RESEARCH ARTICLE

The Assessment of Sugar Beet Half-sib Families based on some Morphophysiological Traits under Drought Stress Conditions

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Study Area: Karaj & Miandoab Iran
Coordinates: $35°59'N; 51°6'E$ & $36°58'N; 46°90'E$

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Abstract

In order to estimate heritability and relationships among traits, 43 diploid sugar beet half-sib families were evaluated in a randomised complete block design with three replications in two locations (Karaj and Miandoab) in drought stress condition. Results of combined analysis of variance showed that there was significant difference between the two locations in terms of root yield, sugar yield, white sugar yield, alkalinity, chlorophyll content, water use efficiency, specific leaf weight and leaf succulence index. There were also significant differences among genotypes for all traits except potassium content, white sugar yield and specific leaf weight. The genotype by environment interaction was significant only for sodium, potassium, alkalinity and extraction coefficient of sugar. The heritability values estimated for root yield, sugar content, white sugar content, sugar yield, extraction coefficient of sugar, white sugar yield and chlorophyll content were 60.61%, 87.10%, 90.88%, 47.90%, 83.91%, 64.0% and 81.11%, respectively. The highest genetic gain belonged to root yield, extraction coefficient of sugar, chlorophyll content and sugar content, respectively. White sugar yield showed a significant positive correlation with root yield, sugar content, sugar yield, extraction coefficient of sugar, white sugar content, chlorophyll content, water use efficiency and specific leaf weight and significant negative correlation with sodium, potassium, alkalinity and molasses sugar. Furthermore, sugar yield, molasses sugar and white sugar content explained 99% of white sugar yield variation and were identified as the most effective traits on white sugar yield. Finally, based on the results of cluster analysis, 43 sugar beet genotypes were divided into three groups with the superior genotypes being placed in the first cluster.

Introduction:

ISugar beet (*Beta vulgaris* L.) has a high capacity for osmotic adjustment and is tolerant to drought and salinity conditions due to having a long growth period, lack of a susceptible flowering stage and deep rooting system. Drought stress is considered a major problem for successful production of field crops in the world including Iran and is known as the main factor for reduced yield in sugar beet (Ober *et al.*, 2004). There is genetic variation for drought tolerance in sugar beet germplasm (Pidgeon *et al.*, 2006; Abdollahian *et al.*, 2011). Rajabi *et al.* (2013) observed significant differences among sugar beet half-sib families in drought stress and non-stress conditions.

Presence of genetic diversity in breeding populations as the primary material for plant breeding is of special importance, a fact that makes it possible for the plant breeder to compare, group and select desirable genotypes from breeding populations. To estimate the genetic gain for a trait, it is necessary to know the correlation of that trait with the other traits and determine the nature of the

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correlation (Agrama, 1996). When the number of independent variables affecting the dependent variable is high, the extent of interdependence of the traits is limited and so the correlations alone cannot explain the relationships among the traits. When the sources of variation for yield and yield components are identified, it would be possible to enhance the yield potential through plant breeding and/or improved cultural practices (Board *et al.,* 1997).

In plant breeding programs, the selection is done based on several agronomic traits among which there may be positive and significant correlations. Therefore, analyses which reduce the number of traits affecting yield without losing a lot of useful information are valuable for researchers. In this regard, it is common to use correlations among traits but there are limitations in grouping and selecting the superior genotypes. These limitations are mainly due to include various traits in the final selection of genotypes. Therefore, multivariate methods such as path and cluster analyses are able to detect the relationships among traits and facilitate the grouping and selection of the genotypes (Moghadam *et al.,* 1994).

Fotouhi *et al.* (2010) studied the direct and indirect effects of different traits on root yield of sugar beet in salt stress condition and found that Sodium (Na) had direct and negative effect and potassium (K) had direct and positive effect on root yield with 96% of the variation of root yield being explained by Na, K, green crop cover and number of plants. Ouda Sohier (2005) introduced root yield and sugar content as the traits with the highest influence on sugar yield. Sharifi (2014) studied the correlation and path analysis of white sugar yield with some traits under irrigation regimes in sugar beet and found that sugar content, Na, extraction coefficient of sugar and canopy temperature in the first order and leaf osmotic potential in the second order had high correlations with white sugar yield. None of these traits had the significant correlation with white sugar yield in severe stress condition. Also, their path analysis showed that in non-stress condition, sugar content, extraction coefficient of sugar and canopy temperature had a high direct effect on white sugar yield.

Rajabi *et al.* (2014) used multivariate analysis for yield and quality traits of sugar beet in drought stress condition and classified the genotypes into four groups among which the one group was found to be superior with respect to yield and quality. Ghasemi *et al.* (2010) found a genetic variation for morphological and physiological traits in sugar beet as revealed by cluster analysis. They assigned the difference between the results of cluster analysis and means comparisons to the likely unequal contribution of the measured traits to white sugar yield.

Rajabi *et al.* (2013) reported a high narrow-sense heritability for morphological as well as quality traits such as Na and extraction coefficient of sugar in sugar beet in late sowing conditions which support our results but they found low heritability values for root yield, sugar yield and white sugar yield. Niazian *et al.* (2012) reported the highest and lowest phenotypic variation for root yield and extraction coefficient of sugar, respectively.

The objective of the current study was to estimate heritability and correlations among traits under drought stress condition and to identify the best genotypes and the most important traits influencing white sugar yield in sugar beet.

Materials and methods:

This study was conducted at Agricultural Research Stations of Karaj and Miandoab, Iran in 2014. The 30-year average temperature and an annual rainfall of the location were 13.5°C and 243 mm, respectively and the soil of the field was clay-loam. Miandoab station is located north-west of the city at an altitude of 1314m. This area has the Ferric temperature regime (the average annual temperature of the soil is 8-15° C) and Xeric moisture regime (semi-arid) with the soil of the field being silty-loam.

In this research, 37 sugar beet half-sib families (Table-1) derived from three selection cycles in drought stress condition along with the original populations and check varieties were evaluated in a randomized complete block design with three replications. Seedbed preparation practices such as ploughing, disking and levelling were uniformly applied. Potassium and phosphorous fertilisers were applied at the time of seedbed preparation and nitrogen fertiliser was applied as topdressing. The between- and within-row spacing was 50 and 15 cm, respectively. Each plot consisted of three rows of 8m length. Cultural practices including irrigation and control of diseases and pests were applied when needed. After plant establishment (4-6-leaf stage), furrow irrigation was applied on the basis of cumulative evaporation from the class A evaporation pan. The inlet and outlet irrigation water was measured by using WSC flumes. During the growing season, some morphophysiological traits such as chlorophyll content (CC), specific leaf weight (SLW) (gr.cm-2) and water use efficiency (WUE) (Y/ET) were measured by taking samples from five fully expanded leaves per plot.

Harvest was done early November. The roots harvested were washed, weighed and used to take brie (pulp) samples. The brie samples were then immediately frozen and sent to the Sugar Beet Technology Lab of Sugar Beet Seed Institute, Karaj, Iran, for determination of root related traits such as root yield (RY) (t.ha-1), sugar content (SC) (gr sugar/100 gr beet), sodium (Na) (meq/100 gr beet),and potassium (K) (meq/100 gr beet). Sugar content (SC) (gr sugar/100 gr beet) was measured by the

Table-1: The list of studied genotypes

No.	Genotype	No.	Genotype	No.	Genotype
1	HSF – 841	16	HSF – 859	31	HSF - 876
2	HSF – 842	17	HSF – 860	32	HSF - 877
3	HSF – 843	18	HSF – 861	33	HSF - 881
4	HSF – 844	19	HSF – 862	34	HSF – 882
5	HSF – 846	20	HSF – 864	35	HSF – 883
6	HSF – 847	21	HSF – 865	36	HSF – 884
7	HSF – 848	22	HSF – 866	37	HSF – 885
8	HSF – 849	23	HSF – 867	38	110
9	HSF – 850	24	HSF – 868	39	191
10	HSF – 851	25	HSF – 869	40	31265
11	HSF – 852	26	HSF – 870	41	32434-91
12	HSF – 854	27	HSF – 871	42	32926-92
13	HSF – 855	28	HSF – 872	43	F – 20505
14	HSF – 856	29	HSF – 873		
15	HSF – 857	30	HSF – 875		

polarimetric method, Na and K by flame photometry and N by blue number method. Molasses sugar (MS) (gr sugar/100 gr beet) was estimated by using the formula of Reinfeld et al. (1974). Sugar yield (SY) (t.ha-1), white sugar yield (WSY) (t.ha-1), white sugar content (WSC) (% in beet), extraction coefficient of sugar (ECS) (% in sugar) and alkalinity (Alk) (% in beet) were calculated based on the following equations (Abdollahian *et al.,* 2005):

SY = Root yield (RY) × SC
WSY = RY × WSC
WSC = SC - (MS + sugar losses in factory)
ECS = (WSC /SC) ×100

Genetic parameters and narrow-sense heritability were estimated after Halluaer & Miranda (1982) on the basis of expected mean squares of the Table of ANOVA (Table 2).

Table 2. Expected mean of squares.

S.O.V	Df	MS	E(MS)
Replication	df_R	MS_R	$_e + g _r$
Genotype	df_G	MS_G	$_e + r _g$
Error	df_E	MS_E	$_e$

$$COVH.S = _g = \frac{MSg - MSe}{r}$$

$$A = 4 _g = 4\,COVH.S$$

$$h^2_n = \frac{_g}{(_g + _g m/r + _e/rm)}$$

Where as h^2_n narrow-sense heritability, $_g$ is genetic variance, $_{gm}$ the variance of genotype by environment interaction, $_e$ is error variance, r is the number of replications and m is the number of environments. Phenotypic (PCV) and genotypic (GCV) coefficient of variation was calculated according to the following equations:

$$PCV = _p/\bar{x} \times 100; \qquad GCV = _g/\bar{x} \times 100$$

Where $_p$ and $_g$ are the phenotypic and genotypic standard deviation, respectively, and $\bar{x}$ is the grand mean of the traits. Genetic gain (Gg) for the selection intensity of 5% was calculated by using the following equation:

$$Gg = K _A / _{ph}$$

Where K is the selection differential, $_p$ is the phenotypic standard deviation, and $_A$ is the additive variance. Before data analysis, normality test was done and then the analysis of variance for the traits was conducted and Duncan's multiple range test was use to separate the means. Then, combined analysis of variance was carried out for the traits over two locations in drought stress condition. The software SPSS, SAS and Excel were used for statistical analysis.

Results & Discussion:

Analysis of variance for agronomic and morpho-physiological traits (Table-3) revealed that the two locations differed significantly at 1% probability level (p=0.01) for root yield, sugar yield, white sugar yield, alkalinity, leaf chlorophyll content, water use efficiency, specific leaf weight and leaf succulence index. There was a significant difference among the genotypes for all of the traits except K, white sugar yield and specific leaf weight. The presence of significant difference among the genotypes indicates the existence of genetic variation among them. Genetic variation is one of the requirements for plant breeding so that successful selection of superior genotypes from a population depends on genetic variation and without that, no progress in plant breeding is realised. In this regard, a higher genetic variation for a trait provides better opportunity for selection. On the other hand, genetic diversity provides a long-term adaptability and survival for a population. Therefore, it is highly important to create and maintain genetic variation in a plant breeding program. The interaction of genotypes by environment was only significant for Na, alkalinity and extraction coefficient of sugar at 1% probability level. The non-significant interaction of genotypes by the environment for most of the traits indicates that the genotypes in the two locations performed similarly with respect to these traits, especially root yield, sugar yield and white sugar yield. Therefore, for most of the traits, the means of two locations were used. Bakshi *et al.* (2012) studied the impact of drought stress on some yield and quality traits of new improved sugar beet varieties and found significant differences among the genotypes for all of the traits studied except alpha-amino nitrogen, Na and molasses sugar. In a similar study, Sharifi (2014) observed significant differences among the sugar beet genotypes for yield and quality traits which is in accordance with our results.

Estimation of genetic parameters: the values of narrow-sense heritability for root yield, sugar content,

Table 3. Combined analysis of variance for the traits measured in Karaj and Miandoab.

S.O.V	Df	MS						
		RY	SC	SY	Na	K	WSC	WSY
Location(L)	1	58295.1**	2.94^{ns}	990.23**	1.93^{ns}	13.05^{ns}	6.67^{ns}	27.51**
Error 1	4	290.3	9.18	8.36	0.28	30.6	20.19	0.35
Genotype (G)	42	354.9**	3.42**	4.50**	0.12**	0.81^{ns}	5.95**	0.10^{ns}
G×L	42	253.16^{ns}	2.98^{ns}	3.24^{ns}	0.13**	1.82**	3.60^{ns}	0.10^{ns}
Error 2	168	130.3	1.52	2.41	0.07	0.58	2.54	0.08
CV (%)	-	21.03	9.69	22.5	13.02	11.36	19.01	14.41

^{ns} Non-siginificant; *significant at 0.05; **significant at 0.01 probability level, respectively.
RY: Root yield, SC: Sugar content, SY: Sugar yield, WSC: White sugar content and WSY: White sugar yield.

Continued table 3.

S.O.V	Df	MS						
		Alk	ECS	MS	CC	WUE	SLW	SI
Location(L)	1	2443.5**	412.47^{ns}	0.75^{ns}	6057.8**	8.06**	0.020**	0.009*
Error 1	4	14.51	623.56	4.01	335.2	0.04	0.015	0.0003
Genotype (G)	42	14.21**	110.96**	0.57**	88.3*	0.04**	0.006^{ns}	0.0002*
G×L	42	14.91**	117.91**	0.38^{ns}	61.9^{ns}	0.02^{ns}	0.005^{ns}	0.001^{ns}
Error 2	168	8.83	54.68	0.25	56.5	0.01	0.005	0.0001
CV (%)	-	25.68	11.4	13.28	21.66	21.7	24.31	18.08

Alk: Alkalinity, ECS: Extraction coefficient of sugar, MS: Molasses sugar, CC: Chlorophyll content, WUE: Water use efficiency, SLW: Specific leaf weight and SI: Succulence index.

Table 4. Estimate of genetic parameters for the traits measured in Karaj and Miandoab.

Parameters	RY	SC	SY	Na	K	WSC	WSY
Best half-sib	75.25	14.24	9.16	5.14	7.3	10.44	5.85
Inferior half-sib	38.16	11.3	4.94	3.04	6.08	6.46	3.43
Range	20.72	1.58	2.27	0.86	0.56	2.17	1.35
$COV_{HS} = {}_g$	31.53	0.63	0.42	0.016	0.076	1.31	0.006
$_A = 4 {}_g$	126.13	2.53	1.46	0.06	0.3	4.54	0.026
h_n	60.61	87.1	47.9	80	60.52	89.88	64
PCV (%)	26.34	13.36	27.13	4.3	20.87	26.8	4.52
GCV (%)	23.75	12.47	25.15	3.84	16.23	25.41	3.62
Gg	18.21	3.06	1.87	0.28	0.71	2.24	0.2
LSD5%	4.41	0.47	0.57	0.1	0.29	0.61	0.1

RY: Root yield, SC: Sugar content, SY: Sugar yield, WSC: White sugar content and WSY: White sugar yield

Continued table 4.

Parameters	Alk	ECS	MS	CC	WUE	SLW	SI
Best half-sib	9.83	73.03	4.22	53.25	0.008	0.0098	0.11
Inferior half-sib	2.9	55.85	3.19	26.71	0.0047	0.006	0.034
Range	4.46	8.57	0.44	18.5	0.0016	0.0034	0.083
$COV_{HS} = {}_g$	1.79	18.76	0.106	10.6	0.01	0.0003	0.0003
$_A = 4 {}_g$	7.17	75.04	0.42	4.42	0.04	0.001	0.001
h_n	78.38	83.91	89.04	81.11	74.11	61.15	59.25
PCV (%)	56.75	14.58	18.36	13.58	32.72	58.92	32.6
GCV (%)	50.24	13.35	17.32	12.23	31.74	46.22	25.1
Gg	3.02	9.45	0.69	7.22	0.2	0.04	0.015
LSD5%	1.14	2.85	2.9	2.97	0.0038	0.027	0.0038

ALK:Alkalinity, ECS: Extraction coefficient of sugar, MS: Molasses sugar, CC: Chlorophyll content, WUE: Water use efficiency, SLW: Specific leaf weight and SI: Succulence index.

white sugar content, sugar yield, extraction coefficient of sugar, white sugar yield and chlorophyll content were estimated to be 60.61, 87.10, 90.88, 47.90, 83.91, 64.00 and 81.11%, respectively (Table-4). Except sugar yield which had a heritability lower than average, the values for the other traits were higher than the average. As narrow-sense heritability is the the ratio of additive variance to phenotypic variance, it can be stated that the above-mentioned traits are mainly governed by additive genetic variance. The highest and lowest phenotypic and genotypic variation was observed in alcalinity and specific leaf weight, respectively. Also, root yield and sugar yield displayed a higher phenotypic and genotypic variation than the other traits. Therefore, the highest genetic gain was found for root yield, extraction coefficient of sugar, chlorophyll content and sugar content, respectively (Table-4). It has been shown that without genetic gain, heritability values will not have practical importance in phenotype-based selection (Ehdaie & Wains, 1997). Thus, in plant breeding programs for concurrent selection, the genetic gain has to be considered along with the heritability. As higher heritability values, as well as optimum quantities of genetic gain, were found for root yield, extraction coefficient of sugar, chlorophyll content and sugar content, selection of genotypes based on these traits will likely be effective in achieving genotypes with high root and sugar yields. MacLachlan (1972) estimated the genetic variance and mode of gene action for root yield, sugar content and components of sugar beet quality and reported that non-additive gene effects had higher importance for sugar yield whereas additive gene effects were more important for sugar content and quality components. Fathi *et al.* (2007) reported that root yield, sugar yield and white sugar yield were more affected by additive effects. Rajabi *et al.* (2013) found higher narrow-sense heritability values for morphological traits as well as root quality traits such as Na and extraction coefficient of sugar which is in line with our results, whereas they reported rather low values for root yield, sugar yield and white sugar yield which are different from our findings. It is necessary to emphasise that additive and dominance effects vary depending on the type of breeding materials, the mating design used and experimental conditions. Therefore, precise knowledge of the genetic structure of yield-related traits and their heritability facilitates selection and success of breeding programs. Niazian *et al.* (2012) evaluated sugar beet genotypes by using the diallel method and found the highest broad-sense heritability for root length with the highest and lowest phenotypic variation for root yield and extraction coefficient of sugar, respectively.

Correlations among traits and path analysis: according to the results of correlation analysis (Table-5), white sugar yield had positive significant correlation with
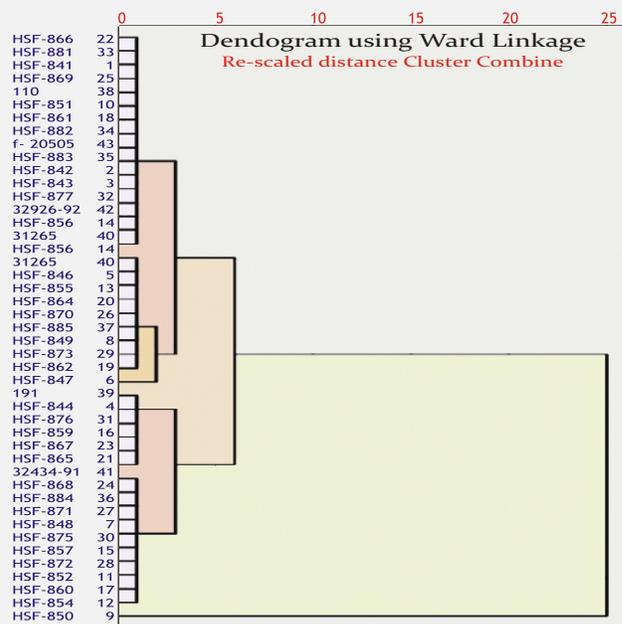

Figure-1: Dendrogram of studied genotypes over the two location based on assayed traits.

root yield, sugar content, sugar yield, white sugar content, extraction coefficient of sugar, chlorophyll content, water use efficiency and specific leaf weight, and negative significant correlation with Na (Sodium), K (Potassium), alkalinity and molasses sugar. As these traits have an acceptable level of heritability, genetic variation and genetic gain, they could be used to select genotypes with high root yield, sugar content, sugar yield, white sugar content, extraction coefficient of sugar and chlorophyll content, and low Na, K, alkalinity and molasses sugar. Ouda Sohier (2005), reported that root yield and sugar content are the most important traits affecting sugar yield which is in line with our results. As simple correlation coefficients do not provide clear information on the nature of cause and effect relationship among the traits of interest, decomposition of the correlation coefficients into direct and indirect effects strengths the degree of impact of independent variables on dependent variable (Ali *et al.,* 2003). Therefore, to identify the traits influencing white sugar yield, stepwise regression analysis was used across the two locations (Table-6). Results showed that sugar yield, molasses sugar and white sugar content totally explaining 99% of the variation of white sugar yield were found to be the most effective traits and thus they were used for path analysis (Table-7). Results of path analysis indicated that sugar yield and sugar content had direct positive, significant effect and molasses sugar had a negative significant effect on white sugar yield. Also, each of the three remaining traits had a positive significant effect on white sugar yield via the other two traits. Baradaran-Firouzabadi (2002) found the highest direct effect on sugar content, molasses sugar, sugar yield

and root diameter in normal condition and for sugar content, molasses sugar and sugar yield in drought stress condition.

Table-5: Correlation coefficients among the traits combined over the two locations.

Trait	1	2	3	4	5	6	7
1	1						
2	-0.08[ns]	1					
3	0.96**	0.17**	1				
4	-0.08[ns]	-0.75**	-0.26**	1			
5	-0.04[ns]	-0.08[ns]	-0.01[ns]	0.20**	1		
6	-0.10[ns]	0.90**	0.13**	-0.83**	-0.29**	1	
7	0.86**	0.37**	0.96**	-0.49**	-0.15*	0.37**	1
8	-0.04[ns]	0.84**	0.16**	-0.86**	-0.42**	0.94**	0.62**
9	-0.54**	-0.30[ns]	-0.29**	-0.35**	-0.24**	-0.60**	-0.33**
10	0.12*	-0.75**	-0.01[ns]	-0.76**	0.70**	-0.77[ns]	-0.86
11	-0.66**	-0.04[ns]	0.66**	0.25**	0.15*	-0.05[ns]	0.12*
12	0.07[ns]	-0.10[ns]	0.06[ns]	0.12*	0.01[ns]	-0.11[ns]	-0.10[ns]
13	0.63**	-0.53**	0.39**	0.14[ns]	0.10[ns]	0.37**	0.84**
14	0.60**	0.44**	0.30*	0.17[ns]	0.16[ns]	0.36**	0.33**

Trait	8	9	10	11	12	13	14
8	1						
9	0.39**	1					
10	0.17**	0.25**	1				
11	0.63**	-0.64**	0.05 ns	1			
12	0.01 ns	0.03 ns	0.10 ns	0.01 ns	1		
13	-0.20 ns	-0.26 ns	-0.10 ns	-0.23 ns	0.10 ns	1	
14	0.17 ns	0.16 ns	0.14 ns	0.14 ns	0.15 ns	0.13 ns	1

[ns] Non-siginificant; *significant at 0.05; **significant at 0.01 probability level, respectively.

1: Root yield, 2: Sugar content, 3: Sugar yield, 4: Na, 5: K, 6: White sugar content, 7: White sugar yield, 8: Alkalinity, 9: Extraction coefficient of sugar, 10: Molasses sugar, 11: Chlorophyll content, 12: Water use efficiency, 13: Specific leaf weight and 14: Succulence index.

Table-6: Stepwise regression for white sugar yield as dependent variable and other traits as independent variables in Karaj & Miandoab.

	1	2	3
Constant	-0.11	2.5	0.43
White sugar yield	0.67	0.66	0.65
Molasses sugar	-	0.69-	0.52-
Sugar content	-	-	0.12
R2	0.91	0.98	0.99

Table-7: Path analysis for white sugar yield as dependent variable and other traits as independent variables in Karaj & Miandoab.

	Direct effect	Indirect effect		
		1	2	3
1-Sugar yield	0.94**	1	0.172	0.04
2-Molasses sugar	-0.20**	0.8	-	0.06
3-White sugar content	0.11**	0.34	0.11	-

Cluster analysis: as the genotypes differ greatly with respect to the traits measured, it doesn't seem to be correct to judge just on the basis of one or a few morphological traits. Therefore, in addition to correlation analysis, various statistical methods are used to select the best genotypes. One of these methods is cluster analysis. As

shown in fig.-1, cut-off at different positions of dendrogram derived from cluster analysis resulted in 3, 4 and 5 groups. To confirm the differences among the groups, multivariate analysis based on randomised complete block design was conducted for the traits measured. on the basis of Wilks Lambda statistic, the highest F value and hence the highest between-group to within-group variance ratio was observed in three-group condition. On this basis, 43 genotypes were divided into three groups. Analysis of variance for the three groups showed that the groups differed significantly in sugar content, Na, white sugar content, extraction coefficient of sugar, white sugar yield and succulence index (Table-8). To precisely determine the differences among the clusters for each trait, means of traits of the clusters was compared using LSD method. When the mean of a trait in a cluster is higher than the grand mean of that trait, it means that the genotypes of the cluster will have a higher value for that trait. Combined over the two locations, the first cluster contained the genotypes 22, 33, 1, 25, 38, 10, 18, 34, 43, 35, 2, 3, 32, 42, 14, 40, 5, 13, 13, 20, 26, 37, 8, 29, 19, 6 and 39. The genotypes of this cluster were higher than the grand mean of all clusters with respect to sugar content, white sugar content, white sugar yield, extraction coefficient of sugar and leaf succulence index, and lower than the grand mean of all clusters for Na and chlorophyll content (Table-8). Therefore, as these genotypes had higher sugar yield than the other two groups and also their sugar content, white sugar content, white sugar yield, extraction coefficient of sugar and leaf succulence index were higher, selection of these genotypes could result in the development of hybrids with higher yield and quality in future. The second cluster included the genotypes 4, 31, 16, 23, 21, 41, 24, 36, 27, 7, 30, 15, 28, 11, 17 and 12. Genotypes of this cluster were higher than the mean of all clusters for Na and lower than the mean of clusters for sugar content, Na, white sugar content and extraction coefficient of sugar (Table-8). Consisted of only one genotype (genotype 9), cluster 3 had higher sugar content, white sugar content and extraction coefficient of sugar than the mean of all clusters, and lower Na and leaf area than the mean of all clusters (Table-8). Rajabi *et al.* (2014), classified sugar beet genotypes into four groups with the first group containing the genotypes 25, 20 and 3 being superior with respect to yield and quality. While clustering sugar beet genotypes, Ghasemi *et al.* (2010) found a different grouping so that the genotypes with higher similarity for the traits studied were grouped together. Results of the current study showed that the genotypes differed significantly for all of the traits studied which indicates the presence of genetic variation for selection of desirable genotypes. The genotype by environment interaction was not significant for white sugar yield and its related traits. In other words, although the two locations were significantly different for most of

Table 8. Analysis of variance and means comparisons of groups for the traits measured over the two locations (Karaj and Miandoab).

S.O.V	Df	MS						
		RY	SC	SY	Na	K	WSC	WSY
Between groups	2	8.53 ns	3.60**	0.31 ns	1.60**	0.05 ns	5.68 **	5.68**
Within groups	40	7.13	0.41	0.77	0.32	0.13	0.75	0.75
Cluster 1	-	52.97	130.09[a]	6.86	4.02[b]	6.7	8.80[a]	4.56
Cluster 2	-	56.59	12.26[b]	6.99	4.5a[b]	6.75	7.76[b]	4.45
Cluster 3	-	51.41	12.07[b]	6.23	4.80[a]	6.41	7.57[b]	3.94
Grand mean	-	54.28	12.76	6.9	4.24	6.71	8.39	4.51

[ns] Non-siginificant; *significant at 0.05; **significant at 0.01 probability level, respectively. Also different letters indicating significant difference, RY: Root yield, SC: Sugar content, SY: Sugar yield, WSC: White sugar content and WSY: White sugar yield.

Continued table 8.

S.O.V	Df	MS						
		Alk	ECS	MS	CC	WUE	SLW	SI
Between groups	2	3.25 ns	89.75**	0.22 ns	26.0 ns	1.35 ns	0.005 ns	0.001**
Within groups	40	3.32	14.92	0.08	14.26	5.08	0.005	0.0001
Cluster 1	-	5.17	66.49[a]	3.68	52.21	0.0061	0.006	0.050[b]
Cluster 2	-	5.71	62.29[b]	3.89	54.14	0.0067	0.0064	0.059[a]
Cluster 3	-	3.46	62.8a[b]	3.9	53.32	0.0062	0.0062	0.048[b]
Grand mean	-	5.33	64.84	3.77	53.22	0.0063	0.0062	0.052

Alk: Alkalinity, ECS: Extraction coefficient of sugar, MS: Molasses sugar, CC: Chlorophyll content, WUE: Water use efficiency, SLW: Specific leaf weight and SI: Succulence index.

the traits, the genotypes reacted similarly with respect to yield. The heritability estimates for root yield, sugar content, white sugar content, extraction coefficient of sugar, white sugar yield and chlorophyll content was found to be mid-to-high. Thus, the non-significant difference between the two environments (locations) could be attributed to the higher heritability of the traits mentioned; because the higher the heritability of a trait, the lower the trait is affected by environmental factors. Due to higher heritability and genetic gain observed for root yield, extraction coefficient of sugar, chlorophyll content and sugar content and also positive significant correlations among these traits, they could be used to select genotypes with high yield and quality. On this basis, genotypes of the first cluster (genotypes 22, 33, 1, 25, 38, 10, 18, 34, 43, 35, 2, 3, 32, 42, 14, 40, 5, 13, 13, 20, 26, 37, 8, 29, 19, 6 and 39) which were higher than the grand mean of the all clusters with respect to sugar content, white sugar content, white sugar yield, extraction coefficient of sugar and leaf succulence index, and lower than the grand mean of the all clusters for Na and chlorophyll content, could be recommended for subsequent development of the hybrids in future.

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