Original Research Article

Comparison of genetic parameters in non-segregating and segregating populations of sugar beet in Egypt.

ABSTRACT

This work aimed mainly at comparison among non-segregating (P1, P2 and F1) and segregating (F2, BC1 and BC2) generations using genetic parameters for four traits in the cross Eg27 x Fc723 cmsduring 2015 to 2018 in Ras-Sudr station, Desert Research Center (DRC), South Sinai and Private Farm in Kafr El Sheikh Governorate. According to combined analysis of variance, highly significant environments (E) for all studied traits and significant or highly significant genotype (G) and GxE interactions for most traits were observed during six generations. In respect to mean performances, Kafr El-Shiekh location was higher than Ras-Sudr location for most studied traits at six generations. Significant differences among six generation means were found for all studied traits in the two locations. The F2 generation was lower than the P1, P2, F1, BC1 and BC2 generations for most studied traits at the two locations. The cross (Eg27 x Fc723 cms) recorded positive and highly significant heterosis, heterobeltiosis and inbreeding depression for most studied traits under two locations. A high broad sense heritability and genetic advance as percent of mean (GAM%) estimates were observed for root diameter/plant at BC1, root weight/plant at BC2 and T.S.S.% at BC1 and BC2. Generally, the values of the all studied genetic parameters for all studied traits during segregating generations were higher than non-segregating generations. The principal component analysis of the relationship between the six generations revealed that the most appropriate generations for selecting these traits ~~are~~ were BC1 and BC2 under the two locations. Backcrossing may be done for 2–5 cycles (BC2 – BC5) at Eg27 parent for improving sugar beet yield in Egypt.

Key words: Comparison ~~—~~; Genetic parameters ~~—~~; non-segregating generations~~—~~; segregating generations ~~—~~; sugar beet.

INTRODUCTION

The genus *Beta* L.~~,~~ of the family Amaranthaceae (formerly Chenopodiaceae), is subdivided into four sections i.e., *Beta*, *Corollinae*, *Nanae* and *Procumbentes*[1]. All cultivated beets are included in the sub-species vulgaris that belongs to the species vulgaris and to the section *Beta*[2]. Beets (*Beta vulgaris spp. vulgaris* L.) are classified by crop type into sugar, fodder, leaf, or table [3]. The sugar beet was recognized as a plant with valuable sweetening properties in the early 1700s [4]. Sugar beet (*Beta vulgaris* L.) has economical importance for sugar production in temperate climate. The plant is usually open-pollinated and rather sensitive to inbreeding due to the presence of self-sterility genes [5].

The total area harvested, yield and production of sugar beet during 2017/2018 growing season are 4894026 ha, 615068 hg/ha and 301015696 tonnes in the worldwide. Russian Federation ranks first in sugar beet production in the world, which ~~was produced~~produces 17.25% of the total world sugarbeet production, followed by France (11.42%), Germany (11.31%) and USA (10.65%). Egypt is ranked ninth country ~~by~~ in sugar beet production in the world. Sugar beet production in Egypt ~~was~~ amounts to 12106661 tonnes that accounts for 4.02 % of the world's sugar beet production. (https://http://www.fao.org; accessed March 20, 2019)

The main objective of plant breeding is the development of varieties with the maximum commercial yield at the lowest economic and environmental cost [6]. Gross sugar yield is the most important trait for growers and it depends on the weight of the roots produced per hectare and on the sugar content, i.e., the percentage w/w of sucrose present in the roots. Varieties must also possess good yield stability across localities and years, which depend on a broad genetic base and on resistances against multiple biotic and abiotic stresses [1]. Procedures for sugar beet breeding are directly applicable to breed beets for alternative and novel uses. Varieties result from repeatedly selecting high sucrose segregants in heterogeneous breeding populations. Sucrose percent is quantitatively controlled with high heritability [3].

The term heterosis was coined by ~~Shull~~ [7], it is the superiority of F1 hybrid over the mid-parents or the better parent or over the standard check with regard to agriculturally useful traits. Inbreeding depression is the decline in the vigor of inbred caused by inbreeding ~~is an opposite phenomenon~~which is the opposite of heterosis and the amount of documented inbreeding depression varies for different species [8]. Heterosis and inbreeding depression are results of the process of changing individual genetic diversity in two reverse ~~(increase and decrease)~~ directions(increase and decrease) [9]. Both heterosis and inbreeding depression are due to dominance and nonallelic interactions[10]. The information on nature and magnitude of inbreeding depression is helpful in determining the effectiveness of selection.

The variances of the measurements of the character in both parents and F1 will thus provide estimates of the non-heritable variation and of its contribution to the variances of later generations like F2, because of segregation of the genetic differences between P1 and P2, heritable variation will also be present [10]. In backcrossing the F1 to either of its true breeding parents half the progeny will be homozygous and half heterozygous in respect of each gene pair by which the parents differ [11]. ~~Dudley~~ [12] stated that if one parent has more loci containing favorable alleles than the other, at least one generation of backcrossing to the recipient population prior to initiation of selection will enhance the probability of recovering a population which outperforms the better parent or a line better than the best line which could be isolated from the better parent. He added, selection starting in the appropriate generation will usually be necessary to either improve the population mean to the desired level or to increase to a reasonable level the probability of obtaining a superior inbred line, and the more diverse the parents, the more useful one or more generations of backcrossing becomes. ~~Meichinger~~[13] reported that the F2 is likely to ~~have~~ be more superior than BC1 and BC2 if 1) the differences in the testcross means of the F2 and BC populations are small compared to the pertinent genetic standard deviations, 2) the heritability of the character is high, and 3) a high selection intensity can he applied.Several statistical descriptors are available to the breeder to aide in making the choice of segregating population. ~~means~~Means, variances, heritabilities, correlations, and selection responses are just a few of the possible statistics that help characterize a population [14].

The development of high yielding varieties requires detailed knowledge of the genetic variability present in the germplasm of the crop, the association among yield components, input requirements and culture practices[15]. Genetic parameters, such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Moreover, knowledge of heritability is essential for selection as it indicates the extent of transmissibility of a character into future generations and the quality of phenotype data in multilocation trials [16]. Heritability coupled with high genetic advance would

be more useful in predicting the resultant effect in the selection of the best genotypes for yield and its attributing traits. It helps in determining the influence of environment on the expression and reliability of characters [17]. The genetic advance is yet another important selection parameter that aids breeder in a selection program [18].The primary objectives of present study were to ~~comparison of~~compare genetic parameters across the P1, P2, F1, F2, BC1 and BC2 generations in sugar beet and ~~comparison~~ between them using principal component analysis ~~during~~ in two different locations in Egypt.

MATERIALS AND METHODS

Genetic Material and Field Procedure:

The experiments were carried out during the four successive seasons from 2015 to 2018.The genetic materials used in the present investigation ~~are~~ were Eg27 multigerm Egyptian genotype and Fc 723 cms American genotype ((cytoplasmic male sterility) and which were obtained from Sugar Beet Breeding Program in Egypt. In 2015 season, the parental cultivars were crossed to produce F1 hybrid seeds (Eg27 x Fc723 cms) under natural conditions of Saint Catherine, South Sinai, Egypt in different locations. In 2016, each F1 was backcrossed to both parents, the parents were also crossed for more hybrid seeds and the F1 plants was selfed to obtain F2 seeds ~~at~~ in the community gardens in Saint Catherine, South Sinai, Egypt. In 2017 year, the six populations (P1, P2, F1, F2, BC1 and BC2) were evaluated separately in a randomized complete blocks design with three replications in the two locations i.e., Ras-Sudr station, Desert Research Center (DRC), South Sinai and Private Farm in Kafr El Sheikh Governorate. Each replicate consisted of 10 rows, one row for each non-segregating generations (P1, P2 and F1) and four rows for F2, three rows for BC1 and BC2 crosses (segregating generations). Each row was 5 meters long and 0.50 m width and comprised 25 hills. Hills were spaced at 20 cm apart and thinned to one plant per hill. Seed drilling was done in the 15th of September 2017 of Ris-Sudir station and Kafer El-Sheikh for the two locations. Agricultural practices namely ; date of cultivation, method of irrigation and application of fertilizer etc -were done ~~as~~ according to ~~research~~ recommended protocols . Harvesting ~~was~~ occurred after 190 days in the two locations (25th of March 2018). The data on ~~an~~ individual plant basis of the six populations were recorded for root length/plant (cm), root diameter/plant(cm), root weight/plant(g) and total soluble solids percentage (T.S.S.% %). T.S.S.% ~~%~~ was determined ~~by~~ using Hand Refractometer and expressed as percentage of the juice.

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Statistical Analysis:

The combined two-way ANOVA was performed considering the effects of locations and genotypes for studied traits in six populations, and computed according to the method of ~~Gomez and Gomez~~ [19]. Heterosis and inbreeding depression (%) were estimated according to ~~Miller et al.,~~[20]. The Phenotypic (σ_P^2), genotypic(σ_G^2), genotype x environment interaction (σ_{GE}^2) and error (σ_E^2)variances were estimated with analysis of variance (ANOVA) by ~~Searle et al.,~~ [21]. Heritability in broad sense (BSH) was estimated from method given by ~~Fehr~~ [22]. The extent of genetic advance to be expected by selecting ten percent of the superior progeny was calculated according to ~~Robinson et al.,~~[23]. Genotypic (GCV%), phenotypic (PCV%) and error

(ECV%) coefficients of variation were calculated according to ~~Burton~~ [24]. Standard error (SE) of genetic parameters was calculated according to Lothrop ~~et al.,~~[25]. Principal component analysis was done using a computer software program PAST version 2.17c.

RESULTS AND DISCUSSION

Analysis of variance:

Combined analysis of variance for registered traits during P1, P2, F1, F2, BC1 and BC2 are shown in Table 1. All studied traits exhibited high~~ly~~ ~~significant~~ significance between environments (E) for all six populations. Significant or highly significant genotypes (G) were found for all studied traits at P1 and BC1 populations, for root length and root weight traits at P2 and F1 populations, for root length and T.S.S.% traits at F2 population~~,~~ ~~:~~ and for root diameter and T.S.S.% traits at BC2 population. The mean squares due to GE interaction were either significant or highly significant for root length trait in all generations except for BC2, ~~for~~ root diameter in P1, F1, BC1 and BC2, and ~~for~~ root weight and T.S.S.% traits in P1, P2 and F2. The EMS error mean squares had the highest share in the total variations of the studied traits at six generations. The mean squares of E, G and GE interaction for segregation generations were higher than non-segregation generations in most studied traits. The CVs values of segregating generations were higher than the CVs values of non-segregating generations for all registered traits (Table 1). Among segregating generations, the CVs values of F2 were higher than BC1 and BC2 for the four traits. These results displayed the environmental influence was large for segregating generations and ~~its~~ lower for non-segregating generations through all studied traits. The magnitude of CV% indicated that the genotypes had exploitable genetic variability in segregation generations during selection of ~~studied~~ traits examined in sugar beet. The genotype x environment interaction ~~can~~ could be detected by differences in the variances of the phenotypes produced by the different genotypes [10].The genetic variability among F2 plants was proven to be significant in all studied traits [26]. ~~Srour and El Hashash~~[27] stated that, the mean squares of F2, F3 and F4 generations showed highly significant (P≤0.01) differences for most studied traits in the two cotton crosses.The analysis of variance showed that all genotypes had significant effects on root traits in sugar beet [5]. Also, significant variations in response of hybrids and lines to the effect of environments showed the right choice of experimental sites for GEinteraction assessment [28].

Table 1. Combined analysis of variance for studied traits during PI, P2, F1, F2, BCl, and BC2 generations over two locations.

Traits	Generations	Environments (E)	Replications within E	Genotype (G)	G x E	Pooled Error	CV%
Root length/p (cm)	P1	239.14**	1.42	3.92**	2.76*	0.62	4.20
	P2	547.84**	0.13	1.52**	3.77**	0.25	2.94
	F1	340.03**	1.70*	1.29*	2.86**	0.36	3.01
	F2	1049.18**	0.60	14.89*	16.47*	6.64	17.00
	BC1	816.41**	0.23	18.78**	9.25**	1.22	5.85
	BC2	385.93**	1.30	5.79	3.32	4.43	12.38
Root	P1	71.46**	1.07*	0.94*	0.82*	0.24	4.32

diameter /p(cm)	P2	57.13**	0.09	0.21	0.21	0.11	3.71
	F1	173.14**	0.19	0.27	1.05**	0.20	3.68
	F2	173.94**	0.95	5.43	6.80	3.32	22.08
	BC1	155.50**	0.58	5.67**	2.12*	0.49	6.10
	BC2	92.93**	0.41	2.23**	2.15**	0.31	6.15
Root weight/ P(g)	P1	11530388.06**	26462.02*	67157.27**	39202.40**	5979.83	5.63
	P2	7303010.76**	2279.99	84348.52**	104634.64**	4202.32	7.54
	F1	18719998.12**	45826.34	86645.77*	89918.26*	18960.09	8.21
	F2	3732271.00**	7418.25	42773.55	59368.38	42202.98	36.41
	BC1	17291994.72**	8208.45	614385.73*	330332.44	158481.22	25.50
	BC2	5080379.01**	16699.98	169625.40	43524.07	65479.24	33.01
T.S.S.%	P1	258.13**	0.23	1.78**	1.22*	0.27	2.44
	P2	154.13**	0.13	0.45	1.05*	0.30	2.23
	F1	168.03**	0.67*	0.47	0.37	0.17	1.78
	F2	866.40**	0.58	19.08**	15.99**	2.73	7.66
	BC1	40.83**	0.73	7.62**	0.92	0.94	4.61
	BC2	158.70**	1.47	4.05**	0.78	0.84	3.79

*** and **: significant at 5% and 1% levels of probability, respectively**

Mean Performances:

In the Table 2, the Kafr El-Shiekh location had the highest mean performances for all studied traits except T.S.S.% in six generations. Significant differences among six generation means were found for all studied traits in the two locations, indicating the presence of genetic variability for these traits in the ~~studied~~ study materials and two locations. The performance of P1 (Eg27) was higher than P2 (Fc723 cms) for all studied traits ~~under~~ in the two locations, except for T.S.S.% trait at Kafr El-Shiekh location. The F2 generation was lower than the respective parents, F1, BC1 and BC2 generations for all the studied traits at the two locations, except T.S.S.% trait at Ras-Sudr location. This result indicated that, the relation between F2 and other generations revealed that there ~~is~~ was different behavior in the ~~studied~~ study materials ~~during~~ of the two locations. The mean values of the two backcross generations ~~comparing~~ in comparison with their parents was higher than the ~~higher~~ superior parent or one of the parents for most studied traits in the two locations, indicating appreciable amount of genetic variability for these characters in the corresponding crosses. The results in combined analysis ~~are~~ were in same direction of the previous~~ly~~ results in the two locations. Generally, the relationship among non-segregating and segregating generation would be more accurate when illustrating the genetic parameters. Thus, it is possible to benefit from the selection in the segregation generations, especially the BC1 and BC2 generations in future breeding programs of improving these traits in sugar beet.

Table 2. Mean Performances and standard errors for studied traits through PI, P2, F1, F2, BCl, and BC2 generations at locations.

Traits	Generation	Ras-sudr	Kafr El-Shiekh	Combined
Root length/P (cm)	P1	15.96±0.23	21.61±0.62	18.78±0.36
	P2	12.83±0.37	21.37±0.46	17.10±0.23
	F1	16.71±0.39	23.45±0.36	20.08±0.21
	F2	10.97±1.23	19.33±0.76	15.15±0.70
	BC1	13.65±0.68	24.09±1.19	18.87±0.79
	BC2	13.41±0.62	20.59±0.48	17.00±0.44

Root diameter /P (cm)	P1	9.73±0.23	12.82±0.26	11.28±0.18
	P2	7.59±0.08	10.35±0.15	8.97±0.08
	F1	9.64±0.24	14.44±0.17	12.04±0.10
	F2	6.55±0.75	9.96±0.50	8.26±0.43
	BC1	9.14±0.28	13.69±0.66	11.42±0.43
	BC2	7.29±0.31	10.81±0.44	9.05±0.27
Root weight /P (g)	P1	754.04±37.22	1993.95±75.53	1374.00±47.31
	P2	365.85±13.66	1352.63±111.41	859.24±53.02
	F1	887.59±21.62	2467.46±106.32	1677.52±53.74
	F2	314.77±43.00	813.59±70.43	564.18±37.76
	BC1	801.70±119.01	2320.12±220.95	1560.91±143.11
	BC2	363.56±48.56	1186.59±108.87	775.08±75.19
T.S.S.%	P1	27.47±0.43	18.60±0.12	21.53±0.24
	P2	26.80±0.27	22.27±0.16	24.53±0.12
	F1	25.27±0.22	20.53±0.08	22.90±0.12
	F2	25.37±1.48	17.77±0.37	21.57±0.80
	BC1	22.20±0.62	19.87±0.43	21.03±0.50
	BC2	26.53±0.44	21.93±0.36	24.23±0.37

Heterosis and inbreeding depression:

Heterosis as percentage over mid-parents (heterosis) and better-parents (heterobeltiosis), and inbreeding depression values are given in Table 3. The significant heterosis and heterobeltiosis towards positive direction and inbreeding depression in negative direction ~~are~~ were desirable (useful) for the studied traits. The relative heterosis was highly significant in positive direction for root length, root diameter and root weight traits under Ras-Sudr and Kafr El-Shiekh locations. While, positive and highly significant heterobeltiosis was found for root weight ~~under~~ in the two ~~studied~~ experimental locations, for root length and root diameter traits for Kafr El-Shiekh location. Estimation of heterobeltiosis ~~is~~ was useful in identifying truly heterotic cross combinations. The values of the heterobeltios ~~is~~ was in Kafr El-Shiekh location were higher than the values of the heterobeltios ~~is~~was in Ras-Sudr location for all ~~studied~~ traits examined. With regard to the inbreeding depression in F2 relative to F1 (Table 2), the results showed highly significant inbreeding depression in positive direction for all studied traits ~~during~~ in the two locations, except T.S.S.% at Ras-Sudr location, which had negative and insignificant. Highly significant heterosis, heterobeltiosis and inbreeding depression in positivedirection, ~~indicates~~ indicated dominance genetic effects for obtaining desirable segregants in sugar beet improvement. In combined analysis specially, the cross (Eg27 x Fc723 cms) exhibited highly significant and positive values of both relative heterosis and heterobeltiosis, which ~~are~~ were helpful for making effective selection in succeeding generations. However, inbreeding depression was found to be significant and positive, indicating less chances for beneficial segregants in F2 population.Positive and highly significant heterosis over the mid-parents and the better parent were found for root length, root diameter, root weight T.S.S.% traits [29]. ~~Smith et al.,~~[30], ~~Skaracis and Smith~~ [31] and ~~Ćurčić et al.,~~ [5] mentioned that, the heterosis and heterobeltiosis values of most hybrid combinations were positive for root traits, indicating that the non-additive gene action was responsible for inheriting those traits in sugar beet. The homozygous parent has only additive effect [32]; while, the both inbred lines and the open

pollinated populations ~~are~~ were used, ~~that~~ the deviation from the full model ~~indicates~~ indicated the existence of epistatic effects [31].

Table 3.Heterosis and inbreeding depression for studied traits at six generations in two locations.

Traits	Parameters	Ras-Sudr	Kafr El-Shiekh	Combined
Root length/P (cm)	HMP	16.08**	9.12**	11.93**
	HBP	4.70	8.51**	6.92**
	ID	34.35**	17.57**	24.55**
Root diameter/P (cm)	HMP	11.32**	24.64**	18.91**
	HBP	-0.92	12.64**	6.74**
	ID	32.05**	31.02**	31.40**
Root weight / P (g)	HMP	58.51**	47.46**	50.23**
	HBP	17.71**	23.75**	22.09**
	ID	64.54**	67.03**	66.37**
T.S.S.%	HMP	-6.87**	0.46	-0.56
	HBP	-8.01**	-7.81**	-6.64**
	ID	-0.40	13.44**	5.81

*** and **: significant at 5% and 1% levels of probability, respectively**

Genetic Parameters:

Variance components for registered traits in six generations are presented in Table 4. Estimates of phenotypic and error variances for all studied traits in six generations were significantly higher than the standard error values. The genotypes × environment variances showed significant for all studied traits in all generations, except root length in BC2, root diameter in P2, root weight in F2, BC1 and BC2, and T.S.S.% in BC1 and BC2. As for genotypic variance, all studied traits had ~~non-~~ insignificant difference in all generations, except root diameter (BC1), root weight (BC2) and T.S.S.% (BC1 and BC2). Estimates of variance components for segregating generations were higher than non-segregating generations for most studied traits. In BC1 generation, the phenotypic and genotypic variances were the highest for all studied traits except T.S.S.%, while GE and error variances for root weight and genotypic variance for T.S.S.% recorded the highest values. Meanwhile, F2 generation recorded the highest estimate of phenotypic variance for T.S.S.% and GE and error variances for studied traits except root weight. The variance components were equal zero for some traits, because their values were negative. ~~Melchinger et al.,~~[33] indicated the backcross generation genetic variance estimates should be equal in the absence of epistasis.

Table 4. Variance components and standard errors (SE) estimates of studied traits during six generations at twolocations.

Traits	Generations	Phenotypic variance ± SE	Genotypic variance ±SE	GxEvariance±SE	Error variance±SE
Root length/P (cm)	P1	0.65±0.38	0.19±0.46	0.71±0.53	0.62±0.21
	P2	0.25±0.15	0.00±0.39	1.17±0.73	0.25±0.08
	F1	0.21±0.12	0.00±0.30	0.83±0.55	0.36±0.12
	F2	2.48±1.06	0.00±1.58	3.28±2.40	6.64±1.52
	BC1	3.13±1.81	1.59±2.01	2.68±1.78	1.22±0.41
	BC2	0.96±0.56	0.41±0.64	0.00±0.81	4.43±1.48
Root diameter/P	P1	0.16±0.09	0.02±0.12	0.20±0.16	0.24±0.08
	P2	0.03±0.02	0.00±0.03	0.03±0.04	0.11±0.04

(cm)	F1	0.05±0.03	0.00±0.10	0.28±0.20	0.20±0.07
	F2	0.91±0.39	0.00±0.62	1.16±1.00	3.32±0.76
	BC1	0.95±0.55	0.59±0.58	0.55±0.41	0.49±0.16
	BC2	0.37±0.21	0.01±0.30	0.61±0.42	0.31±0.10
Root weight/ P (g)	P1	11192.88±6462.21	4659.14±7482.65	11074.19±7573.71	5979.83±1993.28
	P2	14058.09±8116.44	0.00±12932.55	33477.44±20142.36	4202.32±1400.77
	F1	14440.96±8337.49	0.00±12015.72	23652.73±17432.5	18960.09±6320.03
	F2	7128.93±3039.78	0.00±5200.13	5721.80±9034.37	42202.98±9682.03
	BC1	102397.62±59119.29	47342.22±67122.70	57283.74±65966.21	158481.22±52827.07
	BC2	28270.90±16322.21	21016.89±16850.96	0.00±11094.75	65479.24±21826.41
T.S.S.%	P1	0.30±0.17	0.09±0.21	0.31±0.24	0.27±0.09
	P2	0.07±0.04	0.00±0.11	0.25±0.20	0.30±0.10
	F1	0.08±0.04	0.02±0.06	0.07±0.07	0.17±0.06
	F2	3.18±1.36	0.51±1.77	4.42±2.28	2.73±0.63
	BC1	1.27±0.73	1.12±0.74	0.00±0.21	0.94±0.31
	BC2	0.67±0.39	0.54±0.40	0.00±0.18	0.84±0.28

The broad sense heritability (h^2) across two locations showed significant difference only for root weight in BC2 generation and for T.S.S.% in BC1 and BC2 generations (Table 5). The h^2 estimates of the two backcross generations were consistently higher than other generations for all traits except root diameter in BC2 generation. While, h^2 estimates of P1 population had low ($h^2 < 0.30$) for root diameter and ~~had~~ moderate for other studied traits ($h^2 \geq 0.30$).It has been emphasized that without a genetic advance, the heritability values would not be of a practical importance for selection based on phenotypic appearance. So, genetic advance should be considered along with heritability in coherent selection breeding program. High values of h^2 coupled with high genetic advance as percent of mean (GAM%) were noticed all studied traits at the two backcross generations, except root diameter in BC2 generation. The highest values of broad sense heritability revealed that greater proportion of the entire variance was due to the greater genotypic variance influenced less by environmental factors and ~~the less~~ contribution of the experimental error in the total phenotypic variability, therefore having high heritable variations. Superior heritability values indicates the greater effectiveness of selection and improvement to be expected for these studied traits at the two BC1 and BC2 generations in future breeding programmes and development of new sugar beet cultivars, as the genetic variance is mostly due to the additive gene action. The increase in genetic variance and decrease in genotype by environment variance resulted in a significant increase in heritability and a significantly greater predicted selection response across selection intensities [14]. ~~Melchinger et al.,~~[33] stated that the BCl and BC2 predicted selection responses should be identical in the absence of epistasis. Heritability values based on F2 data were found to be moderate magnitude for all traits of most crosses [26]. ~~Bayomi~~[29] reported that heritability estimates in broad sense were moderate for root length, root diameter and root weight traits.

The values of coefficients of phenotypic variation (PCV%) were higher than their corresponding coefficients of genotypic variation (GCV%) for all studied traits in six generations (Table 5), indicating that the phenotype was different ~~of~~ from the genotype, and environmental influence was high for four studied traits ~~at~~ in six generations. The values of the GCV%, PCV% and error coefficients of variation (ECV%) for all studied traits during segregating generations were higher than non-segregating generations. From previous published results, the values of the relative

coefficient of variation (RCV= GCV%/ECV%) were higher than unity for all studied traits in BC1 generation, except root weight trait, ~~indicate~~ indicating that environmental variation among the genotypes was lower than the genetic variation. The genetic parameters were equal to zero for some traits, because the genotypic variance values were equal to zero.

The variation of the measurements of true breeding parental lines and their F1 must be exclusively non-heritable [34]. The variances of these measurements consequently afforded ~~estimates~~ estimation of the non-heritable contribution to the variances of the measurements in families of later generations, such as F2, where because of segregation heritable components of variation ~~will~~ would also be present [11]. Assuming that non-allelic genes make independent contributions to it, the heritable variance produced by all the genes segregating in the F2 will be the sum of their individual contributions [10]. The choice of base populations between F2 and first backcrosses ~~can~~ could be made on the distributions of ~~testerosses~~ test crosses from the first segregating generation [13].~~Hassani et al.,~~ [28] stated that, the variance components and heritability estimates were meaningfully high for the all studied traits. They added that, due to high heritability estimates, genotype selection might lead to improvement of these traits and development of new sugar beet cultivars. ~~Williams and Hussain~~[35] reported that the amount of available genetic variation, even among the small sample of BC1 families tested so far, ~~is~~ was encouraging and ~~is~~ was likely to make selection successful. The ability to backcross to a range of elite genotypes ~~will~~ would further improve genetic variation, and ~~will~~ would enable the addition of new genetic diversity from the species.

Table 5. Heritability with standard errors and other genotypic parameters for studied traits at six generations in two locations.

Traits	Generations	Genetic Parameters						
		h^2	GA	GAM%	GCV%	PCV%	ECV%	RCV
Root length/P (cm)	P1	0.30±0.86	0.42	2.25	2.35	4.31	4.20	0.56
	P2	0.00±1.89	0.00	0.00	0.00	2.95	2.94	0.00
	F1	0.00±1.72	0.00	0.00	0.00	2.31	3.01	0.00
	F2	0.00±0.18	0.00	0.00	0.00	10.40	17.00	0.00
	BC1	0.51±0.79	1.58	8.38	6.68	9.38	5.85	1.14
	BC2	0.43±0.82	0.74	4.34	3.77	5.78	12.38	0.30
Root diameter/P (cm)	P1	0.12±0.94	0.09	0.77	1.24	3.51	4.32	0.29
	P2	0.01±1.00	0.00	0.02	0.17	2.08	3.71	0.05
	F1	0.00±2.80	0.00	0.00	0.00	1.77	3.68	0.00
	F2	0.00±0.76	0.00	0.00	0.00	11.52	22.08	0.00
	BC1	0.63±0.76	1.07	9.38	6.74	8.52	6.10	1.10
	BC2	0.03±0.98	0.04	0.41	1.25	6.74	6.15	0.20
Root weight/ P (g)	P1	0.42±0.82	77.51	5.64	4.97	7.70	5.63	0.88
	P2	0.00±1.13	0.00	0.00	0.00	13.80	7.54	0.00
	F1	0.00±1.02	0.00	0.00	0.00	7.16	8.21	0.00
	F2	0.00±0.81	0.00	0.00	0.00	14.97	36.41	0.00
	BC1	0.46±0.80	260.39	16.68	13.94	20.50	25.50	0.55
	BC2	0.74±0.73	219.99	28.38	18.70	21.69	33.01	0.57
T.S.S.%	P1	0.32±0.86	0.30	1.42	1.43	2.53	2.44	0.59
	P2	0.00±1.80	0.00	0.00	0.00	1.12	2.23	0.00
	F1	0.21±0.90	0.11	0.46	0.56	1.22	1.78	0.31
	F2	0.16±0.62	0.51	2.36	3.33	8.27	7.66	0.43
	BC1	0.88±0.71	1.74	8.29	5.02	5.36	4.61	1.09

	BC2	0.81±0.72	1.17	4.81	3.04	3.39	3.79	0.80

h^2: ~~broad~~ Broad sense heritability; GA: ~~genetic~~ Genetic advance; GAM%: ~~genetic~~ Genetic advance as percent of mean; GCV%: ~~genotypic~~ Genotypic coefficients of variation; PCV%: ~~phenotypic~~ Phenotypic coefficients of variation; ECV%: ~~error~~ Error coefficients of variation; RCV: ~~relative~~ Relative coefficient of variation.

Principle Component Analysis (PCA):

Principal component analysis simplifies the complex data by transforming the number of correlated variables into a smaller number of variables called principal components. To assess the relationship between studied traits and six generations, principal component analysis was utilized that condensed them to only two components (PCA1 and PCA2).The eigenvalues for PC1 and PC2 were 3.09 and 0.90, respectively (Table 6). The PCA1 and PCA2 explained 99.77% of the total variation between six generation based on all studied traits, mainly distinguished the generations in different groups. Thus, the PCA1 and PCA2 were employed to draw a biplot (Fig. 1). The analysis displayed that the PCA1 contributed in77.20% of the total variation with P1, F1 and BC1 generations. On the other hand, the PCA2 explained 22.57% of the total variability with P2, F1 and BC2. Hence, selection of these studied traits with high PCA1 and PCA2 ~~are~~ were more suitable and effective ~~from~~ than BC1 and BC2 generations. In practice, the choice of F2 vs. backcross based populations in "second cycle" breeding is complicated by the fact that the breeder regards not only a single trait but several characters simultaneously [13].

Table 6. Results of principal component analysis for six generations based on the studied traits during the two locations.

Principal component analysis (PCA)	Eigen value	Percent of variance	Cumulative variance
PCA1	3.09	77.20	77.20
PCA2	0.90	22.57	99.77

The relationships (similarities and dissimilarities) between six generations and studied traits ~~during~~ in two locations are graphically displayed in abiplot of PCA1 and PCA2 (Fig.1).According to biplot analysis, the correlation coefficients between root length (RL), root diameter (RD) and root weight (RW) traits were positive and highly significant ~~during~~ in six generations (smallest acute angles~~),~~). ~~this~~ This means that selection based on these traits ~~will~~ would result in an increasing sugar beet yield in both locations. While, root traits were negatively associated with T.S.S %, where the angles between them were slightly less than 90 degrees or obtuse. Using the biplot diagram (Fig.1), F1 generation ~~had~~ was located between all studied traits. Whilst, the roots traits ~~are~~ were located near the P1 and BC1 generations, T.S.S.% ~~is~~ was located near the P2 and BC2 generations. On the other hand, the F2 generation ~~is~~ was located away from the all studied traits. The biplot analysis of the relationship between the six generations revealed that the most appropriate generations for selecting these traits ~~are~~ were BC1 and BC2 ~~under~~ in the two locations. The Backcross method works best for qualitative traits [36] such as root traits in sugar beet. ~~Melchinger~~[13] indicated that F2 and backcross populations offer equal alternatives regarding time, labor, level of inbreeding, and amount of genetic variance released within lines in subsequent selfing generations if linkage and epistasis ~~are~~ were of minor importance. The choice of segregating population ~~can~~ could therefore be based on properties of the first segregating generations.

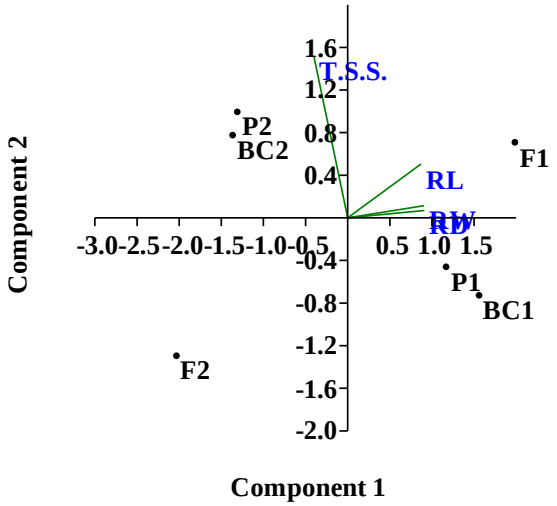

Fig. 1.Biplot diagram based on first two principal component axes of six generations according to mean measured of studied traits ~~under~~ in two locations.

CONCLUSIONS

Significant differences among six generations for all studied traits were found ~~under~~ in two locations. The values of variance components, heritability and other genotypic parameters for all studied traits during segregating generations (F2, BC1 and BC2) were higher than non-segregating generations (P1, P2 and F1). The mean performances and principal component analysis of the relationship between the six generations exhibited that the most appropriate generations for selecting these traits ~~are~~ were BC1 and BC2 ~~under~~ in the two locations. Future studies examining epistasis and linkage should also utilize selfing generations derived from the F2 and backcross populations for improving sugar beet yield in Egypt.

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