



Genotype by environment interaction for physiological traits in sugar beet (*Beta vulgaris* L.) parents and hybrids using additive main effects and multiplicative interaction model

Zahra Abbasi¹ · Jan Bocianowski²

Received: 5 August 2021 / Revised: 17 August 2021 / Accepted: 27 August 2021 / Published online: 12 September 2021
© The Author(s) 2021

Abstract

The objective of this study was to assess genotype by environment interaction for 21 physiological traits in sugar beet (*Beta vulgaris* L.) parents and hybrids grown in Rodasht Agricultural Research Station in Iran by the additive main effects and multiplicative interaction model. The study comprised of 51 sugar beet genotypes [10 multigermline pollen parents, four monogerm seed parents and 36 F1 hybrids], evaluated at four environments in a randomized complete block design, with three replicates. The additive main effects and multiplicative interaction analyses revealed significant environment main effects with respect to all observed traits, except extraction coefficient of sugar. The additive main effects and multiplicative interaction stability values ranged from 0.009 (G17 for leaf Ca²⁺) to 9.698 (G09 for extraction coefficient of sugar). The parental forms 2 7233-P.29 (G38) and C CMS (G49) as well as hybrids 2(6)*C (G27) and 5*C (G33) are recommended for further inclusion in the breeding programs because of their stability and good average values of observed traits.

Keywords *Beta vulgaris* L. · Discriminating ability · AMMI model · Stability · CMS lines

Introduction

Sugar beet approximately supplies about 30 percent of the world's sugar [24]. In the chenopodiaceae family, sugar beet is considered as salt-tolerant plant. This plant with deep root system shows high tolerance to water stress conditions, such as salinity and drought [8]. The previous study was shown that about 50 mM NaCl can stimulate plant growth in sugar beet [32]. Therefore, this plant could be a good resource to explore salt tolerance mechanisms to product salt tolerant hybrid seeds.

Environmental instability causes a variety of genotype reactions during the growing season, which complicates understanding of the physiological traits of sugar beet. The additive main effects and multiplicative interaction (AMMI) model have analyzed the main effects of genotype and environment as well as the genotype-by-environment interaction (GEI) [7, 34]. The AMMI model as a reliable way combines the analysis of variance and the principal component analysis (PCA) in a particular single analysis to dedicate cultivars to different environments or locations. There is little information about how sugar beet varieties respond to different conditions [14, 17, 18, 31].

Evaluation of genotypes in different years and locations (different environments) is one of the important part of breeding programs. In fact, the assessment of the adaptation abilities of cultivars in mega-environment, is a reliable criterion in the detection of stable or specific cultivars in the area. The most stable cultivars are characterized by a negligible effect of genotype by environment interaction [16]. The specifically adapted genotype is known when a genotype shows superior rank in an area over several years particularly under a restricted set of condition that related to the phenomenon of genotype-by-environment interaction (GEI). By changing the rank

Zahra Abbasi and Jan Bocianowski have contributed equally to this work.

✉ Jan Bocianowski
jan.bocianowski@up.poznan.pl

¹ Horticulture Crops Research Department, Isfahan Agricultural and Natural Resources Research and Education Center, (AREEO), Esfahan, Iran

² Department of Mathematical and Statistical Methods, Poznań University of Life Sciences, Wojska Polskiego 28, 60-637 Poznań, Poland

of genotypes in different environments (due to GEI), the interpretation of the information obtained becomes difficult and complicated [21]. Thus, an understanding of GEI using multi environmental trails (METs) will leads to achievement of guaranteed superior genotypes across a range of environmental conditions [21, 30, 33].

The additive main effect and multiplicative interaction model (AMMI) is effective method for studying GEI, stability and adaptation analysis and identifying the specifically adapted cultivars or mega-environments [10]. So far, the variability assessment of genotypes for different environments and stability analysis has been carried out for sugar beet to study the interaction of the genotype per environment. In a study on nine sugar beet genotypes in 52 different environments, the value of total variance for environment, genotype and their interaction were shown 80%, 5%, and 3%, respectively [18]. Mostafavi et al. [25] studied the interaction of nine sugar beet cultivars with six regions using GGE biplot and AMMI methods, and (I13*A37.1) * SH-1-HSF.5 genotype was introduced as the best genotype for stability. From the stability analysis of white sugar yield and the adaptation of 36 sugar beet cultivars under 11 examined locations, four mega-environments and high compliance of the sugar yield rankings were distinguished [31].

The objective of this study were: (1) to assess genotype by environment interaction for the 21 physiological traits

in 51 sugar beet genotypes across four environments and 2 years grown in Rodasht Agricultural Research Station in Iran by the AMMI model, and (2) to select genotypes combining a high stability with good average values of observed traits.

Materials and methods

Plant materials and experimental conditions

Four CMS lines and 10 populations [S_0 = open-pollinated (parental) and S_2 = the second generation of selfing] were subjected to crossing in this study using North Carolina mating design II [9]. The description of these parent populations are shown in Table 1. The drought tolerant and salinity tolerant lines displayed in Table 1 were derived from two independent recurrent selection programs.

To carry out the crosses, the pollen parents were divided into two groups each with five populations. Biparental mating and bulk mating schemes were employed for the first and second group, respectively. In biparental mating, 10 plants were randomly selected from each male parent and independently crossed with four CMS lines in a cross section. Thus, 40 crosses (4×10) from each male parent and a total of 200 cross combinations is expected to produce from five pollen parents of the first group. In bulk mating, 20 crosses

Table 1 Description of 10 multigerm pollen parents and four monogerm seed parents of sugar beet used in this study

ID code	Pollen parents	Characteristic	Germplasm description
1	181	Salt sensitive	S_0
2	7233-P.29	Salt tolerant	S_0
3	BP-Mashhad	Drought tolerant	S_0
4	M249	Drought sensitive	S_2 family selected from BP-Mashhad population
5	191	Salt sensitive	S_0
6	M224	Drought tolerant	S_2 family selected from BP-Mashhad population
7	29,823-P.5	Salt sensitive	S_2 family selected from 7233-P.29 population
8	29,819-P.17	Salt tolerant	S_2 family selected from 7233-P.29 population
9	M193	Drought tolerant	S_2 family selected from BP-Mashhad population
10	M203	Drought sensitive	S_2 family selected from BP-Mashhad population
	Seed parents		
	MS26039	Salt tolerant	CMS line
	MS26051	Salt tolerant	CMS line
	MS26564	Salt sensitive	CMS line
	MS25944	Salt sensitive	CMS line
ID code	Pollen parents	Characteristic	Germplasm description
	Seed parents		
	MS26039	Salt tolerant	CMS line
	MS26051	Salt tolerant	CMS line
	MS26564	Salt sensitive	CMS line
	MS25944	Salt sensitive	CMS line

Table 2 Codes of sugar beet (*Beta vulgaris* L.) genotypes

Code	Origin	Code	Origin	Code	Origin
G01	4 (1)*C	G18	8(3)*C	G35	10*C
G02	4 (2)*C	G19	8(4)*C	G36	10*D
G03	4 (3)*C	G20	8(5)*D	G37	1 181—parent (male)
G04	4 (4)*C	G21	8(6)*D	G38	2 7233-P.29—parent (male)
G05	4 (5)*C	G22	2(1)*A	G39	3 BP-Mashhad—parent (male)
G06	6 (1)*C	G23	2(2)*C	G40	4 M249—parent (male)
G07	6 (2)*C	G24	2(3)*C	G41	5 191—parent (male)
G08	6 (3)*C	G25	2(4)*C	G42	6 M224—parent (male)
G09	6 (4)*C	G26	2(5)*C	G43	7 29,823-P.5—parent (male)
G10	7*B	G27	2(6)*C	G44	8 29,819-P.17—parent (male)
G11	7 (2)*C	G28	3*C	G45	9 193—parent (male)
G12	7 (3)*C	G29	3*D	G46	10 203—parent (male)
G13	7 (4)*C	G30	1*B	G47	A CMS—parent (female)
G14	7 (5)*C	G31	1*C	G48	B CMS—parent (female)
G15	7 (6)*D	G32	5*A	G49	C CMS—parent (female)
G16	8 (1)*C	G33	5*C	G50	D CMS—parent (female)
G17	8 (2)*C	G34	10*A	G51	7233-P.29-hybrid—control

(5 × 4) from five pollen parents of the second group with four CMS lines were obtained. Due to lack of reproductive synchronization between some of the female and male lines, in a number of crosses, the hybrid seed was not formed. In a number of crosses, seed was only sufficiently evaluated for 1 year. Therefore, a total of 51 genotypes including 36 F1 hybrids along with 14 parents and 1 control (Table 2) were grown in two environments saline (EC of soil and water was 8 and 12 dSm⁻¹, respectively) and normal (soil ECe = 4 and irrigation water ECw = 3 dSm⁻¹) field conditions during the 2011 and 2012 growing seasons at Rodasht Agricultural Research Station, Iran (65 km East of Isfahan, 32° 82' 90" N and 52° 81' 00" E, 1560 m altitude). A complete block design with three replications was used. Each plot contained three 5 m long rows and spaced 0.5 m between rows.

Standard cultural practices were followed for seed-bed preparation, sowing, irrigation and control of weed and pests. Thinning was conducted at 6-leaf stage by hand to settle 17 cm plant distance. The salinity treatment was commenced at 4 weeks after emergence.

Agro-physiological traits

The physiological traits (leaf Ca²⁺, leaf Na⁺, leaf K⁺, Ca²⁺/Na⁺, leaf K⁺/Na⁺, net CO₂ assimilation rate, transpiration rate), root related traits (root Na⁺, root K⁺, root α-N, root K⁺/Na⁺, sugar content (SC), white sugar content (WSC), molasses sugar (MS), extraction coefficient of sugar (ECS), alkaline level content (ALC), dry matter (DM) and yield related traits (root number, root yield, sugar yield, white sugar yield) were evaluated in this study. Measurements of

physiological traits were performed at the 5–7-leaf stage which corresponded to about 2 months after applying salinity stress.

Leaf gas exchange parameters (net CO₂ assimilation rate (P_N) and transpiration rate (E)) were measured using a Li-Cor 6400 gas-exchange portable photosynthesis system (Li-Cor, Lincoln, Nebraska, USA).

The concentration of Na⁺, K⁺ and Ca²⁺ ions in leaf tissue were measured about 3 months after sowing in the both experiments in 2011 and 2012. Samples of dried tissues of the four uppermost leaves were ashed for 6 h at 550 °C, dissolved in 1% (v/v) hydrochloric acid (HCl) and made to volume with distilled water. The leaf Na⁺ and K⁺ concentrations were determined by flame photometer (JENWAY Clinical PFP7 model) and Ca²⁺ concentration was determined by atomic absorption spectrometer (Perkin-Elmer 2380 Atomic Absorption).

The sugar beet root yield (RY) was determined after harvest. Root pulps were quickly frozen and stored at – 26°C until analysis of quality-related traits.

Sugar beet root quality-related traits [Na⁺ and K⁺, α-amino-N and sucrose (sugar) contents] in the saline and non-saline experiments conducted in 2011 and 2012 were determined using an automatic beet laboratory system (Venema, Groningen, the Netherlands) linked to Betalyser system (W. Kernchen, GmbH, Seelze, Germany). Molasses sugar (MS), extraction coefficient of sugar (ECS) and alkaline level content (ALC) were calculated using the following formula [29]:

$$MS = 0.343 (K^+ + Na^+) + 0.094 (\alpha - a \text{ min } o - N) - 0.31$$

$$ECS = (WSC/SC) \times 100$$

$$ALC = (K^+ + Na^+)/\alpha - a \text{ min } o - N$$

Roots were oven dried to a constant weight at 80 °C for 48 h to measure dry matter (DM). White sugar content (WSC), sugar yield (SY) and white sugar yield (WSY) were calculated according to the following formulas [29]:

$$WSC = SC - MS$$

$$SY = RY \times SC.,$$

$$WSY = RY \times WSC.$$

The details of other measurements are as described earlier [2].

Statistical analysis

A two-way fixed effect model was fitted to determine the magnitude of the main effects of variation and their interaction on the 21 physiological traits. Least-squares means

were simultaneously produced for the AMMI model. The AMMI model is fitted in two stages. In first stage, the main additive effects of genotypes (G) and environments (E) are fitted by least squares through analysis of variance (ANOVA). In the second stage, genotype-by-environmental interaction GEI, the non-additive residuals will be subjected to singular value decomposition to obtain multiplicative terms referred to as interaction principal components (IPC) scores for genotypes and environments. The traditional AMMI model for fixed effects [13, 26] is given by

$$y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^N \lambda_n \gamma_{gn} \delta_{en} + Q_{ge},$$

where y_{ge} is the mean value of observed trait of genotype g in environment e , μ is the grand mean, α_g is the genotypic mean deviations, β_e is the environmental mean deviations, N is the number of PCA axis retained in the adjusted model, λ_n is the eigenvalue of the PCA axis n , γ_{gn} is the genotype score for PCA axis n , δ_{en} is the score eigenvector for PCA axis n , and Q_{ge} is the residual, including AMMI noise and pooled experimental error (with expected normal distribution).

The AMMI stability value (ASV) was used to compare the stability of genotypes as described by Purchase et al. [28]:

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA_1) \right]^2 + (IPCA_2)^2},$$

where SS is the sum of squares, $IPCA1$ and $IPCA2$ is the first and the second interaction principal component axes, respectively; and the $IPCA_1$ and $IPCA_2$ scores were the genotypic scores in the AMMI model. Lower ASV score indicate a more stable genotype across environments.

Genotype selection index (GSI) was calculated for each genotype which incorporates both mean 1000-kernel weight and ASV index in single criteria (GSI_i) as [12]

$$GSI_i = RM_i + RASV_i,$$

where GSI_i is genotype selection index for i th genotype, RM_i is rank of trait mean (from maximal to minimal for: leaf Ca^{2+} , leaf K^+ , leaf Ca^{2+}/Na^+ , leaf K^+/Na^+ , net CO_2 , root number, root yield, root Na^+ , sugar yield, white sugar yield, white sugar content, extraction coefficient of sugar, dry matter, and from minimal to maximal for: leaf Na^+ , transpiration rate, sugar content, root K^+ , root α -N, root K^+/Na^+ , alkaline level content and molasses sugar) for i th genotype, $RASV_i$ is rank for the AMMI stability value for the i th genotype. Finally, total genotype selection index (TGSI) was calculated for each genotype as sum of GSIs for all 21 physiological traits of study.

The relationships between the particular 21 physiological traits were assessed based on Pearson's correlation coefficients, independently for four environments. All the analyses were conducted using the GenStat v. 18 statistical software package.

Results

The three sources of variation (genotypes, environments and GEI) were statistically significant for: net CO_2 , transpiration rate, root number, root yield, root α -N, sugar yield and white sugar yield (Table 3). The differences between genotypes explained from 2.92% (for leaf K^+/Na^+) to 25.21% (for root yield) of the total quantitative trait variation (Table 3). The differences between genotypes were significant for: leaf Ca^{2+} , leaf K^+ , net CO_2 , transpiration rate, root number, root yield, sugar content, root K^+ , root α -N, sugar yield, white sugar yield, white sugar content, extraction coefficient of sugar and molasses sugar (Table 3). The sums of squares for environment main effect were highly significant for all observed traits, except extraction coefficient of sugar and ranged from 1.30% (for white sugar content) to 79.35% (for leaf K^+/Na^+) of the total physiological trait variation (Table 3). The GEI was statistically significant for ten from 21 observed traits: leaf Na^+ , net CO_2 , transpiration rate, root number, root yield, root α -N, alkaline level content, sugar yield, white sugar yield and dry matter (Table 3). The effects of GEI explained form 7.32% (for leaf K^+/Na^+) to 54.79% (for net CO_2) of the total variation.

The first principal component (IPCA 1) was significant for all observed traits except sugar content and white sugar content and accounted from 43.61% (for dry matter) to 63.61% (for extraction coefficient of sugar) of the variation caused by interaction (Table 3), while $IPCA 2$ was significant for: net CO_2 , transpiration rate, root number, root yield, molasses sugar and dry matter and 3 accounted from 22.94% (for root Na^+) to 47.06% (for root number). Values for the first two principal components were accounted jointly from 78.01% (for transpiration rate) to 99.56% (for leaf Ca^{2+}) of the whole effect it had on the variation of observed trait (Table 3).

Lack of significant change in genotype rank in different environmental and climatic conditions and stability against stresses indicate genotype stability. In this study, climatic conditions were considered as the source of this variation component. The analysis showed that some genotypes have high adaptation; however, most of them have specific adaptability. ASVs revealed variations in observed physiological trait stability among the 51 genotypes were calculated. According to Purchase et al. [28], a stable genotype is defined as one with ASV close to zero. ASV ranged different

Table 3 Mean squares (m.s.) from analysis of variance of main effects and interactions for 21 physiological traits of sugar beet (*Beta vulgaris* L.) genotypes and variability explained (ve, in %)

Trait	Source of variation	df	Treatments	Genotypes	Environments	GE interactions	GE interactions parts:				Error	
							IPCA 1		IPCA 2			Residuals
							50	52	50	52		
Leaf Ca ²⁺	m.s	4.31***	1.79**	201.19***	1.21	2.21***	1.33	0.02	0.97			
	ve (%)	81.48	8.34	56.19	16.95	63.04	36.52					
Leaf Na ⁺	m.s	1.356***	0.364	67.712***	0.36*	0.541***	0.373	0.15	0.279			
	ve (%)	82.25	5.44	60.70	16.11	52.12	34.56					
Leaf K ⁺	m.s	3.97***	1.14*	210.55***	0.78	1.16*	0.76	0.39	0.79			
	ve (%)	82.07	5.83	64.34	11.91	51.58	32.34					
Leaf Ca ²⁺ /Na ⁺	m.s	2.27***	0.62	120.91***	0.45	0.72*	0.58	0.01	0.47			
	ve (%)	82.23	5.54	64.77	11.95	56.05	43.35					
Leaf K ⁺ /Na ⁺	m.s	5.86***	0.78	351.04***	0.65	1.1**	0.69	0.12	0.67			
	ve (%)	89.60	2.92	79.35	7.32	58.64	35.49					
Net CO ₂	m.s	20.51***	21.78***	88.37***	18.73***	30.23***	19.22***	5.77	4.8			
	ve (%)	81.19	21.23	5.17	54.79	55.94	34.20					
Transpiration rate	m.s	2.039***	1.699***	36.593***	1.461***	2.17***	1.163**	1.004*	0.699			
	ve (%)	74.43	15.27	19.74	39.42	51.46	26.55					
Root number	m.s	1330***	755***	55,866***	431***	633***	609***	28	201			
	ve (%)	86.77	12.13	53.86	20.78	50.88	47.06					
Root yield	m.s	295***	412.6***	3232.9***	197.1***	330.9***	151.9*	99	107			
	ve (%)	73.17	25.21	11.85	36.11	58.22	25.70					
Sugar content	m.s	7.002	9.229*	36.163***	5.677	8.404	6.238	2.137	6.401			
	ve (%)	52.60	17.07	4.01	31.51	51.32	36.63					
Root Na ⁺	m.s	3.33***	2.16	94.72***	1.89	3.03**	1.3	1.28	1.77			
	ve (%)	65.26	10.43	27.42	27.42	55.42	22.94					
Root K ⁺	m.s	1.753***	1.779**	30.799***	1.164	1.8***	1.293	0.339	0.946			
	ve (%)	63.53	15.89	16.49	31.15	53.64	37.02					
Root α-N	m.s	1.757***	1.172**	49.356***	1*	1.645***	0.937	0.367	0.708			
	ve (%)	70.79	11.63	29.39	29.77	57.00	31.27					
Root K ⁺ /Na ⁺	m.s	1.928***	1.116	61.921***	0.998	1.604**	1.217	0.114	0.891			
	ve (%)	68.29	9.74	32.43	26.14	55.67	40.65					
Alkaline level content	m.s	4.684**	2.533	48.424***	4.526*	7.965***	4.502	0.826	3.255			
	ve (%)	59.28	7.90	9.06	42.32	61.01	33.16					
Sugar yield	m.s	11.08***	14.73***	168.23***	6.71***	11.47***	5.36	2.97	4.06			
	ve (%)	72.94	23.90	16.37	32.67	59.24	26.60					
White sugar yield	m.s	8.02***	10.79***	116.43***	4.93**	8.04***	4.23	2.28	3.1			
	ve (%)	71.81	23.80	15.41	32.60	56.58	28.63					

Table 3 (continued)

Trait	Source of variation	Treatments	Genotypes	Environments	GE interactions	GE interactions parts:			Error
						IPCA 1	IPCA 2	Residuals	
	d.f	203	50	3	150	52	50	48	200
White sugar content	m.s	7.043	10.406*	11.803***	5.827	7.948	6.855	2.458	6.4
	ve (%)	52.66	19.16	1.30	32.19	47.29	39.21		
Extraction coefficient of sugar	m.s	41.15	67.19**	135.76	30.57	56.09*	26.87	6.79	36.81
	ve (%)	52.34	21.05	2.55	28.74	63.61	29.31		
Molasses sugar	m.s	0.713***	0.737***	12.881***	0.462	0.655**	0.547*	0.164	0.385
	ve (%)	64.24	16.35	17.15	30.74	49.18	39.45		
Dry matter	m.s	3.088***	1.953	39.807***	2.732**	3.437**	2.92*	1.772	1.86
	ve (%)	61.56	9.59	11.72	40.24	43.61	35.63		

* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; *d.f.* number of degrees of freedom

for particular physiological traits, for: leaf Ca^{2+} : from 0.009 (for G17) to 1.582 (for G20), leaf Na^+ : from 0.038 (for G50) to 1.105 (for G07), leaf K^+ : from 0.089 (for G13) to 1.297 (for G01), leaf Ca^{2+}/Na^+ : from 0.056 (for G27) to 0.815 (for G22), leaf K^+/Na^+ : from 0.073 (for G22) to 1.719 (for G38), net CO_2 : from 0.100 (for G46) to 3.748 (for G35), transpiration rate: from 0.044 (for G03) to 2.486 (for G11), root number: from 0.106 (for G44) to 4.517 (for G24), root yield: from 0.211 (for G18) to 8.279 (for G11), sugar content: from 0.162 (for G26) to 2.198 (for G31), root Na^+ : from 0.025 (for G39) to 3.272 (for G30), root K^+ : from 0.078 (for G03) to 1.178 (for G44), root α -N: from 0.068 (for G37) to 1.821 (for G42), root K^+/Na^+ : from 0.057 (for G34) to 1.435 (for G15), alkaline level content: from 0.078 (for G38) to 3.150 (for G42), sugar yield: from 0.147 (for G20) to 3.659 (for G11), white sugar yield: from 0.080 (for G05) to 2.671 (for G11), white sugar content: from 0.045 (for G14) to 1.856 (for G09), extraction coefficient of sugar: from 0.135 (for G28) to 9.698 (for G09), molasses sugar: from 0.097 (for G10) to 0.932 (for G16), and dry matter: from 0.035 (for G36) to 1.612 (for G31) (Table 4).

The genotype selection index ranged different for particular physiological traits, for: leaf Ca^{2+} : from 18 (for G01) to 98 (for G11), leaf Na^+ : from 13 (for G31) to 97 (for G40), leaf K^+ : from 11 (for G13) to 89 (for G19), leaf Ca^{2+}/Na^+ : from 21 (for G27) to 101 (for G11), leaf K^+/Na^+ : from 3 (for G22) to 93 (for G11), net CO_2 : from 19 (for G12) to 76 (for G32), transpiration rate: from 11 (for G17) to 101 (for G35), root number: from 19 (for G29) to 101 (for G11), root yield: from 6 (for G44) to 91 (for G17), sugar content: from 9 (for G26) to 93 (for G17), root Na^+ : from 9 (for G26) to 97 (for G05), root K^+ : from 9 (for G41) to 101 (for G48), root α -N: from 6 (for G37) to 100 (for G42), root K^+/Na^+ : from 13 (for G06) to 100 (for G15), alkaline level content: from 2 (for G38) to 100 (for G16), sugar yield: from 10 (for G10) to 90 (for G37), white sugar yield: from 9 (for G10) to 88 (for G37), white sugar content: from 7 (for G41) to 102 (for G09), extraction coefficient of sugar: from 11 (for G50) to 102 (for G09), molasses sugar: from 8 (for G03) to 98 (for G48), and dry matter: from 6 (for G36) to 95 (for G31) (Table 4).

The stability of tested genotypes can be evaluated according to biplot for physiological trait. The most interesting results were obtained for seven traits: net CO_2 , transpiration rate, root number, root yield, sugar yield, white sugar yield and dry matter. Figure 1 shows distribution of the first two interaction principal components for net CO_2 . Sugar beet parents and hybrids interacted differently with climate conditions in the observed environments. The genotypes G15, G22, G24, G27, G35 and G45 interacted positively with the S1 environment, but negatively with the N2 and S2 (Fig. 1). The genotypes G03, G05, G17, G21, G42 and G43

Table 4 Rank of the AMMI stability value (RA), rank of trait mean [RM, from maximal to minimal for: leaf Ca²⁺, leaf K⁺, leaf Ca²⁺/Na⁺, leaf K⁺/Na⁺, net CO₂, root number, root yield, root Na⁺, sugar yield, white sugar yield, white sugar content, extraction coefficient of sugar, dry matter, and from minimal to maximal for: leaf Na⁺, transpiration rate, sugar content, root K⁺, root α-N, root K⁺/Na⁺, alkaline level content and molasses sugar] and total genotype selection index (TGSI)

Code	Leaf Ca ²⁺		Leaf Na ⁺		Leaf K ⁺		Leaf Ca ²⁺ /Na ⁺		Leaf K ⁺ /Na ⁺		Net CO ₂		Transpiration rate		Root number		Root yield		Sugar content		Root Na ⁺	
	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM
G01	3	15	34	45	51	4	6	17	6	34	5	36	45	30	38	48	43	46	39	28	22	16
G02	17	25	36	42	8	23	36	31	7	36	4	31	3	24	23	31	24	35	47	41	23	18
G03	19	36	42	31	19	32	42	18	16	25	48	13	1	25	27	39	49	23	45	22	15	50
G04	11	38	14	30	47	37	3	38	10	30	37	15	41	37	48	5	18	22	12	13	30	9
G05	5	30	27	13	16	47	18	24	41	27	18	19	47	50	30	2	33	7	44	18	48	49
G06	41	2	28	47	12	20	31	7	31	48	19	33	11	22	26	46	11	51	25	45	10	12
G07	32	46	51	7	13	49	39	32	39	17	15	12	28	42	11	37	5	38	49	4	45	2
G08	9	40	39	48	48	21	24	40	30	7	26	42	24	41	18	15	45	39	33	6	43	1
G09	15	35	6	32	24	16	15	41	3	41	10	16	2	36	41	20	14	34	50	1	12	28
G10	30	49	17	18	40	9	33	48	50	1	40	10	16	26	37	19	32	2	38	12	40	42
G11	47	51	12	17	34	51	50	51	43	50	32	25	51	31	50	51	51	31	30	9	46	14
G12	39	20	38	33	6	27	14	28	47	23	2	17	38	32	3	23	3	18	10	44	17	43
G13	45	27	10	50	1	10	49	35	37	40	36	38	13	20	16	28	10	5	28	39	29	51
G14	10	19	30	34	2	28	32	22	12	43	23	39	10	44	9	17	4	19	4	43	27	32
G15	23	22	48	40	45	18	30	16	14	12	41	14	32	17	13	42	15	45	26	46	49	22
G16	33	18	22	36	33	26	17	39	8	44	21	47	39	18	2	32	6	42	46	5	44	7
G17	1	24	43	3	46	38	4	34	45	26	47	18	8	3	28	45	48	43	43	50	19	19
G18	38	8	26	37	17	8	27	6	42	9	9	50	37	15	32	25	1	33	48	3	14	31
G19	2	26	21	28	41	48	9	14	5	31	14	24	9	34	42	36	35	47	36	27	18	44
G20	51	1	50	44	39	1	43	2	46	46	29	28	43	46	44	50	7	50	17	51	25	46
G21	44	48	20	10	15	22	44	49	35	28	39	4	42	33	14	29	21	6	24	19	3	10
G22	43	9	49	11	29	7	51	5	1	2	43	2	31	27	21	1	8	3	18	10	41	47
G23	50	4	7	14	4	29	48	4	2	35	3	46	26	29	25	44	37	40	22	40	21	11
G24	18	37	33	49	32	19	12	36	49	14	45	7	4	39	51	9	47	9	14	47	31	45
G25	34	17	15	22	11	14	5	26	26	18	22	43	6	13	22	38	42	37	35	35	34	27
G26	12	14	4	25	30	15	11	19	21	8	16	48	20	14	31	33	38	27	1	8	6	3
G27	21	11	19	27	10	5	1	20	33	22	42	8	19	49	12	27	20	17	42	25	13	23
G28	42	12	40	43	43	34	13	9	11	38	7	29	23	23	36	49	27	49	13	17	28	38
G29	22	39	31	19	5	30	2	25	38	10	31	37	27	45	8	11	46	16	8	23	24	29
G30	7	41	16	15	21	39	10	29	29	11	12	51	14	4	17	13	17	13	29	24	51	25
G31	26	47	9	4	36	33	41	46	23	4	30	20	21	48	40	47	44	12	51	2	39	41
G32	16	43	11	6	35	25	8	42	4	15	35	41	40	11	45	24	13	26	6	14	33	8
G33	36	10	35	24	31	6	35	8	19	20	6	35	30	5	35	7	16	29	23	11	7	30
G34	31	5	41	21	25	45	37	1	32	45	20	21	34	19	7	30	39	28	3	7	37	21
G35	27	23	5	20	50	24	23	23	27	29	51	6	50	51	43	43	50	21	27	33	8	37
G36	46	28	13	35	23	44	29	33	28	39	34	27	48	16	46	41	19	24	19	42	2	39
G37	14	29	2	26	20	13	25	27	15	16	28	11	46	21	24	12	41	41	31	26	50	17
G38	20	45	37	2	14	41	19	44	51	3	27	34	12	10	5	22	9	15	11	21	11	48
G39	49	7	18	46	7	36	45	12	24	42	11	32	7	47	39	35	25	11	7	38	1	40
G40	29	44	46	51	37	2	20	47	22	19	25	45	35	9	34	40	28	32	32	34	32	34
G41	25	42	8	39	38	43	16	45	40	49	13	30	25	12	15	21	23	44	2	48	9	26
G42	13	34	24	23	26	35	46	11	48	6	46	9	44	40	29	14	30	20	37	15	42	6
G43	6	31	45	29	27	11	21	43	17	21	50	1	15	28	49	6	36	14	41	36	47	5
G44	4	32	23	16	9	12	22	37	34	24	44	3	18	43	1	26	2	4	40	30	5	13
G45	28	33	25	9	49	31	26	30	25	13	49	22	17	8	33	4	31	10	5	29	38	33

Table 4 (continued)

Code	Leaf Ca ²⁺		Leaf Na ⁺		Leaf K ⁺		Leaf Ca ²⁺ / Na ⁺		Leaf K ⁺ / Na ⁺		Net CO ₂		Transpira- tion rate		Root number		Root yield		Sugar content		Root Na ⁺	
	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM
G46	24	21	32	8	44	40	47	13	44	33	1	40	22	2	6	18	22	30	15	32	26	35
G47	37	3	29	12	42	17	40	3	18	37	38	26	36	6	19	10	40	25	20	37	20	4
G48	8	13	3	41	18	46	7	21	36	51	8	49	33	1	10	16	29	36	21	31	16	15
G49	35	16	44	5	28	3	28	15	20	5	33	23	49	35	20	8	12	8	16	20	36	36
G50	48	6	1	38	22	42	38	10	13	47	17	44	29	38	4	34	26	48	34	49	35	24
G51	40	50	47	1	3	50	34	50	9	32	24	5	5	7	47	3	34	1	9	16	4	20
Code	Root K ⁺		Root α-N		Root K ⁺ / Na ⁺		Alkaline level content		Sugar yield		White sugar yield		White sugar content		Extraction coefficient of sugar		Molasses sugar		Dry matter		TGSI	
	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM		
G01	4	42	7	14	41	23	16	41	32	48	29	49	43	30	40	35	15	37	39	31	1227	
G02	24	20	30	44	24	4	33	4	28	28	30	29	46	12	25	29	2	33	45	7	1062	
G03	1	22	27	19	36	43	34	22	47	21	48	22	39	22	7	12	3	5	14	27	1108	
G04	14	40	49	39	21	13	48	50	20	25	22	27	14	43	32	44	16	41	37	16	1156	
G05	12	9	38	12	50	48	47	32	9	12	1	11	48	29	47	16	43	2	8	35	1122	
G06	40	13	45	6	10	3	44	47	4	51	7	51	33	8	15	21	22	31	6	12	1047	
G07	6	32	50	26	40	2	50	49	17	41	23	43	50	50	49	48	18	42	38	17	1304	
G08	49	19	19	41	32	1	41	45	44	42	40	44	36	48	30	50	12	51	33	15	1331	
G09	25	50	24	38	26	30	29	37	26	45	32	50	51	51	51	51	7	40	10	2	1167	
G10	13	21	33	35	33	25	45	42	6	4	4	5	42	36	26	26	1	16	41	22	1085	
G11	15	36	18	32	14	24	3	14	51	32	51	35	31	44	37	41	32	36	42	49	1464	
G12	27	18	25	21	44	47	31	27	3	11	8	9	16	7	35	5	19	12	13	23	926	
G13	28	1	10	4	46	51	9	23	31	6	37	1	38	9	46	1	30	1	26	51	1066	
G14	31	26	32	9	43	37	22	35	2	13	5	12	1	10	22	8	41	22	5	24	903	
G15	16	7	11	8	51	49	13	29	12	40	10	39	37	6	48	6	44	15	40	26	1137	
G16	47	4	5	3	7	10	49	51	5	46	3	48	26	46	34	39	51	27	46	45	1177	
G17	44	49	6	40	4	18	20	36	48	36	49	37	41	4	19	32	36	44	32	18	1248	
G18	38	38	39	30	22	21	37	19	15	39	18	40	47	49	33	40	33	32	3	9	1118	
G19	45	16	4	10	23	38	23	16	34	47	36	45	25	17	13	14	37	7	48	46	1135	
G20	26	27	9	1	17	20	21	48	1	50	2	46	10	1	12	2	17	6	50	1	1126	
G21	39	46	43	48	15	8	28	5	22	9	14	19	15	41	16	46	27	48	20	48	1116	
G22	42	30	40	33	29	34	46	43	10	5	6	6	27	37	38	28	39	11	29	32	1024	
G23	33	45	41	50	20	31	12	3	35	37	31	38	28	19	31	37	31	45	47	34	1189	
G24	18	14	22	36	45	46	4	2	43	7	47	2	3	5	23	4	24	10	43	41	1086	
G25	41	44	48	42	28	32	24	17	40	35	38	32	17	25	4	34	45	38	4	28	1158	
G26	46	43	47	45	5	9	18	12	37	29	33	33	12	47	41	47	46	46	49	21	1070	
G27	36	23	12	15	13	19	25	34	7	19	9	20	45	27	27	25	29	26	2	8	887	
G28	32	3	44	28	35	5	36	8	27	49	28	47	8	33	1	11	14	3	35	10	1081	
G29	9	11	8	2	12	33	19	44	45	18	44	16	6	23	10	17	5	9	36	14	907	
G30	37	8	23	24	48	35	43	13	24	14	26	13	40	24	43	22	42	19	28	3	1017	
G31	20	31	46	17	30	29	35	31	49	22	43	18	7	31	3	20	34	23	51	44	1248	
G32	48	33	35	43	9	12	5	24	18	26	21	26	20	42	29	42	47	39	24	25	1069	
G33	29	24	21	29	6	27	6	6	13	34	16	31	29	38	21	31	20	25	15	11	890	
G34	7	5	3	16	1	22	40	39	41	27	39	28	2	40	18	30	10	20	11	37	985	
G35	34	29	31	13	31	40	32	30	50	16	50	15	32	16	28	19	28	21	31	39	1256	
G36	43	41	37	27	8	39	15	20	16	20	20	21	21	11	20	24	38	30	1	5	1132	
G37	21	2	1	5	47	44	26	40	46	44	46	42	30	21	42	13	35	14	17	47	1118	

Table 4 (continued)

Code	Root K ⁺		Root α-N		Root K ⁺ /Na ⁺		Alkaline level content		Sugar yield		White sugar yield		White sugar content		Extraction coefficient of sugar		Molasses sugar		Dry matter		TGSI
	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	RA	RM	
G38	2	10	13	37	18	26	1	1	11	17	15	14	19	26	5	7	8	4	30	29	794
G39	22	37	20	34	19	42	14	7	33	3	35	3	9	13	8	23	9	28	7	42	987
G40	10	25	16	7	49	45	42	38	29	31	25	30	35	15	36	15	23	17	19	6	1210
G41	3	6	15	22	34	17	27	28	21	38	17	36	5	2	9	3	4	13	34	38	985
G42	8	48	51	49	39	7	51	46	23	24	13	24	44	45	44	49	21	50	21	19	1274
G43	35	15	29	18	37	36	10	26	39	15	45	17	49	20	50	33	50	35	9	43	1190
G44	51	47	42	51	11	14	39	11	14	1	12	7	34	35	24	45	48	47	18	50	1043
G45	30	17	34	25	42	50	30	10	38	8	41	8	22	18	45	18	40	18	22	33	1097
G46	11	12	17	20	27	41	2	15	25	30	24	25	13	14	39	10	25	8	25	4	942
G47	5	39	26	46	16	16	38	18	42	23	42	23	18	28	14	38	11	43	16	20	1041
G48	50	51	36	47	2	28	7	9	36	33	34	34	4	34	17	43	49	49	23	13	1108
G49	23	34	2	11	38	15	8	33	8	10	11	10	23	32	11	27	6	24	27	30	878
G50	19	28	14	23	25	6	11	25	19	43	19	41	24	3	2	9	26	29	44	36	1093
G51	17	35	28	31	3	11	17	21	30	2	27	4	11	39	6	36	13	34	12	40	908

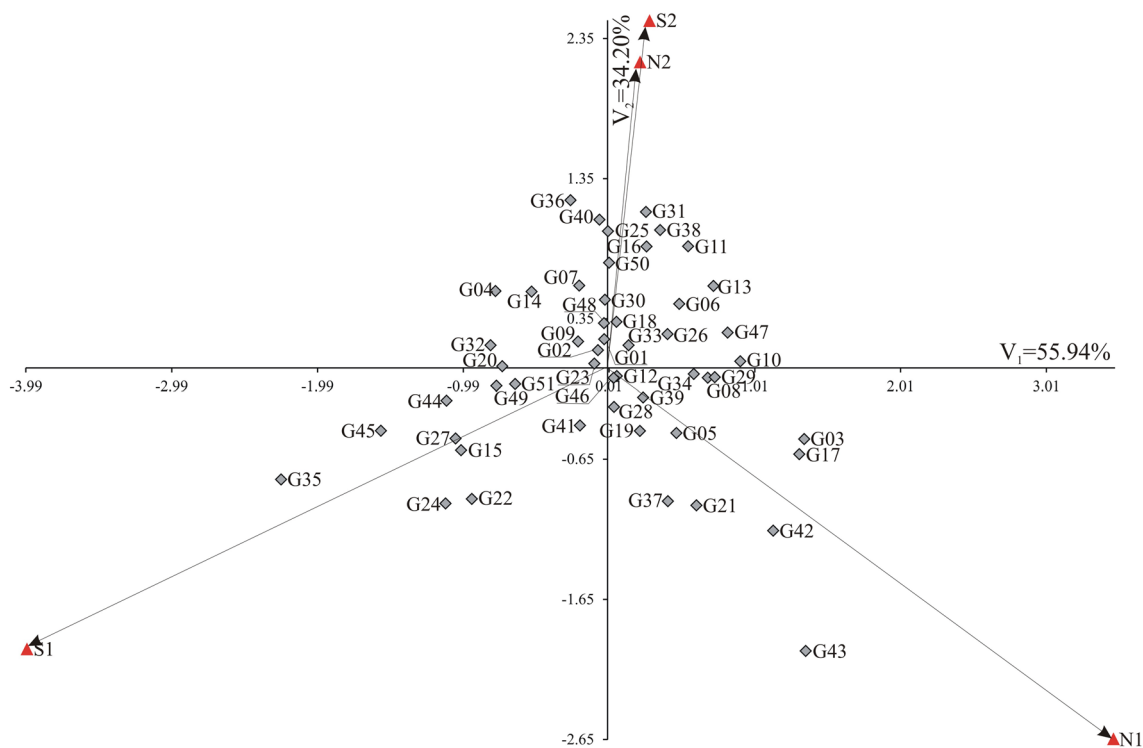


Fig. 1 Biplot for genotype by environment interaction of net CO₂ in sugar beet (*Beta vulgaris* L.) parents and hybrids in four environments [saline (S) and non-saline (N) experiments conducted in 2011

and 2012], showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

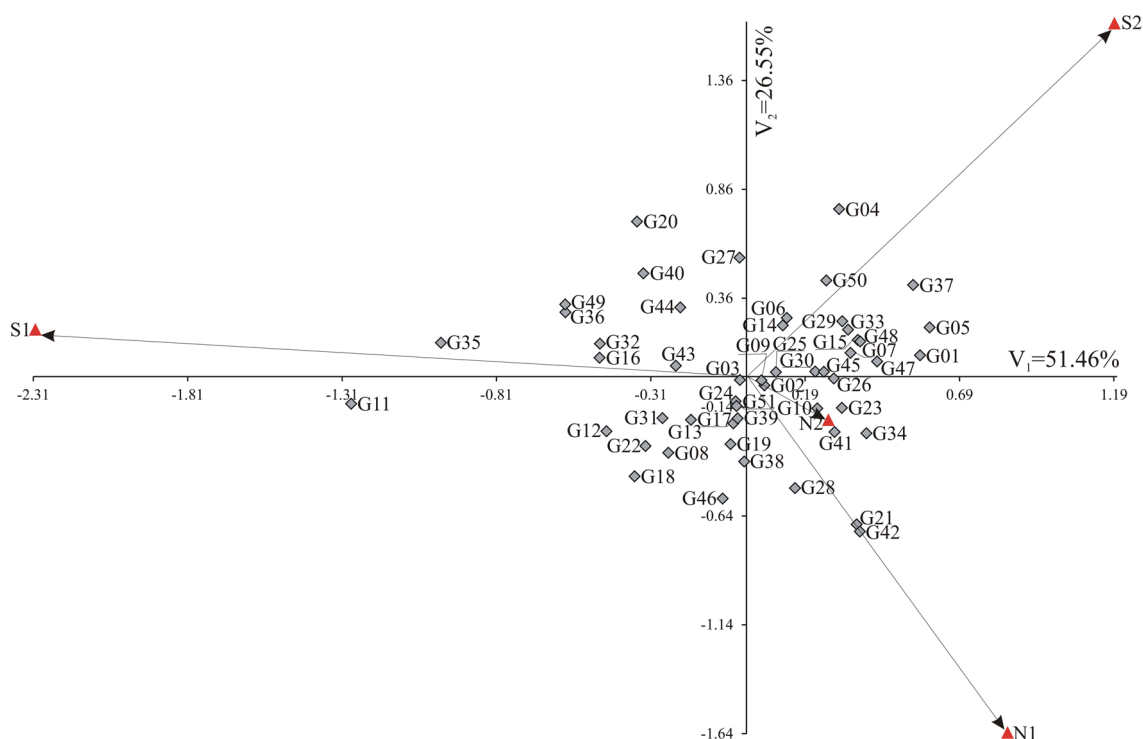


Fig. 2 Biplot for genotype by environment interaction of transpiration rate in sugar beet (*Beta vulgaris* L.) parents and hybrids in four environments [saline (S) and non-saline (N) experiments conducted in

2011 and 2012], showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

interacted positively with the N1 environment, but negatively with the both saline and non-saline experiments in 2012.

The first two interaction principal components for transpiration rate accounted jointly for 78.01% of the variation caused by interaction (Fig. 2). The genotypes G11 and G35 interacted positively with the S1 environment, but negatively with the N1 and S2. The genotypes G21, G28 and G42 interacted positively with the N1 environment. Genotypes G04 and G50 interacted positively with the S2 environment.

The stability of tested genotypes can be evaluated according to biplot for root number (Fig. 3). The genotypes G24 and G43 interacted positively with the N2 environment, but negatively with the N1 and S1. The genotypes G04, G09, G18, G19 and G32 interacted positively with the S2 environment. Genotypes G01, G03, G06, G17 and G31 interacted positively with the S1 and N1 environments.

For root yield we observed that the genotype G11 interacted positively with the N1 environment, but negatively with the S2 as well as the genotype G35 interacted positively with the S1 environment, but negatively with the N2 (Fig. 4). The first two interaction principal components for this trait accounted jointly for 83.92% of the variation caused by interaction (Fig. 4, Table 3).

Figures 5, 6 present the biplots of the stability of tested genotypes for sugar yield and white sugar yield, respectively. Only the first interaction principal component, IPCA1, was statistically significant for these traits. The saline and non-saline experiments in both years of study were strongly different (Figs. 5, 6). The genotype G35 interacted positively with the S1 environment; the G03 and G11 interacted positively with the N1; and genotypes G24 and G43 with N2 environment for both traits.

The first two interaction principal components for dry matter accounted jointly for 79.24% of the variation caused by interaction (Fig. 7). The genotypes G15, G17, G20 and G45 interacted positively with the S1 environment, but negatively with the saline environment in 2012. The genotypes G24, G29, G38, G41 and G49 interacted positively with the N1 environment. Genotypes G11, G23 and G35 interacted positively with the S2 environment, but negatively with the saline environment in 2011. The genotypes G16 and G19 interacted positively with the N2 environment (Fig. 7).

The best total genotype selection index calculated for all 21 physiological traits was observed for genotype G38 (TGSI=794), while the worst—G11 (TGSI=1464) (Table 4). The parental forms 2 7233-P.29 (G38) and C CMS (G49) as well as hybrids 2(6)*C (G27) and 5*C (G33) are recommended for further inclusion in the breeding

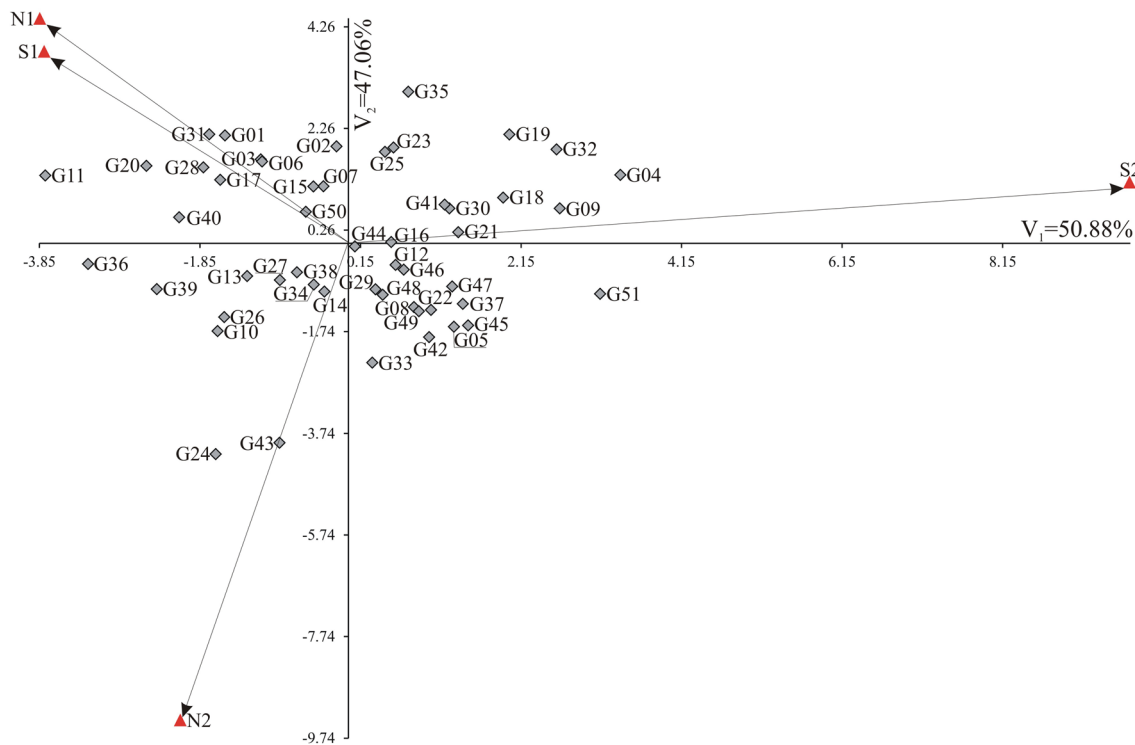


Fig. 3 Biplot for genotype by environment interaction of root number in sugar beet (*Beta vulgaris* L.) parents and hybrids in four environments [saline (S) and non-saline (N) experiments conducted in 2011

and 2012], showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

programs because of their stability and good average values of observed traits.

The positive statistical significant ($\alpha=0.05$) correlation coefficients in all four environments (saline and non-saline experiments conducted in 2011 and 2012) were observed between: leaf Ca^{2+} and leaf Na^+ , root number and root yield, root number and sugar yield, root yield and sugar yield, root yield and white sugar yield, sugar content and white sugar content, sugar content and extraction coefficient of sugar, root Na^+ and alkaline level content, root Na^+ and molasses sugar, root K^+ and root $\alpha\text{-N}$, root K^+/Na^+ and extraction coefficient of sugar, sugar yield and white sugar yield, white sugar yield and extraction coefficient of sugar as well as white sugar content and extraction coefficient of sugar (Tables 5, 6). Negative correlation coefficients in all four environments were observed between: leaf Na^+ and leaf K^+/Na^+ , root Na^+ and root $\alpha\text{-N}$, root Na^+ and extraction coefficient of sugar, root $\alpha\text{-N}$ alkaline level content, root K^+/Na^+ and molasses sugar as well as extraction coefficient of sugar and molasses sugar (Tables 5, 6).

Discussion

Genotype by environment interaction is one of the unifying challenges facing plant breeders [19, 20]. The quantity and quality traits of sugar beet (*Beta vulgaris* L.) are determined by genotype and environment that sugar beet varieties usually differ in different environments. To introduce new varieties in the final stages of breeding program, they must be tested in several environments to identify their stability across different environments. If the genotypes ranking do not vary the environment that is a GEI is absent or low, showing general adaptation [4]. As an advantage of the change of ranks in different environments (crossover) is the availability of special varieties which are adapted to certain areas stress situations [3]. Thus, GEI is of major importance to improve sugar beet production. The aim of this study was to disclose the importance of environment on quantity and quality traits of sugar beet genotypes. For that purpose, 21 traits of 53 sugar beet genotypes were investigated in four environments (combination of two locations and 2 years) in field trials.

AMMI allow for a large set of technical interpretations, and they used more commonly to evaluate the genotype–environment interactions. The additive main effects and multiplicative interaction (AMMI) model

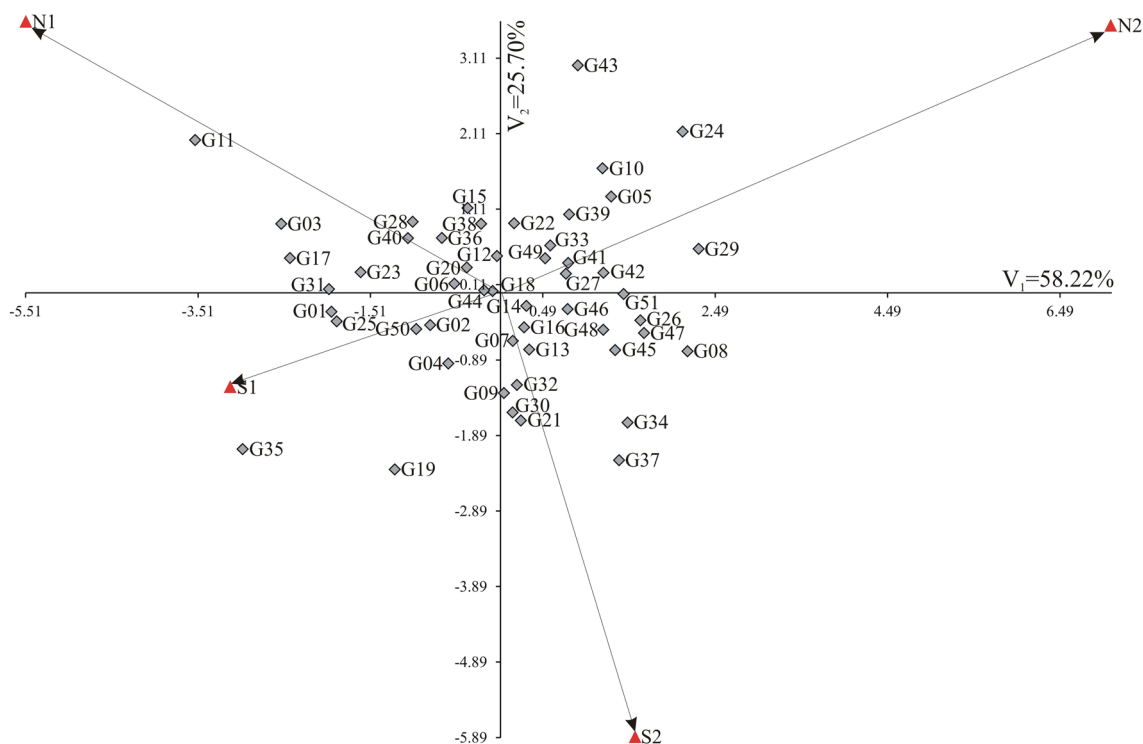


Fig. 4 Biplot for genotype by environment interaction of root yield in sugar beet (*Beta vulgaris* L.) parents and hybrids in four environments [saline (S) and non-saline (N) experiments conducted in 2011

and 2012], showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

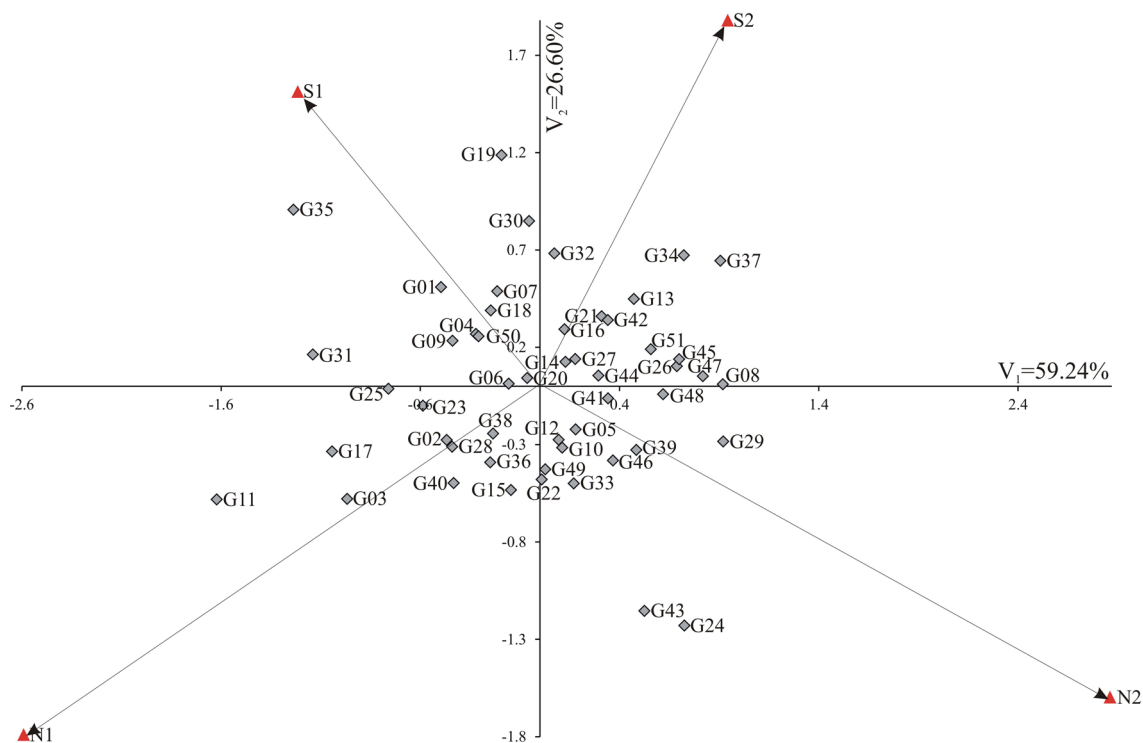


Fig. 5 Biplot for genotype by environment interaction of sugar yield in sugar beet (*Beta vulgaris* L.) parents and hybrids in four environments [saline (S) and non-saline (N) experiments conducted in 2011

and 2012], showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

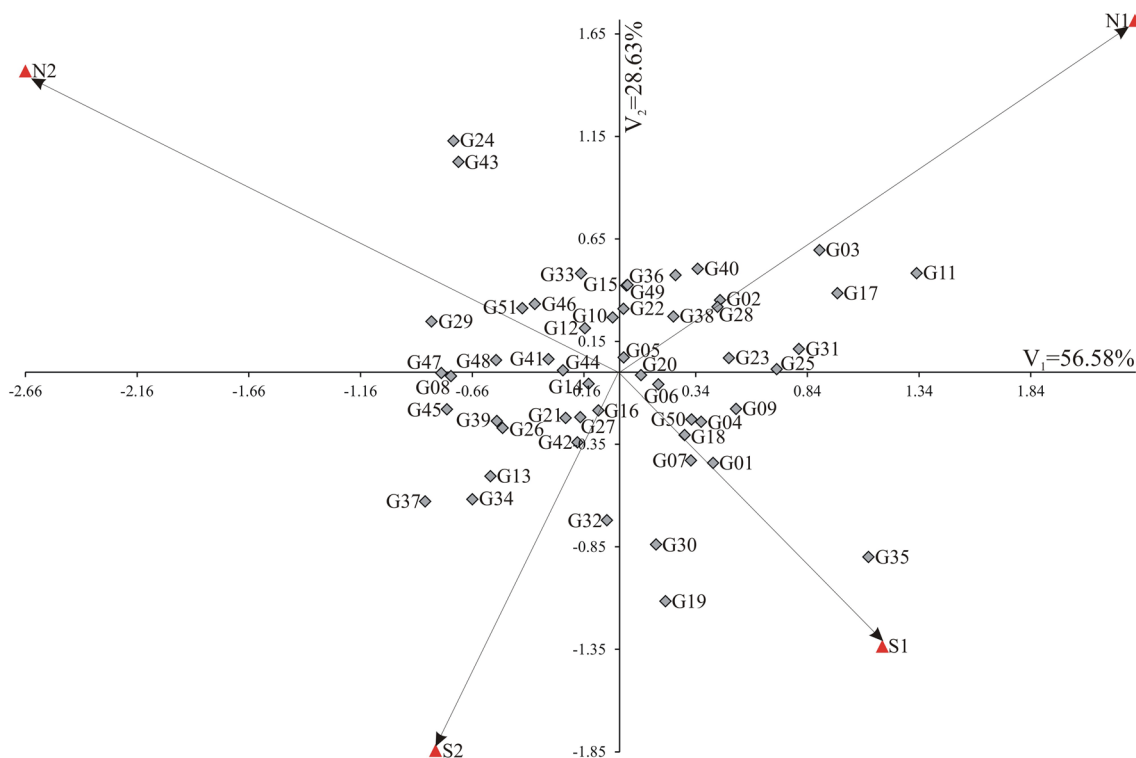


Fig. 6 Biplot for genotype by environment interaction of white sugar yield in sugar beet (*Beta vulgaris* L.) parents and hybrids in four environments [saline (S) and non-saline (N) experiments conducted in

2011 and 2012], showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

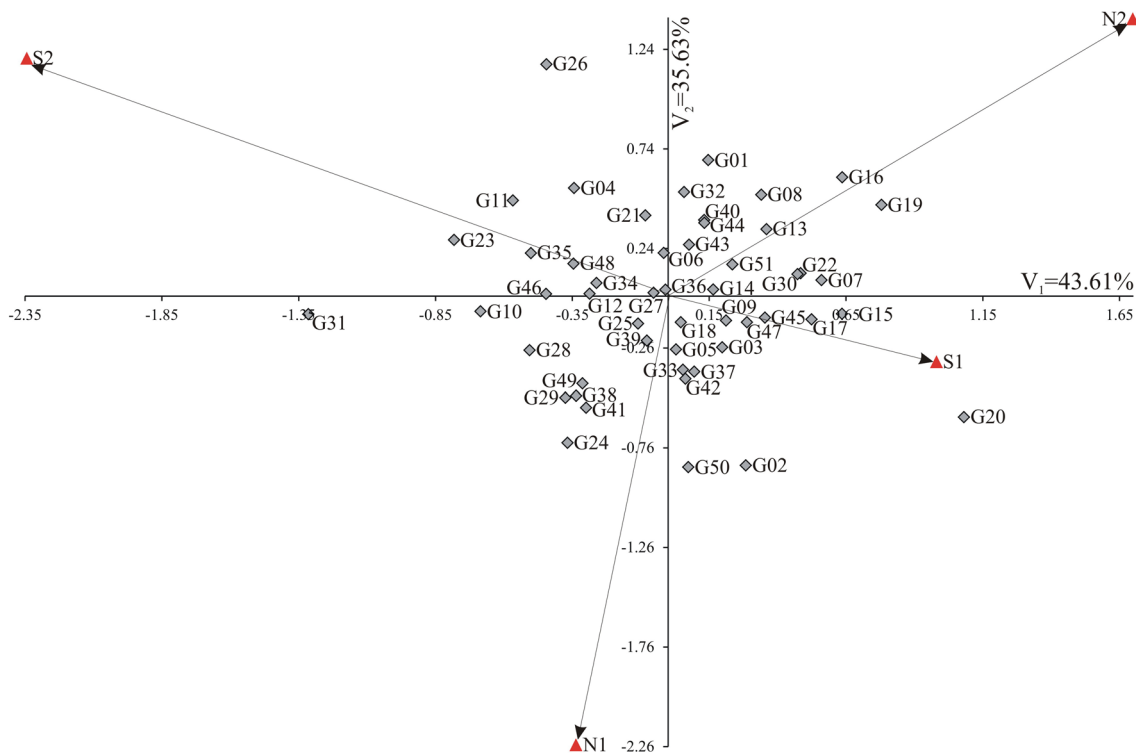


Fig. 7 Biplot for genotype by environment interaction of dry matter in sugar beet (*Beta vulgaris* L.) parents and hybrids in four environments [saline (S) and non-saline (N) experiments conducted in 2011

and 2012], showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

Table 5 Correlation matrix for the traits observed in non-saline experiments conducted in 2011 (above diagonal) and 2012 (below diagonal)

Trait	Leaf Ca ²⁺	Leaf Na ⁺	Leaf K ⁺	Leaf Ca ²⁺ /Na ⁺	Leaf K ⁺ /Na ⁺	Net CO ₂	Transpiration rate	Root number	Root yield	Sugar content
leaf Ca ²⁺	1	0.48***	0.49***	0.32*	0.06	0.25	0.04	-0.21	-0.02	-0.16
leaf Na ⁺	0.67***	1	0.42**	-0.49***	-0.47***	-0.07	-0.09	0.07	-0.07	-0.01
leaf K ⁺	0.45***	0.63***	1	-0.09	0.43**	0.1	-0.15	0	0.16	-0.08
leaf Ca ²⁺ /Na ⁺	0.83***	0.24	0.26	1	0.64***	0.22	0.18	-0.11	0.08	-0.07
leaf K ⁺ /Na ⁺	-0.35*	-0.66***	0.08	-0.04	1	0.18	0.03	0	0.23	0.04
net CO ₂	-0.21	-0.22	-0.15	-0.19	0.21	1	0.45*	-0.17	0.11	-0.13
transpiration rate	-0.07	-0.16	-0.08	0.05	0.11	0.2	1	-0.27	-0.11	0.03
root number	-0.03	-0.04	0.23	0.01	0.25	0.02	-0.07	1	0.55***	0.34*
root yield	-0.11	-0.08	0.2	-0.09	0.29*	0.1	-0.05	0.89***	1	0.15
sugar content	0.23	0.33*	-0.01	0.06	-0.44**	-0.29*	-0.12	-0.14	-0.3*	1
root Na ⁺	-0.11	-0.24	-0.16	0	0.21	0.05	0.02	-0.16	-0.05	-0.31*
root K ⁺	0.08	-0.04	-0.16	0.11	-0.02	0.13	0.12	-0.25	-0.21	0.02
root α-N	-0.09	0.03	-0.13	-0.14	-0.15	-0.01	0.24	-0.43**	-0.37**	0.22
root K ⁺ /Na ⁺	0.05	0.11	0.18	0.03	-0.05	-0.1	0.09	0.16	0.05	0.35*
alkaline level content	0.07	-0.23	0.01	0.27	0.33*	0.2	-0.17	0.26	0.31*	-0.46***
sugar yield	-0.04	0.03	0.23	-0.07	0.17	0.01	-0.08	0.89***	0.95***	-0.02
white sugar yield	-0.04	0.05	0.23	-0.09	0.15	0.03	-0.06	0.86***	0.92***	0.02
white sugar content	0.17	0.3*	-0.02	-0.05	-0.41	-0.19	-0.01	-0.16	-0.3*	0.91***
extraction coefficient of sugar	0.03	0.1	0	-0.07	-0.16	-0.2	-0.12	0.08	0.01	0.55***
molasses sugar	-0.03	-0.16	-0.2	0.04	0.09	0.1	0.11	-0.29*	-0.19	-0.14
dry matter	0.25	0.19	0.14	0.17	-0.07	-0.14	-0.22	-0.22	-0.21	-0.01
Trait	Root Na ⁺	Root K ⁺	Root α-N	Root K ⁺ /Na ⁺	Alkaline level content	White sugar yield	White sugar content	Extraction coefficient of sugar	Molasses sugar	Dry matter
leaf Ca ²⁺	0.12	0.07	-0.2	-0.03	0.28*	-0.06	-0.08	-0.18	0.13	-0.1
leaf Na ⁺	0.01	-0.1	-0.12	-0.03	0.08	-0.08	-0.08	0.02	-0.05	0.12
leaf K ⁺	-0.07	0.12	-0.29*	0.11	0.17	0.11	-0.05	0	-0.06	-0.05
leaf Ca ²⁺ /Na ⁺	-0.03	0.15	0.17	0.12	-0.02	0.05	-0.08	-0.09	0.07	-0.12
leaf K ⁺ /Na ⁺	-0.14	0.25	0.09	0.2	-0.08	0.21	0.04	0.02	-0.01	-0.08
net CO ₂	0.04	0.1	0.14	-0.01	-0.02	0.06	-0.15	-0.13	0.11	-0.07
transpiration rate	-0.1	0	0.23	0.05	-0.18	-0.09	0.05	0.07	-0.07	0.1

Table 5 (continued)

Trait	Root Na ⁺	Root K ⁺	Root α-N	Root K ⁺ /Na ⁺	Alkaline level content	sugar yield	White sugar yield	White sugar content	Extraction coefficient of sugar	Molasses sugar	Dry matter
root number	-0.32*	0.15	0.17	0.27	-0.37**	0.59***	0.61***	0.36**	0.33*	-0.23	0.28*
root yield	-0.36**	0.55***	0.1	0.42**	-0.31*	0.97***	0.95***	0.17	0.16	-0.1	-0.01
sugar content	-0.4**	0.29*	0.18	0.44**	-0.31	0.39**	0.44**	0.96***	0.62***	-0.25	0.77***
root Na ⁺	1	-0.33*	-0.03	-0.89***	0.45***	-0.41**	-0.49***	-0.61***	-0.88***	0.86***	-0.56***
root K ⁺	0.36**	1	0.33*	0.55***	-0.39**	0.56***	0.52***	0.21	0	0.18	0.19
root α-N	0.21	0.58***	1	0.11	-0.8***	0.14	0.12	0.08	-0.13	0.27	0.14
root K ⁺ /Na ⁺	-0.82***	-0.27	-0.25	1	-0.41**	0.47***	0.54***	0.58***	0.71***	-0.64***	0.54***
alkaline level content	0.48***	0.01	-0.61***	-0.33*	1	-0.35*	-0.37**	-0.32*	-0.28*	0.16	-0.31*
sugar yield	-0.18	-0.23	-0.31*	0.19	0.15	1	0.99***	0.38**	0.29*	-0.13	0.16
white sugar yield	-0.28	-0.29*	-0.32*	0.27	0.08	0.99***	1	0.46***	0.39**	-0.24	0.24
white sugar content	-0.48***	-0.14	0.15	0.49***	-0.56***	-0.02	0.07	1	0.82***	-0.52***	0.81***
extraction coefficient of sugar	-0.57***	-0.52***	-0.21	0.49***	-0.34*	0.21	0.31*	0.73***	1	-0.91***	0.69***
molasses sugar	0.8***	0.83***	0.58***	-0.66***	0.2	-0.28	-0.36**	-0.34*	-0.64***	1	-0.46***
dry matter	0.24	0.07	-0.14	-0.02	0.24	-0.22	-0.28*	-0.16	-0.25	0.16	1

* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$

Table 6 Correlation matrix for the traits observed in saline experiments conducted in 2011 (above diagonal) and 2012 (below diagonal)

Trait	leaf Ca ²⁺	leaf Na ⁺	leaf K ⁺	leaf Ca ²⁺ /Na ⁺	leaf K ⁺ /Na ⁺	net CO ₂	transpiration rate	root number	root yield	sugar content
leaf Ca ²⁺	1	0.4**	0.13	0.21	-0.19	-0.17	-0.08	-0.01	-0.07	-0.08
leaf Na ⁺	0.76***	1	0.25	-0.64***	-0.56***	-0.15	-0.13	0.08	-0.05	0.11
leaf K ⁺	0.42**	0.38**	1	-0.24	0.59***	0.12	-0.01	-0.09	0.04	-0.01
leaf Ca ²⁺ /Na ⁺	0.91***	0.45***	0.42**	1	0.46***	0.1	0.23	0.08	-0.02	-0.11
leaf K ⁺ /Na ⁺	-0.29*	-0.56***	0.51***	-0.01	1	0.29*	0.2	0	0.12	-0.12
net CO ₂	-0.15	0.06	0.01	-0.25	-0.05	1	0.3*	-0.03	0.08	-0.02
transpiration rate	0.24	0.25	0.01	0.18	-0.2	0.17	1	0.08	0.33*	-0.16
root number	-0.1	-0.1	-0.02	-0.02	0.06	-0.31*	0.07	1	0.5***	0.02
root yield	-0.33*	-0.35*	-0.02	-0.2	0.3*	-0.08	-0.08	0.66***	1	-0.46***
sugar content	0.25	0.18	-0.11	0.18	-0.21	-0.1	0.23	-0.25	-0.25	1
root Na ⁺	0.1	0.21	0.12	0.03	-0.11	0.33*	-0.03	0	-0.09	-0.24
root K ⁺	-0.1	-0.08	-0.04	-0.1	-0.02	0.23	-0.13	0.03	0.11	-0.03
root α-N	-0.21	-0.17	-0.11	-0.2	0.01	0.04	-0.09	0.04	0.16	0.01
root K ⁺ /Na ⁺	-0.2	-0.23	-0.16	-0.17	0.08	-0.27	0.08	0.2	0.28*	0.3*
alkaline level content	0.17	0.29*	0.18	0.08	-0.09	0.31*	0.1	0.07	-0.1	-0.11
sugar yield	-0.21	-0.3*	-0.11	-0.12	0.19	-0.14	-0.01	0.49***	0.89***	0.13
white sugar yield	-0.19	-0.29*	-0.13	-0.09	0.17	-0.2	0.02	0.44**	0.83***	0.22
white sugar content	0.24	0.15	-0.1	0.18	-0.18	-0.18	0.24	-0.24	-0.24	0.96***
extraction coefficient of sugar	0.13	-0.02	-0.07	0.17	0.01	-0.27	0.12	-0.19	-0.14	0.63***
molasses sugar	-0.03	0.04	0.02	-0.06	-0.06	0.3*	-0.1	0.02	0.04	-0.13
dry matter	-0.01	-0.11	-0.01	0.09	0.13	-0.12	-0.15	-0.14	-0.01	-0.18
Trait	Root Na ⁺	Root K ⁺	Root α-N	Root K ⁺ /Na ⁺	Alkaline level content	Sugar yield	White sugar yield	White Sugar content	Molasses sugar	Dry matter
leaf Ca ²⁺	-0.08	-0.21	-0.01	-0.04	-0.16	-0.1	-0.09	-0.02	0.15	-0.05
leaf Na ⁺	-0.08	-0.21	-0.08	-0.03	-0.09	-0.04	-0.01	0.17	0.26	-0.04
leaf K ⁺	-0.12	0.15	0.09	0.09	-0.08	0.03	0.03	-0.01	0.03	-0.18
leaf Ca ²⁺ /Na ⁺	0.07	-0.01	0.02	-0.05	0.01	-0.04	-0.05	-0.12	-0.12	0.06
leaf K ⁺ /Na ⁺	0	0.27	0.17	0.09	-0.01	0.09	0.07	-0.18	-0.22	-0.15
net CO ₂	0.13	0.15	0.2	-0.07	-0.03	0.08	0.05	-0.09	-0.21	-0.04
transpiration rate	-0.12	-0.02	-0.14	0.1	0.03	0.32*	0.32*	-0.12	0.02	-0.27

Table 6 (continued)

Trait	Root Na ⁺	Root K ⁺	Root α-N	Root K ⁺ /Na ⁺	Alkaline level content	Sugar yield	White sugar yield	White Sugar content	extraction coefficient of sugar	Molasses sugar	Dry matter
root number	-0.23	-0.23	-0.06	0.25	-0.2	0.53***	0.55***	0.13	0.31*	-0.32*	-0.31*
root yield	-0.51***	-0.01	0.19	0.53***	-0.55***	0.96***	0.95***	-0.32*	0.13	-0.39***	-0.73***
sugar content	0.13	0.07	-0.03	-0.17	0.21	-0.24	-0.19	0.94***	0.39**	0.14	0.61***
root Na ⁺	1	-0.08	0.03	-0.88***	0.63***	-0.54***	-0.59***	-0.13	-0.66***	0.78***	0.28*
root K ⁺	0.57***	1	0.52***	0.41**	-0.13	0.07	0.02	-0.12	-0.47***	0.56***	0.03
root α-N	0.34*	0.74***	1	0.18	-0.64***	0.22	0.17	-0.17	-0.41**	0.44**	-0.17
root K ⁺ /Na ⁺	-0.72***	-0.23	-0.12	1	-0.62***	0.57***	0.59***	-0.01	0.35*	-0.47***	-0.29*
alkaline level content	0.45***	-0.02	-0.54***	-0.25	1	-0.57***	-0.58***	0.09	-0.24	0.36**	0.37**
sugar yield	-0.24	0.06	0.15	0.43**	-0.19	1	1***	-0.11	0.22	-0.37**	-0.62***
white sugar yield	-0.38**	-0.09	0.03	0.52***	-0.22	0.98***	1	-0.04	0.32*	-0.45**	-0.59***
white sugar content	-0.46***	-0.29*	-0.19	0.41**	-0.14	0.14	0.27	1	0.67***	-0.19	0.53***
extraction coefficient of sugar	-0.71***	-0.62***	-0.44**	0.5**	-0.22	0.16	0.32*	0.79***	1	-0.85***	0.09
molasses sugar	0.84***	0.92***	0.69***	-0.49**	0.14	-0.06	-0.23	-0.4**	-0.74***	1	0.23
dry matter	0.03	0.03	-0.02	-0.15	0.03	-0.07	-0.08	-0.18	-0.09	0.03	1

P* < 0.05; *P* < 0.01; ****P* < 0.001

addresses the limitations of ANOVA and PCA. The AMMI model effectively explains the GEI patterns. The AMMI method used for three primary purposes for stability. The first is that the model involves variance analysis and principal component analysis. Second, AMMI clarifies GEI and summarizes G and E patterns and relationships, and the third use is the accuracy of yield estimates. AMMI model is more suitable and simplifies genotypes' instantaneous choice for stability. The model helps establish the relationship of genotypes, environment and their interaction. The AMMI model as the most popular multiplicative models was initially proposed by Gollob [15] and [22, 23] in the context of fixed effects. AMMI can have several models: AMMI0, which estimates the main additive effect of genotypes and environments and does not include any major axis (IPCA) AMMI1, which combines AMMI0 genotype additive effects with environmental interactions estimated and combines from the first major axis (IPCA 1). AMMI2 and others up to the full model with all IPCA axes. In this paper we used the traditional AMMI model for fixed effects. The traditional AMMI model has been used extensively for many species [1, 5, 11, 26].

Researchers apply the proposed strategy to extract specific cultivars with competitive performance across different environments that can extract more information from GE interaction [27]. Hassani et al. [17] using AMMI model analyzed GEI for 49 sugar beet genotypes in four different geographical locations in 2 years for three morphological traits: root yield, sugar yield and white sugar yield. Ghareeb et al. [14] also analyzed root yield, sugar yield and white sugar yield by AMMI model. Seven sugar beet cultivars were appraised in eight environments: two consecutive seasons and four locations. Their results showed that the AMMI model clarified most of the GEI (85.97%, 83.34% and 86.47%) for root yield, sugar content and, sugar yield, respectively. Hoffmann et al. [18] analyzed GEI of nine genotypes in 52 environments for yield and quality (sugar, K, Na, amino N, total soluble N, betaine, glutamine, invert sugar and raffinose) of sugar beet in Europe. According to their results, the GEI with about 3% was less than the main effect of genotypes (about 80%).

High genotypes stability is linked with the AMMI stability value. AMMI stability value is the distance of the coordinates of each genotype from the origin of the bi-plot coordinate diagram of the two principal components of the interaction is based on the scores of the first and second for interaction principal component axis (IPCA) model for each genotype. Genotypes with the lowest ASV values are identified by their shortest projection from the bi-plot origin and considered the most stable. Using GE bi-plot displayed based on the AMMI results, the main effect of the genotype, the environment, and

the most significant GEI could be determined. Regarding the AMMI model, the results of the analysis of variance indicated that significant genotype \times environment interaction for all considering physiological traits.

Authors' contributions Conceptualization, ZA and JB; methodology, ZA and JB; software, JB; formal analysis, JB; data curation, ZA and JB; writing—original draft preparation, ZA and JB; writing—review and editing, ZA and JB; visualization, JB. All authors have read and agreed to the published version of the manuscript.

Declarations

Conflict of interest Zahra Abbasi declares that she has no conflict of interest. Jan Bocianowski declares that he has no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

References

1. Abakemal D, Shimelis H, Derera J (2016) Genotype-by-environment interaction and yield stability of quality protein maize hybrids developed from tropical-highland adapted inbred lines. *Euphytica* 209:757–769. <https://doi.org/10.1007/s10681-016-1673-7>
2. Abbasi Z, Majidi MM, Arzani A, Rajabi A, Bocianowski J (2015) Association analysis of morpho-physiological traits with salinity tolerance using SSR markers in sugar beet (*Beta vulgaris* L.). *Euphytica* 205:785–797. <https://doi.org/10.1007/s10681-015-1408-1>
3. Annicchiarico P (2007) Wide-versus specific-adaptation strategy for lucerne breeding in northern Italy. *Theor Appl Genet* 114:647–657. <https://doi.org/10.1007/s00122-006-0465-1>
4. Baker RJ (1988) Tests for crossover genotype-environmental interactions. *Can J Plant Sci* 68:405–410. <https://doi.org/10.4141/cjps88-051>
5. Bocianowski J, Niemann J, Nowosad K (2019) Genotype-by-environment interaction for seed quality traits in interspecific cross-derived *Brassica* lines using additive main effects and multiplicative interaction model. *Euphytica* 215:7. <https://doi.org/10.1007/s10681-018-2328-7>
6. Bocianowski J, Nowosad K, Szulc P (2019) Soil tillage methods by years interaction for harvest index of maize (*Zea mays* L.) using additive main effects and multiplicative interaction model. *Acta Agric Scand B Soil Plant Sci* 69(1):75–81. <https://doi.org/10.1080/09064710.2018.1502343>

7. Bocianowski J, Warzecha T, Nowosad K, Bathelt R (2019) Genotype by environment interaction using AMMI model and estimation of additive and epistasis gene effects for 1000-kernel weight in spring barley (*Hordeum vulgare* L.). *J Appl Genet* 60(2):127–135. <https://doi.org/10.1007/s13353-019-00490-2>
8. Brar NS, Dhillon BS, Saini KS, Sharma PK (2015) Agronomy of sugarbeet cultivation—A review. *Agricul Rev* 36(3):184–197. <https://doi.org/10.5958/0976-0741.2015.00022.7>
9. Comstock RE, Robinson HF (1952) Estimation of average dominance of genes. In: Gowen JW (ed) *Heterosis*. Iowa State College Press, Ames, pp 494–516
10. Crossa J, Cornelius PL, Yan W (2001) Biplot of linear-bilinear models for studying crossover genotype \times environment interaction. *Crop Sci* 41:158–163. <https://doi.org/10.2135/cropsci2002.6190>
11. Edwards JW (2016) Genotype \times environment interaction for plant density response in maize (*Zea mays* L.). *Crop Sci* 56:1493–1505. <https://doi.org/10.2135/cropsci2015.07.0408>
12. Farshadfar E, Sutka J (2003) Locating QTLs controlling adaptation in wheat using AMMI model. *Cereal Res Commun* 31:249–256. <https://doi.org/10.1007/BF03543351>
13. Gauch HG, Zobel RW (1990) Imputing missing yield trial data. *Theor Appl Genet* 79:753–761. <https://doi.org/10.1007/BF00224240>
14. Ghareeb ZE, Ibrahim HEA, Elsheikh SRE, Bachoash SMI (2014) Genotype \times environment interaction for characteristics of some sugar beet genotypes. *J Plant Prod* 5(5):853–867. <https://doi.org/10.21608/jpp.2014.55434>
15. Gollob HF (1968) A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika* 33:73–115. <https://doi.org/10.1007/BF02289676>
16. Götz P, Rücknagel J, Wensch-Dorendorf M, Märländer B, Christen O (2017) Crop rotation effects on yield, technological quality and yield stability of sugar beet after 45 trial years. *Eur J Agron* 82:50–59. <https://doi.org/10.1016/j.eja.2016.10.003>
17. 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(4):79. <https://doi.org/10.1007/s10681-018-2160-0>
18. Hoffmann CM, Huijbregts T, van Swaaij N, Jansen R (2009) Impact of different environments in Europe on yield and quality of sugar beet genotypes. *Eur J Agron* 30(1):17–26. <https://doi.org/10.1016/j.eja.2008.06.004>
19. Lin CS, Binns MR (1988) A superiority measure of cultivar performance for cultivar \times location data. *Canad J Plant Sci* 68:193–198. <https://doi.org/10.4141/cjps88-018>
20. Lin CS, Binns MR (1994) Concepts and methods for analyzing regional trial data for cultivar and location selection. *Plant Breed Rev* 12:271–297. <https://doi.org/10.1002/9780470650493.ch10>
21. Malosetti M, Ribaut JM, van Eeuwijk FA (2013) The statistical analysis of multi-environment data: modeling genotype-by-environment interaction and its genetic basis. *Front Physiol* 4(44):1–17. <https://doi.org/10.3389/fphys.2013.00044>
22. Mandel J (1969) The partitioning of interactions in analysis of variance. *J Res Nat Bureau Standards Series B* 73:309–328
23. Mandel J (1971) A new analysis of variance model for non-additive data. *Technometrics* 13:1–18
24. Monteiro F, Frese L, Castro S, Duarte MC, Paulo OS, Loureiro J, Romeiras MM (2018) Genetic and genomic tools to assist sugar beet improvement: the value of the crop wild relatives. *Front Plant Sci* 9:74. <https://doi.org/10.3389/fpls.2018.00074>
25. Mostafavi K, Orazizadeh M, Rajabi A, Ilkaei MN (2018) Stability and adaptability analysis in sugar beet varieties for sugar content using GGE-biplot and AMMI methods. *Bulg J Agric Sci* 24(1):40–45
26. Nowosad K, Liersch A, Popławska W, Bocianowski J (2016) Genotype by environment interaction for seed yield in rapeseed (*Brassica napus* L.) using additive main effects and multiplicative interaction model. *Euphytica* 208:187–194. <https://doi.org/10.1007/s10681-015-1620-z>
27. Nowosad K, Tratwal A, Bocianowski J (2018) Genotype by environment interaction for grain yield in spring barley using additive main effects and multiplicative interaction model. *Cereal Res Commun* 46(4):729–738. <https://doi.org/10.1556/0806.46.2018.046>
28. Purchase JL, Hatting H, van Deventer CS (2000) Genotype \times environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *South African J Plant Soil* 17:101–107. <https://doi.org/10.1080/02571862.2000.10634878>
29. Reinefeld E, Emmerich A, Baumgarten G, Winner C, Beiß U (1974) Zur voraussage des melassezuckers aus rübenanalysen. *Zucker* 27:2–15
30. Rodrigues PC, Malosetti M, Gauch HG, van Eeuwijk FA (2014) A weighted AMMI algorithm to study genotype-by-environment interaction and QTL-by-environment interaction. *Crop Sci* 54(4):1555–1570. <https://doi.org/10.2135/cropsci2013.07.0462>
31. Studnicki M, Lenartowicz T, Noras K, Wójcik-Gront E, Wyszynski Z (2019) Assessment of stability and adaptation patterns of white sugar yield from sugar beet cultivars in temperate climate environments. *Agronomy* 9(7):405. <https://doi.org/10.3390/agronomy9070405>
32. Wu GQ, Feng RJ, Liang N, Yuan HJ, Sun WB (2015) Sodium chloride stimulates growth and alleviates sorbitol-induced osmotic stress in sugar beet seedlings. *Plant Growth Regul* 75:307–316. <https://doi.org/10.1007/s10725-014-9954-4>
33. Yan W (2016) Analysis and handling of G \times E in a practical breeding program. *Crop Sci* 56(5):2106–2118. <https://doi.org/10.2135/cropsci2015.06.0336>
34. Zobel RW, Wright MJ, Gauch HG (1988) Statistical analysis of yield trial. *Agron J* 80:388–393. <https://doi.org/10.2134/agronj1988.00021962008000030002x>

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.