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Genotype by environment interaction components underlying variations in root, sugar and white sugar yield in sugar beet (*Beta vulgaris* L.)

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Abstract The success of plant breeding programs depends on the ability to provide farmers with genotypes with guaranteed superior performance in terms of yield across a range of environmental conditions. We evaluated 49 sugar beet genotypes in four different geographical locations in 2 years aiming to identify stable genotypes with respect to root, sugar and white sugar yields, and to determine discriminating ability of environments for genotype selection and introduce representative environments for yield comparison trials. Combinations of year and location were considered as environment. Statistical analyses including additive main effects and multiplicative interactions (AMMI), genotype main effects and genotype × environment interaction effects (GGE) models and AMMI stability value (ASV) were used to dissect genotype by environment interactions (GEI). Based on raw data, root, sugar and white sugar yields varied from 0.95 to 104.86, 0.15 to 20.81, and 0.09 to 18.45 t/ha across environments, respectively. Based on F-Gollob validation test, three interaction principal components (IPC) were significant for each trait in the AMMI model whereas according to F ratio (F_R) test two significant IPCs were identified for root yield and sugar yield and three for white sugar yield. For model diagnosis, the actual root mean square predictive differences (RMS PD) were estimated based upon 1000 validations and the AMMI-1 model with the smallest RMS PD was identified as the most accurate model with highest predictive accuracy for the three traits. In the GGE biplot model, the first two IPCs accounted for 60.52, 62.9 and 64.69% of the GEI variation for root yield, sugar yield and white sugar yield, respectively. According to the AMMI-1 model, two mega-environments were delineated for root yield and three for sugar yield and white sugar yield. The mega-environments identified had an evident ecological gradient from long growing season to intermediate or short growing season. Environment-focused scaling GGE biplots indicated that two locations (Ekbatan and Zarghan) were the most representative testing environments with discriminating ability for the three traits tested. Environmentally stable genotypes (i.e. G21, G28 and G29) shared common parental lines in their pedigree having resistance to some sugar beet diseases

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(i.e. rhizomania and cyst nematodes). The results of the AMMI model were partly in accord with the results of GGE biplot analysis with respect to mega-environment delineation and winner genotypes. The outcome of this study may assist breeders to save time and costs to identify representative and discriminating environments for root and sugar yield test trials and creates a corner stone for an accelerated genotype selection to be used in sweet-based programs.

Keywords AMMI · GGE biplot · Model diagnosis · Hybrid · Stability · Representativeness · Discriminating ability

Introduction

The sugar beet share in the global sugar market is significant. Exact sugar contents can vary between 12 and 21%, depending on genotype of the cultivar and growing conditions (FAO 2009; Biancardi et al. 2010). Based on genotype, sugar beet can differ in yield and quality traits. These are additionally modified by biotic and non-biotic parameters of the environment (Stevanato et al. 2017; Broccanello et al. 2018). The aim of growing many crops is to achieve high and stable yields in different environmental conditions. Although the principal aim of sugar beet breeding programs from 1950 until 1970 was to raise yields, since the early 1970s more emphasis has been placed on increasing the sugar and extractable sugar content (Zimmermann and Zeddies 2002). From this point of view, it is necessary to produce varieties adapted to environmental conditions and pathogens that threaten sugar beet growing areas (Brewbaker 1944; Biancardi et al. 2005). For genetic breeding programs, an inherent difficulty in identifying varieties with superior performance is the interaction of different genotypes with various environmental conditions (Eberhart and Russell 1966). In the last stage of a breeding program ending with cultivar release, where there is a large amount of material available for each advanced genotype, it is possible to characterize each genotype in terms of its stability in coping with different environmental conditions (Cooper and Delacy 1994; Acosta-Pech et al. 2017; Zoric et al. 2017). Genotype by environment interaction (GEI) has a significant effect on the efficiency of crop improvement through plant breeding, largely because it confounds comparisons among genotypes with the test environment and complicates the definition of breeding objectives. It is argued that overcoming these constraints needs a better understanding of the differences in plant adaptation associated with variations in the performance and in particular the GEI (Xu 2016). GEI complicates the process of genotype selection and superior performance. Multi environment trials (MET) are widely used by plant breeders to evaluate different aspects of the GEI puzzle (Finaly and Wilkinson 1963; Eberhart and Russell 1966; Perkins and Jinks 1968).

Many tools have been used to characterize environments and discriminate stable from unstable genotypes in different crops (Phuke et al. 2017). Regression-based and multivariate statistical analyses are certainly the most popular methods for assessment of yield stability in cultivar release programs. Multivariate statistical analyses provide options to incorporate different reactions of genotypes to environmental conditions. GGE stands for genotype main effect (G) and genotype by environment interaction (GE) method and was developed by Yan (2002) for graphical analysis of MET. METs are widely used by plant breeders to evaluate the relative performance of a genotype for a target environment (Delacy et al. 1996; Akter et al. 2014). The additive main effects and multiplicative interaction (AMMI) model is the other most widely used statistical method (Gauch 1992). It can be used to understand the structure of interactions between genotypes and environments. The reason for the extensive use of AMMI is that the model can justify a major part of the total deviation of interaction and differentiate the main interactions from one another (Ebdon and Gauch 2002a, b). Yan et al. (2007) concluded that both GGE biplot and AMMI analyses combine rather than separate G and GE in mega-environment analysis and genotype evaluation.

The most important components of sugar beet yield are root weight and sugar content. The combination of a high root yield and high sugar content gives a higher sugar yield per hectare. At the sugar factory, higher sugar content leads to lower energy consumption during the extraction processes. Sugar beet quality is improved by the increase in sucrose concentration reducing the concentration of impurities such as amino acids, potassium and sodium. These impurities often cause a reduction in extractable sugar. Root yield,

sugar content and yield improvements are the main goals of plant breeders targeting higher sugar production. In GEI studies on sugar beet, different univariate statistical methods have been used (Barocka 1978; Beckett 1982; Campbell and Kern 1982; Ggyllenspetz 1998; Ahmad et al. 2012; Hoberg et al. 2016). In a study, the results of univariate statistical analyses revealed that environment had a significant effect on sugar yield variations irrespective of a non-significant interaction between the variety and environment effects (Hoberg et al. 2016). In another study, the lack of interaction between genotype and harvesting and between genotype and irrigation demonstrated that there was no need to consider the planned harvest date or climatic factors in the growing region for variety choice (Bloch and Hoffmann 2005). Ahmad et al. (2012) used simple statistics for stability analysis of sugar beet varieties for agronomic traits and sugar contents and no multivariate analysis was performed for better understanding of GEI. Liebe and Varrelmann (2016) assessed the effects of environmental variations and type of sugar beet genotypes on pathogens during storage in three consecutive years but no attempt was made to evaluate sugar yield and content. The AMMI model has been used for GEI analysis of sugar yield and content in sugar beet monogerm cultivars and the results indicated that genotype and environment had significant effects on these traits, although only a few genotypes were used for stability analysis (Moradi and Jalilian 2012).

A review of the recent literature shows that few attempts have been made to dissect the effects of GEI on sugar related traits using sophisticated multivariate statistical methods in sugar beet (Hoffmann and Marlander 2005; Ahmad et al. 2012; Moradi and Jalilian 2012). The objectives of this study were therefore to dissect genotype by environment interactions for root yield and sugar yield and content and to assess the stability of different sugar beet varieties under variable geographical conditions. The data from MET have three main objectives that are more accurate to estimate and predict yield based on limited experimental data, to determine yield stability and the pattern of response of genotypes across environments and provide reliable guidance for genotypes selection with respect to agronomic related traits for commercial cultivations (Crossa 1990).

Materials and methods

Plant materials and field trials

Forty-nine sugar beet (*Beta vulgaris* L.) genotypes including 32 new hybrids, five single crosses, seven pollinators and five commercial varieties provided by the Iranian Sugar Beet Seed Institute (www.sbsi.ir) were used in this research (Table 1). All genotypes were evaluated for quantitative and qualitative traits in eight field trials in Iran at the four locations of Ekbatan, Torogh, Miandoab and Zarghan. The same number of replications for the forty-nine genotypes was used in each experiment. Each trial was replicated in two growing seasons. To analyze genotype by environment interactions, combinations of year and location were considered as environmental trials. Standard sugar beet agronomic practices were followed at each site. Deep plowing (40 cm) and distribution of phosphate fertilizer (200–300 kg/ha) were applied in all trials. In the spring, field preparation included shallow plowing, disking and leveling. After leveling, 100–200 kg ha^{-1} urea (46% nitrogen) was distributed, which was determined following soil analysis tests. Each experimental plot consisted of three 8- m rows with 50 cm row spacing. After seedling emergence and at the 4–6 leaf growth stage plants were manually thinned to obtain a density of 85,000–86,000 ha^{-1}. Weed control, pest management and irrigation were practiced according to local standard procedures. The experimental design in each site was a randomized complete block with two replications per genotype. In mid-October, an area of 8 m^2 was harvested from in the middle rows. Twenty-five root samples were randomly pulled out of the soil in each plot. The beets were hand washed and root yield was determined (t/ha). Pulps were prepared and kept frozen in a freezer, then transferred to the laboratory until analysis. After extraction of 26 g pulp and clarifying the extract by acetate (II) lead, different parameters were measured such as sugar content (polarimetric method), sodium and potassium concentration SC (using flame photometry), and amino nitrogen α-N (using Betalyzer). Crude syrup purity was measured by dividing sugar content by brix. The dry matter of each sample was determined through drying a part of pulp at 85 °C for 48 h (Abdollahian-Noghabi et al. 2005).

Table 1 Genotype code, and origin of 49 sugar beet genotypes in 8 environments (2 years and 4 locations) in Iran

Genotype code	Type	Parentage/name	Genotype code	Type	Parentage/name
1	Hybrid	SC MH070 * SHR01-P.12	26	Hybrid	SC MH41 * F-8738
2	Hybrid	SC MH076 * SHR01-P.12	27	Hybrid	(7112*SB36) * F-8738
3	Hybrid	SC MH7 * SHR01-P.12	28	Hybrid	SC MH070 * SB27
4	Hybrid	SC MH41 * SHR01-P.12	29	Hybrid	SC MH076 * SB27
5	Hybrid	SC MH070 * SHR02-P.4	30	Hybrid	SC MH7 * SB27
6	Hybrid	SC MH076 * SHR02-P.4	31	Hybrid	SC MH41 * SB27
7	Hybrid	SC MH7 * SHR02-P.4	32	Hybrid	(7112*SB36) * SB27
8	Hybrid	SC MH41 * SHR02-P.4	33	Pollinator	SHR01-P.12
9	Hybrid	SC MH070 * S1-24	34	Pollinator	SHR02-P.4
10	Hybrid	SC MH076 * S1-24	35	Pollinator	S1-24
11	Hybrid	SC MH7 * S1-24	36	Pollinator	S1-88605
12	Hybrid	SC MH41 * S1-24	37	Pollinator	F-8726
13	Hybrid	SC MH070 * S1-88605	38	Pollinator	F-8738
14	Hybrid	SC MH076 * S1-88605	39	Pollinator	SB 27
15	Hybrid	SC MH7 * S1-88605	40	Single crosses (MS)	SC MH070
16	Hybrid	SC MH41 * S1-88605	41	Single crosses (MS)	SC MH076
17	Hybrid	(7112 * SB36) * S1-88605	42	Single crosses (MS)	SC MH7
18	Hybrid	SC MH070 * F-8726	43	Single crosses (MS)	SC MH41
19	Hybrid	SC MH076 * F-8726	44	Single crosses (MS)	SC (7112 * SB36)
20	Hybrid	SC MH7 * F-8726	45	Check	Pars
21	Hybrid	SC MH41 * F-8726	46	Check	Torbat
22	Hybrid	(7112*SB36) * F-8726	47	Check	Ekbatan
23	Hybrid	SC MH070 * F-8738	48	Check	Tous
24	Hybrid	SC MH076 * F-8738	49	Check	Kermit
25	Hybrid	SC MH7 * F-8738			

SC single cross, *MS* male sterile

Statistical analysis

Descriptive statistics

The resulting sugar beet data set were collected for the repeated experiments in four locations and two growing seasons. The mean, range and standard deviation (STD) were calculated for the three traits tested. These statistics were obtained in Statistical Analysis System (SAS) software. In analysis of variance, the effects of year and location were considered as random and genotype as fixed.

Analysis of AMMI model

The AMMI model (Gauch 1988) was used to dissect variance components contributing towards genotype by environment interactions and the stability of sugar related yield across trials. AMMI combines univariate analysis of variance (ANOVA) and multivariate principal component analysis (PCA). ANOVA model was used to analyze the trait data with main effects of genotype and environment without the interaction, a PCA was then integrated using the standardized residuals. These residuals include the experimental error and effect of the GEI. The analytical model for the ith genotype in the jth environment can be written as (Zobel et al. 1988; Gauch 1992; Yan et al. 2007):

$$Y_{ijr} = \mu + g_i + e_j + b_r(e_j) + \sum_{n=1}^{k} \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij} + \varepsilon_{ij}$$

where Y_{ijr} is the root yield, sugar content or sugar yield of genotype i in environment j for replicate r, μ is the

grand mean, g_i is the deviation of genotype i from the grand mean, e_j is the environment main effect as deviation from μ, λ_k is the singular value for the interaction principal component (IPC) axis k, α_{ik} and γ_{jk} are the genotype and environment IPC scores (i.e. the left and right singular vectors) for axis k, $b_r(e_j)$ is the effect of the block r within the environment j, r is the number of blocks, ρ_{ij} is the residual containing all multiplicative terms not included in the model, n is the number of axes or IPCs retained in the model, and ε_{ijr} is the error under independent and identical distribution assumptions,

$$\varepsilon_{ij} \sim \left(N, \frac{\delta^2}{r}\right)$$

In the AMMI analysis of variance, the number of degrees of freedom (df) for component m was simply defined to be df = g + e − 1 − 2m, where g and e stand number of genotype and environment, respectively (Gollob 1968).

AMMI stability value (ASV) was calculated followed by a formula developed by Purchase et al. (2000):

$$ASV = \sqrt{\left[\left[\frac{SSIPCA-1}{SSIPCA-2}\right](IPCA-1\ score)\right]^2 + IPCA-2\ score}$$

where SSIPCA-1 is the sum of squares for interaction principal component analysis 1 (IPCA-1) and SSIPCA-2 is the sum of squares for IPCA-2.

GGE biplot analysis

A genotype main effect plus genotype environment interaction bi-plot based on MET data visualizes the (i) which-won-where pattern of the MET, (ii) interrelationship among test environments, and (iii) ranking of genotypes based on both mean performance and stability parameters. Proper visualization of such aspects, however, requires appropriate singular value (SV) partitioning between the genotype and environment eigenvectors (Yan 2002). Singular value decomposition (SVD) of the first two PCs was used to fit the GGE bi-plot model (Yan 2002),

$$Y_{ij} = \mu + \beta j + \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

where Y_{ij} is the trait mean for genotype i in environment j, μ is the grand mean, β_j is the main effect of environment j, $\mu + \beta_j$ being the mean yield across all genotypes in environment j, λ_1 and λ_2 are the singular values (SV) for the first and second PCs, respectively, ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC1 and PC2, respectively, η_{1j} and η_{2j} are eigenvectors of environment j for PC1 and PC2, respectively, ε_{ij} is the residual associated with genotype i in environment j. In GGE bi-plot analysis, PC1 scores were plotted against PC2 (Yan and Tinker, 2006). The GGE bi-plot analyses were performed by GENSTAT 12th Edition (GENSTAT 2009). The means of environments and genotypes for sugar related traits were compared using the least significant differences (LSD) test in SAS (V 9.2) software.

Model diagnosis

In the AMMI analysis, model diagnosis and accuracy gain (accurate for predicting the true means) to identify most appropriate AMMI family were performed followed Ebdon and Gauch (2002a, b) and Gacuh (2013) descriptions. The actual root mean square predictive differences (RMS PD) were estimated based upon 392,000 validations with the 392 treatment actual data. The softwares MATMODEL V. 3 (Gauch 2007) and AMMISOFT (Gauch 2013) were used for model diagnosis and accuracy gain. Beside cross validation, the resultant robustness tests including F_R (Cornelius 1993) and Gollob (1968) F-test were used to assess model diagnosis and to identify significant IPCs. The ratio as the yield for AMMI winners within each environment (identified in the first column of AMMI ranks) was calculated by dividing the yield for the overall winner (Gauch 2013).

In the GGE biplot analysis, several considerations were imposed so that a feasible number of mega-environments (or groups of environments) were identified (Yan et al. 2007). By definition, the GGE biplot always displays the most important patterns of the G + GE in GEI analysis. Accordingly, the pattern in the biplot means the adequacy of the biplot. If no pattern is seen it means it means there is no clear pattern in the data. For correct interpretation of the biplot obtained, several parameters including centering, scaling and singular-value partitioning associated with the biplot along with the goodness of fit were imposed according to Yan et al. (2007) descriptions. For the mean versus stability view of the GGE biplot, the data were not scaled but environments were centered (centering = 2) and the biplot was based on

genotype-focused singular value partitioning (SVP = 1). SVP = 1 indicates that the singular value to enhance the suitability of the biplot for comparing the genotypes. In the which-won-where biplot, the data not scaled (scaling = 0), not transformed (transform = 0) and environments centered (centering = 2). To better visualizing the relationship between environments, the biplot was based on environment-focused singular value partitioning (SVP = 2). For the discriminating ability vs. representativeness view of the GGE biplot, the data were not transformed (transform = 0) and not scaled (scaling = 0), environments centered (centering = 2) and the biplot was based on genotype-focused singular partitioning (SVP = 2).

Estimation of heritability

Broad-sense heritability across environments was estimated for each tested trait. Five variance components ($\sigma_e^2, \sigma_g^2, \sigma_{gl}^2, \sigma_{gy}^2, \sigma_{gly}^2$) were estimated using the expected mean squares in combined analysis of variance for each of three traits (Falconer and McKay 1996).

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gy}^2}{y} + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_{gly}^2}{ly} + \frac{\sigma_e^2}{rly}}$$

where $\sigma_e^2, \sigma_g^2, \sigma_{gl}^2, \sigma_{gy}^2, \sigma_{gly}^2$ stand for error variance, genotypic variance, variance of genotype by location interactions, variance of genotype by year interaction and variance of genotype by year by location interaction, respectively. The letters r, l and y stand for number of replications, location and year, respectively.

Results

Meteorology data and variations in traits

The meteorology data revealed that annual average rainfall ranged between 193.6 mm and 462.8 mm demonstrating wide variations between study sites (Table 2). Mean temperature was from 12.5 to 19.13 °C. The lowest temperatures occurred mostly in autumn, varying between − 8.8 and − 23.4 °C. Three soil textures were identified including silt loam, clay loam and silty clay loam. The presence of such variability demonstrates the need to identify stable genotypes with relatively consistent performance across a range of environments.

Descriptive statistics for the traits tested in the eight environments are presented in Table 3. Root yield varied between 4.52 and 96.04 t/ha across environments. The range for sugar yield and white sugar yield were 0.8–18.96 and 0.56–16.66 t/ha, respectively. The heritability estimates were meaningfully high for the three traits.

Predictive accuracy, model diagnosis and AMMI analysis of variance

The results of AMMI analysis indicated that variations in environmental conditions and the GEI significantly affected root, sugar and white sugar yields (Table 4). The share of main variance components in the AMMI model analysis showed that 58.2, 59.7 and 61.63% of the total variation in root yield, white sugar yield and sugar yield data were attributed to the environment component (E), respectively. GEI contributed to 17.87, 16.83 and 19% of the total variation of root yield, sugar yield and white sugar yield, respectively. Genotype had the lowest share in the total variations of the three traits. Results from model diagnosis through cross validation identified AMMI-1 model as having the smallest RMS PD and therefore the best predictive accuracy for root yield (Table 5). This model is more close to true means than the raw data (AMMI-F model). The AMMI gain factor for root yield was 2.39. This accuracy gain amounts the number of replications required to achieve the same predictive accuracy without AMMI. Likewise, the AMMI-1 model had the smallest RMS PD with 1.91 and 6.09 gains for sugar yield and white sugar yield, respectively.

The results of F-tests for determining the best predictive truncated model are displayed in Table 4. The results of F_R test were in accord with the results obtained by Gollob's F-test for white sugar yield where both demonstrated three significant IPCAs. The only discrepancy identified between the results of two F-tests was related to root yield and sugar yield data where three IPCAs were detected as significant in the Gollob's F-test whereas two IPCAs were selected by F_R test.

For the root yield data, the residual mean square was 107 demonstrating GE interaction contains 47% noise statistically. Accordingly, GEI captured 53% signal for root yield data (Table 4). The genotype and

Table 2 Meteorology data, description of the field trial sites and USDA soil classifications

Environment	Location	Year	Altitude (m)	Latitude (°N)	Longitude (°E)	Low temp (°C)	High temp (°C)	Mean temp (°C)	Annual rainfall (mm)	Soil classification[a]
E1	Torogh (Mashhad)	2013	990	36° 16″	59° 38″	− 8.8	39.8	16.1	193.6	Silt loam
E2	Zarghan (Shiraz)	2014	1596	29° 47″	52° 43″	− 15	41.6	19.13	205.5	Silt loam
E3	Miandoab (West Azerbayjan)	2013	1300	36° 58″	46° 03″	− 20	37.4	14.34	197.3	Silt loam
E4	Ekbatan (Hamedan)	2013	1757	34° 52″	48° 32″	− 17.8	39.6	12.5	268.6	Clay loam
E5	Torogh (Mashhad)	2014	990	36° 16″	59° 38″	− 17.4	39.6	15.6	213.2	Silt loam
E6	Zarghan (Shiraz)	2015	1596	29° 47″	52° 43″	− 17	40.2	19.1	340	Silt loam
E7	Miandoab (West Azerbayjan)	2014	1300	36° 58″	46° 03″	− 17.4	39.6	14.86	462.8	Silt Loam
E8	Ekbatan (Hamedan)	2014	1757	34° 52″	48° 32″	− 23.4	39.1	12.8	238.6	Silty clay loam

			Month											
			Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
E1	Temp (°C)	Max	19.6	19.8	27	29.3	36.3	39.8	39.5	39.6	39	35.9	22.7	19.9
		Min	− 8.6	− 0.2	− 8.8	1.3	8.8	15	18.4	11.6	12.5	1.8	− 3.5	− 8.2
		Mean	4.4	7.3	10.9	14.5	21.2	26.9	29.1	26	24.8	15.1	9.7	3.3
	Rain (mm)		6.5	34	58.3	28.2	26.6	0.4	0	2.8	0	26.4	3.2	7.2
E2	Temp (°C)	Max	17.5	20	23.5	31	35.5	40	41.6	41.6	36.6	34.5	21	19.2
		Min	− 15	− 5.6	− 1.8	1	8	11.4	17	10.4	12	3	− 2.4	− 4.4
		Mean	2.1	7.8	13.4	19.4	24.4	30.3	32.6	30.8	27.3	21.5	11.1	8.8
	Rain (mm)		72.3	19.6	15.2	34	0	0	0	0	0	0.6	63.8	0
E3	Temp (°C)	Max	14.8	16.6	23.4	26	30.2	35.4	37.4	37.2	35.6	28.2	20.8	16
		Min	− 10.4	− 6.8	− 6.6	− 1.4	6	7.6	10.8	8.4	2.4	− 1.6	− 1.4	− 20
		Mean	2.7	6.2	10	14.3	18.2	24.6	27.8	26.4	22.6	13.9	9.7	− 4.3
	Rain (mm)		20.6	42.5	9.1	30.6	16.2	0.4	0	4	0	3.8	38.4	31.7
E4	Temp (°C)	Max	14.4	16.7	22.3	24.1	29.8	37.3	39.6	36.8	34.9	28.5	18	15.8
		Min	− 15.7	− 9.6	− 10.5	− 2.4	3	6.8	11.5	11.6	3	− 2.9	− 1.8	− 17.8
		Mean	0.7	3.6	8.2	11.3	15.1	22.3	27.1	25.1	19.9	12.6	7	− 3.4
	Rain (mm)		12.5	4.3	25.3	26.1	23.1	0	0	0	0	11.4	85.3	80.6
E5	Temp (°C)	Max	21.1	21.2	27.1	32.9	37.1	39.6	41.6	39	35.6	28.6	21	18.7
		Min	− 6.6	− 17.4	− 3.4	1	12.1	14.4	16.9	15.8	11.9	− 0.9	− 0.3	− 4.9
		Mean	4.8	1.1	9.1	15.5	23.1	27.7	28.4	27.8	23.8	14.3	7	5.1
	Rain (mm)		5	2.9	73.7	35.1	22.4	4.3	0	0	0	16.9	42.4	10.5
E6	Temp (°C)	Max	21.6	22	22	31.6	37	40.2	40	38.6	37.5	33.5	24.5	22.6
		Min	− 17	− 5.4	− 4.2	4.2	8.6	15	15.8	14.6	9	6.8	− 1.6	− 5
		Mean	8.5	9.7	12.6	20.3	25.1	30.2	30	30.7	24	20.3	11.3	6.5
	Rain (mm)		28	57.2	68.7	0	8.4	0	3.8	0	4	8	85.3	76.3
E7	Temp (°C)	Max	11.8	18	19.8	26.8	31.2	36	39.6	37.2	36.4	26.4	17.6	13.2
		Min	− 17.4	− 11.6	− 1.4	− 4.8	5.2	9.6	11.6	10.6	6	1.4	− 5	− 4.4
		Mean	0.1	2.9	10.1	15	20.6	25.2	28.3	28	23.4	13.7	6.5	4.5
	Rain (mm)		34.1	7	57.1	16.4	22.8	0.9	3.3	0	0.7	133.2	138.9	48.4

Table 2 continued

			Month										
			Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
E8	Temp (°C)	Max	10.5	17	19.7	25.3	30.4	36.9	38.8	39.1	34.6	28.2	17.8	14.4
		Min	− 23.4	− 21.7	− 4.5	− 6.1	3.7	7.4	11.7	11.2	6.9	0.1	− 7.1	− 6.5
		Mean	− 4.1	− 2.5	7.1	12.3	16.7	22.9	26.6	25.8	21	12.4	4.3	2.5
	Rain (mm)		30.1	50	46.3	13.9	27.3	0.4	0.3	0.2	0	31.4	20.3	18.4

[a]Soil types by clay, silt and sand composition as used by the United States Department of Agriculture

Table 3 Variance components and heritability estimates of traits

Traits	Min	Max	Mean	STD	σ_g^2	σ_{yg}^2	σ_{lg}^2	σ_{ylg}^2	H^2
Root yield (t/ha)	4.52	96.04	42.95	19.14	534.79	1.15	21.20	27.17	97.37
Sugar yield (t/ha)	0.80	18.96	7.26	3.49	31.94	0.04	0.74	0.83	98.59
White sugar yield (t/ha)	0.56	16.66	5.87	2.97	23.43	0.02	0.56	0.63	98.60

Min minimum, *Max* maximum, *STD* standard deviation, σ_g^2 variance of genetic, σ_{yg}^2 variance of genetic and years interaction, σ_{lg}^2 variance of genetic and location interaction, σ_{ylg}^2 variance of genetic, year and location interaction, h^2 heritability in broad-sense

environment main effects contain 11 and 0.3% noise for root yield, respectively. For the sugar yield data, GEI, genotype and environment contained 44, 10 and 0.2% noise, respectively. The estimated sum of squares for GEI, environment and genotype effects noise with respect to white sugar yield data were 37.5, 9 and 0.2%, respectively. Accordingly, GE interaction captured 56 and 62.5% signal for sugar yield and white sugar yield data, respectively.

Dissection of GEI mean squares revealed that the first two IPCAs captured 57.68 and 58.19% of the total GEI for root yield and sugar yield, respectively. For white sugar yield, the three significant IPCAs contributed to 75.47% of the total variation of GEI.

AMMI winners and mega environments

The winner genotypes for AMMI model family are listed in IPC1 order (Table 6). Genotypes at the top and bottom in Table 6 have opposite GE interaction patterns. This contrast of genotypes has an evident agricultural interpretation. The results indicated that 43 genotypes never win for root yield and sugar yield. For root yield, AMMI-1 shows G29 won in six environments and G21 in two. Accordingly, two mega-environments was distinguishable for root yield based on AMMI-1. AMMI-4, AMMI-6 and AMMI-F had 5 winners and accordingly these families divided the eight environments into 5 mega-environments with respect to root yield. The results indicated that 42 genotypes never win for white sugar yield in the eight environments tested. According to AMMI-1, the most accurate member of this family, three genotypes won for sugar yield and white sugar yield demonstrating 3 mega-environments identified for these traits.

Table 7 is a ranking table illuminating the top 5 genotypes in each of the environments according to AMMI-1 and AMMI-F. The environments are listed in IPC1 order. Accordingly, those at top and bottom have opposite GE interaction patterns. These models are of particular interest because the first is suited for mega-environment delineation and the later represents the raw data. According to AMMI-1 for root yield data, the first mega-environment comprised of E1, E2, E4, E5, E6 and E8 and the second contained E3 and E7. G29 won in the first mega-environment and G21 in the second. G29 stood third rank in E3. The ratio for G21 was 1.06 and 1.38 in E3 and E7, respectively. Based on AMMI-F, G29 and G21 won only in E5 and E7, respectively. The three mega-environments delineated

Table 4 AMMI analysis of variance and in 49 sugar beet genotypes under 8 environments for root, sugar and white sugar yields

Source	df	Root yield (t/ha)				Sugar yield (t/ha)				White sugar yield (t/ha)			
		MS	Proportion (%)	Noise (%)	F-test Gollob	MS	Proportion (%)	Noise (%)	F.test Gollob	MS	Proportion (%)	Noise (%)	F-test Gollob
Rep/Env	8	1266***	–	–		27.94***	–	–		17.22***	–	–	
Genotype (Gen)	48	766***	11.17	11[a]		24.62***	11.08	10[a]		18.06***	11.3	9[a]	
Environment (Env)	7	27,370***	58.2	0.3[a]		937.27***	61.63	0.2[a]		654.04***	59.7	0.2[a]	
Interactions	336	175***	17.87	47[a]		5.33***	16.83	44[a]		4.34***	19	37.5[a]	
IPCA1	54	369***	33.90	–	3.61***	12.19***	36.75	–	4.38***	10.46***	38.75	–	4.86***
IPCA2	52	269*	23.78	–	2.63***	7.4***	21.44	–	2.65***	5.35***	19.09	–	2.66***
IPCA3	50	–	–	–	1.69**	–	–	–	1.95***	5.14**	17.63	–	2.14***
Residuals	230	107	42.32	42.32[a]		3.26	41.81	41.81[b]		1.99[C]	24.53	24.5[b]	
Error	384	83				2.37				1.63			

	Normality test statistic		
	Root yield	Sugar yield	White sugar yield
Shapiro–Wilk	0.9797 (p value < 0.5543)	0.9796 (p value < 0.5481)	0.966 (p value < 0.1667)
Anderson–Darling	0.3256 (p value < 0.5132)	0.4785 (p value < 0.5481)	0.82 (p value < 0.5905)

Significance of IPCA were tested based on F_R, IPCA: interaction principal component axis

Rep replication

*, ** and *** significant at 0.05, 0.01 and 0.001, respectively

[a]Calculated by [(df × MS error)/SS] × 100

[b]Calculated as SS residual/(Env × Gen SS) × 100

[c]df for white sugar yield residual was 180

Table 5 AMMI model and root mean square predictive difference (RMS PD) of 49 sugar beet genotypes in 8 environments for root, sugar and white sugar yields

Model	DF	RMS PD		
		Root yield (t/ha)	Sugar yield (t/ha)	White sugar yield (t/ha)
AMMI-1	54	13.252	2.146	1.987
AMMI-2	52	13.455	2.217	2.153
AMMI-3	50	13.912	2.284	2.263
AMMI-4	48	14.195	2.326	2.338
AMMI-5	46	14.316	2.337	2.388
AMMI-F	391	14.638	2.380	2.457

AMMI additive main effects and multiplicative interaction, *DF* degree of freedom

Table 6 Winner genotypes in the AMMI model families for root, sugar and white sugar yields

	Genotype		AMMI model family						
			1	2	3	4	5	6	F
Root yield	G32								1
	G49					1		1	
	G48			1	1	1	2	2	2
	G29		6	5	3	2	2	1	1
	G28			1	3	3	3	3	3
	G21		2	1	1	1	1	1	1
		Mega-environment	2	4	4	5	4	5	5
Sugar yield	G48		2	2	2	2	2	2	2
	G49				1	1	2	2	2
	G29		4	4	3	1		1	
	G14								1
	G28			1	1	3	3	2	2
	G21		2	1	1	1	1	1	1
		Mega-environment	3	4	5	5	4	5	5
White sugar yield	G48				1	1	2	2	2
	G47		2	2	3	3	2	2	2
	G28		4	3	1			1	
	G27			1	1	2	2	1	1
	G13								1
	G20			1	1	1	1	1	1
	G49		2	1	1	1	1	1	1
			3	5	6	5	5	6	6

AMMI additive main effects and multiplicative interaction, *F* full model

by AMMI-1 ranks for sugar yield were identical to those identified for white sugar yield. The only discrepancy was the order of E2, E4, E6 and E8 in the second mega-environment. The first mega-environment comprised of E1 and E5, whereas the third comprised of E3 and E7. G29 and G28 were overall winners of AMMI-1 for sugar yield and white sugar yield, respectively. In the AMMI-F, the raw data, 5 of 49 genotypes won first rank for sugar yield. AMMI-1 had three winners, G48, G29 and G21, for sugar yield

Table 7 Ranking genotypes in environments for AMMI1 and AMMIF of 49 sugar beet genotypes in 8 environments for root, sugar and white sugar yields

Root Yield		Ratio	AMMI-1 Ranks					AMMI-F Ranks				
	Environment		1	2	3	4	5	1	2	3	4	5
	E1	1	G29	G30	G48	G49	G32	G48	G29	G30	G4	G24
	E5	1	G29	G30	G28	G48	G49	G29	G49	G28	G22	G31
	E6	1	G29	G30	G28	G48	G49	G28	G14	G36	G39	G29
	E2	1	G29	G28	G30	G48	G49	G28	G30	G14	G4	G31
	E4	1	G29	G28	G30	G48	G14	G32	G49	G28	G29	G17
	E8	1	G29	G28	G30	G14	G22	G48	G29	G31	G45	G22
	E3	1.06	G21	G28	G29	G19	G45	G28	G29	G47	G13	G24
	E7	1.38	G21	G28	G25	G19	G2	G21	G19	G25	G7	G45
Sugar yield	E1	1.07	G48	G30	G29	G49	G31	G48	G30	G29	G24	G32
	E5	1.02	G48	G29	G30	G49	G31	G49	G29	G28	G22	G31
	E6	1	G29	G48	G28	G30	G49	G14	G39	G29	G36	G28
	E4	1	G29	G48	G28	G30	G49	G49	G30	G31	G32	G28
	E2	1	G29	G28	G48	G30	G49	G28	G30	G14	G31	G29
	E8	1	G29	G28	G48	G30	G49	G48	G31	G29	G18	G22
	E3	1.08	G21	G28	G29	G19	G45	G28	G29	G47	G14	G13
	E7	1.4	G21	G19	G28	G25	G45	G21	G19	G25	G7	G45
White Sugar Yield	E5	1.09	G47	G48	G28	G29	G30	G48	G27	G28	G21	G30
	E1	1.08	G47	G48	G28	G29	G30	G47	G29	G28	G23	G31
	E4	1	G28	G47	G27	G48	G29	G48	G29	G47	G30	G27
	E8	1	G28	G47	G27	G48	G29	G47	G28	G30	G17	G48
	E6	1	G28	G27	G47	G48	G29	G13	G28	G38	G35	G30
	E2	1	G28	G27	G47	G20	G13	G49	G27	G29	G13	G30
	E3	1.11	G49	G20	G27	G28	G18	G27	G28	G13	G46	G3
	E7	1.44	G49	G20	G18	G27	G44	G20	G18	G6	G24	G44

AMMI additive main effects and multiplicative interactions, *E* environment, *F* full, *G* genotype, each mega-environment is separated by blank lines

and three; G47, G28 and G49, for white sugar yield. In AMMI-1, G29 also stood second and third AMMI-1 ranks in E5 and E3 for sugar yield, respectively. Among sugar yield AMMI-1 winners, G48 and G21 won only in E1 and E7 according to AMMI-F ranks. G48, stood second AMMI-1 rank in E4 and E6, respectively. According to the AMMI-1 ranks, the overall winner for white sugar yield was G28 being identified first rank in the second mega-environment. Based on AMMI-1 ranks, this genotype also stood third and fourth ranks in the first mega-environment and E3. G47 and G49 won in the first and second mega-environments with respect to white sugar yield. G47 stood second AMMI-1 rank in the second mega-environment.

Results of AMMI-2 family model indicated that G48 had specific adaptation to E1 (Fig. 1). Several genotypes were specifically adapted to E2 (G4, G10,

G26, G29 and G36), E4 (G3, G9, G22 and G23), and E8 (G5 and G18). According to AMMI-2 biplot analysis, E1 (Torogh-2013), E3 (Miandoab-2013) and E7 (Miandoab-2014) and the genotypes G48, G28, G33, G21 and G25 gave the highest contribution to GE interaction for root yield. In the AMMI-2 biplot, the furthest away genotypes indicated that they were more susceptible to the interactive forces of the environment (Miranda et al. 2009). G8, G21, G28 and G48 for sugar yield, G8, G13, G21 and G48 for white sugar yield gave the highest contribution to GE interaction. Accordingly, these genotypes were relatively susceptible to changes in environmental conditions. According to the AMMI-2 family model, G16, G27, G34, G40 and G42 for root yield, G16, G17, G24, G27 and G42 for sugar yield and G3, G9, G17, G35 and G44 for white sugar yield were identified as stable genotypes. E2, E4 and E8 were close to the center of the AMMI-2 biplot for both root and sugar yield and hence were stable environments with respect to these traits. E2, E6 and E8 were stable environments for white sugar yield (Fig. 1). E1, E3 and E7 for root and sugar yields, and E1, E3, E5 and E7 for white sugar yield were identified as unstable environments (Fig. 1).

IPCA scores and stability value (ASV) of the AMMI model for the three traits are presented in Suppl. Tables 1, 2 and 3. G16 had lowest ASV and was accordingly the most stable genotype for root yield, whereas G21 was unstable (Suppl. Table 1). G17 and G42 were stable for sugar yield whereas G48 was unstable (Suppl. Table 2). G48 was likewise unstable for white sugar yield whereas G44 was the most stable genotype (Suppl. Table 3).

GGE biplot: genotypic discriminating ability and representativeness of the test environments

The GGE biplot analysis indicated that the first two of PCs were attributable to 60.52, 62.90 and 64.69% of total GEI variation for root, sugar and white sugar yields, respectively (Figs. 2, 3, 4). Stable genotypes and environments with low IPCA-1 and IPCA-2 scores are near the origin of the GGE biplot graph (Yan and Tinker 2006). Which-won-where GGE biplot graphs are divided by an equality line into sectors in which different mega environments can be detected (Yan and Tinker 2005, 2006). In this study, the equality line divided the test environments into four mega- environments for the studied traits (Figs. 2, 3, 4). For root yield, the first mega environment consisted of E1, whereas the second included E2, E4, E5, E6 and E8 (Fig. 2). The third root yield mega-environment was E3, and E7 was the fourth. E7 was the first sugar yield mega- environment and E3 the second. E2, E4, E5 and E6 and E8 were identified as the third mega- environment for sugar yield and the fourth was E1 (Fig. 3). Likewise, two single environments were the first (E7) and second (E3) mega-environments for white sugar yield. The third (E2, E4, E6, E8) and fourth (E1, E5) mega- environments for white sugar yield were also identified (Fig. 4).

The ability of test environments to discriminate genotypes and representativeness of the environments for root yield are shown in Suppl. Fig. 1. Concentric circles in Suppl. Fig. 1 help visualize the distance between each environment and the ideal environment, "ideal test environment", which is at the center of the concentric circles. Hence, E8 was the best representative environment and had the highest ability for discriminating genotypes with respect to root yield whereas E7 was the poorest. Likewise, E2 and E8 for sugar yield and E2 and E4 for white sugar yield were the best representative and discriminating test environments (Suppl. Figs. 2, 3).

GGE biplot: winners and mega-environments

In the GGE biplot model, the ideal genotype might have the highest mean performance stability (Yan and Kang 2003). Although such a genotype may not exist in reality, it can be used as a reference for evaluation of genotype. If a genotype is closer to the ideal genotype, it becomes more desirable than others that are located further away. The concentric circles in GGE biplot for genotype-focused scaling help to identify an ideal genotype for a trait of interest. The average environment coordination (AEC) view of GGE biplot indicated that G29 (SC MH076 * SB27) was closest to the ideal genotype and was accordingly identified as the most desirable genotype with respect to root yield (Suppl. Fig. 4). G28 was the next nearest to the ideal genotype and accordingly may be considered as the second desirable genotype for higher root yield. Although G34, G35 and G40 were low yielding genotypes they were highly stable as positioned on the AEC abscissa. Likewise, G28 and G29 were located at the center of the concentric circles of AEC view of GGE biplot and were accordingly the most desirable

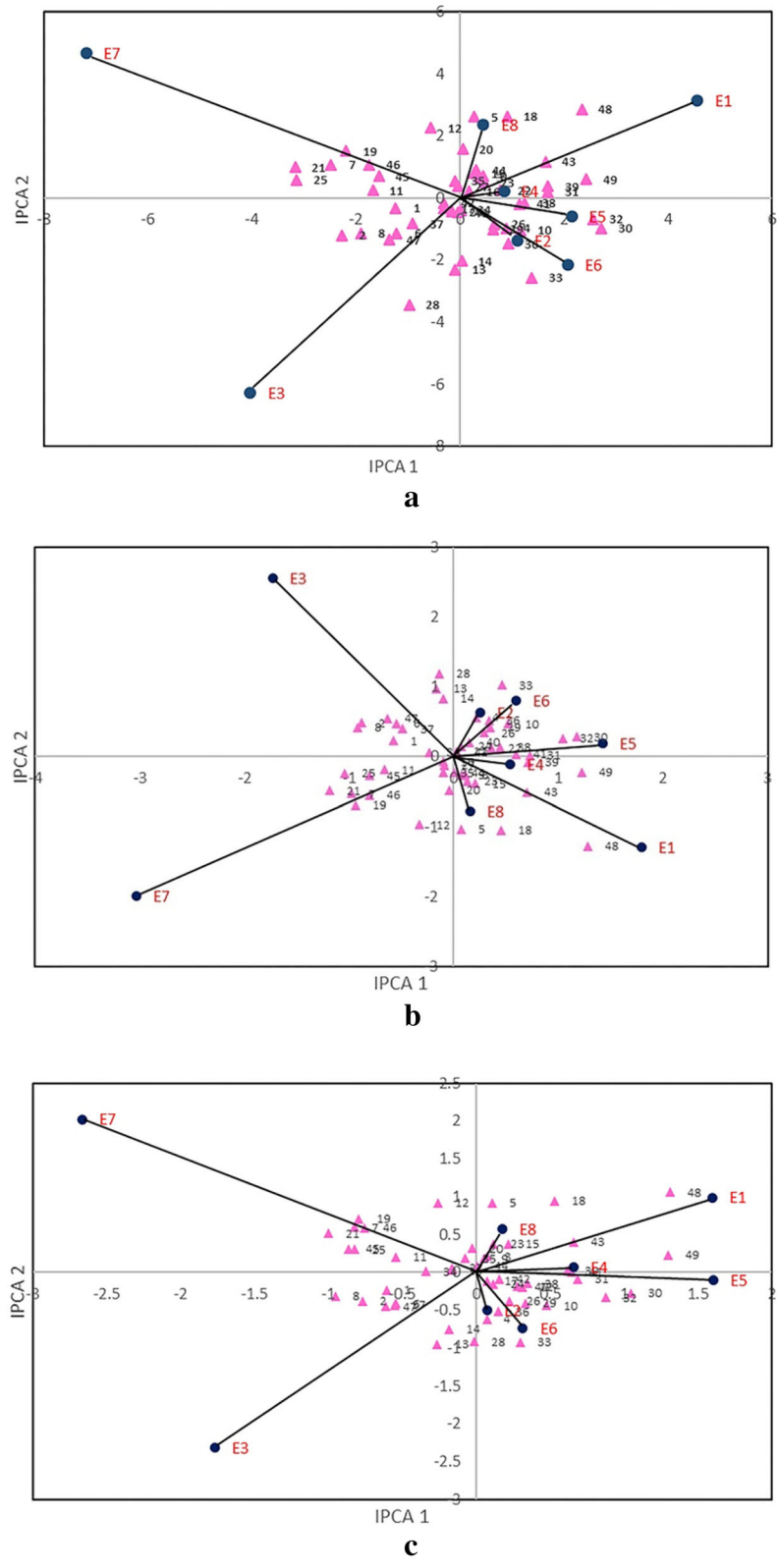

Fig. 1 AMMI-2 biplot for root yield (**a**), sugar yield (**b**) and white sugar yield (**c**), of 49 sugar beet genotypes (G) and 8 environments (E)

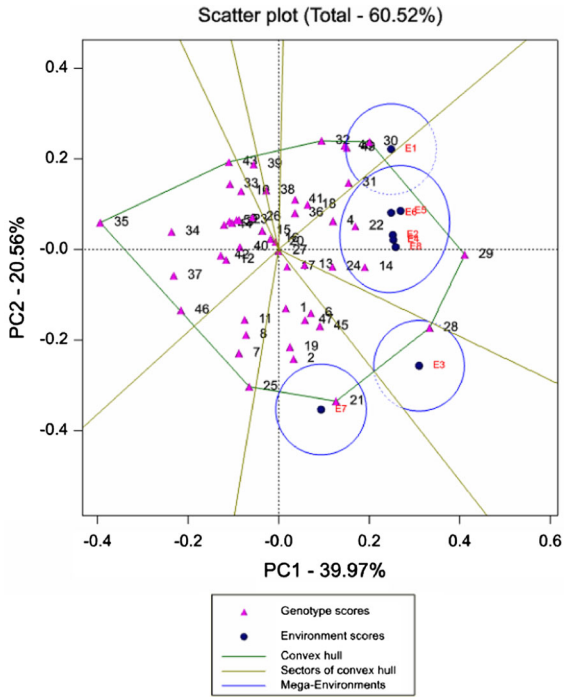

Fig. 2 Which-won-where polygon view of the GGE biplot for root yield of 49 sugar beet genotypes (G) in 8 environments (E) to show which genotype performed best in which environment and meaningful mega environment. The perpendicular of the polygon facilitates visual comparison of the distance between genotypes and environments. Different mega environments are located in different biplot sectors

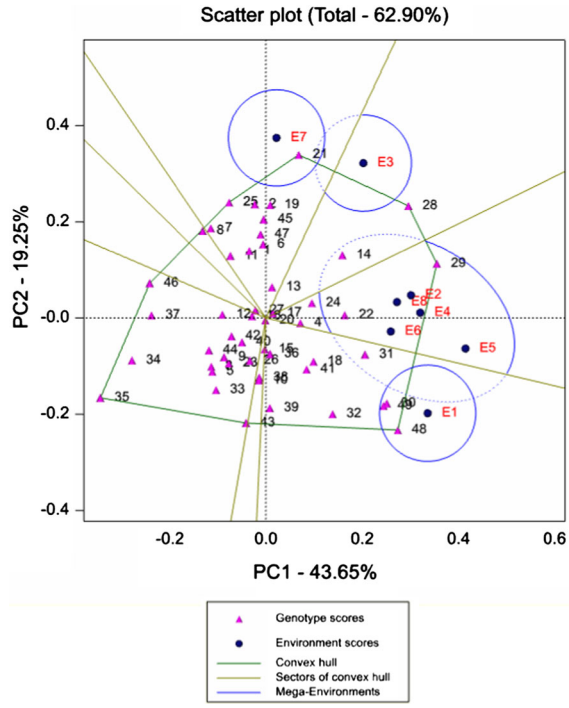

Fig. 3 Which-won-where polygon view of the GGE biplot for sugar yield of 49 sugar beet genotypes (G) in 8 environments (E) to show which genotype performed best in which environment and meaningful mega environment. The perpendicular of the polygon facilitates visual comparison of the distance between genotypes and environments. Different mega environments are located in different biplot sectors

genotypes for both sugar and white sugar yield traits (Suppl. Figs. 5, 6). Instead, G30, G48 and G49 were deemed unstable for these two traits as they were far from the AEC abscissa although they were high yielding.

Environmental means and correlations

Mean comparison of the environments showed that E4 and E5 yielded significantly higher root and sugar with respect to the grand mean (Suppl. Tables 1 and 2). E5 showed the highest mean for white sugar yield (Suppl. Table 3). E8 for root and sugar yields and E2 for white sugar yield had lower IPCA-1 showing that these environments were more stable for these traits because low IPCA-1 score means higher environmental stability (Yan and Tinker 2006; Jamshidmoghaddam and Pourdad 2013). Analysis of correlation between environments with respect to each trait indicated that E2 and E6 (r = 0.70**), and E4 and E8 (r = 0.69**) had relatively stronger correlations for root yield (Suppl. Table 4). Likewise, these two environments showed stronger correlations for sugar and white sugar yields.

Discussion

Genotype by environment interaction is one of the unifying challenges facing plant breeders (Lin and Binns 1988, 1994). Many agriculturally important traits are affected by external factors at some time during the life cycle of plants (Kumar et al. 2015). The extent to which genotype by environment interaction affects a trait is an important determinant of the degree of testing over years and locations. The present study aimed to identify environmental stability of sugar beet genotypes with respect to root, sugar and white sugar yields and to understand the factors leading to a good sugar yield phenotype. The experiment was performed

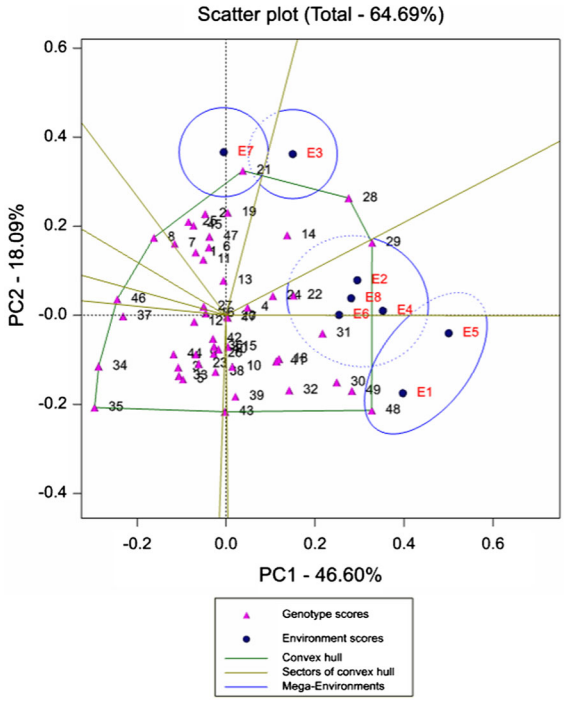

Fig. 4 Which-won-where polygon view of the GGE biplot for white sugar yield of 49 sugar beet genotypes (G) in 8 environments (E) to show which genotype performed best in which environment and meaningful mega environment. The perpendicular of the polygon facilitates visual comparison of the distance between genotypes and environments. Different mega environments are located in different biplot sectors

in eight environmental conditions (combination of location and year). The data were collected from four geographically different locations replicated in 2 years. Descriptive statistics for root, sugar and white sugar yields revealed that wide variations for the three traits exist in the genotypes tested. Although sugar is the primary product of sugar beet little information is available regarding the contribution of environmental conditions to sugar yield variation and analysis of genotype by environment interactions. Improvements in yield and chemical properties of the root by plant breeding continue to increase the amount of white sugar extracted at the processing factories (Dryacott 2006). The biggest breakthrough by plant breeders is the introduction of new cultivars of hybrids allowing higher sugar yield and content under a wide range of environmental conditions. Evaluations of genotypes in different environments must be employed to satisfactorily quantify their performance. Discarding genotypes evaluated in just one environment in the early stages of breeding programs may lead to losing genetic variations because these might do well in another environment. Some useful genes could thus be lost due to limited testing. Including genotype by environment analysis will therefore further improve the progress of genotype selection towards cultivation in a target environment. In the present study, two multivariate statistical analyses including the AMMI and GGE biplot models were used to assess stability of root and sugar yield. The results from the AMMI model for root, sugar and white sugar yields showed that the main components of AMMI analysis of variance: genotype (G), environment (E) and their interactions (GEI) were significant. In the AMMI model, 58.20% of the total sum of squares was attributable to the environment component, indicating the significant effect of environmental variables on changes in root yield. Likewise, environment components gave the largest contribution to the total variation of sugar and white sugar yields. Similar results from other studies indicate the large proportion of environmental conditions in the total variation of GEI with respect to yellow passion fruit and durum wheat (Oliviera et al. 2014; Bassi and Sanchez-Garcia 2017). In the present study, the first two IPC (IPCA-1 and IPCA-2) for the interaction component cumulatively contributed to higher than 55 and 60% of the total variation of GEI for each trait in the AMMI and GGE biplot models, respectively. But, in a study with soybean, the results revealed that the AMMI model was better than the GGE biplot at retaining the greatest amount of variation in the first two principal components (Sousa et al. 2015). In another study with soybean, a genotype-by-trait biplot explained 52–63% of total variation of the data in the GGE biplot analysis (Yan and Rajcan 2002). Dissection of genotype by environment interaction component in barley showed that the IPCA-1 and IPCA-2 were cumulatively contributed to 61.07% of the GEI variance with respect to grain yield data (Kiliç 2014).

Analysis of model diagnosis is required to identify which model family is the best for a given dataset and research objective. Two basic approaches, cross validation and test of hypothesis about the number of components, have evolved to identify the optimal number of multiplicative terms in dissection of GEI mean squares (Gauch and Zobel 1988; Cornelius 1993; Dias and Krzanowski 2003; Gauch 2013). In the present study, the two approaches were used for model

diagnosis and optimizing predictive accuracy of AMMI model families. The results showed that the estimated sum of square (SS) for GEI signals were somewhat larger than IPCA-1 SS for the three traits tested. Accordingly, IPCA-1 was strongly dominated by signal rather than noise. Results of cross validation identified the AMMI-1 model, with the smallest RMS PD, as the best predictive accuracy for the three traits. The aim of achieving maximum predictive accuracy is to balance underfitting real structure and overfitting spurious noise (Gauch and Zobel 1988; Ebdon and Gauch 2002a, b). The AMMI-1 model left residuals SS that are 42.33, 41.81 and 24.5% of the GE interaction for root yield, sugar yield and white sugar yield, respectively; which are close to the target noise. This accuracy gain improves cultivar recommendations. In the Ebdon and Gauch (2002a, b) study, 36.4 and 43.7% noise were estimated for Kentuchy bluegrass and ryegrass data sets, respectively. In our study, distribution of F tests, Gollob's F-test and F_R, came up with different results; indicating two significant IPCs based on F_R test for each of root yield and sugar yield traits and three significant IPCs identified according to Gollob's F-test results. For white sugar yield, the results of both F-tests demonstrated three significant IPCs. In the GEI studies, there is a large discrepancy between the results of different methods used for model diagnosis and predictive accuracy (Vargas and Crossa 2000). In a study, distribution of F-tests indicated two components as optimum whereas the RMS PD estimates demonstrated three or four (Dias and Krzanowski 2003). In another study with GEI in barley, the results of F_R and Gollob's F- tests were relatively similar with respect to significant IPCs but the results of these tests were not in accord with the results obtained by cross validation procedure (Akbarpour et al. 2014). It has been shown that F-test methods are rely on distributional assumptions, normality of data, and some of F-tests, i.e. F_R could be liberal (Akbarpour et al. 2014) or conservative in detection of significant IPCs (Anicchiarico 1997). Here, in our study distribution of the data were normal based on the results of several normality tests; i.e. Shapiro–Wilk (1965) and Anderson–Darling (1954), with respect to the three traits tested (Table 4). Of the two approaches used for model diagnosis, predictive accuracy merits special attention (Gauch 2013). It can be concluded that the three tests for model diagnosis agreed on AMMI-1 for the three traits, whereas AMMI-2 and AMMI-3 were also selected as significant models by F-tests for sugar yield and white sugar yield, respectively. Practical constraints limit the number of workable mega-environments to only 2 or 3 or perhaps a few more which requires a lower AMMI model (AMMI-1 or maybe AMMI-2) than that identified solely by statistical considerations (Gauch 2013). Thereby, this illuminates a tradeoff between statistical and practical considerations might assist choosing appropriate and parsimonious models in GEI studies.

Winners for the AMMI model family identified in this study demonstrated more complex AMMI models have more genotype winners or mega-environments. In the AMMI-0 model, the eight environments tested were distinguished as a mega-environment but, AMMI-0 captures no GEI signal. Five mega-environments were identified according to AMMI-F, a model which captures all noise and signals. Accordingly, a parsimonious intermediate model, i.e. AMMI-1 or AMMI-2 might have the most predictive accuracy (Gauch 2013). Rankings of environments based on IPC scores in the AMMI-1 model demonstrated 2 mega-environments for root yield and 3 for each of sugar yield and white sugar yield traits which are tidy and practical for assessment of GEI trials. The AMMI-1 mega-environments identified have an evident agricultural interpretation with respect ecological gradient from long growing seasons (E1, E5) to intermediate (E2, E4, E6 and E8) and short growing seasons (E3 and E7). The AMMI-1 winners in the short growing seasons outperformed the overall AMMI-1 winner for the three traits. The meteorology data of the environments tested indicated that the long growing season mega-environment had higher mean temperature and lower annual rainfall than the short growing season one. In some studies with GEI, precipitation distribution, temperature differences and relative humidity are known to significantly contribute to total GEI variations (Saeed et al. 1984; Dehghani et al. 2006; Jalata 2011).

Low IPCA-1 scores that are related to stable environments (Yan and Tinker 2006; Naroui Rad et al. 2013) demonstrated E4 (Ekbatan-2013) and E8 (Ekbatan-2014) as being the most stable environments for root yield and E4 (Ekbatan-2013) for both sugar and white sugar yield. Assessment of meteorological and soil data indicates that Ekbatan had a nutrient enriched soil accompanied by suitable weather conditions and it

can be a good candidate for growing sugar beet. Furthermore, E8 (Ekbatan-2014) and E2 (Zarghan-2014) were also stable environments for all traits tested.

The prediction assessment with AMMI has shown that only two IPCs could be the best predictive model in GEI studies (Zobel et al. 1988; Kiliç 2014). The AMMI-2 which is a graphical representation of the IPCA-1 versus IPCA-2 explains the magnitude of interaction of each genotype and environment (Gauch and Zobel 1988). Based on AMMI-2, E2 (Zarghan-2014), E4 (Ekbatan-2013) and E8 (Ekbatan-2014) were stable for root and sugar yield and E2 (Zarghan-2014), E6 (Zarghan-2015) and E8 (Ekbatan-2014) were more stable for white sugar yield. Therefore, E2 (Zarghan-2014), E4 (Ekbatan-2013) and E8 (Ekbatan-2014) and partly E6 (Zarghan-2015) could be good environments for testing sugar beet genotypes. These four environments were also detected as mega-environment according to the truncated AMMI-1 model.

Which-won-where graphs identified through analysis of GGE biplot facilitate the visual comparison of distance between genotypes and environments and helps identify the representativeness of environments and their discriminating ability (Yan and Tinker 2005, 2006). The polygon view of a GGE biplot clearly displays the which-won-where pattern, based on mega-environments that allow breeders to identify discriminating and representative environments which are good test environments for detection of generally adapted genotypes or breeding for adaptation to specific environmental factors (Akinwale et al. 2014; Xu 2016). In addition, by adding mega-environment boundaries, breeders can determine whether a test location is predictive for a given environment or else frequently crosses mega-environment boundaries from year to year (Gauch et al. 2008). Accordingly, analysis of which-won-where GGE biplot in our study revealed that E2 and E6 (Zarghan) and E4 and E8 (Ekbatan) could be considered as a mega-environment for root yield. Environment-focused scaling GGE biplots indicated E8 (Ekbatan- 2014), which was closest to the center of the concentric circles, as an ideal environment for root yield followed by E4 (Ekbatan-2013) and E2 (Zarghan-2014) as the most representative testing environments. E2 (Zarghan-2014) and E4 (Ekbatan-2013) followed by E8 (Ekbatan-2014) were identified as most representative testing environments for sugar and white sugar yields. These results were in accord with the results of the AMMI model analysis. E1 (Torogh-2013) and E7 (Miandoab-2014) were the poorest representative environments although most discriminating for all the traits studied in this research. Assessment of discriminating ability and representativeness of environments are the most important features of the GGE biplot analysis, providing not only valuable but also unbiased information about tested genotypes and environments (Yan and Hunt 2001; Yan and Kang 2003; Abate et al. 2015). From this point of view, a favorable test environment must have high IPCA-1 scores (more discriminating genotypes) and near zero IPCA-2 scores (more representative environment). The results of our GGE bi-plot analysis showed that E2, E4, E8 and partly E6 were the best test environments where the best genotypes could easily be identified with respect to each sugar and root trait. Similar results were obtained based on the AMMI-1 and AMMI-2 family models demonstrating these four environments identified as a mega-environment for sugar and root yield.

According the truncated AMMI-1 model, G29 and G21 for root yield, G48, G29 and G21 for sugar yield, and G47, G28 and G49 for white sugar yield were identified as the first ranked winners. G29 was the overall AMMI-1 winner for root yield and sugar yield with ratio equal 1. Both parents of G29 have shown resistance to rhizomania (www.sbsi.ir). Among AMMI-1 winners, G21 and G28 and G29 have shown resistance to rhizomania in their pedigrees. SB27 which was the common parental line used in production of G28 and G29 has shown resistance to both rhizomania and cyst nematodes diseases (www.sbsi.ir). Hence, crossing hybrids with SB27 might increase root and sugar yields, and also resistance to aforementioned diseases under different environmental conditions. G21 with narrow adaptation to one of mega-environments (E3 and E7) identified in this study outperformed the overall AMMI-1 winner genotype (G29) with respect to root yield and sugar yield. G48 that was a check high yielding variety (www.sbsi.ir), was another AMMI-1 winner for sugar yield outperformed the overall winner in E1 and E5.

Beside multivariate statistics, the AMMI stability value (ASV) assists selection of stable genotypes in the AMMI model. Genotypes with lowest ASV are stable (Naroui Rad et al. 2013). Hence, the results of this study revealed that G16, G17 and G44 with lowest

ASV, were stable genotypes for root, sugar and white sugar yields, respectively. Although G16 and G21 had a common parental line in their pedigree they showed different ASV values. One possible justification for this might be the contribution of different pollinators being used during the improvement of these two genotypes in breeding programs. The results of ASV were partly different from the results of AMMI-1 and somewhat GGE biplot analyses. This is because; IPC scores are used in the ASV formula whereas the AMMI-1 model is based on both the mean of traits and IPC scores. Similar results were found in a study on safflower (Jamshidmoghaddam and Pourdad 2013). The results of ASV scores were in accord with the AMMI-2 family model with respect to stable genotypes.

Winner genotypes were also identified based on the results of GGE biplot analysis. G14, G22 and G29 had specific adaptability to the second mega-environment (E2, E4, E6 and E8) identified for root yield in GGE biplot whereas G28 and G21 adapted to E3 and E7, respectively. According to which-won-where GGE biplot, G21 and G28 had specific adaptability to E7 (Miandoab-2014) and E3 (Miandoab-2013) for sugar yield. This result was partly in accord with results of the truncated AMMI-1 model indicating G21 had narrow adaptation to E3 and E7 as the third mega-environment identified for sugar yield. G28 stood second and third ranks in E3 and E7 in the AMMI-1 model with respect to sugar yield respectively. G14, G22, G29 and G31 in third GGE biplot mega-environment (E2, E4, E5, E6 and E8) and G30, G43 and G48 in E1 had the best sugar yield. Results of a study indicated that the genotype rankings by the GGE biplot and AMMI analyses were significantly correlated in wheat (Roostaei et al. 2014). Identification of mega- environments are important for breeders to verify discriminating and representative environments that could potentially be good test environments to select generally adapted genotypes and breeding for adaptation to specific environmental factors (Akinwale et al. 2014; Xu 2016). G21 was the best specific adapted genotype under E3 and E7 for white sugar yield. The third GGE biplot mega-environment comprised of E2, E4, E6 and E8 with G22, G29 and G31 were identified as the best specific adapted genotypes for white sugar yield. E1 (Torogh-2013) and E5 (Torogh-2014) constituted the fourth mega-environment for white sugar yield and the two G48 and G49 genotypes were superior with respect to this trait. G48 was identified as one of the AMMI-1 first ranked genotypes for sugar yield in E1 and E5 whereas G49 stood fourth rank.

Conclusion

The results of both AMMI and GGE biplot demonstrated that several genotypes had broad and narrow adaptation to environments. G28 for white sugar yield and G29 for root yield and sugar yield were identified as the best genotypes in most environments. Analysis of model diagnosis through cross validation demonstrated the truncated AMMI-1 model as the most accurate model with highest predictive accuracy, although AMMI-2 and AMMI-3 were also detected as significant models based on F_R and Gollob's F-tests. In the GGE biplo, the first two PCs explained large proportion of GEI variations. Results of the AMMI and GGE biplot models were partly in accord with respect to winner genotypes and mega-environment delineation. Most sugar beet lines in the present study were environmentally stable although low yielding. They could therefore be used in the development of stable but moderate yielding hybrids. Due to high heritability estimates, genotype selection might lead to improvement of traits and development of new sugar beet cultivars. Also, significant variations in response of hybrids and lines to the effect of environments show the right choice of experimental sites for genotype by environment interactions assessment. According to AMMI-1, AMMI-2 and GGE biplot based on environment-focused scaling, Zarghan and Ekbatan could be good representative environments for testing sugar beet genotypes. Most sugar beet lines in the present study were low yielding. They can therefore be bred for higher root and sugar content in future breeding programs.

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Compliance with ethical standards

Conflict of interests The authors declare no conflict of interest associated with this publication.

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