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Genetic and phenotypic assessment of quantitative and qualitative characteristics of new sugar beet (*Beta vulgaris* L.) genotypes

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ABSTRACT

This experiment aimed to identify the genetic relationship between sugar beets' quantitative and qualitative traits and their association with sugar yield (WSY). In this study, 13 sugar beet genotypes were grown in a randomised complete block design in Iran's Karaj, Mashhad, Miandoab, Zarghan, and Hamedan stations in the 2022 and 2023 crop seasons. Based on the heat map cluster analysis results in both years, the Genotypes were classified into three groups. Genotypes G5, G6, G7, and G13 exhibited the highest values of sugar yield (SY), sugar content (SC), white sugar content (WSC), WSY, and purity (PUR) compared to other groups. According to the biplot analysis, the first two components accounted for 83.4% and 82.8% of the total data variance. The estimated values of the phenotypic (PCV) and genotypic coefficient of variance (GCV), heritability (h^2b), and genetic advance as a percentage of the mean (GAM) for WSY in the first year were 9.37%, 11.97%, 66%, and 16.3%, and in the second year, were 9.39%, 11.68%, 64%, and 15.55%. In both years, there were positive and significant genetic and phenotypic correlations of WSY with SC, α-amino-N (N), PUR, WSC, and WSY, and negative with alkalinity (ALC) and molasses sugar (MS). In addition to SY's positive genetic and phenotypic direct effect on WSY, traits such as RY, SC, N, PUR, and WSC indirectly showed a positive genetic and phenotypic effect on WSY through this trait. Sodium (Na) had the highest PCV, GCV, heritability, and GAM value; this trait's correlations and direct genetic and phenotypic effects on WSY were negative and significant, so selecting genotypes based on low Na is more effective.

Keywords: biplot, sugar content, heritability, variability

INTRODUCTION

Sugar beet (*Beta vulgaris* L.) is a crucial crop for sugar production (Akyüz and Ersus 2021), accounting for 20-30% of global sugar production after sugarcane (Ribeiro et al., 2016). In 2020-21, global sugar production reached 181 million tons, with 26% of it coming from sugar beet (FAO, 2021). The genetic diversity within different genotypes of the same species can be assessed based on morphological variations. This is because different individuals may have contrasting phenotypes due to contrasting alleles of a gene (Mulusew et al., 2014; Nag et al., 2015; Bhandari et al., 2017).

Diversity in plant genetic resources allows plant breeders to develop new and improved cultivars with desirable characteristics, including farmer-preferred and breeder-preferred traits (Rahman et al., 2016; Bhandari et al., 2017). Genetic variation is crucial for biodiversity. Without it, a population cannot adapt to environmental changes and is more likely to become extinct. Planning a breeding program requires considering the genetic variation and mode of inheritance of quantitative and qualitative traits (Shah et al., 2015; Kumar et al., 2016). Genetic parameters such as genotypic coefficient of

variation (GCV) and phenotypic coefficient of variation (PCV) help detect the variability in the germplasm (Kumar et al., 2019; Upadhyay et al., 2019). Assessing the variability in yield and other characteristics is essential before planning an appropriate breeding strategy for genetic improvement (Kumar et al., 2019).

Various factors, such as polygenes, environmental conditions, and genetic variation, influence crop yields (Usman et al., 2017). Understanding the relationship between crops' inherited traits and their direct and indirect impact on yield is essential for making successful selections in breeding programs (Binodh et al., 2008). Moreover, investigating genotypic and phenotypic correlations among targeted crop plant traits in breeding programs aids in planning, assessing, and creating selection criteria (Tarekegne, 2001). However, selecting for high yield based solely on correlation coefficients, without considering interactions among yield components, may lead breeders astray from their main goals (Majumder et al., 2008). Path coefficient analysis is a statistical technique used to quantify the interrelationship of different components and their direct and indirect effects on yield. Path coefficient analysis allows the partitioning of total correlation into direct and indirect effects, facilitating effective selection (Verty et al., 2017).

Considering these facts, a planned effort was undertaken to evaluate different sugar beet genotypes under Iran's agro-climatic conditions. This information is crucial for selecting better genotypes for breeding programs. A small number of studies have investigated the genetic relationship between quantitative and qualitative traits with white sugar yield. The article innovatively investigates genetic relationships between traits in sugar beets over two years and across multiple environments, a novel approach not previously explored in research. Identifying the exact relationships between traits and evaluating the parameters between them is influential in determining a breeding strategy. Therefore, the current research was designed and implemented to identify the phenotypic and genetic relationships between traits and to identify the most effective trait on WSY.

MATERIALS AND METHODS

Plant materials

This experiment evaluated 13 sugar beet genotypes in Value for Cultivation and Use (VCU) experiments (Table 1). The Iranian Seed Registration and Certification Institute provided seeds of these genotypes to this project. Genotypes with superior quantitative and qualitative traits compared to the control and other genotypes in this experiment are introduced to farmers for cultivation as cultivars.

Table 1. List of the studied sugar beet genotypes

Row	Genotype	Cod
1	G1	F-21370
2	G2	F-21371
3	G3	F-21372
4	G4	F-21373
5	G5	F-21374
6	G6	F-21375
7	G7	F-21376
8	G8	F-21377
9	G9	F-21410
10	G10	F-21411
11	G11	F-21412
12	G12	F-20940
13	G13	F-21092

Research sites and experimental design

The plant materials used in the study were grown in Iran's agricultural research stations located in five provinces: Karaj (Alborz province), Zarghan (Fars province), Miandoab (West Azerbaijan province), Mashhad (Razavi Khorasan Province), and Hamedan (Hamedan province), during two consecutive growing seasons, 2022 and 2023. Genotype evaluation was conducted using a randomized complete block design with four replications at every station. Table 2 presents environmental data of the research stations where trials were located.

Table 2. Geographical characteristics and rainfall of the research stations during the 2022-2023 seasons

Location	Rainfall (mm)	Altitude (m)	Coordinate		Temperature (°C)			Texture
			Longitude	Latitude	Min	Max	Ave	
Karaj - 2022	252.3	1244	50°52´E	35°50´N	10.4	26.5	18.45	Clay-loam
Karaj - 2023	263.7				9.5	27.3	18.4	
Hamedan-2022	261.1	1818	48°30′ E	34°47′ N	5.27	22.9	14.085	Silty-loam
Hamedan-2023	258.3				6.14	28.5	17.32	
Mashhad-2022	214.9	998	60°48´E	35°12´N	12.30	25.7	19	Silty-loam
Mashhad-2023	228.9				10.22	28.8	19.51	
Miandoab-2022	166.8	1294	46°06´E	36°57´N	9.0	25.3	17.15	Silty-loam
Miandoab-2023	258.1				9.5	27.1	18.3	
Shiraz-2022	207.3	1598	52°42´E	29°46´N	11.1	28.9	20	Clay-loam
Shiraz-2023	221.4				10.5	28.5	19.5	

Each genotype was planted in three rows, 8 m long, with a distance of 0.5 m between the rows. The spacing between the plants within the rows was set at 0.2 m. The seeds were sown in mid-April in all locations. Betanal Progress was used to control weeds during the growing season, while diazinon and Avant pesticides were applied early to manage pests, particularly caradrina and fleas. The pesticide Calexin was used in late July and early August to control powdery mildew. Drip irrigation (tape type) was also used in all locations.

Trait measurements

Harvesting occurred in mid-October across all locations. Before the harvest, half-meter margins were removed from the rows' beginning and end. Harvesting was done over an area of 3.5 m^2, and the roots were counted by hand. They were then weighed and considered as the root yield (RY). The collected roots were promptly cleaned and weighed, and then finely ground into a paste using a saw. The brei samples were rapidly frozen at −70 °C and subsequently transported to the Sugar Technology Laboratory, where they were kept at −18 °C. To assess the sugar content, 26 g of the frozen samples were meticulously mixed with 177.8 ml of lead (II) hydroxide acetate, $Pb(C_2H_3O_2)_2$, and blended for 3 minutes using a suitable mixer. As a consequence of this procedure, a transparent liquid was produced, which was subsequently filtered through a sieve to guarantee the elimination of any contaminants. Subsequently, the transparent solution was analysed using the Betalyser device, which enabled precise measurement of SC (sugar content), N (root alpha-amino N content), Na^+ (root sodium content), and K^+ (root potassium content) following the official ICUMSA protocol (Marlander et al. 2003).

The values obtained were used to estimate the quantitative and qualitative characteristics listed below (according to Eqs 1 to 5) (Cooke and Scott 1993).

$$SY = RY \times SC \quad (1)$$

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

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

$$WSY = WSC \times RY \quad (4)$$

$$PUR = (WSC / SC) \times 100 \quad (5)$$

$$ALC = (K^+ Na) / N \quad (7)$$

RY, SY, and WSY = root, sugar, and white sugar yield (t/ha)

SC and WSC = sugar and white sugar content (%)

MS = molasses sugar (%)

K^+, Na^+, and alpha-amino-N are root potassium, sodium, and nitrogen content, respectively (milliequivalents/100 g)

PUR = extraction of sugar coefficient (%)

ALC = Root alkalinity.

Data analysis

Before analysing combined variance, the normal distribution of variables and homogeneity of variance were investigated using Shapiro-Wilk and Bartlett's tests.

The software SAS version 9.4 (SAS Institute Inc., USA) was used to perform analysis of variance (ANOVA) and mean comparison (least significant differences, LSD; $P < 0.05$). Using principal component analysis (PCA) with the FactoMineR package (v.1.34) in R Studio (v. 3.4.4) (http://www.rstudio.com/) followed by conducting hierarchical cluster analysis (HCA) and visualising with a heat map through the ClustVis web tool (Metsalu and Vilo 2015).

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2b), genetic advance (GA), and genetic advance as a percentage of the mean (GAM) were calculated according to the equations (1-5) given by Johnson et al. (1955) and Acquaah (2012) as follow:

$$PCV = \frac{\sqrt{\sigma_P^2}}{\mu} \times 100 \quad (8)$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\mu} \times 100 \quad (9)$$

$$h_b^2 = \frac{\sigma_g^2}{\sigma_P^2} \times 100 \quad (10)$$

$$GA = K \times \sigma_P \times h_b^2 \quad (11)$$

$$GAM = \frac{GA}{\mu} \times 100 \quad (12)$$

where

σ_p^2 = phenotypic variance,

σ_g^2 = genotypic variance,

μ = the mean of the trait,

k = the efficacy of selection, which was 2.06 at 5% selection intensity.

Phenotypic and genotypic correlation coefficients for each pair of traits were computed as described by Singh and Chaudhury (1996) using a variability package in RStudio software.

$$r_{pxy} = \frac{p\,cov_{xy}}{\sqrt{\sigma_{Px}^2 \times \sigma_{Px}^2}} \times 100 \quad (13)$$

$$r_{gxy} = \frac{g\,cov_{xy}}{\sqrt{\sigma_{gx}^2 \times \sigma_{gx}^2}} \times 100 \quad (14)$$

where r_{pxy} = phenotypic correlation coefficient between two attributes (x, y), r_{gxy} = genotypic correlation coefficient between x and y. *Pcov(x,y)* and *Gcov(x,y)* = phenotypic and genotypic covariance between x and y, $\sigma^2_p x$ and $\sigma^2_p y$ = phenotypic variance for traits x and y; $\sigma^2_g x$ and $\sigma^2_g y$ = genotypic variance for traits x and y, respectively.

According to Dewey and Lu's (1959) method, path analysis was conducted to calculate direct and indirect path coefficients based on genotypic correlation coefficients. WSY was treated as the response variable, while the other traits were considered causal or independent variables. All statistical analyses were performed using R software (Lavaan package).

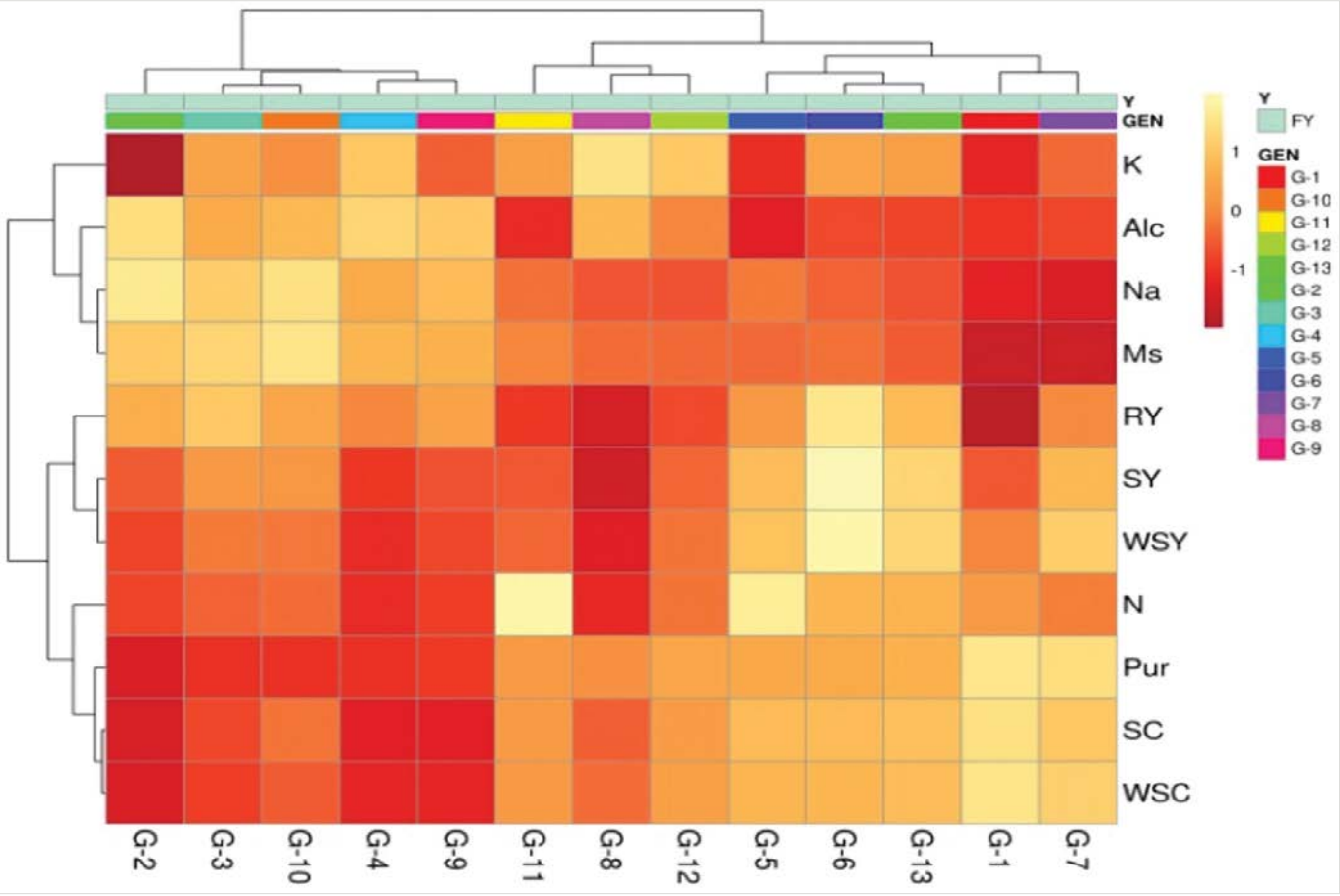
RESULTS

Before conducting a combined variance analysis in two years and five locations, Bartlett's test was performed to check the experimental data error variance uniformity. In this study, the test error was not uniform between the two years in five locations (significance of Bartlett's test). Also, the interaction effect of genotypes with the environment was significant for all investigated traits. Therefore, all analyses of this study were done separately for each year (results not shown).

Hierarchical clustering and Principal component analysis

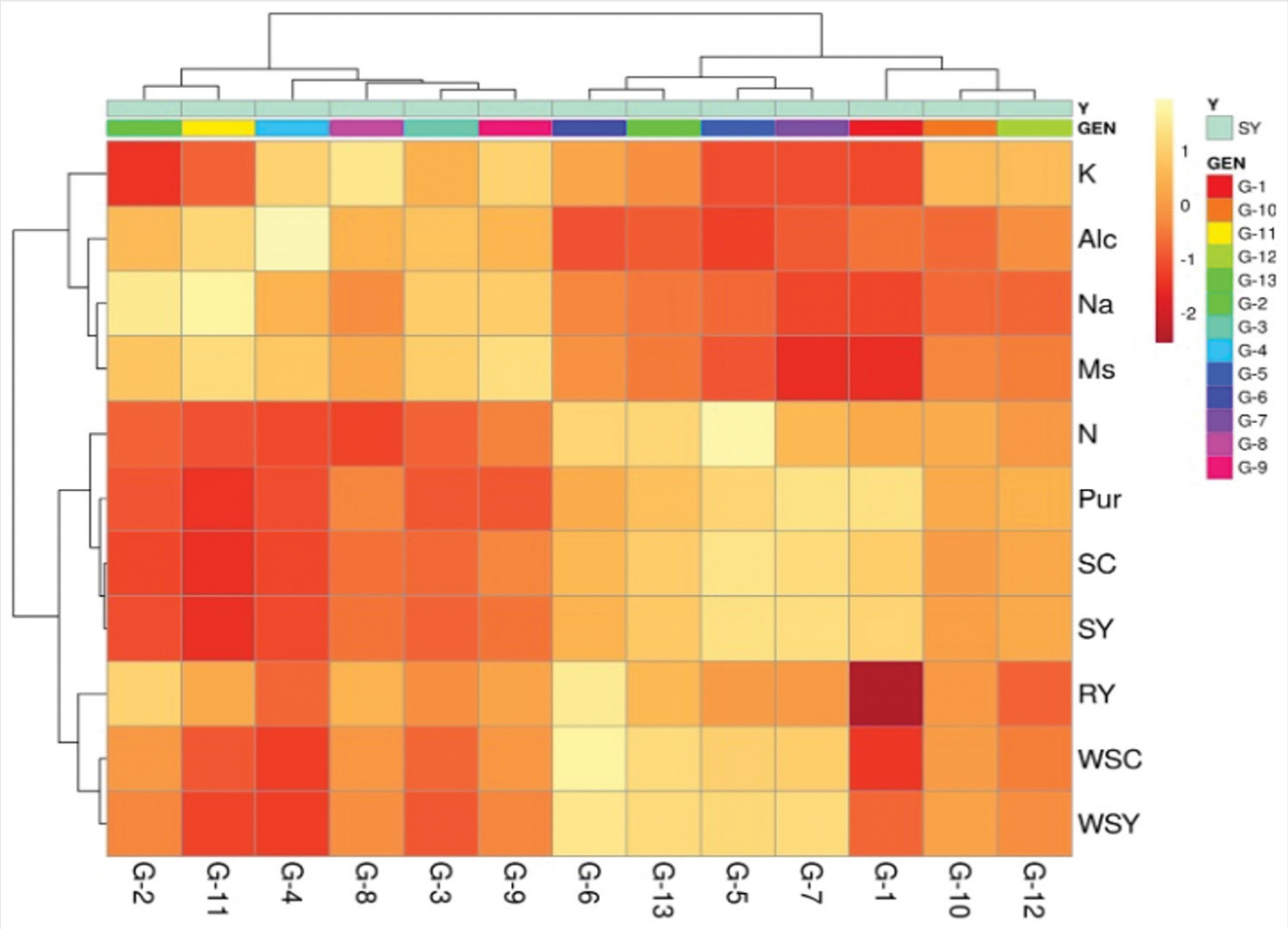
Based on the results of heat map analysis in the first year, genotypes were classified into three groups and traits into two groups (Figure 1). The difference between groups was significant regarding SY ($P < 0.05$) and SC, WSC, WSY, Na, ALC, PUR, and MS ($P < 0.01$) (results not shown). The third group, which included G5, G6, G13, G1, and G7 genotypes, had the highest values of RY, SY, SC, WSC, WSY, and PUR and the lowest values of Na, Alc, and MS compared to other groups. Cluster one obtained the lowest RY, SY, SC, WSC, WSY, and PUR values and the highest Na, ALC, and MS. This Cluster included genotypes G2, G3, G10, G4, and G9. In the first year, traits K, ALC, Na, and MS were in the first cluster, and RY, SY, WSY, N, PUR, SC, and WSC were in the second cluster (Table 3).

In the second year, genotypes and traits were classified into three clusters based on heat map analysis (Figure 2). Variance analysis of the clusters in terms of investigated traits showed that the difference between genotypes was significant in terms of RY, WSC, N, and ALC ($P < 0.05$) and SC, SY, WSY, Na, PUR, and MS ($P < 0.01$) (results not shown). Among the three clusters, the second cluster, which included G6, G5, G7, and G13 genotypes, had high values of RY, SY, SC, WSC, WSY, PUR, and N and low values of Na, Alc, and MS. Also, the first cluster had fewer SC, SY, WSC, WSY, N, and PUR and higher RY, Na, ALC, and MS than the other two clusters (Figure 2). In the second year, K, AC, Na, and MS were in the first cluster, N, PUR, SC, and SY were in the second cluster, and RY, WSY, and WSC were in the third cluster (Table 3).



Note: RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar

Figure 1. Hierarchical clustering analysis and heat map of quantitative and qualitative characteristics of the 13 studied genotypes in the first year and five environments



Note: RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar

Figure 2. Hierarchical clustering analysis and heat map of quantitative and qualitative characteristics of the 13 studied genotypes in the second year and five environments

Based on the biplot analysis, the first two components accounted for 83.4% and 82.8% of the total data variance in the first and second years, respectively. In both years, the first and third zones of the bi-plot were occupied by WSC, WSY, N, SC, SY, and PUR traits. G5, G6, G13, and G7 genotypes were located in this area of the biplot; the placement of these traits and genotypes in the vicinity indicates their close relationship (Figures 3 and 4). The traits ALC, Na, and MS in the first year and K, ALC, Na, and MS in the second year were placed in the first and fourth regions of the bi-plot. In the first year, genotypes G4, G9, G2, G10, and G3 were located near ALC, Na, and MS traits. In the second year, G4, G9, G8, G2, G11, and G3 were located near K, ALC, Na, and MS.

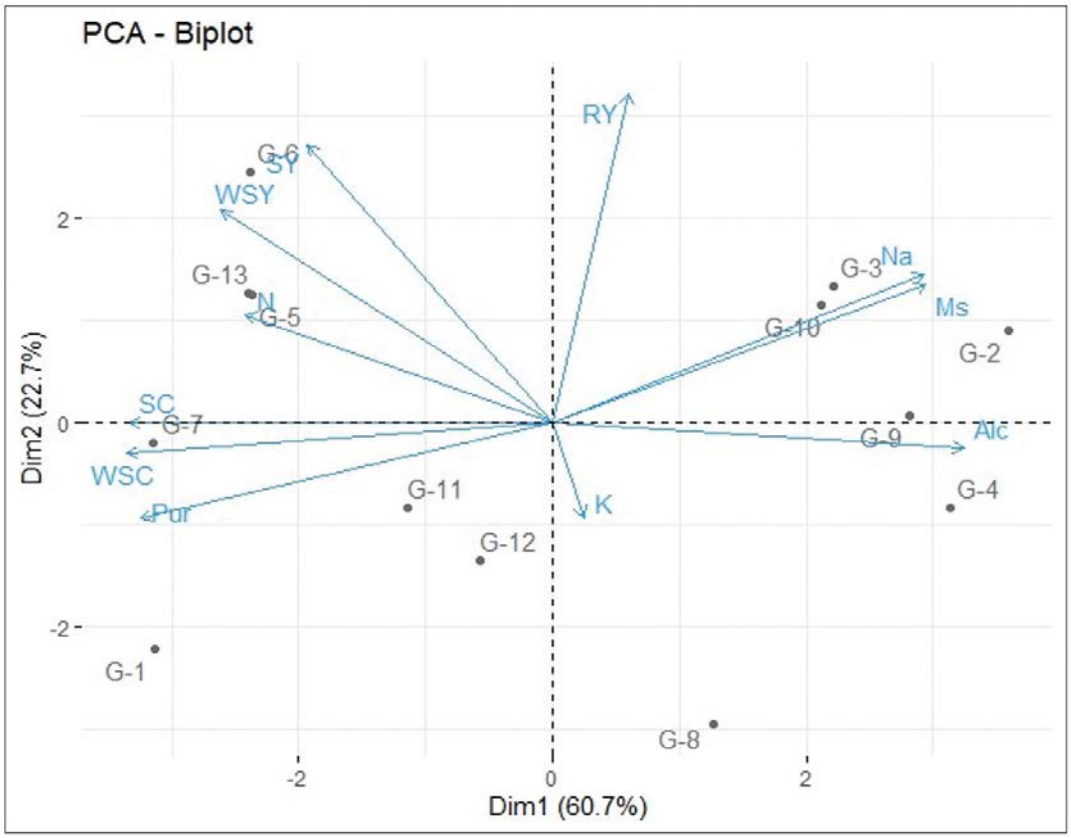
Biplot analysis conducted over two years revealed that the first two components accounted for 87.8% of the variance in the data (Figure 5). Over two years, the genotypes G5, G6, and G13 were positioned in an area of the biplot near the SY, WSY, and N trait vectors (Second region). Genotypes G1, G11, G12, and G7 were located in a different area of the biplot (Third region), adjacent to the vectors for PUR, WSC, and SC traits. Genotypes G10, G2, G3, and G9 were located in a distinct area of the biplot (First region), adjacent to the RY, MS, and Na trait vectors. Finally, Genotypes G8, G11, and G4 were positioned separately in the biplot, close to the K vector (Fourth region).

Table 3. Analysis of variance and mean comparison of groups from cluster analysis for studied traits in the first and second year and five environments

	RY (t/ha)	SC (%)	SY (t/ha)	WSC (%)	WSY (t/ha)	Na (meq/100)	K (meq/100)	N (%)	ALC (%)	PUR (%)	MS (%)
First-year											
Cluster1	88.66^{a}	16.81^{c}	14.88^{b}	13.54^{c}	11.92^{b}	4.37^{a}	4.17	1.44	6.65^{a}	79.35^{c}	2.76^{a}
Cluster2	79.16^{b}	18.02^{b}	14.22^{b}	15.06^{b}	11.88^{b}	2.83^{b}	4.48	1.67	5.19^{b}	83.27^{b}	2.35^{b}
Cluster3	86.66^{a}	19.15^{a}	16.52^{a}	16.38^{a}	14.12^{a}	2.57^{b}	4.13	1.82	4.20^{b}	85.12^{a}	2.16^{b}
Mean	84.82	17.99	15.20	14.99	12.64	3.19	4.26	1.64	5.34	82.58	2.42
Second year											
Cluster1	83.06^{a}	17.16^{b}	14.01^{b}	14.05^{b}	11.41^{b}	3.57^{a}	4.34	1.44^{b}	7.37^{a}	81.26^{b}	2.54^{a}
Cluster2	84.57^{a}	19.02^{a}	16.35^{a}	15.82^{a}	13.53^{a}	2.37^{b}	4.03	1.88^{a}	4.82^{b}	85.73^{a}	2.06^{b}
Cluster3	75.95^{b}	18.32^{a}	15.63^{a}	13.69^{b}	11.60^{b}	2.28^{b}	4.28	1.64^{ab}	5.63^{b}	85.08^{a}	2.09^{b}
Mean	81.09	18.16	15.33	14.52	12.18	2.74	3.35	1.65	5.94	84.02	2.23

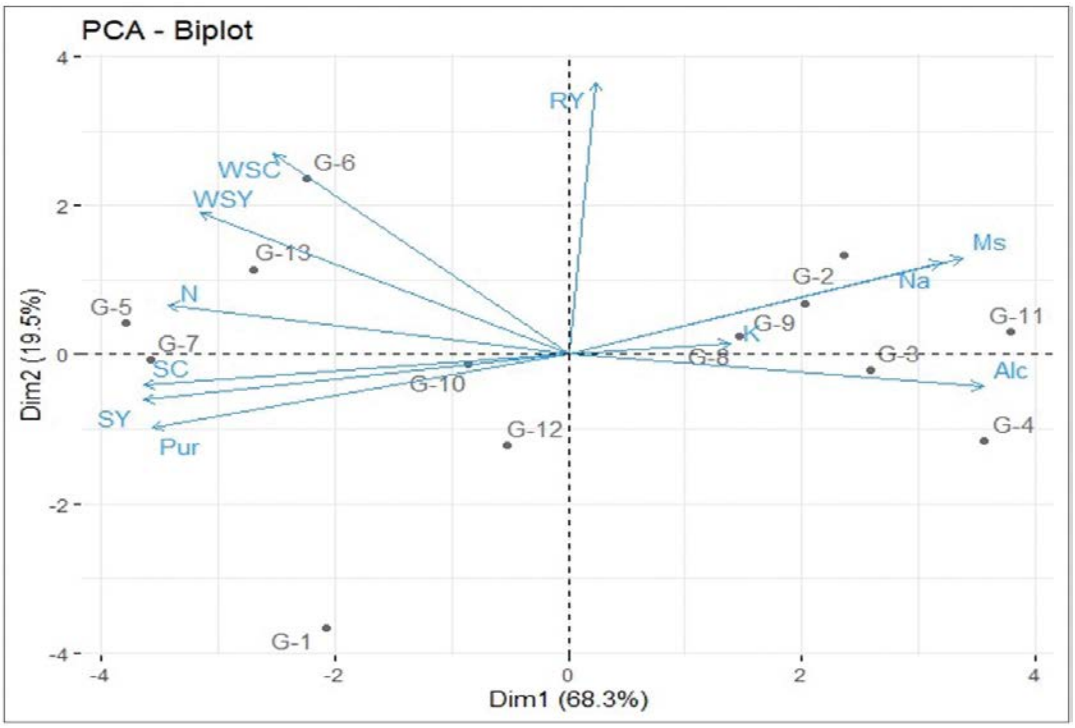
Note: Means in each column, followed by a similar letter(s), are not significantly different at the 5% probability level

RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar.



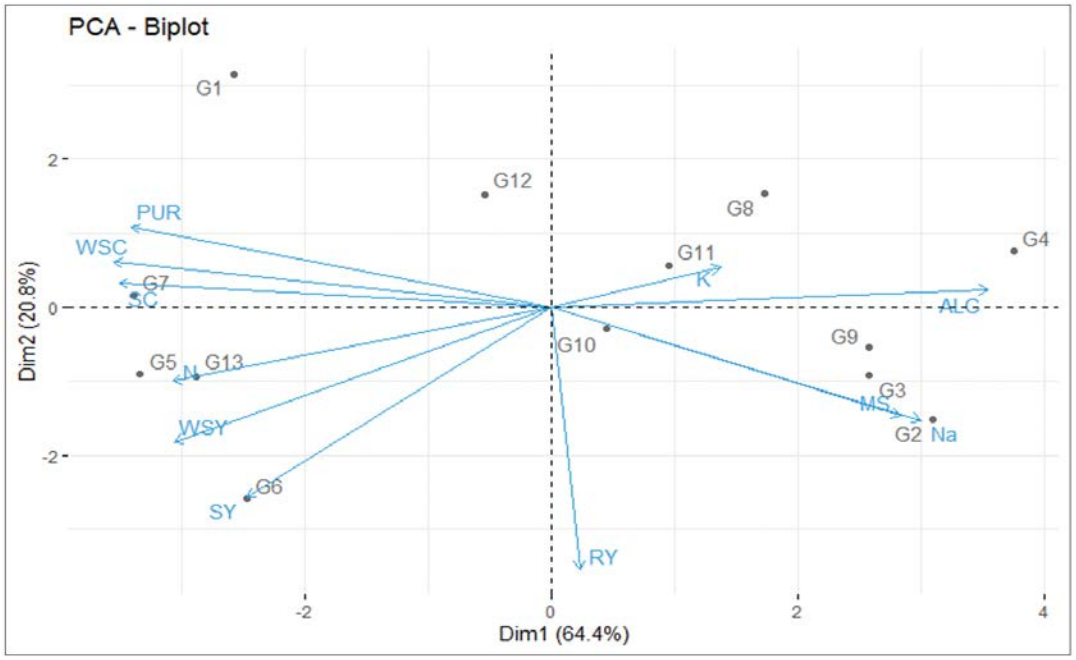
Note: RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar

Figure 3. Principal component analysis (PCA) to elucidate the variable treatment and genotype relationships in the first year and five environments



Note: RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar

Figure 4. Principal component analysis (PCA) to elucidate the variable treatment and genotype relationships in the second year and five environments



Note: RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar

Figure 5. Principal component analysis (PCA) to elucidate the variable treatment and genotype relationships in a total of two years and five environments

Diversity of traits and genetic parameters

Crop breeding success relies on genetic variation and trait inheritance. Analyzing this variation helps breeders improve target traits. The study found that the examined traits had substantial differences in genetic and phenotypic diversity coefficients; all traits had a lower GCV than PCV. Tables 4a and 4b estimate various parameters, such as the σ_e^2, σ_g^2, σ_p^2, ECV, PCV, GCV h^2b, GA, and GAM for eleven investigated traits. Significant genetic and phenotypic diversity was observed in most traits during the first year of examination.

The two traits with the highest and lowest ECV values were N (13.13%) and PUR (1.61%), respectively. The ECV values for RY and WSY were 5.64% and 6.97%, respectively (Table 4a).

Na and ALC had the highest GCV values, with 28.1% and 22.79%, respectively, while PUR and K had the lowest, with 3.32% and 5.61%, respectively.

The GCV values for RY and WSY were 6.56% and 9.73%, respectively. This study documented the highest (30.06%) and lowest (3.69%) PCV values for the Na and PUR traits, respectively. The recorded PCV values for RY and WSY were 8.66% and 11.97%, respectively.

In the second year, sugar beet genotypes had significant phenotypic and genotypic diversity. In this year of the experiment, the ALC and N traits had the highest ECV values of 16.32% and 12.47%, respectively, while the lowest ECV values were observed in PUR and SC traits with 1.13% and 2.94%, respectively. Na and ALC had the highest values (27.65% and 21.44%, respectively),

Table 4a. Estimation of some genetic and phenotypic parameters of measured traits in sugar beet genotypes in the first year and five environments

Parameters	RY	SC	SY	WSC	WSY	Na	K	N	ALC	PUR	MS
Maximum	99.06	19.86	18.73	17.6	16.14	5.37	4.94	2.42	8.15	88.58	3.1
Minimum	72.49	15.46	12.66	12.08	9.94	1.36	3.53	1.12	3.16	76.35	1.65
GM	85.7	17.99	15.36	14.9	12.76	3.32	4.23	1.64	5.37	82.47	2.43
SEm	2.42	0.23	0.47	0.29	0.44	0.17	0.1	0.1	0.33	0.66	0.08
CD5%	6.94	0.68	1.37	0.84	1.27	0.5	0.3	0.3	0.96	1.91	0.23
σ_e^2	23.44	0.22	0.92	0.34	0.79	0.12	0.04	0.04	0.44	1.77	0.02
σ_g^2	31.65	1.27	1.57	1.92	1.54	0.87	0.05	0.06	1.5	7.5	0.09
σ_p^2	55.09	1.5	2.49	2.27	2.33	1.00	0.1	0.11	1.95	9.28	0.11
ECV	5.64	2.64	6.24	3.94	6.97	10.66	5.02	13.13	12.46	1.61	6.65
GCV	6.56	6.27	8.16	9.27	9.73	28.1	5.61	15.5	22.79	3.32	12.33
PCV	8.66	6.81	10.28	10.08	11.97	30.06	7.53	20.31	25.97	3.69	14.01
h^2b	0.57	0.84	0.63	0.84	0.66	0.87	0.55	0.58	0.76	0.8	0.77
GA	8.78	2.14	2.05	2.62	2.08	1.8	0.36	0.4	2.21	5.07	0.54
GAM	10.24	11.91	13.36	17.58	16.3	54.13	8.63	24.37	41.19	6.15	22.36

Note: RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar.

GM = Grand Mean, SEm = Standard Error of Mean, CD 5% = Critical Difference, σ_e^2 = environment variance, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance, ECV = Environmental Coefficient of Variance, GCV = Genotypic Coefficient of Variance, PCV = Phenotypic Coefficient of Variance, h^2b = Heritability (Broad Sense), GA = Genetic Advance, GAM = Genetic Advance as a percentage of the mean.

while PUR and RY had the lowest GCV values (3.17% and 5.77%, respectively). The GCVs of RY and WSY were 5.77% and 9.39%, respectively. The study showed that the highest and lowest PCV values were observed in Na and PUR traits, respectively, with values of 28.57% and 3.37%. The PCV values for RY and WSY were 7.9% and 11.69%, respectively (Table 4b).

Na and WSC had the highest heritability values (87% and 84%), while K and RY traits had the lowest (55% and 57%) in the first year of examination (Table 4a). The estimated h^2b values for RY and WSY were 57% and 66%, respectively. In the second year, the range of h^2b for the studied traits varied from 53% for RY to 93% for Na. The estimated h^2b value for WSY was 64% (Table 4b).

The maximum GA in the first year was recorded for RY (8.78) and PUR (5.07), and the minimum was for K (0.36) and N (0.4). The estimated GA value for WSY was equal to 2.08. Based on the results of this study, Na recorded the highest GAM (54.13%), followed by the ALC trait (41.9%). PUR and K (6.15% and 6.83%) obtained the lowest GAM index values. The GAM values for RY and WSY were estimated to be 10.24% and 16.3%, respectively (Table 4a).

In the second year, the highest and lowest GA values obtained were 7.11 and 0.35 for RY and N, respectively (Table 4b). The GA value estimated for WSY was equal to 1.85. In this study, GAM was the maximum value for Na (55.14%) and the minimum value for PUR (6.15%). The GAM value estimated for RY and WSY was equal to 8.69 and 15.55, respectively.

Table 4b. Estimating some genetic and phenotypic parameters of measured traits of sugar beet genotypes in the second year and five environments

Parameters	RY	SC	SY	WSC	WSY	Na	K	N	ALC	PUR	MS
Maximum	94.2	19.74	16.83	17.06	14.37	4.59	5.28	2.37	12.56	87.68	2.98
Minimum	61.65	15.98	11.74	12.63	9.48	1.8	3.26	1.09	3.87	77.69	1.74
GM	81.77	17.85	14.37	14.92	11.94	3	4.26	1.59	6.38	83.17	2.3
SEm	2.2	0.26	0.46	0.27	0.41	0.1	0.11	0.09	0.52	0.47	0.01
CD5%	6.32	0.75	1.33	0.79	1.19	0.3	0.33	0.28	1.49	1.35	0.17
σ_e^2	19.46	0.27	0.86	0.3	0.68	0.04	0.05	0.03	1.08	0.89	0.05
σ_g^2	22.31	1.07	1.11	1.72	1.25	0.68	0.11	0.05	1.87	6.96	0.04
σ_p^2	41.78	1.35	1.98	2.03	1.94	0.73	0.16	0.09	2.96	7.86	0.1
ECV	5.39	2.94	6.47	3.71	6.95	7.19	5.48	12.47	16.32	1.13	5.35
GCV	5.77	5.8	7.35	8.8	9.39	27.65	7.79	14.23	21.44	3.17	12.52
PCV	7.9	6.5	9.79	9.55	11.68	28.57	9.53	18.92	26.95	3.37	13.52
h^2b	0.53	0.79	0.56	0.84	0.64	0.93	0.66	0.56	0.63	0.88	0.87
GA	7.11	1.9	1.63	2.49	1.85	1.65	0.55	0.35	2.24	5.11	0.52
GAM	8.69	10.65	11.37	16.7	15.55	55.14	13.13	22.04	35.15	6.15	23.77

Note: RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar.

GM = Grand Mean, SEm = Standard Error of Mean, CD 5% = Critical Difference, σ_e^2 = environment variance, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance, ECV = Environmental Coefficient of Variance, GCV = Genotypic Coefficient of Variance, PCV = Phenotypic Coefficient of Variance, h^2b = Heritability (Broad Sense), GA = Genetic Advance, GAM = Genetic Advance as a percentage of the mean.

Genetic and phenotypic correlation

In the first year, there were positive and significant genetic and phenotypic correlations of WSY with RY (r_g=0.39* and r_p=0.57**), SC (r_g=0.77** and r_p=0.68**), N (r_g=0.73** and r_p=0.40*), PUR (r_g=0.59** and r_p=0.56**), WSC (r_g=0.66** and r_p=0.72**) and WSY (r_g=0.95** and r_p=0.96**). On the other hand, there were negative and significant correlations of WSY with AlC (r_g=-0.60** and r_p=-0.78**) and MS (r_g=-0.60** and r_p=-0.88**). The highest positive genetic and phenotypic correlation coefficient (r_g=0.99** and r_p=0.98**) was detected between WSC and SC. Also, the highest genetic and phenotypic negative correlation coefficient (r_g=-0.96** and r_p=-0.94**) was seen between PUR and Na traits (Table 5).

In the second year, there were strong genetic and phenotypic correlations between WSY and RY (r_g=0.44* and r_p=0.58**), SC (r_g=0.80** and r_p=0.73**), N (r_g=0.93** and r_p=0.70**), PUR (r_g=0.70** and r_p=0.64**), SY (r_g=0.95** and r_p=0.96**) and WSC (r_g=0.77** and r_p=0.71**). In addition, there were negative and significant correlations between WSY and ALC (r_g=-0.90** and r_p=-0.77**) and MS (r_g=-0.63** and r_p=-0.52**). The highest positive correlation coefficients were found between WSC and PUR (r_g=0.98** and r_p=0.96**), while the highest negative correlation coefficients were found between PUR and MS traits (r^g=-0.96** and rp=-0.94**) (Table 6).

Table 5. Genetic (top) and phenotypic (bottom) correlation coefficients of investigated traits in the first year and five environments

	cor	RY	SC	Na	K	N	ALC	PUR	WSC	SY	WSY
SC	rg	-0.2^{ns}									
	rp	-0.16^{ns}									
Na	rg	0.33^{ns}	-0.81**								
	rp	0.47*	-0.79**								
K	rg	-0.12^{ns}	-0.05^{ns}	-0.24^{ns}							
	rp	-0.08^{ns}	-0.08^{ns}	-0.10^{ns}							
N	rg	0.05^{ns}	0.75**	-0.21^{ns}	-0.26^{ns}						
	rp	0.01^{ns}	0.52**	-0.48*	-0.04^{ns}						
ALC	rg	0.18^{ns}	-0.96**	0.76**	0.10^{ns}	-0.89**					
	rp	0.09^{ns}	-0.82**	0.67**	0.09^{ns}	-0.83**					
PUR	rg	-0.45*	0.93**	-0.96**	0.04^{ns}	0.59**	-0.89**				
	rp	-0.30^{ns}	0.90**	-0.94**	-0.12^{ns}	0.46*	-0.75**				
WSC	rg	-0.29^{ns}	0.99**	-0.87**	-0.04^{ns}	0.71**	-0.95**	0.97**			
	rp	-0.21^{ns}	0.98**	-0.86**	-0.11^{ns}	0.47*	-0.81**	0.95**			
SY	rg	0.66*	0.57*	-0.18^{ns}	-0.13^{ns}	0.64**	-0.59*	0.33^{ns}	0.51^{ns}		
	rp	0.76**	0.50**	-0.20^{ns}	-0.12^{ns}	0.46*	-0.45*	0.43*	0.46*		
WSY	rg	0.44*	0.77**	-0.35^{ns}	-0.12^{ns}	0.73**	-0.78**	0.59**	0.72**	0.95**	
	rp	0.58**	0.68**	-0.43*	-0.15^{ns}	0.40**	-0.60**	0.56**	0.66**	0.96**	
MS	rg	0.33^{ns}	-0.82**	0.97**	-0.01^{ns}	-0.33^{ns}	0.77**	-0.96**	-0.88**	-0.18^{ns}	-0.46*
		0.35*	-0.78**	0.94**	0.21^{ns}	-0.20^{ns}	0.63**	-0.96**	-0.86**	-0.20^{ns}	-0.45*

Note: ns, * and **: non-significant, significant at 1% and 5% of probability levels
RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY =white sugar yield, MS = molasses sugar

Table 6. Genetic (top) and phenotypic (bottom) correlation coefficients of investigated traits in the second year and five environments

	cor	RY	SC	Na	K	N	ALC	PUR	WSC	SY	WSY
SC	rg	-0.23^{ns}									
	rp	-0.11^{ns}									
Na	rg	0.31^{ns}	-0.88**								
	rp	0.25^{ns}	-0.82**								
K	rg	0.05^{ns}	-0.38^{ns}	0.02^{ns}							
	rp	0.04^{ns}	-0.21^{ns}	0.04^{ns}							
N	rg	0.03^{ns}	0.97**	-0.73**	-0.50^{ns}						
	rp	0.13^{ns}	0.77**	-0.54**	-0.16^{ns}						
ALC	rg	-0.01^{ns}	-0.97 **	0.81**	0.40^{ns}	-0.97 **					
	rp	-0.12^{ns}	-0.78**	0.69**	0.27*	-0.81**					
PUR	rg	-0.35^{ns}	0.97**	-0.93**	-0.35^{ns}	0.90**	-0.93**				
	rp	-0.21^{ns}	0.92**	-0.92**	-0.36**	0.62**	-0.77**				
WSC	rg	-0.27^{ns}	0.99**	-0.90**	-0.39^{ns}	0.95**	-0.96**	0.98**			
	rp	-0.15^{ns}	0.99**	-0.87**	-0.27*	0.73**	-0.79**	0.96**			
SY	rg	0.62**	0.60**	-0.38^{ns}	-0.21^{ns}	0.80**	-0.76**	0.28^{ns}	0.56**		
	rp	0.74**	0.56**	-0.45*	-0.07^{ns}	0.62**	-0.62**	0.43**	0.53**		
WSY	rg	0.39*	0.80**	-0.61**	-0.28^{ns}	0.93**	-0.90**	0.70**	0.77**	0.95**	
	rp	0.57**	0.73**	-0.55**	-0.16^{ns}	0.70**	-0.74**	0.64**	0.71**	0.96**	
MS	rg	0.32^{ns}	-0.90**	0.93**	0.38^{ns}	-0.84**	0.87**	-0.99**	-0.39^{ns}	-0.96**	-0.63**
		0.27^{ns}	-0.79**	0.90**	0.46*	-0.48**	0.69**	-0.96**	-0.44*	-0.86**	-0.52**

Note: ns, * and **: non-significant, significant at 1% and 5% of probability levels
RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY =white sugar yield, MS = molasses sugar

Genetic and phenotypic path analysis

Path analysis was performed on all studied traits to accurately evaluate the internal relationships between traits and divide the correlation of the studied traits with WSY into direct and indirect effects.

In the first year (Table 7), the direct genetic and phenotypic effect of RY on WSY was negative. However, this trait had a positive indirect genetic and phenotypic effect on WSY through SC and SY and a negative indirect genetic and phenotypic effect on WSY through WSC. It is important to note that the indirect genetic effect of RY on WSY was negative through Na and positive through K, ALC, and PUR.

SC had a negative effect on WSY directly from the genetic and phenotypic pathways; this trait showed a positive effect on WSY indirectly through the genetic and phenotypic pathways via RY, WSC, and SY. The study results indicate that SC has a positive indirect genetic effect on WSY through Na and K and a negative impact through N, ALC, PUR, and MS (Table 7).

Table 7. Direct (diagonal) and indirect (off-diagonal) phenotypic and genetic effects of Traits under investigation on WSY of sugar beet genotypes evaluated in the first year and five environments

Trait	Path	RY	SC	Na	K	N	Alc	Pur	WSC	SY	Ms	COR
RY	g	-3.85	1.23	-4.57	0.27	-0.02	0.21	0.79	-1.44	3.54	4.27	0.43
	p	-0.368	0.28	0.16	-0.01	0.00	0.00	-0.04	-0.39	0.98	-0.03	0.58
SC	g	0.85	-5.59	6.96	0.12	-0.23	-1.11	-1.60	4.83	3.08	-6.53	0.78
	p	0.06	-1.74	-0.34	-0.01	0.01	0.00	0.13	1.84	0.65	0.07	0.68
Na	g	-2.05	4.53	-8.58	0.52	0.13	0.88	1.65	-4.24	-0.99	7.70	-0.45
	p	-0.13	1.39	0.43	-0.01	-0.00	-0.00	-0.13	-1.60	-0.26	-0.09	-0.43
K	g	0.49	0.32	2.09	-2.12	0.08	0.12	-0.08	-0.21	-0.73	-0.08	-0.12
	p	0.03	0.143	-0.04	0.12	-0.00	0.00	-0.01	-0.20	-0.15	-0.02	-0.15
N	g	-0.20	-4.23	3.52	0.57	-0.31	-1.03	-1.02	3.45	3.41	-3.43	0.73
	p	-0.00	-0.91	-0.12	-0.00	0.03	0.00	0.05	0.88	0.47	0.02	0.41
Alc	g	-0.69	5.40	-6.58	-0.22	0.28	1.15	1.54	-4.64	-3.17	6.16	-0.77
	p	-0.03	1.43	0.28	0.01	-0.02	-0.00	-0.10	-1.51	-0.59	-0.06	-0.60
Pur	g	1.76	-5.22	8.25	-0.10	-0.18	-1.03	-1.71	4.72	1.79	-7.69	0.59
	p	0.11	-1.58	-0.40	-0.01	0.01	0.00	0.14	1.78	0.43	0.09	0.56
WSC	g	1.14	-5.55	7.47	0.09	-0.22	-1.10	-1.66	4.86	2.72	-7.04	0.71
	p	0.07	-1.72	-0.37	-0.01	0.01	0.00	0.139	1.86	0.59	0.08	0.66
SY	g	-2.57	-3.24	1.61	0.29	-0.20	-0.69	-0.58	2.49	5.32	-1.48	0.95
	p	-0.28	-0.88	-0.08	-0.01	0.012	0.00	0.048	0.85	1.29	0.02	0.96
Ms	g	-2.07	4.60	-8.33	0.02	0.13	0.89	1.66	-4.31	-0.99	7.94	-0.46
	p	-0.12	1.36	0.40	0.02	-0.00	-0.00	-0.14	-1.60	-0.27	-0.09	-0.45

Note: The upper underlined numbers indicate the direct phenotypic effect, and the lower underlined numbers indicate the direct genotypic effect

p = phenotypic effects, g = genotypic effects

RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar

COR: correlation with WSY

The results showed that Na's direct genetic effect on WSY was positive, and its direct phenotypic effect was negative. Na's indirect genetic and phenotypic impact on WSY was positive through the SC pathway and negative through the RY, WSC, and SY pathways.

The indirect genetic effect of Na on WSY from the K, N, Alc, Pur, and Ms pathways was positive, while the indirect phenotypic effects of Na on WSY from the K, Pur, and Ms pathways were negative (Table 7).

In this experiment, K exhibited a negative direct genetic and positive direct phenotypic effects on WSY. The results showed that the indirect genetic and phenotypic effect of K on WSY was positive from the RY and SC pathways and negative from the Pur, WSC, SY, and Ms pathways.The indirect genetic effect of K on WSY from the Na, N, and Alc pathways was positive, while the indirect phenotypic impact of K on WSY from the Na pathway was negative (Table 7).

In this study, N's direct genetic effect on WSY was negative, and its direct phenotypic effect was positive and insignificant. The results showed that N had a negative indirect genetic and phenotypic effect on WSY through SC and a positive indirect genetic and phenotypic effect on WSY through WSC and SY. N showed a positive genetic indirect effect through Na and K, and a negative genetic indirect effect on WSY through RY, ALC, PUR, and MS. Notably, the indirect phenotypic effect of N on WSY through Na was also negative (Table 7).

The results of the present study showed that ALC had a positive direct genetic effect and a (negligible) negative phenotypic effect on WSY. ALC's indirect genetic and phenotypic effects on WSY were positive through SC and negative through RY, WSC, and SY. ALC's indirect genetic and phenotypic effects on WSY were positive through SC and negative through WSC and SY. It should be noted that the indirect genetic effect of ALC on WSY was negative through Na and K, and positive through N, Pur, and Ms. In contrast, the indirect phenotypic effect of ALC on WSY was positive through Na and K, and negative through N, Pur, and Ms (Table 7).

In this research, the direct genetic effect of PUR on WSY was negative, and the direct phenotypic effect of this trait was positive. PUR's genetic and phenotypic indirect effect on WSY was positive through RY, WSC, and SY and negative through SC. It should be noted that PUR had a negative effect genetically and indirectly through K, N, ALC, and MS on WSY and a positive effect through Na. Also, the indirect phenotypic effect of PUR on WSY through Na was negative (Table 7).

WSC had a positive direct genetic and phenotypic effect on WSY. This trait's indirect genetic and phenotypic effect on WSY was positive through SY and RY and negative through SC. The genetic indirect effect of WSC on WSY was positive through the Na pathway and negative through the N, ALC, PUR, and MS pathways. It should be noted that WSC had a positive indirect phenotypic effect on WSY through PUR but a negative impact through Na (Table 7).

In this study, SY had a positive direct genetic and phenotypic effect on WSY, and this trait's indirect genetic and phenotypic effect on WSY was positive through WSC and negative through RY and SC. SY had a positive indirect genetic effect through Na and K, and a negative genetic indirect effect on WSY through N, ALC, PUR, and Ms (Table 7).

Ms directly had a significant positive genetic effect on WAY; the direct phenotypic effect of this trait on WSY was not significant. Ms indirectly had a positive genetic and phenotypic effect through SC and an indirect negative genetic and phenotypic effect through RY, WSC, and SY on WSY. In this investigation, the genetic indirect effect of Ms on WSY was positive from the K, N, ALC, and PUR pathways and negative from the Na pathway. It should be noted that the indirect effect of MS phenotypically on WSY was positive through the Na pathway and negative through the PUR pathway (Table 7).

In the second year (Table 8), the direct genetic and phenotypic effect of RY on WSY was negative. The indirect effect of RY on WSY was positive through SY. Also, the direct genetic effect of RY on WSY was positive through PUR and WSC and negative through SC and Na.

This research showed that SC had a positive direct genetic effect and a negative direct phenotypic effect on WSY. SC's indirect genetic and phenotypic effect on WSY was negative through PUR and positive through RY and SY. Additionally, SC had a positive genetic indirect effect through Na and K, and a negative genetic indirect effect through N and WSC, on WSY. It should be noted that the indirect phenotypic effect of SC on WSY was positive through WSC and Ms (Table 8).

The results showed that Na's direct genetic effect on WSY was negative, and its direct phenotypic effect was positive. In this experiment, the indirect genetic and phenotypic effects of Na on WSY were positive through the Pur pathway and negative through the RY, SY, and Ms pathways. The results indicated that the indirect genetic effect of Na on WSY was positive through the WSC and N pathways, but negative through the SC and K pathways. It is important to note that the indirect phenotypic effect of Na on WSY was positive through the SC pathway, but negative through the WSC pathway (Table 8).

Table 8. Direct (diagonal) and indirect (off-diagonal) phenotypic and genetic effects of traits under investigation on WSY of sugar beet genotypes evaluated in the second year and five environments

Trait	Path	RY	SC	Na	K	N	Alc	Pur	WSC	SY	Ms	COR
RY	g	-0.15	-0.78	-0.50	-0.02	-0.00	0.00	0.11	1.14	0.63	-0.02	0.39
	p	-0.23	0.02	0.00	0.00	-0.00	0.001	0.03	-0.03	0.84	-0.07	0.57
SC	g	0.03	3.38	1.08	0.18	-0.14	0.00	-0.30	-4.10	0.61	0.04	0.80
	p	0.02	-0.18	-0.03	-0.00	-0.01	0.00	-0.14	0.20	0.64	0.22	0.73
Na	g	-0.06	-2.97	-1.22	-0.01	0.10	0.00	0.29	3.71	-0.38	-0.04	-0.61
	p	-0.06	0.15	0.03	0.00	0.00	0.00	0.15	-0.17	-0.39	-0.26	-0.56
K	g	-0.00	-1.31	-0.03	-0.48	0.07	0.00	0.11	1.60	-0.21	-0.02	-0.28
	p	-0.01	0.03	0.00	0.02	0.00	.00	0.05	-0.05	-0.08	-0.13	-0.17
N	g	-0.00	3.28	0.90	0.24	-0.14	0.00	-0.28	-3.92	0.81	0.04	0.94
	p	-0.03	-0.14	-0.02	-0.00	-0.01	0.00	-0.10	0.14	0.71	0.14	0.70
Alc	g	0.00	-3.30	-0.99	-0.19	0.14	0.00	0.29	3.97	-0.77	-0.04	-0.91
	p	0.02	0.14	0.02	0.00	0.01	-0.01	0.12	-0.16	-0.71	-0.20	-0.74
Pur	g	0.05	3.30	1.15	0.17	-0.13	0.00	-0.31	-4.07	0.48	0.05	0.71
	p	0.05	-0.16	-0.03	-0.00	-0.00	0.00	-0.16	0.19	0.49	0.27	0.64
WSC	g	0.04	3.37	1.10	0.19	-0.13	0.00	-0.31	-4.11	0.57	0.05	0.77
	p	0.03	-0.18	-0.03	-0.00	-0.01	0.00	-0.15	0.20	0.60	0.25	0.72
SY	g	-0.09	2.05	0.47	0.10	-0.11	0.00	-0.15	-2.33	1.00	0.02	0.96
	p	-0.17	-0.10	-0.01	-0.00	-0.00	0.00	-0.07	0.10	1.13	0.08	0.97
Ms	g	-0.06	-3.18	-1.14	-0.18	0.12	0.00	0.31	3.96	-0.40	-0.05	-0.64
	p	-0.06	0.14	0.03	0.00	0.00	0.00	0.15	-0.17	-0.34	-0.28	-0.53

Note: The upper underlined numbers indicate the direct phenotypic effect, and the lower underlined numbers indicate the direct genotypic effect
p = phenotypic effects, g = genotypic effects
RY = root yield, SC = sugar content, SY = sugar yield, Na = root sodium content, K = root potassium content, N root alpha-amino N content, PUR = extraction of sugar coefficient, ALC = Root alkalinity, WSY white sugar yield, MS = molasses sugar
COR: correlation with WSY

In this experiment, K exhibited an adverse direct genetic and positive direct phenotypic effects on WSY. The results showed that the indirect genetic and phenotypic impact of K on WSY was positive from the Pur pathways and negative from the SY and Ms pathways.

The indirect genetic effect of K on WSY from the N and WSC pathways was positive, whereas it was negative from the SC, Na, and K pathways. The indirect phenotypic impact of K on WSY from the SC and K pathways was positive, whereas it was negative from the WSC pathway (Table 8).

In this study, the direct genetic and phenotypic effect of N on WSY was negative. The results indicated that the indirect genetic and phenotypic impact of N on WSY was negative through PUR and positive through SY. The genetic indirect effect of N on WSY was positive through SC, Na, and K and negative through WSC. The indirect phenotypic impact of N on WSY was positive through WSC, SY and Ms and negative through SC (Table 8).

Alc's direct phenotypic effect on WSY was negative and insignificant. However, Alc's indirect genetic and phenotypic effect on WSY was positive through Pur and

negative through SY. The indirect genetic effect of ALC on WSY was positive through N and WSC, and negative through SC, Na, and K. It is worth noting that the indirect phenotypic effect of ALC on WSY was positive through SC and negative through WSC and Ms (Table 8).

In the current study, PUR had a negative direct effect on WSY both genetically and phenotypically. The genetic and phenotypic indirect effect of PUR on WSY was positive through RY and SY. In this study, the indirect genetic effect of PUR on WSY was positive through SC, Na, K and Ms and negative through N and WSC. The phenotypic indirect effect of PUR on WSY was positive from the WSC and Ms pathways and negative from the SC pathway (Table 8).

The results indicated that WSC had a negative genetic impact but a positive phenotypic effect on WSY. The genetic and phenotypic indirect effect of WSC on WSY was positive through RY, SY, and Ms and negative through PUR. The genetic indirect effect of WSC on WSY was positive from the SC, Na, and K pathways and negative from the N pathway. It should be noted that the phenotypic indirect effect of WSC on WSY was negative from the SC pathway (Table 8).

SY had a direct positive genetic and phenotypic effect on WSY. The indirect genetic and phenotypic effects of SY on WSY were positive through the RY pathway and negative through the MS pathway. The indirect genetic effect of SY on WSY was positive from the SC, Na, and K pathways and negative from the N, PUR, and WSC pathways. Also, the indirect effect of SY on WSY was positive from the WSC path and negative from the SC paths (Table 8).

In this study, Ms's direct genetic and phenotypic effect on WSY was negative. Ms's genetic and phenotypic indirect effect on WSY was positive from the Pur pathway and negative from the RY and SY pathways. The results showed that Ms's genetic indirect effect on WSY was positive through N and WSC and negative through the SC, Na, and K pathways. Also, the indirect effect of MS on WSY was positive through the SC path and negative through the WSC path (Table 8).

DISCUSSION

The study's results showed that in both years of testing, the genotypes G5, G6, G7, and G13 exhibited the highest values of SY, SC, WSC, WSY, and PUR and the lowest values of Na, ALC, and MS compared to other groups. Thus, the genotypes mentioned have the potential to produce high and stable economic yields in five locations over two years. The results of cluster analysis overlapped with biplot analysis. In both analyses, G5, G6 and G13 were located next to each other and near WSY and SY traits. Genotypes G5, G6, and G13 were found in a region adjacent to the WSY and SY traits over two years and five locations. It can be concluded that the identified genotypes exhibit WSY and SY stability over two years across five regions. Considering the above and the experiment's purpose, genotypes G5, G6, and G13 can be used in future breeding and cultivar introduction programs. Previous studies have used cluster analysis and biplot to group sugar beet genotypes under different conditions (Bassiony et al., 2020; Tayyab et al., 2023; Aycan et al., 2023; Hamze et al., 2024). Najari et al. (2025) classified 18 sugar beet genotypes into three groups based on a heat diagram and seven studied traits into two groups.

In both years of the experiment, the highest and lowest GCV and PCV were recorded for N and PUR, respectively. High variability suggests an appropriate chance to select and improve certain traits or characteristics. The higher PCV compared to GCV indicates that the environment has a more significant influence on the characteristics. A low to moderate level of variability suggests that the base population needs improvement. The genetic variability in breeding materials is essential for selection, and the use of PCV and GCV measures the total variation observed in a trait under evaluation. However, they do not differentiate between the portions of variation that are heritable (genotypic variance) and non-heritable (environmental variance). Numerous studies have shown that there is genetic diversity among different genotypes of sugar beet.)Mohammadian et al., 2024; Ebmeyer et al., 2021; Sadeghzadeh Hemayati et al., 2024(.

The heritability parameter is commonly used to separate phenotypic variation's genetic and environmental components (Regmi et al., 2021). Breeders aim to minimise environmental impact by identifying genes responsible for efficient agronomic traits.

As indicated by Tessema et al. (2022), heritability is classified as low (0–30%), moderate (30– 60%), and high (>60%). In the current study, the heritability value in the first year varied from 55% for K to 87% for Na. In this environment, the estimated heritability for K, RY, and N was moderate; for SY, WSY, ALC, PUR, SC, WSC, and Na, it was high. Heritability changes in the second year varied from 53% for RY to 93% for Na. In this environment, heritability estimates were medium for RY, SY, and N and high for ALC, WSY, K, SC, WSC, MS, and PUR. The estimated heritability values for WSY in the first and second years were 66% and 64%.

The heritability values for RY, SC, SY, WSY, N, and ALC traits were higher in the first year, whereas the heritability values for Na, K, PUR, and MS traits were lower in the first year than in the second year. The change in the heritability of these traits over two years shows the effect of the year on their gene expression. However, the heritability value for WSC remained constant in both years. In this study, Na had high heritability in both environments, which indicated that genetic factors played a more critical role than environmental factors in controlling this trait. This suggests that selection for these traits is highly desirable. The results showed that the estimated heritability for RY was moderate in both years. It can be stated that the role of genetic and environmental factors in controlling this trait is almost the same (Acquaah, 2012). The high general heritability may be attributed to this study's inability to account for the genotype x environment interaction and the uniformity of the test environment (low CV).

GAM reflects the prediction of genetic gain for a specific trait under selection cycles and its stability under selection intensity. Genetic coefficient of variation, heritability, and selection differential determine the impact of this parameter. GAM, which coincides with high heritability, is more valuable than heritability alone in predicting the resultant effect when selecting the best individual genotype revealed in the present study. High heritability characteristics coupled with the moderate genetic advance in per cent of mean offered the scope of the traits for improvement through selection so that these characteristics could be improved more quickly than others (Singh et al., 2016). Abbasi et al. (2019) discovered that the narrow-sense heritability (Hn) estimate for RY, SY, and WSY under optimal conditions was 19.47%, 11.47%, and 10.75%, and under saline conditions was 7.04%, 7.41%, and 8.0%.

Tessema et al. (2022) classified the GAM as low (0-10%), moderate (10-20%), or high (>20%). Accordingly, in the first year, the amount of GAM was low for PUR and K, moderate for RY, SC, SY, WSY, and WSC, and high for MS, N, ALC, and Na. In the second year, GAM values were low for PUR and RY, medium for SC, SY, K, WSY, and WSC, and high for N, MS, ALC, and Na. In our study, Na had the highest genetic and phenotypic diversity and heritability among the 11 traits, with the highest GAM value. Selecting genotypes with low Na content can help obtain germplasm with suitable quality properties. Singh et al. (2018) reported the highest heritability estimate for root yield (94.3%), followed by SRW (94.0%). They also found the highest GA for SRW and RY (41.54%). Ganapati et al. (2015) reported high heritability and genetic advance for days to germination, germination, brix, and yield, except root length in sugarbeet. El Mouhamady et al. (2021) reported high heritability for sugar content, apparent purity, and root yield and moderate heritability for sucrose% and sugar yield in two years. In Rajabi et al.'s (2023) study, the general heritability estimated for all quantitative (RY, SY, and WSY) and qualitative (SC, WSC, Na, K, and ALC) characteristics of sugar beet was high.

In this study, the positive and significant correlation of WSY with SC and PUR is due to the common component of these WSC traits, which increases the mentioned traits. The reason for the positive correlation between WSY and SY is the common component of these two attributes, namely RY, and WSC is also one of the constituent components of WSY, along with RY. The negative correlation between ALC and MS with WSY is due to their

impact on reducing the WSC content. It should be noted that genetic factors played a significant role in creating a strong relationship between the mentioned traits and WSY, and environmental factors could not change this strong relationship.

In the study by Singh et al. (2018), RY showed a positive genetic and phenotypic correlation between SC and PUR. Hassani et al. (2023) found a negative correlation between root yield and key traits such as sugar content, sodium, potassium, and alpha-amino nitrogen.

In the first year, SY had the highest genotypic and phenotypic correlation with WSY. Separating this correlation into direct and indirect effects indicated that this trait's direct genetic effect is far higher than its indirect effect, but the indirect negative effects of SY through some investigated traits, such as RY and SC, reduced this direct effect. Additionally, the division of WSC correlation into direct and indirect effects revealed that the direct impact of this trait was mediated indirectly by genetic and phenotypic effects through other characteristics, such as SC decreasing and SY increasing. Another component of WSY is RY. Although this trait's direct genetic and phenotypic effect on WSY was negative, due to the positive and significant indirect effect, primarily through SC and SY, this trait was finally able to have a genetic positive correlation and phenotype on WSY.

In the second year of the experiment, the highest genotypic and phenotypic correlation was found for the two traits, WSY and SY. In this situation, the indirect and negative effects of traits such as WSC and PUR genetically and traits such as RY and SC phenotypically reduced the direct impact of SY on WSY. In the case of WSC, this trait had a high negative genetic direct effect on WSY. However, this trait moderated this negative direct effect due to indirect positive genetic effects, especially through RY, SC, and SY, and finally had a positive correlation with WSY. The direct phenotypic effect of WSC on WSY was insignificant. However, this trait can eventually have a positive phenotypic correlation with WSY due to the indirect impacts through traits such as SY and MS. In this research, like the experiment in the first year, RY had a direct negative effect on WSY genetically and phenotypically. However, this trait indirectly and through traits such as SY positively affected WSY, which finally showed a positive correlation with WSY.

A study on sugar beets found that four variables, root diameter, SY, MS, and SC, had the highest direct effects on WSY under normal conditions. Additionally, three variables, SC, SY, and MS, directly affected white sugar yield under drought-stress conditions (Baradaran Firouzabadi et al., 2011). Ghaffaria et al.'s study (2020) introduced RY and SC as two traits influencing WSY changes.

CONCLUSION

G5, G6, G7, and G13 genotypes displayed favorable characteristics such as RY, WSC, WSY, N, SC, SY, and PUR with low Na levels in the roots across two years and five regions. It is recommended that these genotypes be chosen in the tested area. There was significant genetic and phenotypic diversity among genotypes regarding the studied traits. This diversity supports a breeding program, enabling the selection of genotypes with desirable characteristics. The current study's results indicate that genetic and environmental factors, as well as the internal relationships between the characteristics, influence the relationship among traits. Therefore, emphasizing correlation coefficients alone does not accurately represent the true relationship between traits. In our study, Na had the highest genetic and phenotypic diversity and heritability among the 11 traits, with the highest GAM value. This trait's phenotypic correlation in the first year and its phenotypic and genotypic correlation in the second year with WSY were negative and significant. In both investigated years, the direct genetic effect of Na on WSY was negative and significant. This trait also showed a negative indirect genetic and phenotypic effect on WSY through RY. Indirect selection of genotypes based on low Na is more effective than direct selection based on WSY.

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