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GENETIC IMPROVEMENT OF SWEET MELON BY INBREEDING AND SELECTION

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ABCTERACT: *This study was conducted during the period from 2012 to 2014 for improving the productivity and fruit quality of local resources of sweet melon by increasing their homogeneity through inbreeding and selecting the best individual genotypes during four successive generations to produce inbred lines was the aim of this investigation. Significant differences between the base populations and selected inbred lines were observed for all studied traits. The round fruits were observed in Bm920, Si819, Bm922 and Bm923 (0.88< fruit shape index < 1.1). Twelve out of 21 genotypes had fruits with cylindrical shape (1.1< fruit shape index < 1.5), while the remaining five inbred lines were oblong shape (1.5< FSI). Concerning the mean values of selected inbred lines ranged from 5.57 to 23.86 ton/feddan and the highest values, i.e., 23.68, 15.03 and 13.2 ton/feddan were observed for Gs48, Kb613 and Fb25, respectively. Estimates of coefficient of variance (C.V %) values in the new selected inbred lines (C_4) for the studied traits revealed higher homogeneity than base populations in all traits viz., Si819 and Bm924. Also, each of Bm920, Bm923, Si818, Si817, Fb25, Fb24, Ab12, Gs48, Ai511, Kb614 and Qi715 were homogeneous in all traits except average fruit weight, while Da1227 was homogeneous in average fruit weight, seed cavity diameter, flesh thickness and fruit shape index. These new inbred lines are enough homogeneous and could be considered as new inbred lines of sweet melon.*

Key words: *Sweet melon. Selection, Coefficient of variance, heritability, inbreeding and homogeneous*

INTRODUCTION

Sweet melon (*Cucumis melo* var. *aegyptiacus* L.) is a local variety of melon in Egypt. It is staple and refreshing fruit in Egypt (Ibrahim 2012). Melon's fruits are consumed in the summer period and are popular because the pulp of the fruit is very refreshing, high nutritional and sweet with a pleasant aroma (Melo *et al* 2000). Also, Melon (*Cucumis melo* L.) is an economically important dicotyledonous vegetable crop in the cucurbitaceae family. At present, melon is cultivated under both tropical and subtropical climatic conditions throughout the world (Reddy *et al* 2013). According to Ibrahim (2012) the presence of genetic variation in the breeding material at hand determines the success or failure of any breeding or bioengineering program. Therefore, the measurement of genetic variation and understanding mode of inheritance of quantitative traits are essential steps in any crop improvement program.

The most of cultivation of sweet melon is based on local open pollinated varieties which are maintained by farmers. The commercially important improved cultivars of sweet melon are Kahera-6, Ananas El-Dokki and Shahd El-Dokki. So, developing local sweet melon, based on local genotypes, may result in very promising outputs, especially because the germplasm of sweet melon is available in Egypt is having high genetic variability (El-Shimi and Ghoneim, 2006). Reddy *et al* (2013) who reported that maximization of yield is one of the most important objectives of melon breeding programmes. Continued yield increases in melon will likely depend on the availability and use of genetic variability and breeding for yield or yield-related traits. Germplasm is an indispensable material to plant breeders and germplasm collection is essential to crop improvement. So, systematic study and evaluation of germplasm is imperative to understand the genetic background and the breeding value of the available germplasm

and is of great importance for current and future agronomic and genetic improvement of the crop. Yield is a complex character influenced by many components. Yield and its components are quantitative characters and are affected by environment (Ahmed and Khaliq 2007). Due to the complex inheritance of yield-related traits, breeding for yield in many crop species has been difficult (Yadav *et al* 1998). Also, Reddy *et al* (2013) found that direct selection for yield is not effective. Efficient selection for yield in crops requires the estimation of genetic parameters for the strategic planning and allocation of limited resources. So, the genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epistasis (non-allelic interaction). Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean. It is important in choosing an appropriate breeding programme for improving the traits in any crop to know the mean value, variability, heritability of the trait. The estimates of heritability alone fail to indicate the response to selection. Therefore, heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance and genetic advance as percentage over mean (Johnson *et al* 1955). Heritability provides an idea to the extent of genetic control for expression of a particular trait and the reliability of phenotype in predicting its breeding value (Tazeen *et al* 2009). High heritability indicates less environmental influence in the observed variation (Songsri *et al* 2008). It also gives an estimate of genetic advance a breeder can expect from selection applied to a population and help in deciding on what breeding method to choose (Hamdi *et al* 2003). Genetic advance which estimates the degree of gain in a trait obtained under a given selection pressure is another important parameter that guides the breeder in choosing a selection program (Shukla *et al* 2004). High heritability and high genetic advance for a given trait indicates that it is governed by additive gene action and, therefore, provides the most effective condition for selection (Panse 1957, Rakhi and Rajamony 2005, Torkadi *et al* 2007 and Tomar *et al* 2008). According to Khatab *et al* (2013) the realized gain of selection of some studied characters showed some inbreeding depression as a result of the two applied cycles of pure line method of selection. On the other hand, the characters height of the first fruiting node, fruit color and shape possessed considerable realized gain on cycle1 (S_1) and cycle2 (S_2) of selection when compared with the base population (S_0).

The aim of this investigation was to improve the productivity and quality of local resources of sweet melon by increasing their homogeneity through self pollination and selecting the best individual genotypes for four successive generations to produce inbred lines. Also, the estimation of the coefficient of variance for fruit quality traits within basic populations and inbred lines derived from it to compare the homogeneity between basic populations and its inbred lines. Beside the estimation of the genotypic and phenotypic components of variance, heritability, expected genetic advance and realized gain (RG %) of selection for all studied traits to find out the selection role in melon improvement with a view to recommending breeding methods for the improvement of the crop.

MATERIALS AND METHODS

Eleven different local genotypes of sweet melon were collected from different regions in Egypt to use as genetic materials for this study (Table 1). Self pollination and selection of desirable horticultural traits were made for individual plants from each genotype for four successive generations under greenhouse conditions during the 2012 and 2013 early and late summer seasons of each year at Kaha Vegetable Research Farm (KVRF), Kalubia. Genotypes seedlings production was carried out in a plastic house for all seasons.

Table 1. The collection regions for different local genotypes of sweet melon used in this study.

Genotype code	Collection region	Developed inbred lines
Ab1	Absheway-Fayoum	Ab11 - Ab12
Fb2	Al Fashn-Beni Sueif	Fb24 - Fb25
Qq3	Qeft-Qena	Qq37
Gs4	Girga-Sohag	Gs48
Ai5	Abu Suweir-Ismaelia	Ai511
Kb6	Al Khatatba-Minufiya	Kb613 - Kb614
Qi7	East Qantara-Ismaelia	Qi715 - Qi716
Si8	Al Salihiya-El Sharkia	Si817 - Si818 - Si819
Bm9	Bani Mazar-El Minya	Bm920 - Bm922 - Bm923 - Bm924
Sa10	Sodfa-Assiut	Sa1025 - Sa1026
Da12	Dirout-Assiut	Da1227

Seed sowing and transplanting dates were, 1 Jan. and 1 Feb. for early summer season and 15 Jun. and 1 Jul. for late summer season in the two years 2012 and 2013, respectively. Thirty seedlings were transplanted from each genotype under greenhouse and both self pollination and selection for four generations were applied in the two years of 2012 and 2013. Finally, according to the results obtained on the degree of homogeneity and the preliminary yielding ability after 4 generations from observations, self pollination and selection for desirable horticultural traits, 21 selected inbred lines (C_4) and their base populations (C_0) were evaluated in the open field condition during the 2014 early summer season at KVRF. A randomized complete block design with 3 replicates was used. Each experimental plot consisted of one bed, 1.5 m. wide and 8 m. long., with 50 cm within plants. They were surface irrigated and given the common agricultural practices. Evaluation of 21 selected inbred lines (C_4) and their base populations (C_0) in the open field were recorded for the following characters:

1. Fruit quality traits: average fruit weight (AFW), seed cavity diameter and flesh thickness, fruit shape index (FSI) calculated as the ratio of fruit length to fruit diameter. Fruits with a fruit shape index less than 0.88 were classified as oblate, those with a FSI ranging from 0.88 to 1.1 were considered round, those with a FSI ranging from 1.1 to 1.5 were classified as cylindrical and those with a FSI above 1.5 were classified as oblong (Rashidi and Seyfi 2007). Total soluble solids (TSS) were determined using a hand refractometer. The remain traits such as netting, rind color, striped, flesh color and flesh texture were measured as descriptive traits depend on the visual method according to description of the international union for the protection of new varieties of plant (UPOV).
2. Yield as total yield (TY) and marketable yield (MY).

Statistical Analysis:

Obtained data were subjected to analysis of variance and the mean comparisons according to Gomez and Gomez (1984). Coefficient of variability (C.V. %) was calculated within and between inbred lines and original populations for some important traits according to Steel and Torrie (1960).

Genotypic (σ^2g), phenotypic (σ^2p) variance, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad sense heritability (h^2bS) were estimated according to Falconer and Mackay (1996). Also, Realized gain (RG) after four selective generations (C_4) relative to the original population (C_0) was calculated as illustrated by Falconer (1989), using the means of the various populations in the following equation:

R.G% (of C_4 relative to C_0) = (C_4-C_0) / C_0

Where; C_0 and C_4 are the mean values of the original population, and after four selective generations, respectively.

RESULTS AND DISCUSSION

Degree of homogeneity

Estimated coefficient of variance (C.V %) for average fruit weight (Table 2) ranged from 24.03 to 76.85 % in the base populations with the mean of 454.50%. The lowest C.V % value was observed for the genotype Bm9 while, the highest C.V % value was recorded for the genotype Gs4. On other hand, in selected inbred lines, data revealed that the genotypes Si819, Bm924 and Da1227 were the highest homogeneous ones, since they showed the lowest variation within their plants. The obtained C.V. % values in these inbred lines ranged from 8.32 to 10.71%., indicating that they were more homogenous than other selected genotypes. These results are in agreement with Abdel-Ghani and Atif (2014). For seed cavity diameter, estimated coefficient of variance (C.V %) ranged from 13.42 to 30.38 % in the base populations. On other hand, in selected inbred lines, variance coefficient (C.V %) values ranged from 4.04 to 12.05 % with an average of 6.96%. The selected inbred lines Bm920, Fb24, Kb613, Kb614, Si819, Si818, Fb25, Da1227, Ai511 and Qi716 were the highest homogeneous ones which had the lowest C.V % values, *ie.*, 4.04, 4.05, 4.46, 5.13, 5.15, 5.43, 5.45, 561,5.66 and 5.85%, respectively.

Regarding flesh thickness, estimated coefficient of variability (C.V %) ranged from 15.11 to 26.17 % in the original populations and from 5.79 to 11.06 % in the selected ones with an average of 7.86%. All selected inbred lines were homogeneous except Sa1025 and Sa1026, indicating that they were more uniform than other both Sa1025 and Sa1026 selected genotypes.

For fruit shape index, estimated coefficient of variability (C.V %) ranged from 9.46 to 40.78 % and from 3.12 to 11.41 % in the original populations and selected inbred lines, respectively. On other hand, The lowest C.V % values, *ie*., 3.12, 4.05, 4.06, 4.78 , 4.82, 5.43, 6.15, 6.78 and 6.95% were recorded for the genotypes, Bm920, Bm923, Qi715, Si819, Si817, Bm922, Si818, Qi716 and Bm924, respectively, indicating that they were more homogeneous than other selected genotypes. Estimated coefficient of variability (C.V %) for total soluble solids (TSS %) ranged from 14.68 to 43.51 % in the base populations and ranged from 3.44 to 12.57 % in C_4 selected generation. On the other hand, the lowest C.V % values in the selected inbred lines, *ie.*, 3.44, 4.92, 5.2, 6.06 and 6.07 % were recorded for the genotypes Ab12, Bm923, Gs48, Bm922 and Kb614, respectively, indicating that they were more homogeneous than other selected ones. In general, estimates of C.V% values in the new selected inbred lines C_4 for the studied traits revealed higher homogeneity than base populations in all traits *viz*., Si819 and Bm924 in all studied traits. Also, each of Bm920, Bm923, Si818, Si81, Fb25, Fb24, Ab12, Gs48, Ai511, Kb614 and Qi715 had homogeneous in all traits except average fruit weight, while Da1227 had homogeneous in average fruit weight, seed cavity diameter, flesh thickness and fruit shape index. These new inbred lines are enough homogeneous and could be considered as new inbred lines of sweet melon.

Morphological description of some studied traits

In both the base populations and selected inbred lines, fruit characters were varied greatly (Table 3), cork formation

varied greatly from present, semi and absent. Skin color varied greatly from deep yellow, orange light yellow, green and yellow. Grooves trait varied greatly from weakly, strongly and absent in original population and selected inbred lines. Flesh color varied greatly from pale orange, greenish white, whitish green and orange in original population, while, in selected inbred lines varied greatly from pale orange, greenish white, whitish green ,orange, white, light green and cream. These findings agreed with those of Burger *et al* (2006). For flesh firmness medium, soft and hard in original populations and selected inbred lines.

Table (2). Estimated coefficient of variance (C.V %) values of the base and selected inbred lines

genotypes\Traits	Average fruit weight	Seed cavity diameter	Flesh thickness	Fruit shape index	Total soluble solids %
Original populations (C_O)					
Ab1	41.24	19.64	15.11	24.18	18.33
Fb2	65.51	21.55	25.83	35.29	26.85
Qq3	49.73	29.69	24.91	40.78	24.19
Gs4	76.85	30.38	26.17	18.51	43.51
Ai5	44.98	24.02	21.36	19.58	18.19
Kb6	36.79	19.75	23.39	9.46	25.16
Qi7	34.69	13.42	20.46	12.49	14.68
Si8	39.76	17.29	20.58	16.32	26.22
Bm9	24.03	19.15	20.56	17.61	24.51
Sa10	51.88	18.15	22.24	20.22	23.50
Da12	35.01	15.11	22.26	17.03	22.26
Mean	45.50	20.74	22.08	21.04	24.31
Selected lines (C_4)					
Ab11	11.28	6.93	6.69	11.41	9.14
Ab12	21.08	7.79	8.88	9.24	3.44
Fb 24	16.42	4.05	5.79	9.09	6.87
Fb 25	21.43	5.45	6.83	7.01	6.64
Qq37	43.49	12.05	6.40	10.76	10.22
Gs48	43.07	7.67	8.64	7.25	5.2
Ai511	29.28	5.66	8.32	8.03	7.24
Kb613	23.14	4.46	7.53	7.59	12.57
Kb614	17.72	5.13	7.28	7.88	6.07
Qi715	21.08	9.81	7.80	4.06	9.23
Qi716	16.10	5.85	6.75	6.78	10.33
Si817	16.58	7.97	9.07	4.82	9.05
Si818	13.46	5.43	7.56	6.15	9.35
Si819	8.32	5.15	8.48	4.78	8.11
Bm920	14.94	4.04	6.49	3.12	6.98
Bm922	14.28	11.14	6.38	5.43	6.06
Bm923	15.46	9.73	7.16	4.05	4.92
Bm924	8.93	6.71	10.13	6.95	7.71
Sa1025	13.33	8.34	10.24	7.08	7.49
Sa1026	14.68	7.23	11.06	8.54	9.22

Da1227	10.71	5.61	7.52	6.98	12.37
Mean	18.80	6.96	7.86	7.00	8.01

Table (3). The morphological description for original populations and selected inbred lines of sweet melon.

Genotypes	Fruit				
	Cork formation	Skin color	Grooves	Flesh color	Flesh firmness
Base populations (C_O)					
Ab1	present	deep yellow	weakly	pale orange	medium
Fb2	semi	Orange	strongly	greenish white	medium
Qq3	semi	Green	strongly	greenish white	soft
Gs4	semi	light yellow	strongly	whitish green	soft
Ai5	absent	Green	strongly	pale orange	soft
Kb6	absent	light green	weakly	whitish green	medium
Qi7	present	Yellow	absent	greenish white	medium
Si8	present	Yellow	weakly	orange	hard
Bm9	present	Yellow	absent	orange	hard
Sa10	absent	Green	absent	pale orange	medium
Da12	semi	deep orange	strongly	whitish green	soft
Selected inbred lines (C_4)					
Ab11	present	Orange	absent	white	soft
Ab12	present	Orange	absent	pale orange	medium
Fb 24	semi	Green	strongly	whitish green	soft
Fb 25	semi	Orange	weakly	white	soft
Qq37	semi	Green	strongly	greenish white	medium
Gs48	semi	Yellow	weakly	greenish white	medium
Ai511	absent	Yellow	strongly	pale orange	medium
Kb613	semi	light green	strongly	greenish white	soft
Kb614	absent	light green	weakly	light green	medium
Qi715	present	Yellow	absent	greenish white	medium
Qi716	present	Yellow	absent	cream	medium
Si817	present	Yellow	weakly	orange	medium
Si818	present	Yellow	absent	pale orange	medium
Si819	semi	Yellow	strongly	orange	hard
Bm920	present	deep yellow	absent	pale orange	medium
Bm922	present	bright yellow	absent	cream	medium
Bm923	present	Yellow	absent	white	medium
Bm924	present	deep yellow	absent	greenish white	hard
Sa1025	absent	deep yellow	absent	cream	soft
Sa1026	absent	Orange	strongly	pale orange	medium
Da1227	semi	deep orange	strongly	whitish green	soft

Mean performance of original and selected- inbred lines

Significant differences between the mean of base population and selected inbred lines were observed for mean values of all

studied traits (Table 4). Average fruit weight ranged from 0.78 kg (Qq3) to 1.95 kg (Ai5) for base populations and the highest values were produced by Ai5 (1.95) followed by Kb6 (1.75), respectively, without significant differences between them. Meanwhile, the mean value of selected inbred lines ranged from 0.76 to 1.63 kg (Table 4). The highest mean values were recorded for inbred lines Si818 followed by Bm922 (1.63 and 1.53kg, respectively) without significant differences between them and the lowest ones were observed for Qi715, Kb613 and Ab12 (0.76, 0.8 and 0.82 kg, respectively). Regarding seed cavity diameter the mean value in base populations ranged from 4.5 to 13.4 cm. The highest mean values were observed in Gs4 followed by Da12 (13.4 and 8.2 cm, respectively), while the lowest mean values were recorded in Qi7 (4.5cm) followed by Bm9 (5.2cm). The mean value of the selected inbred lines ranged from 4.1 to 7.6 cm. The highest values, *i.e.,* 7.6 followed by 7.0, 6.8 and 6.7 cm were observed for both Gs48 and Ai511 (the same value), Fb25, Ab12 and Ab11, respectively, without significant differences between them. While, the lowest ones were obtained in Qi715, Qi716, Bm923 and Bm924 (4.1, 4.2, 4.2 and 4.4 cm, respectively).

Concerning the mean value of flesh thickness (Table 4) base populations ranged form 2.4 (Ai5) to 3.9 (Bm9) cm. The highest values were observed for Bm9 followed by Gs4 and Qq3 (3.9, 3.8 and 3.5 cm, respectively), without significant differences between them. The lowest values were observed for Ai5 (2.4 cm) followed Fb2 and Sa10 (2.5cm) without significant differences between them. The selected inbred lines ranged from 2.1cm (Ai511 and Sa1026) to 4.0 cm (Kb613). The highest values, *i.e.,* 4.0, 3.8 were recorded for Kb613 and Bm924, 3.7 (Fb25 and Bm922) and 3.5 cm for Fb24, without significant differences between them. The lowest values were observed in (Ai511 and Sa1026 the same value 2.1 cm) followed by Sa1025 (2.3 cm) without significant differences between them.

Regarding the mean value of fruit shape index (Table 4), the original populations ranged from 1.05 to 2.12 (cylindrical to oblong fruit shape). Generally, a great diversity was observed among the 21 selected inbred lines for fruit shape. The selected inbred lines ranged from 0.97 to 2.29. The round fruits were observed in Bm920, Si819, Bm922 and Bm923 (0.88< FSI < 1.1). Twelve out of 21 genotypes had fruits with cylindrical shape (1.1< FSI < 1.5), while the remaining five inbred lines were oblong shape (1.5< FSI). These results are in agreement with those of Rashidi and Seyfi (2007). For total soluble solids% (Table 4), the mean values of base populations ranged from 5.5 to 10.0%.The highest mean value was observed in Ab1 (10.0%) followed by Kb6 (9.9%) without significant difference between them. The lowest mean value was recorded in Gs4 (5.5%) followed by Qq3 (5.6%) without significant differences between them. The 21 selected inbred lines ranged from 5.2% (Fb24) to 10.9% (Si819). The highest mean values, *i.e.,* 10.9, 10.2 and 10.0% were observed for Si819, Si817 and Bm924 without significant differences between them and the lowest values, *i.e.,* 5.2, 6.0, 6.3 and 6.5% were observed for Fb24, Qi716, Si818 and Fb25 respectively. Significant differences among the base populations and selected inbred lines were observed for total yield/feddan (Table4). The mean values of base populations ranged from 6.07 to 18.85 ton/feddan and the highest values, *i.e.,* 18.85, 11.3 and 11.02 ton/feddan were observed for Gs4, Da12 and Fb2, respectively, while the lowest one was in both Kb6 (6.07 ton/feddan) and Si8 (7.03 ton/feddan) without any significant differences between them. The mean values of selected inbred lines ranged from 5.57 to 23.86 ton/feddan and the highest values, *i.e.,* 23.68, 15.03 and 13.2 ton/feddan were observed for Gs48, Kb613 and Fb25 respectively, while the lowest one was in Si819 (5.57 ton/feddan) and Qi716 (5.96 ton/feddan) without significant differences between them. On the other hand, in marketable yield/feddan (Table4), origial populations ranged from 5.52 to 17.18 ton/feddan. Gs4 genotype gave the highest value (17.18 ton/feddan) followed by Da12

(9.98 ton/feddan) and Fb2 (9.32 ton/feddan). The lowest mean values were observed for Kb6, Si8 and Qi7 (5.52, 6.6 and 6.62 ton/fedan, respectively), without significant between them. Meanwhile, the selected inbred lines ranged from 4.91 to 16.53 ton/feddan. The highest values, *i.e.,* 16.53, 13.73 and 11.43 were observed for Gs48, Kb613 and Fb25, respectively. The lowest mean values, *i.e.,* 4.91, 5.23, 5.42, 5.90, 5.97 and 5.98 ton/feddan were observed for Ab11, Qi716, Si819, Ab12, Bm920 and Kb614, respectively, without significant between them.

Table (4). Mean performances for base populations and selected inbred lines of sweet melon.

Genotypes	Average fruit weight(Kg)	Seed cavity diameter (cm)	Flesh thickness (cm)	Fruit shape index	Total soluble solids %	Total yield ton/feddan	Marketable yield ton/feddan
Base populations (C_O)							
Ab1	1.18	6.1	2.7	1.23	10.0	10.06	8.65
Fb2	1.33	6.0	2.5	1.69	6.8	11.02	9.32
Qq3	0.78	7.7	3.5	1.93	5.6	10.12	8.65
Gs4	0.94	13.4	3.8	1.05	5.5	18.85	17.18
Ai5	1.95	6.5	2.4	1.77	6.2	7.81	6.51
Kb6	1.75	6.3	3.3	1.48	9.9	6.07	5.52
Qi7	1.23	4.5	3.2	1.38	7.6	7.60	6.62
Si8	0.95	5.8	3.3	1.29	7.3	7.03	6.60
Bm9	1.0	5.2	3.9	1.27	8.3	7.99	7.48
Sa10	1.19	6.4	2.5	2.12	7.2	10.56	7.45
Da12	1.16	8.2	2.8	1.17	6.8	11.30	9.98
Mean	1.22	6.92	3.08	1.49	7.38	9.86	8.54
Selected lines (C_4)							
Ab11	1.29	6.7	2.8	1.25	9.6	6.75	4.91
Ab12	0.82	6.8	2.7	1.17	8.5	6.58	5.90
Fb 24	1.25	6.3	3.5	1.77	5.2	9.05	7.92
Fb 25	1.00	7.0	3.7	2.29	6.5	13.20	11.43
Qq37	1.35	5.1	3.1	1.37	6.8	9.29	7.36
Gs48	0.94	7.6	2.6	1.12	9.5	23.68	16.53
Ai511	1.25	7.6	2.1	1.44	7.0	10.10	8.40
Kb613	0.80	6.0	4.0	1.15	7.3	15.03	13.73
Kb614	0.94	5.2	3.4	1.19	8.3	6.37	5.98
Qi715	0.76	4.1	3.3	1.47	7.4	8.82	8.29
Qi716	1.18	4.2	3.1	1.68	6.0	5.69	5.23
Si817	1.30	5.3	3.3	1.11	10.2	7.33	6.57
Si818	1.63	5.1	2.9	1.30	6.3	11.03	10.43
Si819	1.10	5.3	3.0	0.98	10.9	5.57	5.42
Bm920	1.40	5.4	3.5	0.97	7.8	6.28	5.97
Bm922	1.53	4.9	3.7	0.99	7.8	10.36	9.33
Bm923	1.14	4.2	3.4	1.03	9.1	6.92	6.50
Bm924	1.18	4.4	3.8	1.12	10.0	7.41	6.77
Sa1025	1.44	4.6	2.3	2.07	7.4	7.56	6.52

Sa1026	0.95	6.7	2.1	1.81	7.9	7.98	7.13
Da1227	1.43	7.0	3.1	1.11	6.6	8.22	6.96
Mean	1.18	5.69	3.11	1.35	7.91	9.20	7.97
LSD at 0.05	0.71	1.46	0.65	0.39	1.52	5.44	5.11

Components of variance

The genotypic and phenotypic coefficients of variation (G.C.V and P.C.V) may serve as a reference point for breeders who try to detect genotypic differences of the most important economic characters, in hybrid plants and mutant populations. It makes also selection of forms with valuable genotypes more effective (Guzhov, 1986).

The obtained results from coefficient of variance for the five studied traits illustrated that the selected inbred lines CV % was very lower than the base populations CV % of these inbred lines. So, this indicated that after four generations of self pollination and selection for base populations, the developed inbred lines showed high homogeneity degree in the five studied traits compared with its base populations.

Estimates of both genotypic and phenotypic coefficient of variance, broad sense heritability and genetic advance for the studied traits are listed in Table (5). The variance was varied from character to another, since the coefficient of variance was ranged from 12.06 to 38.33%. The highest variations among the studied genotypes were observed in each of the traits marketable yield/feddan, average fruit weight and total yield/feddan (38.3, 36.4 and 35.38%, respectively). While, each of seed cavity diameter, (14.67%), flesh thickness (12.86%) and total soluble solids (12.06%). had the lowest ones. Estimated genotypic coefficient of variance (GCV %) vs. phenotypic one (PCV %) for the studied traits were 34.01 vs. 49.77% for average fruit weight, 27.29 vs. 30.98% for seed cavity diameter, 15.3 vs. 19.99 for flesh thickness, 23.98 vs. 29.43% for fruit shape index, 17.23 vs. 21.03% for total soluble solids, 35.42 vs. 50.07% for total yield/feddan and 29.0 vs. 48.06% for marketable yield/feddan. The results coincided with those obtained by Ibrahim (2012).

Broad sense heritability (H^2_b) 46.9% for average fruit weight, 77.59% for seed cavity diameter, 58.61% for flesh thickness, 66.39% for fruit shape index, 67.1% for total soluble solids, 50.05% for total yield/feddan and 36.41% for marketable yield/feddan were obtained. Small difference were observed between GCV and PCV in seed cavity diameter, flesh thickness and total soluble solid, indicating the importance of the genetic effects in controlling the inheritance of these traits resulting in the high value of (H^2_b) in these traits. Therefore, these traits can be improved through selection based on phenotypic observation. These results are in agreement with those of panse (1957), Rakhi and Rajamony (2005), Torkadi *et al* (2007), Tomar *et al* (2008) and Tazeen *et al* (2009). On contrast, high deference was observed between GCV and PCV in the remaining traits and resulting in the low value of (H^2_b) in these traits, indicating a major environmental effect. Therefore, selection may be not effective for these traits. These results are in agreement with those of Yadav *et al* (1998), Ahmed and Khaliq (2007). Songsri *et al* (2008) and Reddy *et al* (2013).

Realized gain (R.G%)

Realized gain values are presented in Table (6). The data showed that the selected inbred lines, *i.e.,* Fb25, Gs48, Kb613, Kb614, , Si817, Si818 and Bm923 had considerable realized gains compared to the base populations for total yield/feddan . While, the inbred lines Qq37, Gs48, Ai511, Si817, Si819, Bm920, Bm924, Sa1025 and Sa1026 for total soluble solid. Meanwhile, the selected inbred lines, *i.e.,* Ab11, Fb24, Fb25, Kb613, Kb614, Qi715, Si817 and Da1227 had considerable realized gains, for flesh thickness trait. These results are in agreement with those of Khatab *et al* (2013).

Table (5). Estimated genotypic and phenotypic variance (GCV and PCV), broad-sense heritability (H^2_b) and genetic advance values of the studied characters in the evaluated populations

Genotypes	Average fruit weight	Seed cavity diameter	Flesh thickness	Fruit shape index	Total soluble solids %	Total yield ton/feddan	Marketable yield ton/feddan
C.V	36.40	14.67	12.86	17.06	12.06	35.38	38.33
σ^2e	0.19	0.80	0.16	0.06	0.87	11.12	9.79
σ^2g	0.17	2.78	0.23	0.11	1.77	11.15	5.60
σ^2p	0.36	3.58	0.39	0.17	2.64	22.27	15.39
GCV%	34.01	27.29	15.30	23.98	17.23	35.42	29.00
PCV%	49.77	30.98	19.99	29.43	21.03	50.07	48.06
H^2_b	46.69	77.59	58.61	66.39	67.10	50.05	36.41
Genetic advance%	32.53	33.65	16.40	27.35	19.76	35.08	24.50

Table (6). Realized gain (RG %) for the studied traits in selected inbred lines of sweet melon.

Genotypes	Average fruit weight(Kg)	Seed cavity diameter	Flesh thickness (cm)	Fruit shape index	Total soluble solids	Total yield ton/feddan	Marketable yield ton/feddan
Ab11	-28.89	9.84	2.69	1.08	-4.01	-32.94	-43.22
Ab12	-34.25	11.48	-2.20	-5.41	-14.38	-34.56	-31.82
Fb 24	99.03	4.42	42.08	4.33	-23.41	-17.85	-14.99
Fb 25	8.52	16.57	48.17	35.04	-5.37	19.81	22.72
Qq37	-49.52	-33.57	-11.48	-29.14	22.75	-8.26	-14.91
Gs48	-61.59	-43.60	-31.14	6.98	72.73	25.60	-3.78
Ai511	42.69	17.01	-12.50	-18.61	14.05	29.33	29.03
Kb613	29.99	-4.26	23.88	-22.47	-26.35	147.69	148.82
Kb614	-5.43	-16.49	3.37	-19.78	-15.88	5.00	8.46
Qi715	19.82	-9.70	2.93	6.78	-2.20	16.15	25.29
Qi716	3.46	-6.00	-1.36	21.79	-20.26	-25.10	-21.01
Si817	-26.63	-9.71	0.71	-13.73	38.64	4.22	-0.51
Si818	-38.70	-12.00	-10.41	0.78	-14.55	56.78	58.03
Si819	-53.17	-10.00	-8.57	-23.58	48.18	-20.81	-17.93
Bm920	-52.30	1.61	-23.09	-22.37	31.45	-30.32	-27.62
Bm922	-20.86	5.16	-11.16	-23.16	-6.05	-21.39	-20.27
Bm923	-27.16	-5.81	-3.78	-22.11	-6.05	29.61	24.72
Bm924	-43.48	-19.35	-12.96	-18.68	10.48	-13.47	-13.14
Sa1025	-33.90	-28.50	-8.87	-2.36	2.76	-28.44	-12.49
Sa1026	3.43	4.15	-17.22	-14.47	9.22	-24.46	-4.21

Da1227	15.41	-14.57	10.32	-5.14	-2.94	-27.29	-30.20

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التحسين الوراثى فى الشمام عن طريق التربية الداخلية و الانتخاب

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الملخص العربى

أجريت هذه الدراسة فى الفترة من 2012 حتى 2014 بمزرعة بحوث الخضرالتابعة لمعهد بحوث البساتين– مركز البحوث الزراعية – قها – القليوبية وذلك بهدف تحسين الصفات البستانية و الجودة فى الشمام. حيث تم تجميع أحد عشر طرز وراثى مختلف من الشمام من مناطق مختلفة بجمهورية مصر العربية.

تم عمل تربية داخلية وانتخاب لبعض الصفات البستانية والجودة لمدة أربعة أجيال متتالية داخل وبين هذه الطرز. ثم تم زراعة الطرزالمنتخبة الجديدة مع االطرز التى تم تجميعها (طرز الاساس) وذلك لدراسة التجانس ومدى التقدم الوراثى للأنتخاب

أوضحت النتائج وجود اختلافات معنوية بين الطرزالمنتخبة الجديدة و طرز الاساس فى كل الصفات المدروسة.

حيث اظهرت السلالات المنتخبة الجديدة Bm920 ، Si819، Bm923، Bm922 ثمار ذات شكل كروى حيث كان معامل شكل الثمرة اكبر من 0.88 واقل من 1.1 ، كما اظهر احد عشر تركيب وراثى منتخب ثمار ذات شكل اسطوانى حيث كان معامل شكل الثمرة أكبر من 1.1 وأقل من 1.5 ، أما باقى السلالات فأعطت ثمار ذات شكل مطاول حيث كان معامل شكل الثمرة أكبر من 1.5 مما يظهر ان الإنتخاب كان فعالا فى إظهار تباينات جديدة فى شكل الثمرة.

أظهرت السلالات المنتخبة الجديدة إنتاجية تراوح من 5.57 إلى 23.68 طن فدان. حيث أعطت السلالات Gs48، Kb613، Fb25 إنتاج 23.68 و 15.03 و13.2 طن /فدان على التوالى.

أوضحت دراسة معامل الاختلاف بين السلالات أن السلالة Si819 ، Bm924 كانت متجانسة بدرجة عالية فى كل الصفات ، كما أظهرت السلالات Bm920، Bm923، Si818، Si817، Fb25، Fb24، Ab12 ، Gs48، Ai511، Kb614 ، Qi715 تجانسا عاليا لكل الصفات عدا صفة وزن الثمرة مقارنة بطرز الاساس.

كما اظهرت السلالات المنتخبة Fb25، Gs48 ، Kb613، Kb614 ،Si817 ، Si818 ، Bm923 عائد انتخابى كبير لصفة المحصول وعدد الثمار/ نبات.

كما اظهرت السلالات Ab11، Fb24، Fb25، Kb613،، Kb614 ،Qi715 ، Si817، Da1227 عائد انتخابى كبير لصفة سمك اللحم.