data variance, respectively. The AMMI stability parameters identified the F-21376 genotype as a stable variety that produces a high white sugar yield in five locations. Also, the first two components of the interaction effect (G×E) explained 80.70% of the variance. The biplot analysis showed that F-21376 was the genotype that produced the greatest white sugar yield and stability in infected conditions. Based on the results of the multi-trait stability index (MTSI), F-21375, and F-21372 genotypes were selected as ideal genotypes. Finally, it can be concluded that two genotypes, F-21375 and F-21376, can be introduced as high-yielding and disease-resistant genotypes in the beet cultivation areas due to their white sugar yield and stability in experimental environments.

Keywords: AMMI analysis, biplot, MTSI index, sugar beet, stability

INTRODUCTION

Sugar beet (*Beta vulgaris* L.) is a crop that is essential for sugar production (Akyüz and Ersus, 2021). After sugarcane, it is considered one of the primary sources of sugar (Monteiro et al., 2018) and accounts for approximately 20% to 30% of global sugar production (Ribeiro et al., 2016). In the 2020-21 year, the global production of sugar amounted to approximately 181 million tons, with about 26% coming from sugar beet (FAO, 2021). The quality and quantity of plant products can be reduced by biotic and abiotic stresses, leading to significant annual losses in agricultural production. Among the biotic stresses, pests and diseases are particularly detrimental to the quantity and quality of plant products (Oerke, 2006).

Sugar beet is vulnerable to diseases that are caused by pathogens. Rhizomania is a global disease that reduces the yield and quality of sugar beet crops (Galein et al. 2018; Rezaei 2007). Polymyxa betaeKeskin is the vector of the Beet Necrotic Yellowing Vein Virus (BNYVV), which is the cause of Rhizomania disease (Tamada, 1975). Sugar beet, on a global scale, could face a significant threat from this disease (McGrann et al., 2009). Izadpanah et al. (1996) reported this illness in Iran for the first time in Fars province. It was later confirmed that it exists in sugar beet fields throughout most country areas (Arjmand and AhunManesh, 1996).

Plants with high yield potential require increased environmental stress tolerance to maintain yield stability. The term genotype × environment nteraction (GEI) refers to how different genotypes respond in various environments. Crop breeding researchers acknowledge that GEI can hinder breeding progress and pose challenges in identifying superior genotypes. Breeders need to develop and release new high-yielding cultivars. Yield, a quantitative trait, is of utmost importance economically and agronomically.

Stability assessment methods are utilized to evaluate the production potential of different cultivars in various environments. As genotypes can exhibit different reactions to environmental changes, it is crucial to identify which ones can adapt and remain stable in diverse conditions. While conventional analysis methods provide limited information, regression-based equations are employed for more comprehensive evaluations of genotype performance (Eberhart and Russell, 1966). Additive mean effect multiplicative interaction (AMMI) and genotype plus genotype-environment interaction-biplot) GGE-biplot(are among the other statistical methods that have gained widespread usage (Fasahat et al., 2015).

The AMMI method is a statistical analysis considering the combined impact of genetics, environment, and their interaction (GxE). It helps understand the GxE interaction more accurately (Ebdon and Gauch, 2002). The AMMI method combines the ANOVA and principal component analysis (PCA) models. Researchers have utilized AMMI analysis to identify stable genotypes in sugar beet (Studnicki et al., 2019; Taleghani et al., 2023; Rajabi et al., 2023).

The GGE-biplot method visually displays the interaction between genotype and environment to assess stability and performance across environments for breeders. It also evaluates the relationship among environments to identify target environments in breeding programs (Yan et al. 2001). Abbas and Bocianowski (2021) used the GGE-biplot method to identify stable genotypes of sugar beet; they introduced 7233-P.29 (G38) and C CMS (G49) parental and 2(6) C (G27) and 5C (G33) hybrids for future cross-breeding programs.

Olivoto et al. (2019) have presented the theoretical foundation of the multi-trait stability index (MTSI), which aids in identifying genotypes with high yield and stability in METs, taking into account multiple traits and fixed and random effects models. The MTSI is determined by measuring how far away a genotype is from the ideal one, which is estimated using factor analysis. Using this index, stable genotypes can be selected with a positive selection for desired traits and an adverse selection for undesired traits.

Genotype-by-environment interaction (GEI) is a unifying challenge for plant breeders (Lin and Binns, 1994). Genetic and environmental factors determine sugar beet's quantitative and qualitative traits. Various sugar beet cultivars exhibit different reactions to different environments. To introduce new varieties into the breeding program, examining them in multiple environments is necessary to determine their stability across other conditions. If the ranking of a genotype does not change in different environments, it means that there is no or very little GEI, and this genotype has a general adaptation (Baker, 1988).

Since rhizomania is a soil-borne disease and the ineffectiveness of conventional methods (such as chemical and agronomical) in managing soil-borne diseases are reported, genetic resistance has been proven as the most effective way to control the disease.

Identifying and selecting disease-resistant genotypes requires evaluating the genetic diversity of breeding lines. The study examined sugar beet genotypes to determine disease resistance and yield stability of modern sugar beet genotypes in areas with high rhizomania contamination.

MATERIALS AND METHODS

Details of experiments and plant materials

In this experiment, 13 modern foreign cultivars were examined based on the list provided by the Iranian Seed Registration and Certification Institute to determine Value for Cultivation and Use (VCU) (Table 1).

Table 1. List of the studied sugar beet genotypes

Row	Genotype
1	F-21370
2	F-21371
3	F-21372
4	F-21373
5	F-21374
6	F-21375
7	F-21376
8	F-21377
9	F-21410
10	F-21411
11	F-21412
12	F-20940
13	F-21092

The plant materials were grown in Iran's agricultural research stations located in Karaj (Alborz province, center of Iran), Mashhad (Razavi Khorasan Province, northeast of Iran), Shiraz (Fars province, south of Iran), Miandoab (West Azerbaijan province, northwest of Iran), and Hamedan (Hamedan province, western Iran). Genotypes were evaluated in a randomized complete block design with four replications at each station.

Rhizomania disease had naturally infected the research stations, apart from the Karaj environment. To ensure that the soil of the experimental site was contaminated with Rhizomania, a cultivar sensitive to Rhizomania Sharif was cultivated around the experiments. The specifications for the research stations are presented in Table 2.

Measurement of quantitative and qualitative root traits

Once the root yield was harvested and recorded, the roots were washed. Following this, a pulp sample was created at random from each plot. The content of sugar, alpha-amino N, and the sodium (Na^+) and potassium (K^+) of samples were measured in the quality control laboratory (Kunz et al., 2002). The values obtained were used to estimate the quantitative and qualitative characteristics listed below (Cook and Scott, 1993).

$$Y = RY \times SC \tag{1}$$

$$MS = 0.0343K^+ + Na^+ + 0.094\ (\text{alpha amino N}) - 0.31 \tag{2}$$

$$WSC = SC - (MS + 0.6) \tag{3}$$

$$WSY = WSC \times RY \tag{4}$$

$$ESC= (WSC / SC) \times 100 \tag{5}$$

where:

- RY, SY and WSY = root, sugar and white sugar yield respectivley ($t.ha^{-1}$),
- SC and WSC = sugar and white sugar content (%),
- MS = molasses sugar (%),
- K^+, Na^+, and Alpha-amino-N are root potassium, sodium, and nitrogen content, respectively (milliequivalents. 100 g^{-1}),
- ESC = extraction of sugar coefficient (%).

Statistical analysis

Bartlett's test (Bartlett, 1937) was used to check the homogeneity of the variances of experimental errors. A combined variance analysis was performed after confirming the homogeneity of error variance for each trait. Considering the economic importance of white sugar yield, AMMI stability and GGE biplot analysis methods were performed based on this trait. AMMI and biplot analysis were conducted using GEA-R (v. 4.0, CIMMYT, Mexico) and GGE biplot software (Yan, 1999, 2001).

Table 2. Geographical characteristics and rainfall of the research stations during the 2021 seasons

Location	Rainfall (mm)	Altitude (m)	Coordinate		Temperature (C°)			Soil type
			Longitude	Latitude	Min	Max	Ave	
Karaj	252.3	1244	50° 52´ E	35° 50´ N	10.4	26.5	18.5	Clay-loam
Hamedan	261.1	1818	48° 30´ E	34° 47´ N	5.27	22.92	14.09	Silty-loam
Mashhad	214.9	998	60° 48´ E	35° 12´ N	12.3	25.7	19.0	Silty-loam
Miandoab	166.8	1294	46° 06´ E	36° 57´ N	9.0	25.3	17.6	Silty-loam
Shiraz	207.3	1598	52° 42´ E	29° 46´ N	11.1	28.9	20.0	Clay-loam

Equation 6 was used to perform stability analysis by the AMMI method (Gauch, 1992):

$$Y_{ij} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn\delta_{en}} + \rho_{ge} \qquad (6)$$

where Y_{ij} is the yield of genotype g in environment e; μ is the grand mean; α_g is the genotype deviation from the grand mean; β_e is the environment deviation; λ_n is the singular value for IPCn, and correspondingly λ_n^2 is its eigenvalue; γ_{gn} is the eigenvector value for genotype g and component n; ρ_{ge} is the eigenvector value for environment e and component n, with both eigenvectors scaled as unit vectors; and δ_{en} is the residual.

During this study, 13 statistics obtained from the AMMI model were used to identify the stable genotype in disease-infected conditions through Equations 7 to 18:

$$\text{AMGE (Sum across environments of GEI modeled by AMMI)} = \sum_{n=1}^{\acute{N}} \lambda_n \gamma_{n\delta_{in}}$$

(Sneller et al., 1997)

$$\text{ASI (AMMI stability index)} = \sqrt{[PC_1^2 + \theta_1^2] + [PC_2^2 + \theta_2^2]}$$

(Jambhulkar et al., 2014)

$$\text{ASV (AMMI stability value)} = \sqrt{\frac{SSIPCA1}{SSAPCA2}(IPC_1)^2 + (IPC_2)^2}$$

(Purchase et al., 2000)

$$\text{ASTAB (AMMI − based stability parameter)} = \sum_{n=0}^{\acute{N}} \lambda_n \gamma_{in}^2$$

(Rao & Prabhakaran, 2005)

$$\text{AVAMGE (Sum across environments of the absolute value of GEI modeled by AMMI)} = \sum_{j=1}^{E} \sum_{n=1}^{\acute{N}} \lambda_n \gamma_{n\delta_{in}}$$

(Zali et al., 2012)

$$\text{Da (Annicchiarico's D parameter)} = \sqrt{\sum_{n=0}^{\acute{N}} (\lambda_n \gamma_{in}^2)^2}$$

(Annicchiarico, 2002)

$$\text{Dz (Zhang's D parameter)} = \sqrt{\sum_{n=0}^{\acute{N}} \lambda_{in}{}^2}$$

(Zhang et al., 1998)

$$\text{EV (Average of the squared eigenvector values)} = \sum_{n=1}^{\acute{N}} \frac{\gamma_{in}^2}{\acute{N}}$$

(Zhang et al., 1998)

$$\text{FA (Stability measure based on fitted AMMI model)} = \sum_{n=1}^{\acute{N}} \lambda_n{}^2 \gamma_{in}^2$$

(Raju, 2002)

$$\text{MASI (Modified AMMI stability index)} = \sqrt{\sum_{n=1}^{\acute{N}} (PC_n^2 \times \theta_n^2)}$$

(Ajay et al., 2018)

$$\text{MASV (modified AMMI stability value)} = \sqrt{\sum_{n=1}^{\acute{N}} (\frac{SSIPCn}{SSAPCn + 1})(IPC_n)^2 + (IPC_{\acute{N}})^2}$$

(Zali et al., 2012)

$$\text{SIPC (Sum of the absolute values of the IPC scores)} = \sum_{n=0}^{\acute{N}} |\lambda_n{}^{0.5} \gamma|$$

(Sneller et al., 1997)

$$\text{Za (Absolute value of the relative contribution of IPCAs to the interaction)} = \sum_{n=0}^{\acute{N}} |\theta_n \gamma_{in}|$$

(Zali et al., 2012)

To estimate the mean yield and simultaneous stability of RY, SY, WSY, SC, WSC, K^+, Na^+, N, MS and ECS, the MSTI index was computed based on equation 7 (Olivoto et al., 2019).

$$MSTI_i = \left[\sum_{j=1}^{f}\left((\gamma_{ij} - \gamma_j)^2\right)\right]^{0.5} \quad (7)$$

where is the multi-trait stability index of genotype *i*, γ_{ij} is the score of genotype *i* in factor *j*, and γ_j is the score of the ideal genotype in factor *j*.

RESULTS

The analysis of variance showed that the difference between genotypes in the five studied regions was significant in terms of white sugar yield. The means comparison of the genotypes showed that the F-21375 and F-21092 genotypes achieved the highest white sugar yield in all five investigated regions. A mean comparison of genotypes in five environments with rhizomania natural contamination showed that the F-21373 genotype in the environment of Karaj, genotype F-21377 in the environment of Mashhad and Miandoab, genotype F-21410 in the environment of Shiraz, and genotype F-21371 in the environment of Hamedan had the lowest white sugar yield (Table 3).

AMMI stability

The results of the variance analysis based on white sugar yield showed that the difference between genotypes and environments and the interaction effect of genotype in the environment in terms of white sugar yield was significant at the 1% probability level (Table 4).

Table 3. Analysis of variance and mean comparison for white sugar yield (t/ha) of sugar beet genotypes

Sources of variation	Karaj	Mashhad	Shiraz	Miandoab	Hamedan
Replication	8.865	16.651	7.900	25.707	3.088
Genotypes	10.579**	12.062**	6.476**	15.40*	20.203**
Error	3.268	3.191	2.286	7.581	1.224
Coefficient of variation	13.258	13.058	11.542	16.808	12.975
Genotypes					
F-21370	14.18^{abc}	14.00^{abc}	14.79^{ab}	14.28^{bc}	8.61^{cde}
F-21371	13.20^{abc}	12.34^{cde}	11.60^{cd}	17.99^{ab}	4.67^{h}
F-21372	13.53^{abc}	13.91^{abc}	12.17^{cd}	17.22^{abc}	7.35^{efg}
F-21373	9.33^{d}	12.98^{bcd}	11.89^{cd}	14.57^{bc}	8.51^{cde}
F-21374	12.72^{bc}	15.88^{a}	13.51^{abc}	17.77^{ab}	11.39^{ab}
F-21375	14.86^{ab}	16.08^{a}	14.56^{ab}	20.79^{a}	11.52^{ab}
F-21376	15.55^{a}	15.41^{ab}	14.93^{a}	17.10^{abc}	9.96^{bc}
F-21377	13.53^{abc}	10.40^{e}	13.38^{abc}	13.40^{c}	5.78^{gh}
F-21410	14.86^{ab}	11.22^{de}	10.71^{d}	16.54^{bc}	6.85^{fg}
F-21411	11.9^{c}	13.8^{abc}	12.8^{bc}	15.9^{bc}	9.1^{cd}
F-21412	14.1^{abc}	13.1^{bcd}	13.1^{abc}	15.3^{bc}	6.8^{fg}
F-20940	14.6^{ab}	13.2^{bcd}	12.9^{abc}	14.8^{bc}	8.2^{def}
F-21092	14.7^{ab}	15.3^{ab}	14.7ab	17.1^{abc}	11.9^{a}

Note: * and ** are significant at 5 and 1% probability levels, respectively
In each column, the mean with common letters has no significant difference at the 5% probability level

Table 4. Analysis of variance based on AMMI model for sugar yield of sugar beet genotypes

Source	Df	Sum of squares	Mean of squares	Relative variance (%)	G×E Relative variance (%)
Total	259	3275.1	12.65		
Treatments	64	2456.7	38.39**	75.015	
Genotypes	12	429.4	35.79**	13.11	
Environments	4	1680	420**	51.29	
Block	15	186.6	12.44**	5.69	
Interactions	48	347.2	7.23**	10.60	
IPCA1	15	182.7	12.18**	5.57	52.62
IPCA2	13	123.5	9.5**	3.77	35.57
Residuals	20	41.1	2.05ns	1.25	11.84
Error	180	631.8	3.51	19.29	

Note: ns, * and **, non-significant, significant at 5 and 1% probability levels, respectively
Df: Degrees of freedom G×E: Genotype× Environment

Genotype and environment explained 13.11 and 51.29% of the total variation of data variance, respectively (Table 4). In this study, the interaction effect of genotype × environment was divided into two factors or components: IPCA1 (AMMI 1) and IPCA2 (AMMI 2), and both the first two components were significant at the probability level of 1%.

The contribution of the first component (IPCA1) and the second (IPCA2) was 5.57 and 3.77% of the total sum of squares and 52.62 and 35.57% of the sum of the squares of the interaction effects of genotype in the environment, respectively. Also, IPCA1 (AMMI 1) and IPCA2 (AMMI 2) accounted for 88.19% of the total variations of variance of genotype × environment interaction (Table 4).

Table 5 shows the white sugar yield mean, IPCA1 and IPCA2 components, and different AMMI stability parameters for 13 sugar beet genotypes across five environments. According to the results of the mentioned table, the highest white sugar yield with an average of 15.57, 14.78, 14.60, and 14.26 t/ha was related to F-21375, F-21092, F-21376, and F-21374 genotypes, respectively; the lowest one was recorded with an average of 11.3 t/ha for F-21377 genotype. In this study, genotypes F-21376 and F-21372 showed the lowest ASTAB, ASI, ASV, AVAMGE, DA, DZ, EV, FA, MASI, MASV, SIPC, ZA and WAAS and were considered stable genotypes in terms of white sugar yield, While F-21371 genotype had the highest values of the mentioned stability parameters and was recognized as unstable genotypes (Table 5).

First four AMMI selections per environment

The average values of white sugar yield and the appropriate four genotypes in each environment are shown in Table 6. In this study, Miandoab and Hamedan experimental environments with an average of 16.38 and 8.53 t/ha exhibited the highest and lowest white sugar yield, respectively.

In this study, the difference between experimental environments in terms of competence and production potential was much higher than the difference between genotypes. Analysis of variance also showed that the environmental factor contributed 51.29% to the total variance. In this study, the F-21375 genotype for all environments investigated and genotype F-21376 for all environments except Miandoab were among the ideal four genotypes (Table 6).

Table 5. White sugar yield mean and different AMMI stability parameters for 13 sugar beet genotypes in five environments

Genotype	white sugar yield (t/ha)	IPCA1	IPCA2	ASTAB	ASI	ASV	AVAMGE	DA	DZ	EV	FA	MASI	MASV	SIPC	ZA	WAAS
F-21370	13	0.02	-0.95	0.90	0.34	0.95	3.99	2.24	0.40	0.08	5.01	0.34	0.95	0.97	0.15	0.40
F-21371	11.96	0.96	1.20	2.36	0.66	1.86	7.59	3.77	0.63	0.20	14.23	0.66	1.86	2.16	0.38	1.06
F-21372	12.84	0.23	0.59	0.40	0.24	0.68	2.66	1.51	0.26	0.04	2.28	0.24	0.68	0.82	0.14	0.37
F-21373	11.46	-1.23	0.01	1.51	0.65	1.82	5.79	3.19	0.47	0.11	10.20	0.65	1.82	1.24	0.25	0.74
F-21374	14.26	-1.11	0.31	1.32	0.59	1.67	5.55	2.97	0.45	0.10	8.80	0.59	1.67	1.42	0.27	0.78
F-21375	15.57	-0.40	0.96	1.08	0.40	1.13	4.75	2.49	0.44	0.09	6.21	0.40	1.13	1.36	0.23	0.63
F-21376	14.60	0.08	-0.37	0.14	0.14	0.39	1.62	0.90	0.16	0.01	0.80	0.14	0.39	0.45	0.07	0.19
F-21377	11.3	0.87	-0.94	1.63	0.56	1.59	6.59	3.15	0.52	0.13	9.95	0.56	1.59	1.80	0.32	0.89
F-21410	12.04	0.97	0.48	1.16	0.54	1.51	5.58	2.75	0.42	0.09	7.58	0.54	1.51	1.44	0.27	0.77
F-21411	12.74	-0.65	0.01	0.42	0.34	0.96	3.06	1.69	0.25	0.03	2.87	0.34	0.96	0.67	0.13	0.39
F-21412	12.52	0.54	-0.32	0.39	0.31	0.86	3.25	1.59	0.25	0.03	2.52	0.31	0.86	0.86	0.16	0.45
F-20940	12.76	0.33	-0.60	0.47	0.28	0.78	3.31	1.66	0.29	0.04	2.75	0.28	0.78	0.93	0.16	0.44
F-21092	14.78	-0.61	-0.39	0.52	0.35	0.98	3.76	1.83	0.29	0.04	3.34	0.35	0.98	1.00	0.18	0.52

Table 6. Score and white sugar yield mean of experimental environments and first four genotypes for each environment

Number	Environment	Mean	Score	1	2	3	4
2	Karaj	13.64	1.88	F-21376	F-21375	F-21092	F-20940
4	Miandoab	16.38	0.30	F-21375	F-21371	F-21374	F-21372
5	Shiraz	13.1	0.16	F-21092	F-21376	F-21375	F-21370
3	Mashhad	13.68	-0.79	F-21375	F-21092	F-21374	F-21376
1	Hamedan	8.53	-1.56	F-21092	F-21374	F-21375	F-21376

Biplot

Figure 1 shows how white sugar yield and genotype adaptation were assessed using biplots of the first and second principal components. A genotype that produces a high white sugar yield and a low genotype-environment interaction is more favourable.

Based on Figure 1, the biplot of average white sugar yield of genotypes against IPCA1 values, F-21370 and F-21376 genotypes had IPCA1 values close to zero and had appropriate yield stability and general compatibility, While F-21373 and F-21374 genotypes had high values of IPCA1 and were identified as unstable genotypes.

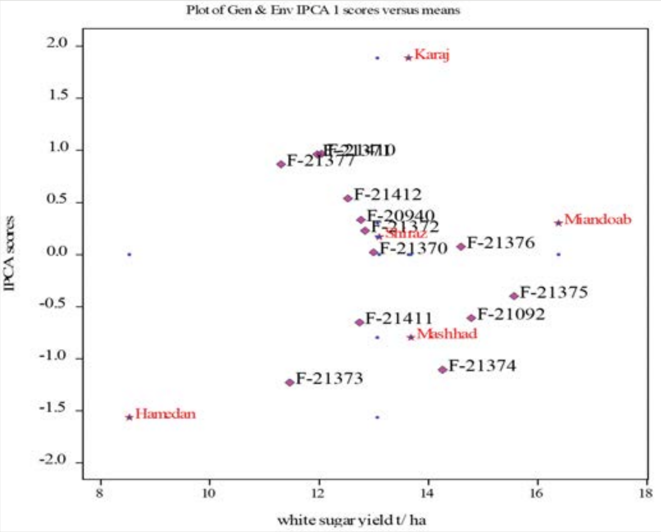

Figure 1. Scatter plot for genotypes and environments based on white sugar yield means and a first principal component

The biplot of the white sugar yield mean of the genotype against the IPCA2 values (Figure 2) showed that the F-21373 and F-21411 genotypes had IPCA2 values close to zero. In contrast, the genotype numbers F-21371, F-21375, and F-21370 had the most significant distance from zero and were identified as unstable genotypes.

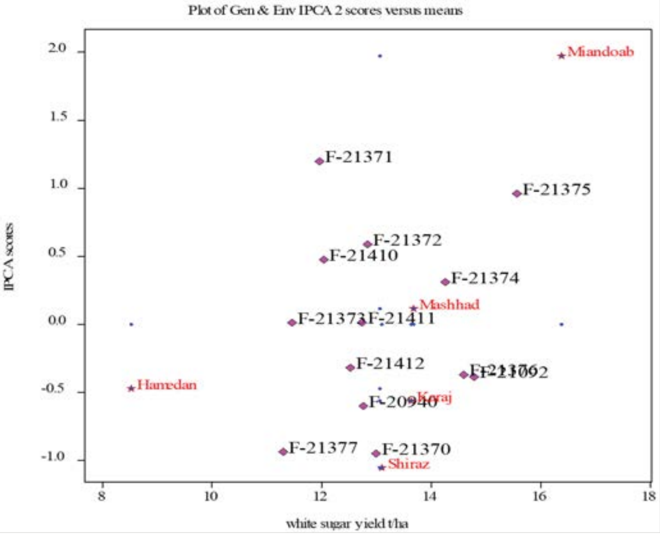

Figure 2. Scatter plot for genotypes and environments based on white sugar yield means and a second principal component

GGE model

The Convex hull resulting from GGE analysis of sugar beet genotypes in five environments is shown in Figure 3. In this diagram, genotypes and environments are determined based on the values of the first and second principal components; Points close to the origin of the first and second principal components have the most negligible GGE interaction. This diagram (the interaction effect's first and second principal components) justified 80.70% of the variance of the interaction effect of genotype and environment. In this diagram, the genotypes located near a location have private compatibility with that environment, and those near the origin of coordinates have general compatibility.

In the current research, F-20940 and F-21412 genotypes were the closest to the coordinate origin and identified as the most stable. The F-21371 genotype had the greatest distance from the coordinate origin and was identified as the most unstable. In this biplot, a polygon can be seen that defines the suitable genotype for each environment. Based on this, the F-21375 genotype was placed at the vertex of the polygon. Due to its high private compatibility, it was recognized as a suitable genotype for each Karaj, Mashhad, Shiraz, Miandoab, and Hamedan environment. F-21373, F-21410, F-21371, and F-21377 were located at the vertex of the polygon near which there was no environment; these genotypes were recognized as inappropriate for the tested environments (Figure 3).

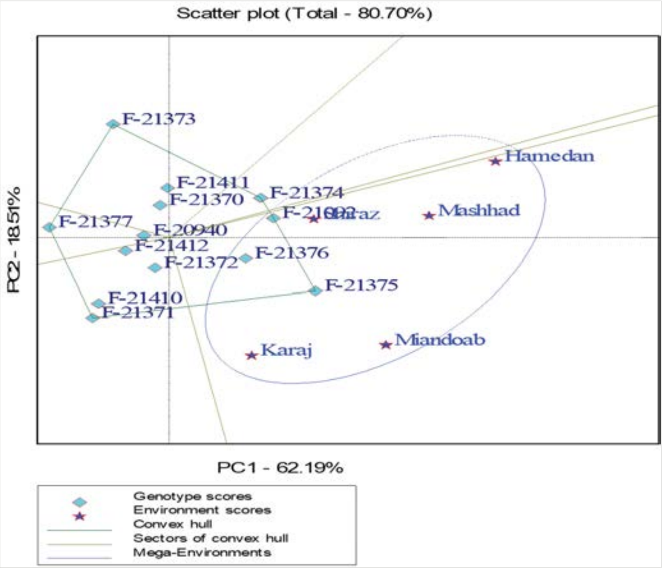

Figure 3. Polygon of GGE biplot method to identify suitable genotypes for each environment

Average yield and stability

The average environment coordination line is the diagonal line that passes through the center of the biplot and the ideal point (the average representative of the coefficients of the first two components of the interaction effect in the GGE biplot model). Genotypes closer to the circle's center on this line yield the highest. Genotypes further from the perpendicular line to the environmental function's average line are less stable and have a more significant impact on interaction. In this study, the three genotypes, F-21375, F-21376, and F-21092 genotypes, had a higher white sugar yield than other genotypes, and due to their small distance from the ACE line, they were recognized as stability genotypes. According to the study, genotypes F-21371 and F-21373 showed the most significant distance from the ACE line and had lower stability (Figure 4).

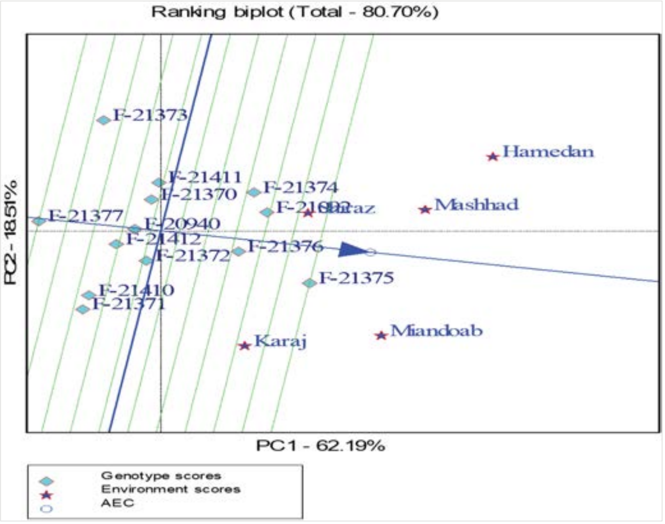

Figure 4. Genotype ranking based on average white sugar yield and stability

Concentric circles have been formed on the biplot to establish the ideal genotype as a reference for evaluation. These circles allow for a visual assessment of the distance between the studied genotypes and the ideal genotype. The concentric circles, with the ideal genotype in the center, help visualize the distance between the studied genotypes and the ideal variety. Based on this, the genotypes F-21375 and F-21092 genotypes were the closest genotypes to the ideal genotype and were more favorable than all the studied genotypes; on the other hand, F-21373 genotype was determined as the most undesirable genotypes because they had the greatest distance from the ideal variety (Figure 5).

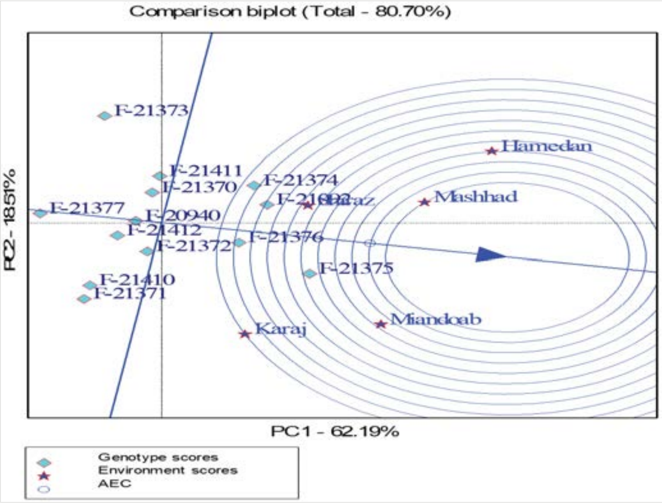

Figure 5. Evaluation of studied genotypes compared to the ideal genotype based on white sugar yield

Multi-trait stability index (MTSI)

In this study, three factors with an eigenvalue higher than one were identified, which explained 80.77% of the total variance of the data. The first factor, with eigenvalues of 3.30, justification of 30.00% of the total variance, had high and positive factor coefficients for sugar content, white sugar content, extraction coefficient of sugar, and white sugar yield and had high and negative factor coefficients Na^+, Alkalinity, and Molasse sugar.

The second factor explained 25.59% of the total data variance and had an eigenvalue of 2.81. This factor had high and negative coefficients for root yield, alpha-amino nitrogen, sugar yield, and white sugar yield. The third factor contributed to 25.17% of data variation and an eigenvalue of 2.77, which showed a high and positive factor coefficient for the K^+ and alkalinity (Table 7).

The factor scores of the above-mentioned factors were used to calculate the MTSI stability index of the genotypes. The MTSI was calculated using both quantitative and qualitative characteristics. In Figure 6, the experimental genotypes have been sorted based on their MTSI values; the genotype with the highest MTSI

Table 7. Factor analysis based on principal component analysis: Eigenvalues, factor coefficients, relative and cumulative variance, after varimax rotation

Traits	Factors			Communality	Uniquenesses
	FA1	FA2	FA3		
Root yield	-0.30	-0.88	0.19	0.91	0.09
Sugar content	0.86	-0.39	0.07	0.89	0.11
Na^+	-0.77	-0.04	0.22	0.64	0.36
K^+	0.04	-0.12	0.90	0.83	0.17
alpha-amino nitrogen	0.47	-0.57	-0.38	0.69	0.31
Alkalinity	-0.60	0.26	0.54	0.72	0.28
White sugar content	0.88	-0.31	0.11	0.88	0.12
Extraction of sugar coefficient	0.93	-0.14	0.01	0.88	0.12
Molasse sugar	-0.78	0.02	0.39	0.77	0.23
Sugar yield	0.32	-0.93	0.01	0.96	0.04
White sugar yield	0.51	-0.83	-0.06	0.95	0.05
Eigenvalue	3.30	2.81	2.77		
Relative Variance (%)	30.00	25.59	25.17		
Cumulative variance (%)	30.00	55.59	80.77		

is in the centre, while the one with the lowest MTSI is in the outermost circle. The genotypes determined in red colour dots were selected based on their MTSI values at 20% selection intensity. In our research, F-21375 and F-21372 genotypes were selected as ideal genotypes. Based on the highest to the lowest value of the MTSI index, genotypes are placed in the outermost circuit to the centre of the Figure, respectively. F-21371 genotype had the lowest stability index score, showing poor stability and mean sugar yield in different environmental conditions (Figure 6).

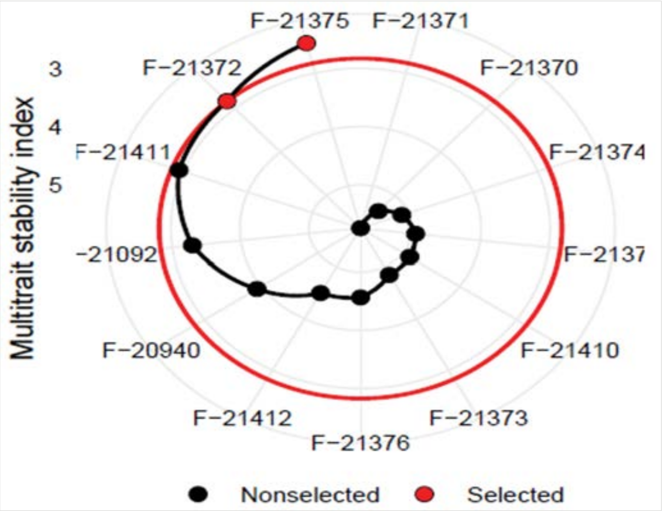

Figure 6. Genotype ranking and selected genotypes based on the MTSI index

DISCUSSION

The results of mean comparisons showed a suitable genetic diversity between the examined genotypes regarding white sugar yield. Genetic diversity provides breeders with a selection of cultivars to choose from. Genetic diversity provides breeders with the option to select from various cultivars. Of all the genotypes studied, F-21375 and F-21092 genotypes had the highest white sugar yield in all five studied locations. Genetic differences between sugar beet cultivars regarding white sugar yield have also been reported in previous studies (Studnicki et al., 2019; Rajabi et al., 2023; Taleghani et al., 2023).

The AMMI analysis results showed a significant interaction effect between genotype and environment. This suggests that genotypes respond differently to varying environments. The existence of this interaction effect indicates the problems faced by breeders in selecting new genotypes for release.

It was found that the residual sum of squares (Noise) from the AMMI model with the lowest mean of squares was not significant, which indicates the model's considerable accuracy (Anandan and Eswaran, 2009). Based on AMMI stability parameters, the F-21376 genotype was recognized as stable, producing a high white sugar yield in five locations. Using the AMMI method, Rajabi et al. (2023) found that the G×E interaction explained 65.10% of the total data variance. Taleghani et al. (2023) showed that the additive main effects of genotype and environment and the multiplicative interaction (AMMI) model were significant for white sugar yield; in their study, the first four components explained 86.30% of the GEI.

In this experiment, the first two significant components justified 80.70% of the total variance of the interaction effect of genotype with the environment. Hence, the drawn biplot had high reliability in explaining the interaction effects of genotype with the environment (Tardieu, 2013). Based on the biplot results of the values of the first and second components and the white sugar yield, the F-21376 genotype had close to zero values of the first and second components and high white sugar yield compared to other genotypes, which indicates that this genotype had a consistent and stable performance, which is higher than the different genotypes that were investigated. In this study, the F-20940 and F-21412 genotypes showed high general compatibility for all regions, while the F-21375 genotypes had significant private compatibility for the Karaj, Mashhad, Miandoab, and Hamedan regions. It has been stated that a biplot can be used to determine MEs when it accounts for at least 60% of the data variance (Yang et al., 2009). Hassani et al. (2018) showed that the first two PCs explain 62.9% of the GEI variations. According to a study by Saremirad et al. (2020), the combined value of the first and second principal components was approximately 74%. Through biplot analysis, Rajabi et al. (2023) demonstrated that the

RM5 genotype had a high white sugar yield and stability, even in infected conditions.

Studnicki et al.)2019(investigated the stability of 36 modern sugar beet cultivars under Polish environmental conditions; they did not find a cultivar or cultivars with a broad adaptation to the environmental conditions. Abbas and Bocianowski (2021) introduced 7233-P.29 (G38) and C CMS (G49) parental and 2(6)C (G27) and 5 C (G33) hybrids as stable genotypes.

According to the Average yield and stability diagram, two cultivars, F-21375, F-21376, and F-21092, had a higher white sugar yield and a small distance from the ACE line; they were recognized as stability genotypes. Furthermore, the cultivars F-21375 and F-21092 were the closest genotypes to the ideal genotype and were more favourable than all the studied genotypes.

Based on the MTSI stability index, F-21375 and F-21372 genotypes were selected as stable and superior genotypes based on all quantitative and qualitative measured characteristics. According to Sharif et al. (2021) and Koundinya et al. (2021), plant breeders can effectively use MTSI to identify superior genotypes for multiple traits based on multi-environment data. Rajabi et al. (2023) identified five sugar beet genotypes that are stable under field conditions and resistant to rhizomania disease based on the MTSI results. Taleghani et al. (2023) identified four ideal sugar beet genotypes using MTSI.

CONCLUSION

Based on the results of all statistical analyses, F-21375 and F-21376 genotypes had acceptable white sugar yield and stability in all test environments. After additional evaluations, these genotypes can be introduced in beet-growing areas infected with Rhizomania.

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