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Analysis of the Genotype by Environment Interactions of Sugar Beet Genotypes under Rhizomania Contamination

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ABSTRACT

The sugar beet crop has always been attacked by various pests and diseases. Rhizomania viral disease, which has spread in different regions of sugar beet cultivation, has become a disease of prime importance for the crop in the last three decades. Resistant cultivar usage is the only reliable way to manage rhizomania disease. In order to identify promising genotypes, eleven sugar beet genotypes with natural infection to rhizomania, in a company with three controls, were assessed in a Randomized Complete Block Design (RCBD) with four replications. The experiment was conducted in six research stations of Karaj, Khoy, Kermanshah, Mashhad, Miandoab, and Shiraz for two cropping seasons (2020 and 2021). Based on the rhizomania score, all genotypes had acceptable resistance to the disease. The Additive Main Effects and Multiplicative Interaction (AMMI) stability analysis illustrated that the first five principal components were significant and specified 88.8% of the total genotype by environment interaction variance. Gen-7, Gen-10, Gen-11, and Gen-2 were selected as stable genotypes based on the AMMI model. Genotype plus Genotype by Environment Interaction (GGE) biplot results also confirmed the superiority of Gen-10 and Gen-11 regarding sugar yield and stability in disease-infected environments. According to the results of the Multi-Trait Stability Index (MTSI), genotypes Gen-4, Gen-1, Gen-2, and Gen-11 were identified as stable genotypes under rhizomania-infected conditions. By applying different stability measurement methods, in addition to identifying the genotypes' adaptation to different environments, accurate decisions for future breeding or cultivar registration can be achieved.

Keywords: Genotype selection, Multi-trait stability index, *Polymyxa betae*, Resistance to rhizomania, Stability parameters.

INTRODUCTION

Sugar is a global bulk commodity that can be stored without loss and transported easily. In 2020-21, global sugar production was about 181 million tons, approximately 26% was obtained from sugar beet (ISO, 2022; Statista, 2022). Global sugar production has risen by nearly 1.5% per year, with vast fluctuations over the years for more than 20 years (Jurgen, 2019). The growth in global consumption is principally due to developing countries with an annual consumption of less than 10 kg of sugar per

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capita. In developed countries, sugar consumption ranges from 25 to 50 kg per person based on eating habits and appetite. In the majority of countries, sugar prices are determined by national import and export regulations and sugar price policies. Therefore, the national profitability of sugar production from sugar beet and its cultivated area varies largely. Sugar beet cultivation is commonly related to agreements between sugar producers and farmers. For sugar beet as an annual crop, there is more flexibility in the cultivated area than sugarcane (Fasahat and Kakueinezhad, 2021; Hoffmann *et al.*, 2021). For decades, the sugar beet crop has been the cornerstone of the activities and income of many farmers and sugar industries around the world. Breeding activities have contributed to maintaining the competitive position of this crop. Continuous increases in yield and improving the crop tolerance to the biotic and abiotic stresses indicate its development over the years.

Rhizomania is one of the main diseases of sugar beet. The disease is caused by the sugar beet necrotic yellow vein virus, which is transmitted to sugar beet through the root fungus *Polymyxa betae*, a soil-borne pathogen. The pathogen mainly attacks the roots of the plant, causing the proliferation of lateral roots along the main root (Norouzi *et al.*, 2017). About half of the lands under sugar beet cultivation in Iran are infected with rhizomania, and the severity of infection in the fields is different from each other. The damage caused by rhizomania differs depending on the cultivar and virus strain and can reduce the crop yield by 90%. Over the past few decades, plant breeders have worked to improve the productivity and quality of rhizomania-resistant cultivars. By 2008, the genetic progress was such that the vast majority of sugar beet growers in Iran, France, Belgium, and the Netherlands planted rhizomania-resistant cultivars in their fields (Norouzi *et al.*, 2017). Nowadays, most commercial sugar beet cultivars carry resistance genes to rhizomania, including Rz_1 and Rz_2, as a priority. Other resistance sources, such as Rz_3, Rz_4, and Rz_5 were also identified (Biancardi and Tamada, 2016).

Evaluation of the adaptability and stability of cultivar production under different environmental conditions is of particular importance in breeding programs. Due to the different responses of the cultivars to environmental changes, their performance varies from one environment to another. Typically, each genotype has the maximum production potential in a particular environment; however, by assessing the stability and adaptability of the genotypes under various environments, it is possible to identify genotypes with acceptable performance in all environments (Fasahat *et al*., 2015). Since traditional statistical methods of analysis, such as using combined ANOVA tables, provide only limited information on the interaction of genotypes in the environment, different methods are used for the stability assessment. Using regression-based equations is one of the first methods used (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). Other statistical multivariate methods such as AMMI and GGE-biplot have also been widely used (Yan, 2001; Fasahat *et al.*, 2015). The AMMI method is a multivariate statistical method that assess the cumulative effects of genotype, environment, and G×E multiplicative effects and interprets G×E interaction (Ebdon and Gauch, 2002). The AMMI method is a combination of ANOVA and Principal Component Analysis (PCA) (Fasahat *et al.*, 2014). The GGE-biplot method graphically illustrates G×E interaction to help breeders simply check the stability of genotypes, and combines stability with a genotype's performance in different environments. It also evaluates the relationships among environments to identify target environments in breeding programs (Yan *et al*., 2001).

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. Therefore, it is essential to evaluate the genetic diversity of breeding lines to distinct disease-resistant genotypes.

In this study, sugar beet genotypes were assessed in terms of the effects of different environmental conditions on resistance to rhizomania disease. Also, analysis was done of genotype by environment interaction for the use of resistant genotypes in breeding programs to recommend them for cultivation in contaminated environments in Iran.

MATERIALS AND METHODS

This study was performed under the Breeding Department, Sugar Beet Seed Institute, Karaj, Iran. Eleven sugar beet genotypes accompanied by three controls were sown across six agricultural research stations in two cropping seasons (2020 and 2021). The selected environments (combination of year and location) covered considerably different conditions regarding temperature, rainfall, and soil properties. Geographical characteristics and rainfall amounts of the experimental sites across the two growing seasons are shown in Table 1.

Trials were performed in a Randomized Ccomplete Block Design (RCBD) with four replications in each environment (Table 1). The name and the given code of each genotype are listed in Table 2. The susceptible cultivar Sharif was sown around the trials in order to confirm the field infection to rhizomania. After reaching the necessary base temperature for germination, seeds were sown in rows at 20 cm spacing. The experimental units consisted of three-row plots, 8 m long and spaced 50 cm apart. Irrigation was performed immediately after planting and adjusted for subsequent irrigation intervals according to the region's thermal regime and evapotranspiration potential. At the 2-leaf stage, thinning was done, and weeds were controlled manually. The experimental fields were managed according to local agronomic practices. At harvest, to eliminate marginal effects, the first row, the last row, the beginning, and the end of each row (one m long) were removed.

The disease score was given to the roots at harvest in accordance with the Luterbacher *et al*. (2005) based on 1-9 scale (score 1 shows plants with healthy roots and 9 as dead plants) at two agricultural research stations of Shiraz and Mashhad. Although the trial in Miandoab was also performed under disease-infected conditions, the data on infection severity was not recorded. Harvested roots were weighed, washed, and pulp samples were taken. Quality analysis was conducted via a Betalyser (Anton Paar, Germany) automatic beet laboratory system based on standard procedures (ICUMSA, 2009). Quality characteristics such as sugar content, sodium (Na^+), potassium (K^+), and

Table 1. Geographical characteristics and rainfall of the research stations during 2020-21 seasons.

Locations	Codes	Cropping season	Rainfall (mm)	Altitude (m)	Coordinate		Temperature (C°)			Soil type
					Longitude	Latitude	Min	Max	Ave	
Karaj	KJ20	2020	252.3	1244	50° 52′ E	35° 50′ N	10.4	26.5	18.5	Clay-
Karaj	KJ21	2021	51.6				12.1	27.9	19.9	loam
Kermanshah	KH20	2020	319.2	1362	46° 48′ E	34° 15′ N	10.8	28.5	19.7	Silty-
Kermanshah	KH21	2021	71.3				10.7	28.9	20	clay
Khoy	KY20	2020	240.2	1147	44° 56′ E	38° 22′ N	11.0	24.9	17.9	Silty-
Khoy	KY21	2021	154.4				11.7	25.9	18.8	loam
Mashhad	MD20	2020	214.9	998	60° 48′ E	35° 12′ N	12.3	25.7	19.0	Silty-
Mashhad	MD21	2021	62.7				13.2	27.4	20.3	loam
Miandoab	MB20	2020	166.8	1294	46° 06′ E	36° 57′ N	9.0	25.3	17.6	Silty-
Miandoab	MB21	2021	107.3				10.7	26.3	18.6	loam
Shiraz	SZ20	2020	207.3	1598	52° 42′ E	29° 46′ N	11.1	28.9	20.0	Clay-
Shiraz	SZ21	2021	28.2				13.0	30.5	21.8	loam

Table 2. List of the studied sugar beet genotypes.

Genotype	Code	Genotype	Code
F-21236	Gen-1	F-21276	Gen-8
F-21237	Gen-2	F-21277	Gen-9
F-21238	Gen-3	F-21278	Gen-10
F-21239	Gen-4	F-21279	Gen-11
F-21242	Gen-5	BTS310	Gen-12
F-21243	Gen-6	Denzel	Gen-13
F-21244	Gen-7	Macumba	Gen-14

amino-Nitrogen (N) were measured. Their values were used to estimate sugar yield, white sugar yield, white sugar content, molasses sugar, and extraction coefficient of sugar based on Equations (1-5) (Cook and Scott, 1993; Reinfeld *et al*., 1974).

$$SY = RY \times \mathrm{SC} \quad (1)$$

$$WSY = \mathrm{RY} \times \mathrm{WSC} \quad (2)$$

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

$$MS = 0.0343(\mathrm{K}^{+} + \mathrm{Na}^{+}) + 0.094 \quad (4)$$

$$ECS = (\mathrm{WSC}/\mathrm{SC}) \times 100 \quad (5)$$

Where, SY is Sugar Yield (t ha^{-1}), RY is Root Yield (t ha^{-1}), SC is Sugar Content (%), WSY is White Sugar Yield (t ha^{-1}), WSC is White Sugar Content (%), MS is Molasses Sugar (%), and K^{+}, Na^{+}, and amino-Nitrogen is N (all in meq 100 g^{-1}), and ECS is Extraction Coefficient of Sugar (%).

Statistical Analysis

Bartlett's test (Bartlett, 1937) was calculated to check the homogeneity of the variances of experimental errors. After confirming the homogeneity of error variance for each trait (RY= 0.7073, SY= 0.6909, SC= 0.0867, WSC= 0.1768, WSY= 0.4540, Na= 0.6608, K= 0.6673, N= 0.5138, MS= 0.8691, and ECS= 0.9933), a combined variance analysis was performed. The genotypes were considered as fixed variables, while the environments were treated as random variables.

The weight of sugar beet root and the sugar content are the two main components of yield formation in sugar beet. A combination of high values obtained from root yield and sugar content will result in a high sugar yield per hectare. Therefore, owing to the importance of sugar yield as the main criterion to distinguish sugar beet cultivars, multivariate stability analysis was conducted graphically on the basis of GGE biplot for this trait using GGE biplot software (Yan, 1999, 2001) and AMMI analysis by GEA-R (v. 4.0, CIMMYT, Mexico). Different statistics from the AMMI model, including AMMI-based stability parameter (ASTAB), AMMI Stability Index (ASI), AMMI Stability Value (ASV), sum across environments of Absolute Value of G×E interaction modeled by AMMI (AV_{AMGE}), Annicchiarico's D parameter (DA), Zhang's D parameter (Dz), average of the squared Eigenvector Values (EV), stability measure based on Fitted AMMI model (FA), Modified AMMI Stability Index (MASI), Modified AMMI Stability Value (MASV), Sums of the absolute value of the IPC scores (SIPC), absolute value of the relative contribution of IPCAs to the interaction (ZA) (Sneller *et al.*, 1997; Zhang *et al.,* 1998; Purchase *et al.*, 2000; Raju, 2002; Rao and Prabhakaran, 2005; Zali *et al.,* 2012; Ajay *et al.*, 2018) were calculated to identify stable genotypes. All statistical analysis was performed using R Statistical Software 4.0.3 (R core Team 2020).

To estimate the average yield and simultaneous stability of RY, SY, WSY, SC, WSC, K^{+}, Na^{+}, N, MS, and ECS, the MSTI index was computed based on Equation (6) (Olivoto, 2019) using R Statistical software 4.0.3 (R core Team 2020).

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

Where, $MSTI_i$ is the Multi-Trait Stability Index of the genotype *i*, γ_{ij} is the score of the genotype *i* in the factor *j*, and γ_j is the score of the ideal genotype in the factor *j*.

RESULTS AND DISCUSSION

Combined Analysis of Variance

After confirming the uniformity of error variances in all trials by performing Bartlett's test (Bartlett, 1937), a combined analysis of variance was performed to determine G×E interaction (Table 3). There was a highly significant difference among genotypes for all traits, and the location had a significant effect on most traits such as root yield, sugar content, white sugar content, sugar yield, white sugar yield, and K^+. The year × location interaction showed significant differences in all studied traits, except for the sugar content trait. The genotype×location interaction had significant differences for Na^+, K^+, N, and the extraction coefficient of sugar. The genotype×year×location (G×E), as a three-way interaction, showed the significance of this effect only for root yield, sugar yield, white sugar yield, and N.

To better understand the G×E interaction, the partitioning of interaction percentage was calculated from the total sum of squares for sugar yield. A remarkable scale of discrepancy was because of location (46.9%), followed by genotype × location (9.6%), and G×E interaction (7.7%). A large difference between locations results in higher variability in genotype performance. Such location effects are in congruence with the results of Oladosu *et al*. (2017) and Khan *et al*. (2021). The genotype effect accounted for 5.4% of the total sum of squares, and the genotype × year, location × year, and the year effect contributed 1.3, 1, and 0.3% of

Table 3. Results of ANOVA for the studied traits of sugar beet genotypes across 12 environments. [a]

Source of variation	df	Mean of squares									
		Root yield	Sugar yield	Sugar content	White sugar content	White sugar yield	Na^+	K^+	alpha-amino nitrogen	Molasses sugar	Extraction coefficient of sugar
Year	1	15.4	20.3	29.7	2.4	3.2	62.9	159.8	0.2	49.1	929.5
Location	5	16629.4**	643.6**	335.1*	320.1	688.4**	93.6	209.8*	32.6	55.3	1407.1
Year×Location	5	1219.1**	14.0	56.1**	94.6**	16.4*	21.9**	29.8*	29.3**	11.0**	508.2**
Error 1	36	242.4	8.4	3.3	4.8	6.3	1.3	1.0	0.8	0.4	20.3
Genotype	13	1081.6**	28.5**	9.7**	15.7**	24.9**	12.1**	5.5**	1.1**	1.4**	67.3**
Genotype×Year	13	189.1	6.6	1.4	1.5	5.3	0.4	0.3	0.09	0.1	4.6
Genotype×location	65	272.9	10.1	1.5	2.2	7.2	0.8**	0.5**	0.3*	0.1	9.3*
Genotype×Year×location	65	245.1**	8.1	1.1	1.4	6.2**	0.4	0.3	0.2**	0.1	5.8
Error 2	468	86.7	3.4	1.0	1.3	2.6	0.3	0.3	0.1	0.1	5.1

[a] ns, *, **: Non-significant and significant at five and one percent probability levels, respectively.

Table 4. Resistance score given to sugar beet genotypes against rhizomania in Agricultural Research Stations of Mashhad and Shiraz.

Genotype	Mashhad		Shiraz		Genotype	Mashhad		Shiraz	
	2020	2021	2020	2021		2020	2021	2020	2021
Gen-1	1	2	2	3	Gen-8	1	2	3	3
Gen-2	1	2	2	3	Gen-9	1	2	2	3
Gen-3	1	2	2	3	Gen-10	1	2	2	3
Gen-4	1	1	2	3	Gen-11	1	2	3	3
Gen-5	1	2	2	3	BTS310	1	1	2	3
Gen-6	1	2	2	3	Denzel	1	2	2	3
Gen-7	1	2	2	3	Macumba	1	1	2	4

the variation, respectively. The low contribution of year showed that the evaluated years in this study were similar. In addition, the lower percent of the sum of squares for the location × year effect than the location effect indicates that there was no variation across locations over the two years. Significant variations in the response of genotypes to the impact of environments demonstrate the right choice of experimental sites for G×E interaction assessment (Hassani *et al*. 2018).

Genotype Response to Rhizomania Disease

Table 4 shows the results of the genotype response to rhizomania disease in accord with the Luterbacher *et al*. (2005) method. In 2020, genotypes evaluation for rhizomania infection in Mashhad showed that all genotypes had a complete resistance with healthy roots and no hairy root or colour variation. Therefore, all genotypes carry the resistance genes related to the disease. However, in Mashhad in 2021, only genotypes Gen-4, BTS310 and Macumba as controls had a perfect resistance, and other genotypes accompanied by control Denzel illustrated a semi-resistant response. This is perhaps because of the environmental situations and the new pathotypes of the disease development, which resulted in the lack of perfect genotype resistance (Norouzi *et al*., 2017). According to the results of genotypes' response to rhizomania infection in Shiraz, the genotypes were grouped in semi-resistant to semi-susceptible with no perfect resistance to the disease during both years of the study. This indicates that the intensity of genotype infection to the disease in Shiraz was higher than that of Mashhad.

Genotype×environment interaction causes significant differences in genotype behavior in different environments, which reduces the relationship between phenotypic and genotypic values. This interaction effect can be ignored if it does not cause a change in the genotype ranking, but if it is large enough to cause a change in the rank of genotypes under different environments, it should be evaluated. Since the conventional statistiscal methods, like combined analysis of variance, only provides information about the existence or lack of G×E interaction, plant breeders are using different stability methods such as GGE-biplot and AMMI stability analysis (Fasahat *et al*., 2014; Fasahat *et al*., 2015).

GGE-Biplot Analysis

The sum of the first and second principal components in the GGE biplot was 64.3%, which indicates that these two components explain a large variation in sugar yield variance. Figure 1 shows the polygon biplot (Yan, 1999) to identify mega-environments as well as top genotypes in different environments. In this biplot, a polygon identifies the top genotypes in each environment. The environmental indicators

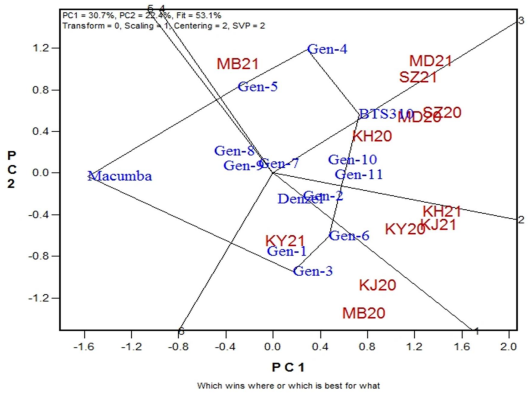

Figure 1. Polygon of GGE biplot method for identification of best genotypes in each environment.

are positioned into four sections, with different genotypes in each section. Based on the 14 genotypes and 12 environments examined here, the GGE-biplot was divided into six clockwise fan-shaped sections. Genotypes Gen-3, Gen-6, Gen-4, BTS310, and Macumba were placed at the polygon sides. In KJ20, MB20, and KY21, Gen-3 was the best genotype, followed by Gen-6 and Gen-1 as the most suitable cultivar in these environments. Genotype Gen-2 in KJ21, KY20, and KH21, Gen-10 and Gen-11 in KH20, MD20, and SZ20, Gen-4 and Gen- in SZ21, MD21, and MB21 were identified as the best genotypes. Surprisingly, the control Macumba showed no superiority or equality over other genotypes in any of the studied areas, and was considered a poor cultivar.

In Figure 2, genotypes were ranked based on the average sugar yield and yield stability in 12 environments. The line that crosses through the biplot's origin and the desired point (which represents the average of PC1 and PC2 of environmental scores) is called the average environment coordinate (AEC) (Yan and Kang, 2003). Genotypes that are closer to the center of the circle on this line have higher yields. The line that is perpendicular to this line and crosses

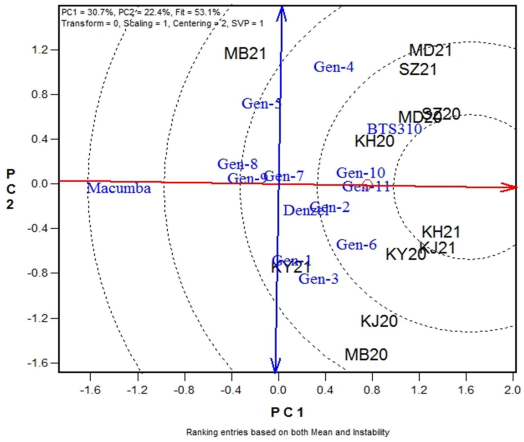

Figure 2. Genotype ranking based on average sugar yield and stability.

through the center of the biplot (line with double arrow) is the criterion for measuring the stability of genotypes. Genotypes that are far from this line are less stable. Based on the GGE biplot model, genotypes with more adaptability should be close to the optimal point on the AEC line and have the least distance from this line. As can be deduced from Figure 2, Gen-11 and Gen-8 had the highest and lowest sugar yield, respectively, compared with other genotypes. Among the studied environments, KH20 showed higher stability, followed by MD20. Such G×E interaction effects are in congruence with the results of Khan *et al*. (2021), who evaluated the stability of Bambara groundnut genotypes in four environments in Malaysia.

AMMI Stability

The sugar yield data of genotypes were subjected to AMMI analysis. Results showed that the G × E interaction for sugar yield was significant (P< 0.01) and explained 25.7% of the variance (Table 5). In a study conducted on the grain yield of finger millet using the AMMI method, the G×E interaction contributed 37.8% of the variance (Anuradha *et al*., 2022). In addition, the analysis unfolded that G × E interaction was significantly specified by the first five Principal Components (PCs). Among them, the first PC contributed 33.5% of the total G×E interaction, while the second to fifth PCs explained 20.1, 14.3, 13.2, and 7.7%, respectively. In a study on G×E assessment for grain quality in rice using the AMMI model, the first principal component significantly contributed 67% of the total of G×E interaction (Fasahat *et al.,* 2014).

In Table 6, the average sugar yield and various AMMI stability parameters for fourteen sugar beet genotypes in twelve environments are shown. Genotypes Gen-2 and Gen-11 had the highest, and Gen-9 and Gen-8 had the lowest sugar yield with an average sugar yield of 15.4 t ha^{-1}. Based on ASTAB, ASI, ASV, FA, ZA, and AVAMGE stability indices, genotypes Gen-7 and Denzel were the most stable genotypes with the lowest value for these indices. Stability indices of DA, DZ, EV, MASI, MASV, and SIPC showed the same results and identified Gen-10 and Gen-8 as the most stable genotypes. However, Gen-2, Gen-3, Gen-9, and Macumba, with the highest values for these statistics, were the most unstable genotypes. The results are in congruence with those achieved by Yadav *et al*. (2022) and Anuradha *et al*. (2022), who

Table 5. Analysis of variance based on AMMI model for sugar yield of sugar beet genotypes.

Source of variation	df	Sum of squares	Mean of squares	Relative variance (%)	Cumulative variance (%)
Environment	11	3308.67	300.78**	-	-
Error 1	36	302.57	8.4	-	-
Genotype	13	371.69	28.59**	-	-
G×E interaction	143	1279.32	8.94**	-	-
PC1	23	428.98	18.65**	33.5	33.5
PC2	21	256.96	12.24**	20.1	53.6
PC3	19	182.71	9.62**	14.3	67.9
PC4	17	168.64	9.92**	13.2	81.1
PC5	15	97.99	6.53*	7.7	88.8
Noise	48	143.71	2.99^{ns}		
Error 2	504	1908.07	3.79^{ns}		
CV (%)	11.9				

*,**and ns: Significant at 5 and 1% probability levels and non-significant, respectively.

Table 6. Average sugar yield and different AMMI stability parameters for 14 sugar beet genotypes in 12 environments.[a]

Genotype	Mean sugar yield (t ha^{-1})	ASTAB	ASI	ASV	AVAMGE	DA	DZ	EV	FA	MASI	MASV	SIPC	ZA
Gen-1	15.8	1.95	0.43	2.12	11.21	4.35	0.46	0.04	18.92	0.43	2.22	2.28	0.19
Gen-2	16.0	3.09	0.08	0.42	13.95	4.59	0.67	0.09	21.04	0.26	1.93	2.22	0.13
Gen-3	15.8	4.81	0.63	3.15	19.51	6.71	0.73	0.11	44.97	0.65	3.68	3.30	0.27
Gen-4	15.9	3.04	0.49	2.45	15.02	5.28	0.59	0.07	27.92	0.50	2.77	3.36	0.26
Gen-5	15.2	1.98	0.31	1.56	10.23	4.01	0.50	0.05	16.05	0.32	2.03	2.74	0.19
Gen-6	15.5	1.81	0.25	1.22	10.24	3.69	0.50	0.05	13.60	0.25	1.83	2.13	0.13
Gen-7	15.2	0.94	0.03	0.14	7.14	2.51	0.38	0.03	6.30	0.14	1.18	1.57	0.09
Gen-8	14.6	1.42	0.04	0.21	8.23	2.70	0.53	0.06	7.29	0.11	1.23	1.77	0.08
Gen-9	14.7	2.47	0.02	0.08	12.00	4.08	0.61	0.07	16.65	0.22	1.78	2.13	0.11
Gen-10	15.8	4.29	0.36	1.80	15.86	5.65	0.78	0.12	31.92	0.40	3.18	4.22	0.27
Gen-11	16.0	2.77	0.16	0.78	11.79	3.90	0.73	0.11	15.21	0.20	1.84	2.75	0.14
BTS310	16.6	1.71	0.33	1.64	11.65	3.86	0.45	0.04	14.87	0.34	2.10	2.35	0.18
Denzel	15.1	1.28	0.20	1.02	8.09	3.14	0.41	0.03	9.86	0.22	1.67	1.85	0.12
Macumba	13.5	5.02	0.43	2.16	16.48	6.27	0.81	0.13	39.29	0.48	3.56	4.36	0.30
LSD (0.05)	1.2												

[a] ASTAB: AMMI based Stability parameter, ASI: AMMI Stability Index, ASV: AMMI Stability Value, AV_{AMGE}: Sum across environments of Absolute Value of G×E interaction modeled by AMMI, DA: Annicchiarico's D parameter, Dz: Zhang's D parameter, EV: Average of the squared Eigenvector Values, FA: Stability measure based on Fitted AMMI model, MASI: Modified AMMI Stability Index, MASV: Modified AMMI Stability Value, SIPC: Sums of the absolute value of the IPC scores, ZA: Absolute value of the relative contribution of IPCAs to the interaction.

reported the importance of the first two principal components in the prediction of the accurate model in AMMI decomposition. Meanwhile, Anuradha *et al*. (2022) found a strong correlation among the AMMI-based indices. According to AMMI-based indices, except Gen-8, the selected genotypes had sugar yield values around the average.

MTSI and Genotype Selection

In Table 7, the results of factor analysis based on principal component analysis are presented. The first factor, with eigenvalue of 4.75 and an explanation of 43.1% of total variance, had high and positive factor coefficients for root yield, sugar yield, Na^+, K^+, alpha-amino nitrogen, and molasses sugar. The second factor explained 27.1% of the total variance and had an eigenvalue of 2.98. This factor had high and negative coefficients for root yield, sugar yield, white sugar yield, and alpha-amino nitrogen. The third factor contributed to 18.2% of the data discrepancy, and an eigenvalue of 2, which showed a high and negative factor coefficient for half of the traits consisting of sugar yield, sugar content, white sugar yield, Na^+, and molasses sugar.

The factor scores of the previously mentioned factors were used to calculate the MTSI stability index of the genotypes. In Figure 3, genotypes ranking based on the MTSI stability index are shown in which Gen-4 and Gen-1 were selected as ideal genotypes using a selection pressure of 20%. Based on the highest to the lowest value of the MTSI index, genotypes are placed in the outermost circuit to the center of the Figure, respectively. Macumba had the lowest stability index score showing poor stability and mean sugar yield in different environmental conditions. Genotype selection by MTSI is important according to the value of traits in genotypes, i.e. traits that have a good appearance (Olivoto *et al*., 2019). The overall results of the stability analysis of pearl millet genotypes from the previous study (Yadav *et al*., 2022) are concordant with the results of this study.

Table 7. Eigenvalues, relative and cumulative variance as well as factor coefficients after varimax rotation in factor analysis based on principal component analysis.

Traits	Factors		
	First	Second	Third
Root yield	0.41	-0.91	0.08
Sugar yield	0.08	-0.99	-0.02
Sugar content	-0.91	0.22	-0.25
White sugar content	-0.98	0.14	-0.07
White sugar yield	-0.19	-0.97	0.03
Na^+	0.72	0.01	-0.51
K^+	0.17	0.15	0.01
alpha-amino nitrogen	0.18	-0.05	0.95
Molasse sugar	0.85	0.11	-0.43
Extraction coefficient of sugar	-0.96	0.0	0.23
Eigenvalue	4.75	2.98	2
Relative Variance (%)	43.1	27.1	18.2
Cumulative variance (%)	43.1	70.2	88.4

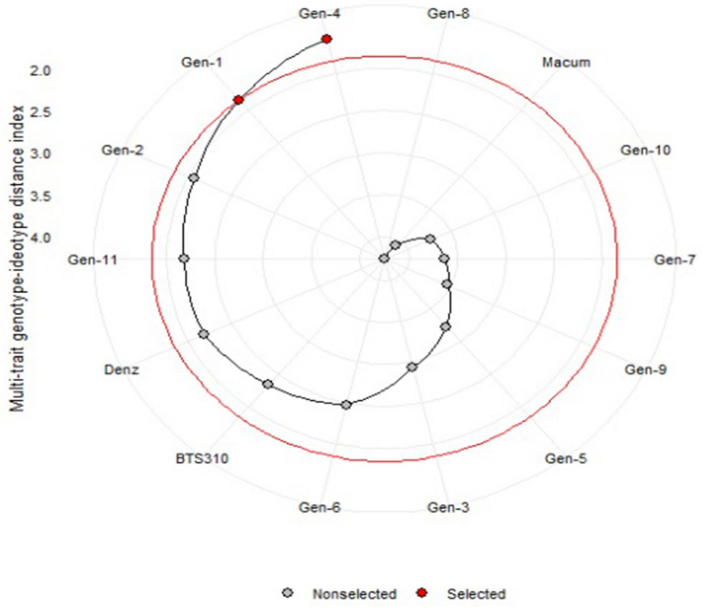

Figure 3. Genotype ranking and the selected genotypes based on multi-trait stability index. Based on this index, genotypes with lower values of this index are less distant form the ideal genotype, and for the ones with higher MTSI value, more distant from the ideal genotype can be observed.

CONCLUSIONS

One of the major accomplishments of plant breeding in sugar beet is the development of cultivars resistant to rhizomania. Since 1970s, this disease has spread rapidly throughout the sugar beet growing areas, and sugar beet breeding companies contributed to its management. Resistance genes pyramiding through the identification of resistance sources and adding them in breeding programs is a promising way to cope with the disease evolution. In this study, genetic diversity was found among genotypes regarding sugar yield under infected environments. The given rhizomania scores indicated a high number of genotypes with resistance

response compared with the susceptible ones. Evaluation of genotypes for yield stability under rhizomania infection using different statistics resulted in identification of different stable genotypes, among which genotypes Gen-10, Gen-11, Gen-4, and Gen-2 were common.

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بررسی اثرات متقابل ژنوتیپ در محیط ژنوتیپ های چغندرقند تحت آلودگی به ریزومانیا

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چکیده

گیاه چغندرقند همواره مورد حمله آفات و بیماری های مختلف بوده است. بیماری ویروسی ریزومانیا که در مناطق مختلف کشت چغندرقند گسترش یافته است، در سه دهه اخیر به مهمترین بیماری این محصول تبدیل شده است. استفاده از رقم مقاوم تنها راه قابل اعتماد برای مقابله با بیماری ریزومانیا است. به منظور شناسایی ژنوتیپ های امیدوارکننده، ۱۱ ژنوتیپ چغندرقند به همراه سه شاهد در قالب طرح بلوک های کامل تصادفی با چهار تکرار در مزارع آزمایشی با آلودگی طبیعی به ریزومانیا در شش ایستگاه تحقیقاتی کرج، خوی، کرمانشاه، مشهد، میاندوآب و شیراز برای دو سال (۱۳۹۹و۱۴۰۰) مورد ارزیابی قرار گرفتند. بر اساس امتیازدهی ریشه ها نسبت به آلودگی به بیماری ریزومانیا، ژنوتیپ ها مقاومت قابل قبولی را به بیماری نشان دادند. تجزیه و تحلیل پایداری AMMI نشان داد که پنج مؤلفه اول معنی‌دار بوده و ۸۸/۸ درصد از اثرات متقابل را بیان می کنند. ژنوتیپ هایGen-7 ، Gen-10، Gen-11 وGen-2 به عنوان ژنوتیپ های پایدار بر اساس مدل AMMI انتخاب شدند. نتیجه حاصل از روش گرافیکی GGE-biplotنیز برتری Gen-10 و Gen-11 را از نظر عملکرد شکر و پایداری در محیط های آلوده به بیماری تایید کرد. نتایج به‌دست‌آمده از شاخص MTSI ژنوتیپ‌های Gen-4، Gen-1، Gen-2 وGen-11 را به عنوان ژنوتیپ‌های پایدار تحت شرایط آلوده به ریزومانیا شناسایی کرد. با بکارگیری روش‌های مختلف اندازه‌گیری پایداری، علاوه بر شناسایی سازگاری ژنوتیپ‌ها با محیط‌های مختلف، می‌توان تصمیم دقیقی برای بهنژادی یا ثبت رقم در آینده گرفت.