



Efficiency of Mass Selection and Selection Indices on Improving Growth, Yield and Quality of Cantaloupe (*Cucumis melo*, L.).

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ABSTRACT: Present investigation was carried out during three successive seasons, in years 2021 and 2022. Two cycles of inbreeding and mass selection program were applied, using the methods of selection indices, on 6 strains of melon (cantaloupe) under the green houses of Sabahya Horticulture Research station, Alexandria. Original population (S0), first and second selection generation (S1 and S2) and Boshra 411 as a check cultivar were sown in experimental evaluation in early summer season in first March of year 2022 to test the progress in the traits under studies in a factorial experiment with two factors (genotypes and selection cycle) in randomized complete block design with three replicates (RCBD) in private farm at Al-Mahmudiyah area in Al-Buhaira governorate. Analysis of variance over all mean performances, estimation of genetic parameters like, heritability; genetic advance (G_A) and inbreeding depression (ID) were estimated, for vegetative, flowering and fruiting, yield, and its components characteristics.

The most important results are summarized as follows: There were significant and highly significant differences between all genotypes in all traits with exception to fruit shape index trait. Differences between original population and selection cycles, were significant and highly significant for all traits under study. By comparing the inbred strains to each other (G, M, Q, S, W and X) it can be noted that line S was superior to other strains in most characteristics. By comparing the same strains with the control variety (Boshra 411), it can be noted that there was a clear superiority of the control variety in all traits under study. First and second selection generations (S1 and S2) had the highest values for traits like flesh thickness %, netting degree (1-10), placenta hardness (1-10) and dray matter%. The highest estimates of heritability in broad sense ($> 75\%$) were observed for dray matter % (93.28%); total soluble solids % (90.67%); total number of fruits / plant (82.94%); placenta hardness (1-10) (77.26%) and flesh thickness % (76.34%). This was consistent with the close values of GCA and PCV and highest values of Genetic advance (GA) for the same traits. Estimates of inbreeding depression were positive in traits, plant length, total number of nodes / plants; fruit set percentage %; total number of fruits / plants; total yield / plant (KG) and fruit shape index. The largest inbreeding depression were in traits total number of fruits/ plant and fruit set percentages % (19.91 and 18.13 % respectively).

Keywords: *cantaloupe* (*Cucumis melo*, L.), *selection index*, *heritability*, *inbreeding depression*, *genetic advance*.

INTRODUCTION

Cantaloupe (*Cucumis melo*, L.) (Mango melon), *C. melo* Var. *dudiam* (Pocket melon) (Sebastian *et al.*, 2010). Melon genotypes is an important vegetable crop, produced worldwide with average total production in 2021, 28.617.598 tons produced from a cultivated area estimated at 2.565.164 fed worldwide. Egyptian cultivated area and total production of all melon genotypes, reached its peak in 2016 it was 100,756 fed (40,774 ha) with total production 1066817 tons and average yield / fed 10.59 tons / fed. This increase in the cultivated area, in addition to the average productivity / fed, was interpreted as an increase during this period in the import of hybrid

seeds. With the import process gradually decreasing by 2021, the harvested area for all melon genotypes has become 15,934 fed (6,452 ha) with total production 179,129 tons and average yield / fed 11.24 tons / fed. These results warn of a problem in this field (the field of improved and hybrid seed production) in general, which calls for the attention of all concerned institutions in an attempt to contribute to finding solutions to improve local breeds and produce selected strains that are later used in the production of hybrids (FAO, 2021). Genetic improvement programs mainly target factors such as modification of mean population. Mass selection considered one of the effective breeding programs in improving cross-pollinated crops, mass selection can be briefly described as, best individuals in terms of some predetermined trait phenotypically selected from population then seeds harvested in bulk to produce next generation, by repeating the selection periodically, improvement happens faster in early selective generation (Naroui Rad. 2022).

Selection indices method aiming to maximize advance in economic traits and effective in selection for several traits at the same time, selection index require knowledge of (i) the genotypic and phenotypic variance (ii) the genotypic and phenotypic covariance (iv) the economic weight for trait. The "economic" values may reflect the market situation, preferences (Magnussen 1990). Numerous investigations was carried out on selection indices in plant breeding like Lal and Singh (1997) on melon, Gomaa *et al.*, (1999) on cotton, Daliya and Wilson, (2004) on eggplant, Rabie *et al.*, (2004) on rice grain, Hussein *et al.*, (2008) on rice, Muhammad and syed, (2010) on sweet corn, Mohammad *et al.*, (2014) on sugarcane, Nyo *et al.*, (2020) on rice grain and Gomes *et al.*, (2021) on melon. The authors reported that there was more success using selection index for increasing expected response to selection than direct selection of different traits at the same time. Heritability in broad sense is very important and should be recognized as a first step before starting any breeding program. Heritability measures are the portion of the total genetic variance that are due to hereditary factors. High values of heritability associated with high genetic advance means high additive gene effects and consequently the scope for improving traits through phenotypic selection is more, (Khomphet *et al.*, 2022). Inbreeding

depression measured the reduction in performance of the F2 generation due to inbreeding. The large amount of inbreeding depression for fruit weight, and fruits yield/plant, were expected since these traits showed large amount of heterosis. (Kustanto., 2023). Current investigation aimed to try to increase the homogeneity of the six inbred lines of cantaloupe cultivar, by selfing and selecting the best genotypes for two successive seasons (selection index model). Evaluate the selection generation and original population behind commercial cultivar in separate evaluation season. Asses the magnitude of genetic variability and use of a certain genetic parameter which play a big role in cantaloupe improvement.

MATERIALS AND METHODS

Present study was carried out during three successive seasons in years of 2021 and 2022. The experimental sites were the green houses and the experimental field of Sabahya Horticulture Research station, Alex, Egypt, and a private farm in Al-Mahmudiyah area in Al-Buhaira governorate. Details of the materials and techniques used in the investigation are briefly described as follow:

Experimental details:

Geographic location, climate and soil and water analysis.

Experimental field of breeding technique (greenhouses of Sabahya Horticulture Research station) situated at latitude of 31°12'54.4"N and longitude of 29°58'26.4"E. regarding evaluation experiment (private farm in Al-Mahmudiyah area in Al-Buhaira governorate) situated at latitude of 31°10'30.1"N and longitude of 30°30'51.6"E. Important weather data during evaluation experiment period (summer season of 2022) is shown in Fig. (1). Soil and water analysis of both farming areas are presented in Table (1).

Plant materials

The original populations for this investigation consist of six strains of melon (cantaloupe) namely G, M, Q, S, W and X genotypes. They are a result of melon breeding program at Cross-Pollination Vegetable Research Department, Horticulture Research Institute, Agriculture Research Center, Egypt. The origin and some special features for the six melon strains under study are listed in Table (2).

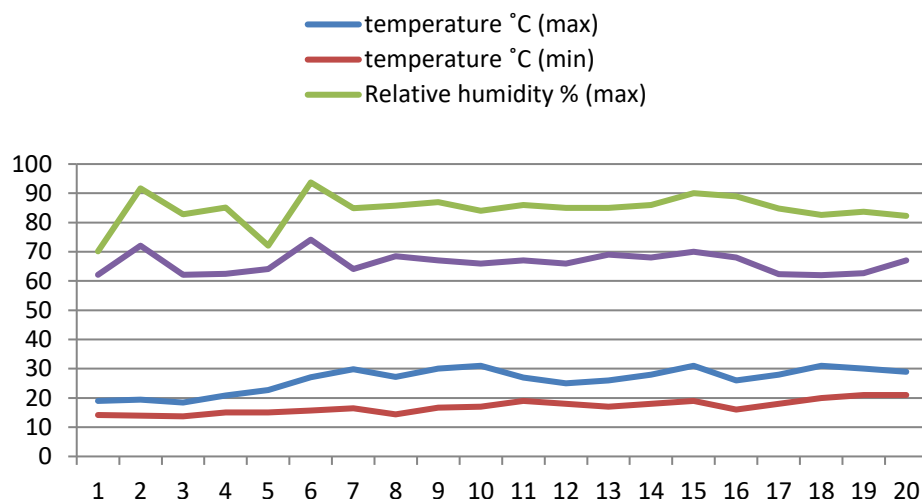


Fig. (1). Average temperature degrees (°C) and relative humidity percentages (%), in Al-Mahmudiyah area in Al-Buhaira governorate on a weekly basis, over a period of 20 weeks, which is the period of the evaluation season for the strains under study.

Table (1). Soil and water analysis of Sabahya Horticulture Research station (pollination site) and Al-Mahmudiyah (evaluation site).

Parameters	Soil analysis		Measuring unit
	Sabahya	Al-Mahmudiyah	
Mechanical analysis			
Sand	56.72	46.72	%
Silt	16	20	%
Clay	27.28	33.28	%
Textural class	Sandy clay loam	Clay loam	
PH(1:2)	7.5	7.8	
EC(1:2 water extract)	1.12	0.953	Ds/m
O.M	1.75	1.1	%
Caco ₃	3.9	2.3	%
Soluble cations			
Calcium (Ca ²⁺)	5	5	Meq/l
Magnesium (Mg ²⁺)	8	4	Meq/l
Sodium (Na ⁺)	2.5	2.6	Meq/l
Potassium (K ⁺)	0.38	0.13	Meq/l
Soluble anions			
Carbonates (Co ₃)+Bicarbonates (Hco ₃)	1	4	Meq/l
Chloride (Cl ⁻)	11	8.4	Meq/l
Sulfate (So ₄ ²⁻)	3.65	0.8	Meq/l
Available nutrients			
Nitrogen (N)	5.2	11.5	Meq/l
Phosphorus (P)	22.3	35.9	Meq/l
Potassium (K)	300	275	Meq/l
Water analysis			
PH	7.1	7.2	-
EC	0.460	0.580	Ds/m
Soluble cations			
Calcium (Ca ²⁺)	2	4	Meq/l
Magnesium (Mg ²⁺)	3	3	Meq/l
Sodium (Na ⁺)	1.1	1.1	Meq/l
Potassium (K ⁺)	0.2	0.26	Meq/l
Soluble anions			
Carbonates (Co ₃)+Bicarbonates (Hco ₃)	1	1	Meq/l
Chloride (Cl ⁻)	10	8	Meq/l
Sulfate (So ₄ ²⁻)	0.12	0.12	Meq/l

Ds/m = Dsi Siemens / m it is a unit of measurement of the degree of electrical conductivity

Meq/l = mille equivalent /liter

Table (2). The origin and some special features for the six melon strains under study.

Genotypes	Characteristics	Genotypes	Characteristics
G_{F4} Segregated by selection in F ₂ primal hybrid down to the fourth generation (F ₄)	<ul style="list-style-type: none"> • Strong vegetative growth. • Moderate maturity duration • High netting degree. • There are hollow ribs in the fruit. • Coppery yellow fruit color • Fruit flesh color is light green. • A medium-sized triangular inner cavity. • The fruit is spherical in shape 	S_{S3} Improved strain segregated by inbreeding and selection in Mostadir Matrouh variety (local variety cultivated in Matrouh governorate) down to the third generation (S ₃)	<ul style="list-style-type: none"> • Strong vegetative growth. • Moderate maturity duration. • Moderate netting degree. • Yellow green fruit color. • Fruit flesh color is light green. • A medium-sized triangular inner cavity with high flesh thickness. • The fruits are slightly oval.
M_{F3} Segregated by selection in F ₂ of hybrid Matrouh variety (improved local variety cultivated in Matrouh governorate) × charantais (imported variety) down to the third generation (F ₃)	<ul style="list-style-type: none"> • Strong vegetative growth. • Short ripening period. • High netting degree. • The fruits have non-hollow ribbing. • Yellow fruit color • Fruit flesh color is dark orange. • Small internal circular cavity. • High flesh thickness. • The fruit is spherical in shape. 	W_{S3} Improved segregated line by inbreeding and selection in Mostadir Matrouh variety but with orange flesh (local variety cultivated in Matrouh governorate) down to the third generation (S ₃)	<ul style="list-style-type: none"> • Moderate vegetative growth. • Moderate maturity duration. • High netting degree. • Coppery yellow fruit color. • Fruit flesh color is light orange. • Small internal circular cavity. • High flesh thickness. • The fruit is spherical in shape.
Q_{F4} Segregated by selection in F ₂ primal hybrid down to the fourth generation (F ₄)	<ul style="list-style-type: none"> • Strong vegetative growth. • Short ripening period. • High netting degree. • The fruits have non-hollow ribbing. • yellow fruit color. • Fruit flesh color is light green. • Small internal circular cavity. • High flesh thickness. • The fruit is spherical in shape. 	X_{F4} segregated by selection in F ₂ of Ideal hybrid down to the fourth generation (F ₄)	<ul style="list-style-type: none"> • Moderate vegetative growth. • Moderate maturity duration. • High netting degree. • Canary yellow fruit color. • Fruit flesh color is Light cream. • A medium-sized triangular inner cavity with high flesh thickness. • The fruit is spherical in shape.
control (Boshra 411) (Commercials cultivar)	<ul style="list-style-type: none"> • Very strong vegetative growth. • Short ripening period. • High netting degree. • Yellow fruit color. • Fruit flesh color is Light orange. • Small internal circular cavity. • High flesh thickness. • The fruit is spherical in shape. 		

Development of Genetic Materials

Two cycles of inbreeding and mass selection program were applied on the six strains (G, M, Q, S, W and X) of melon (cantaloupe) in the summer and autumn season of 2021. The original population (S0) of the six strains were planted in green house at the mid of February 2021 direct by seeds on ridges 1 meters wide and 40 cm apart. Mass selection and selfing techniques was conducted as follows: 10 % of the original population from each genotype were selected and its seeds were mixed (mass selection) to get the first selection generation (S1), the same practices was done to get second selected generation (S2) which was planted at end of July 2021. Selection was based on characters; plant length, total number of nodes/plants, total number of branches/plants, total number of fruits/plant, total yield (kg), netting degree (1-10), flesh thickness (%), placenta hardness (1-10), total soluble solids (TSS) and Fruit set percentages (%). Selection was carried out using the methods of selection indices, and its reference was also mentioned.

Evaluation of Genetic Materials:

Seeds of the original population (S0), first and second selection generations (S1 and S2 and Boshra 411 (check cultivar) were sown in experimental evaluation in early summer season in first March of 2022 in foam plates. After one month, in private farm at Al-Mahmudiyah area in Al-Buhaira governorate the transplants were sown on ridges 1.5 meters wide and 50 cm apart to test the progress in the traits under studies in an factorial experiment with two factors (genotypes and selection cycle) in randomized complete block design with three replicates (RCBD). Each replicate contained 24 rows 4 rows for each of the 6 genotypes So, S1, S2 and Boshra 411 (control cultivar), the rows were 12 m long and 150 cm wide. The hills were thinned to one plant each, after three weeks from transplanting.

Recorded Data

Vegetative growth traits

Plant length (cm) was measured from end of root zone to the terminal buds of the main stem. Number of branches per plant and total number of nodes per plant were counted at the end of the harvest season.

Earliness traits

Maturity duration was determined as a number of days from planting to the pick of first fruit. Number of nodes from cotyledon leaves to the picked first fruit was also determined.

Yield and its components traits

At the end of the harvest season, four traits were determined as follow: Fruit set percentage (the ratio between the number of total

fruits obtained at the end of the harvest season and the number of total female flowers produced by the same plant), average fruit weight (KG), total number of fruits/plant and total yield/plant (KG).

Fruit characteristics:

Fruit shape index was determined by dividing fruit length by fruit diameter according to Winger and Ludwig (1974). Flesh thickness % was determined as a ratio between flesh thickness and fruit diameter. Netting degree (1-10) was rating from 1 to 10, 1 denoted the extreme smooth fruit skin and 10 the heavily rough fruit. Placenta hardness: rating from 1 to 10, 1 denoted the juicy placenta tissues and 10 is the hard placenta. Total soluble solids (TSS) were determined using the Zeiss hand refractometer. Dray matter % was determined by weighting 100 gm of fruit flesh then chopped and dried at 70 °c for 5 days until constant weight.

Statistical procedures and Estimation of Genetic Parameters:

All the collected data were statistically analyzed according to the following:

1- Selection indices

Classical selection index was performed according to **Smith (1936)** and as illustrated by **Singh and Choudhary (1985)** Smith described the method as follow:

1- First function

$$H \text{ (Genetic worth)} = a_1G_1 + a_2G_2 + \dots + a_nG_n$$

Were,

G_1, G_2 and G_n = genotypic variation values for analysis of variance and covariance for individual character and a_1, a_2 and a_n = economic weight for all studied traits.

2 - Second function

$$I \text{ (Phenotypic performance of various characters)} = b_1p_1 + b_2p_2 + \dots + b_np_n$$

Were,

b_1, b_2 and b_n = correlation between H and I, *ie*, $r(H, I)$.

p_1, p_2 and p_n the phenotypic variation values for analysis of variance and covariance.

The maximization of $r(H, I)$ lead to a set of simultaneous equation which upon solving give the desired values of b_n . Considering 10 characters.

Selection index values formula.

$$(S.I) = b_n x_{ij}$$

Were,

b_n = the column vector for correlation between $r(H, I)$,

x_{ij} = the matrix which contain the values for several traits for each genotype.

2- Analysis of variance Analysis of variance for individual character of 6 populations was done on

the basis of the mean values as suggested by Sendecor and Cochran (1980).

3- Estimation of genetic parameters

Components of variance

- Genotypic and phenotypic variances were computed from ANOVA table based on the expected mean sum of squares as follows:

$$- \text{Genotypic variance (VG)}(\sigma_g^2) = \frac{M1-M3}{rs}$$

$$- \text{Selection cycle variance (VSc)} = \frac{M2-M3}{rg}$$

$$- \text{Interaction variance (VGS)} = \frac{M3-M4}{r}$$

$$- \text{Phenotypic variance (VP)}(\sigma_{ph}^2) = VS + VG + V(GS) + VE$$

Where: M1, M2, M3 and M4 are the mean square of the Genotypes, Selection cycle, Genotypes x Selection cycle and experimental error, respectively.

1- Coefficient of variation

Genotypic and phenotypic of variations were computed according to Burton (1952).

$$\text{Genotypic coefficient of variance (GCV)} = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sqrt{\sigma_{ph}^2}}{\bar{x}} \times 100$$

Where: \bar{x} = General mean of the trait, σ_g^2 = Genotypic variance and σ_{ph}^2 = Phenotypic variance

2- Heritability

Broad sense heritability values were estimated for all studied traits as the ratio of genotypic variance (σ^2g) to the phenotypic variance (σ^2ph) and was expressed in percentage Hanson *et al.*, (1956).

$$(\text{Heritability in broad sense}) H_{bs}^2 = \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$$

Where, σ_g^2 = Genotypic variance and σ_{ph}^2 = Phenotypic variance

3- Genetic advance (G_A)

Was computed according to the formula given by Johanson *et al.*, (1955).

$$G_A = i \sqrt{\sigma_{ph}^2 H_{bs}^2}$$

Where: H_{bs}^2 = Broad sense heritability, i = Selection differential 1.76 at 10% selection intensity and σ_{ph}^2 = Phenotypic standard deviation.

4- Genetic advance as percentage of mean (GAM)

Were calculated as illustrated by Falconer, (1989). Using the following formula:

$$GAM = \frac{G_A}{\bar{x}} \times 100$$

Where: G_A = Genetic advance and \bar{x} = General mean of the trait

5- Inbreeding depression (ID)

Calculated by formula suggested by Bernstein *et al.*, (1985).

$$GAM = \frac{S0 - S2}{S0} \times 100$$

Where, S0 = General mean of original population and S2 = General mean of second selection generation

RESULTS AND DISCUSSION

Efficiency of Mass Selection and Selection Indices:

Data presented in tables (3) and (4) showed the selection index values for lines selected to get the first selection generation (S1) and second selection generation (S2), respectively, from each genotype under study (10 % from lines which have a best performance in characters which selection was based on it and 90 % of lines which was neglected) with selection intensity 10%. Lines selected to get first selection generation were, G30, G14 and G18 with selection index values 267.54, 252.23 and 221.96 respectively; M30, M21 and M3 with selection index values 141.38, 140.65 and 140.42 respectively; Q6, Q4 and Q13 with selection index values 207.44, 142.04 and 135.33 respectively; S8, S24 and S16 with selection index values 70.38, 68.55 and 67.29 respectively; W7, W28 and W21 with selection index values 53.49, 52.70 and 52.67 respectively and X14, X4 and X9 with selection index values 58.02, 57.90 and 57. Lines selected to get second selection generation were, G19, G3 and G12 with selection index values 521.10, 494.92 and 394.88 respectively; M17, M19 and M4 with selection index values 118.96, 118.74 and 118.48 respectively; Q9, Q28 and Q10 with selection index values 32.23, 31.12 and 30.19 respectively; S1, S4 and S21 with selection index values 172.51, 169.32 and 167.18 respectively; W16, W20 and W4 with selection index values 28.88, 28.66 and 28.57 respectively and X8, X12 and X22 with selection index values 35.67, 8.31 and 8.19. Individual "lines" of each population were arranged discerningly in order to the selection index value.

Data of analysis of variance of cantaloupe genotypes under study, in addition to control variety presented in table (5) showed that there were significant and highly significant differences between all genotypes in all traits with exception to fruit shape index trait. Concerning differences between selection cycles data of mean squares values were significant in number of branches / plant and fruit shape index traits and highly significant in remaining traits. The interaction between genotypes x selection cycle, mean squares values were significant in trait, total soluble solids (TSS) (2.165*) and highly

significant in traits, total number of nodes / plant (24.458**), Total yield / plant (KG) (0.221**), Placenta hardness (1-10) (0.521**) and Dry matter % (1.991**) from these results it can be noted that There are differences between the strains under study, and this is considered a fertile environment for starting a breeding program, as the basis for any breeding program is the presence of differences in a high degree. Similar results were found by Metwally *et al.*, (2015), Abo Sedera *et al.*, (2016) and Khomphet *et al.*, (2022) who reported that the phenotypic differences are high between the strains at the beginning of the breeding program, and this is considered good for the breeder, and sometimes the breeder resorts to creating differences to obtain genetic isolations in which the selection is made for the distinguished ones and to reach a satisfactory degree.

The effectiveness of a plant breeding programs depends on the ability of a breeder to select superior individuals or families for many traits of interest (Rabiei *et al.*, 2004) and (Gomes *et al.*, 2021) who reported that the high values of selection index, means that these genotypes had strong correlation between genetic worth and phenotypic performances. And also found that the several cycles of inbreeding using mass selection and selection index method, reduced the variability among individuals. Generally, the data prove that all studied traits could be improved through mass selection method and selection index, but with different degrees depending upon the amount of variation present in each population. So, selection index has been shown to be the most efficient method to achieve aggregate genetic progress compared with any other direct single trait selection methods

Mean performances

Mean performances of all Cantaloupe genotypes for all studied characters are presented in table (6). The results clarified that, line S followed by Q scored the highest plant length (2.61 and 2.6 m respectively), line S followed by line X scored the highest number of branches / plant (4.56 and 4.44 branches / plant, respectively), line S followed by line M and Q

scored the highest number of nodes / plant (29.11 and 28.39 nodes /plant respectively), line S followed by Q scored the lowest maturity duration (100.67 and 100.78 days respectively), line S and Q scored the lowest number of nodes to pick first fruit (3.44 nodes).

Line Q followed by S scored the highest fruit set percentage (3.22 and 3.11 respectively), line X followed by S scored the highest average fruit weight (KG) (1.10 and 1.03 respectively), line S followed by line M scored the highest total number of fruits / plant (3.61 and 3.48 fruits / plant respectively), line S followed by Q scored the highest total yield / plant (KG) (3.69 and 3.41 kg respectively). Regarding fruit shape index, data showed that all genotypes tend to be oval in shape, as a result of approaching the fruit shape index the unity, line W followed by G scored the highest flesh thickness % (37.85 and 34.97 respectively), line Q followed by S scored the netting degree (1-10) (8.60 and 8.58 respectively), line W followed by M scored the highest placenta hardness (1-10) (8.71 and 8.48 respectively), line S followed by line W and line X scored the highest total soluble content (TSS%) (12.98 and 11.78 % respectively), line W followed by line S scored the highest dry matter % (8.34 and 8.14 respectively)

By comparing the studied strains with the control variety (Boshra 411), it can be noted that there was a clear superiority of the control variety in all traits under study, same trends of these study were by Hatem, *et al.*, (2014), Kevin *et al.*, (2017), wang *et al.*, (2021) They attributed the reason for the superiority of the test variety to, it is mostly a hybrid, and thus it is possible for it to be superior in the characteristics of the strength of growth as a result of the hybrid strength, in addition to that it has completed its improvement program, and thus it is superior in the quality characteristics of the fruits. Singh *et al.*, (2023) Reported that there are isolates that are present in the population and are superior to the test variety, and these are targeted by selection to increase their genetic replication in the advanced selective generations.

Table (3). Selection index values for the six genotypes of cantaloupe (G, M, Q, S, W and X) obtained from the analysis of the selection indices on the basis of selection in original population (S0) to get seeds of first selection generation (S1).

Selection intensity %	Sequence	G strain	selection index	M strain	selection index	Q strain	selection index	S strain	selection index	W strain	selection index	X strain	selection index
10% selected	1	G30	267.54	M30	141.38	Q6	207.44	S8	70.38	W7	53.49	X14	58.02
	2	G14	252.23	M21	140.65	Q4	142.04	S24	68.55	W28	52.70	X4	57.90
	3	G18	221.96	M3	140.42	Q13	135.33	S16	67.29	W21	52.67	X9	57.00
90% neglected	4	G20	220.07	M12	139.41	Q22	134.64	S11	60.33	W14	51.49	X19	56.56
	5	G26	215.94	M27	130.66	Q5	108.81	S9	60.08	W24	50.95	X5	55.64
	6	G2	215.18	M9	129.96	Q14	108.66	S19	59.79	W3	50.04	X29	55.01
	7	G4	213.58	M18	126.61	Q23	107.20	S3	59.56	W17	50.03	X24	54.73
	8	G16	207.01	M16	125.38	Q9	106.10	S27	58.23	W10	49.84	X18	54.59
	9	G24	206.22	M25	121.83	Q27	105.46	S25	57.86	W1	49.64	X23	54.56
	10	G10	202.81	M7	116.45	Q18	102.68	S17	57.06	W15	49.37	X15	54.07
	11	G23	202.68	M17	114.41	Q17	90.91	S10	56.86	W16	49.33	X7	53.93
	12	G22	198.45	M26	113.38	Q26	89.85	S1	56.36	W8	49.33	X20	53.74
	13	G8	195.77	M8	111.59	Q7	87.25	S18	54.39	W22	49.24	X10	53.65
	14	G7	194.51	M14	108.33	Q16	86.94	S26	51.69	W9	49.11	X30	52.73
	15	G28	193.17	M23	108.06	Q25	84.60	S12	50.37	W30	48.92	X8	52.69
	16	G27	192.24	M5	106.58	Q8	84.42	S20	50.03	W29	48.70	X13	52.61
	17	G19	190.91	M1	106.19	Q11	81.27	S2	49.61	W23	48.67	X3	52.58
	18	G12	184.63	M28	103.81	Q29	81.09	S4	49.61	W2	48.53	X28	52.53
	19	G29	184.35	M19	103.05	Q24	80.33	S28	49.48	W4	48.32	X2	52.41
	20	G25	182.73	M10	102.91	Q15	80.17	S5	45.49	W20	48.07	X22	51.94
	21	G3	182.59	M22	101.39	Q20	79.72	S13	44.15	W25	47.49	X17	51.54
	22	G11	180.98	M4	99.15	Q2	71.06	S29	43.80	W11	46.51	X25	51.23
	23	G6	180.09	M20	98.87	Q1	68.21	S21	43.64	W6	46.35	X6	51.17
	24	G13	179.25	M29	98.74	Q28	66.11	S22	42.64	W13	45.95	X12	51.12
	25	G1	175.69	M11	97.22	Q19	66.01	S15	41.98	W27	44.49	X21	50.32
	26	G9	174.78	M2	96.39	Q10	64.19	S6	41.32	W18	44.22	X27	50.04
	27	G21	172.71	M13	94.40	Q3	58.68	S14	40.46	W26	40.03	X16	49.93
	28	G17	171.12	M15	93.92	Q30	57.07	S30	40.09	W12	39.83	X11	49.45
	29	G5	164.66	M6	93.79	Q12	56.79	S23	39.14	W19	39.71	X26	47.01
	30	G15	164.3548	M24	93.764	Q21	56.47	S7	38.70	W5	38.173	X1	46.758

Table (4). Selection index values for the six genotypes of cantaloupe (G, M, Q, S, W and X) obtained from the analysis of the selection indices on the basis of selection in first selection generation (S1) to get seeds of second selection generation (S2).

Selection intensity %	sequence	G strain	selection index	M strain	selection index	Q strain	selection index	S strain	selection index	W strain	selection index	X strain	selection index
10% selected	1	G19	521.10	M17	118.96	Q9	32.23	S1	172.51	W16	28.88	X8	35.67
	2	G3	494.92	M19	118.74	Q28	31.12	S4	169.32	W20	28.66	X12	8.31
	3	G12	394.88	M4	118.48	Q10	30.19	S21	167.18	W4	28.57	X22	8.19
90% neglected	4	G6	391.52	M24	117.55	Q2	28.69	S6	148.05	W5	28.50	X29	7.84
	5	G7	388.10	M10	114.13	Q14	28.25	S12	147.94	W24	27.89	X11	7.74
	6	G11	386.10	M22	113.99	Q5	25.62	S26	146.69	W3	26.81	X2	7.55
	7	G21	375.73	M20	110.46	Q29	25.59	S5	146.19	W13	26.34	X13	7.20
	8	G1	374.57	M29	106.49	Q20	25.53	S15	146.03	W11	26.22	X24	7.08
	9	G15	369.81	M13	103.68	Q11	24.93	S23	144.27	W27	25.61	X21	6.25
	10	G9	361.56	M15	97.66	Q12	24.68	S14	143.06	W19	24.94	X14	6.08
	11	G30	361.21	M30	96.35	Q4	24.28	S8	141.48	W29	24.89	X6	5.94
	12	G18	360.59	M9	95.06	Q8	23.40	S27	134.18	W21	24.84	X30	5.93
	13	G27	357.40	M7	93.56	Q16	22.16	S17	131.33	W30	24.68	X26	5.89
	14	G22	353.08	M8	91.85	Q24	21.61	S28	130.96	W23	24.25	X18	5.83
	15	G29	348.37	M23	90.49	Q1	19.23	S29	130.49	W6	23.29	X7	5.69
	16	G10	345.32	M16	89.99	Q27	18.92	S3	130.36	W7	23.10	X1	5.25
	17	G14	344.80	M3	89.93	Q22	18.75	S24	130.01	W8	22.84	X5	5.04
	18	G16	342.98	M27	89.82	Q26	17.96	S11	126.54	W1	22.82	X20	4.73
	19	G17	335.79	M2	88.85	Q3	17.83	S22	123.72	W26	22.57	X9	4.61
	20	G8	332.70	M14	88.65	Q19	17.78	S2	109.93	W17	21.93	X16	4.42
	21	G28	307.89	M28	88.33	Q23	15.61	S18	109.87	W10	21.09	X27	4.29
	22	G26	296.39	M21	87.66	Q13	14.89	S16	109.25	W15	20.78	X15	4.29
	23	G24	278.34	M1	84.95	Q15	12.96	S20	109.23	W2	20.31	X23	4.27
	24	G25	276.66	M6	84.57	Q21	12.89	S30	108.84	W12	19.66	X19	4.18
	25	G23	271.91	M26	84.02	Q18	12.35	S10	104.91	W9	19.59	X3	4.09
	26	G20	266.57	M12	83.48	Q17	11.89	S19	103.89	W22	16.95	X10	4.09
	27	G5	260.92	M11	82.55	Q30	11.64	S7	102.51	W18	15.76	X4	3.85
	28	G13	249.92	M5	79.68	Q6	11.38	S13	101.29	W25	15.12	X17	3.49
	29	G4	239.25	M18	79.64	Q7	11.17	S9	99.24	W28	15.08	X25	2.69
	30	G2	141.4974	M25	79.286	Q25	10.363	S25	86.26	W14	14.60	X28	1.64

Table (5). Combined analysis of variance of 6 cantaloupe genotypes, original population (S0) and 2 selection generations (S1 AND S2) in addition to control variety (boshra411) in all traits under studied.

Sources of variance	Blocks	Genotypes	Selection cycle	Genotype × Selection cycle	Error
Degrees of freedom	2	5	2	10	34
Plant length (m)	0.0005	0.299**	0.373**	0.027	0.027
Number of branches / plant	0.241	1.585**	1.407*	0.985	0.319
Total number of nodes / plant	2.00	35.578**	102.931**	24.458**	7.794
Maturity duration (days)	6.24	107.14**	28.69	13.82	14.52
Number of nodes to pick first fruit	0.352	3.041**	1.1296*	0.5296	0.313
Fruit set percentage %	0.028	1.526**	1.537**	0.247	0.142
Average fruit weight (KG)	0.013	0.045**	0.088**	0.035	0.018
Total number of fruits / plant	0.032	1.645**	2.354**	0.078	0.063
Total yield / plant (KG)	0.361	1.187**	0.711**	0.221**	0.072
Fruit shape index	0.0003	0.007	0.014*	0.008	0.004
Flesh thickness %	12.710	84.038**	82.94**	16.43	9.28
Netting degree (1- 10)	0.336	0.910**	8.472**	0.136	0.244
Placenta hardness (1-10)	0.109	0.618**	6.021**	0.521**	0.131
TSS	0.623	10.8096**	132.779**	2.165*	0.8896
Dray matter %	0.326	14.22**	23.004**	1.991**	0.224

*, ** Significant at 5% and 1% levels of probability, respectively.

Table (6). Mean performances of all Cantaloupe genotypes under study in addition to control variety (boshra411) for vegetative measurements, earliness traits, yield and its components and fruit characteristics.

Genotypes	Vegetative measurements			Earliness		
	Plant length (m)	Number of branches / plant	Total number of nodes / plant	Maturity duration (days)	Number of nodes to pick first fruit	
G	2.45 _{ab}	3.78 _{cd}	26.89 _{ab}	104.33 _b	3.78 _b	
M	2.58 _a	3.89 _{bcd}	28.39 _{ab}	102.11 _b	3.67 _b	
Q	2.60 _a	3.44 _d	28.39 _{ab}	100.78 _b	3.44 _b	
S	2.61 _a	4.56 _a	29.11 _a	100.67 _b	3.44 _b	
W	2.37 _b	4.11 _{abc}	25.67 _{bc}	104.44 _b	3.89 _b	
X	2.14 _c	4.44 _{ab}	23.89 _c	109.89 _a	5.00 _a	
(control)	3.10 _a	4.33 _{abcd}	39.00 _a	99 _{bc}	3.33 _{bc}	
Genotypes	Yield and its components					
	Fruit set percentage %	Average fruit weight (KG)	Total number of fruits / plant	Total yield / plant (KG)		
G	2.66 _c	0.98 _b	3.26 _b	3.20 _{bc}		
M	2.92 _{bc}	0.92 _b	3.48 _{ab}	3.19 _{bc}		
Q	3.22 _{ab}	0.95 _b	3.60 _a	3.41 _b		
S	3.11 _a	1.03 _{ab}	3.61 _a	3.69 _a		
W	2.66 _c	0.92 _b	3.26 _b	2.95 _c		
X	2.20 _d	1.10 _a	2.47 _c	2.64 _d		
(control)	4.7 _a	1.15 _b	3.83 _{ab}	4.37 _a		
Genotypes	Fruit characteristics					
	Fruit Shape index	Flesh thickness%	Netting degree 1- 10	Placenta Hardness (1-10)	TSS%	Dray matter%
G	1.05 _a	34.97 _a	7.74 _b	8.11 _c	9.78 _c	4.92 _d
M	1.01 _{ab}	30.74 _b	8.40 _a	8.48 _{ab}	10.67 _c	6.32 _c
Q	0.99 _{ab}	30.65 _b	8.60 _a	8.10 _c	11.67 _b	7.11 _b
S	0.97 _b	30.81 _b	8.58 _a	8.34 _{bc}	12.98 _a	8.14 _a
W	0.99 _{ab}	37.85 _a	8.38 _a	8.71 _a	11.78 _b	8.34 _a
X	1.00 _{ab}	30.84 _b	8.18 _{ab}	8.04 _c	11.78 _b	6.99 _b
(control)	1.03 _{abc}	61.53 _{def}	9.07 _a	9.17 _a	15.33 _a	7.37 _{bc}

Means with the same alphabetical litter are not significantly different from each other, using Duncan's Multiple Range Test at 5% probability.

Mean performances, ranges and standard deviation for vegetative measurements, yield and its components and fruit characteristics, of original population (S0) 2 selection cycles (S1 and S2) of 6 cantaloupe genotypes under study, are presented in table (7) data showed that the original population (S0) was superior to the selection generation (S1 and S2) in plant length (2.59 m); total number of nodes / plant (29.14); number of nodes to pick first fruit (3.61); fruit set percentage (3.15%); total number of fruits / plant (3.63) and total yield / plant (3.4 kg). Although these traits have been selected on the basis of each other, such as plant length; total number of nodes / plant; total number of fruits / plant; total yield (kg) and Fruit set percentages However, inbreeding depression had a negative impact on it, same trend of these finding were reported by Abd Rabou and El-Sayd, (2021); Naroui Rad, (2022), who showed that the introduction of traits such as plant height and high yield within the selection program is to reduce the effect of inbreeding depression that occurs and will be to a higher degree if it is accompanied by a lack of interest in selection for crop related traits, and therefore it can be concluded that by selecting for plant height and higher yield it is not guaranteed to obtain selective generations with higher plant lengths or a higher crop, but what will certainly happen is obtaining selective generations with high quality characteristics, and that's what happened, where first and second selection generations (S1 and S2) get the highest values for traits like flesh thickness % (35.08% for second selective generation), netting degree (1-10) (8.75 for first selective generation and 8.67 for second selective generation), placenta hardness (1-10) (8.86 for second selective generation) and dray matter (7.84 % for second selective generation). Thus, at the end of the breeding program, there will be strains with an acceptable level of strength in growth, in addition to being highly distinguished in terms of quality) Kustanto, (2023)

Regarding values of ranges and standard deviation, it can be noted that the differences between values became closer in the selection generations (S1 and S2) compared to the original population, and this was reflected in the values of the standard deviation, where, the value decreased in the second selection generation than the first selection generation and the original population, similar results were discussed by Khomphet *et al.*, (2021) who reported that the goals of self-inbreeding in cross-pollinated crops are summarized in, Obtaining pure strains whose genetic composition does not change when self-propagated in cross-pollinated crops, Increasing the genetic variations of the individuals of the plant population (i.e. the formed strains) which increases the efficiency of the selection process and Reducing the genetic frequency of genes responsible for undesirable traits. **Table (7).**

Variability, heritability, genetic advance and inbreeding depression.

Estimates of genotypic variance, genotypic and phenotypic coefficient of variance (GCV and PCV), heritability in broad sense (H^2_{bs}), genetic advance and inbreeding depression (ID) are presented in table (8). Genetic variability is essential to realize response to selection pressure. It has also been pointed out that the magnitude of genetic variability present in base

population of any crop species is important in crop improvement and must be exploited by plant breeders for yield improvement (Abd El-Salam and Marie 2002). The highest values of genotypic variance were in traits, flesh thickness % (41.27), total number of nodes / plant (11.15), maturity duration (days) (10.96), total soluble solids (TSS) (8.64) and dray matter % (3.12). Values of genotypic and phenotypic Coefficient of variance (GCV and PCV) may serve as a bright spot and an important statistical measure for plant breeders seeking to discover genetic variation for the most important economic traits. It also makes selection of forms with valuable genotypes more effective (Reddy *et al.*, 2013).

Data of genotypic and phenotypic coefficient of variance (GCV and PCV) revealed that, in general, the magnitude of phenotypic coefficients of variation (PCV) was higher than the corresponding genotypic coefficients of variation (GCV) for all the fifteen characters under study. The estimates of PCV were high in magnitude (>20%) for total soluble solids (TSS) (26.99%); dray matter (26.21%); fruit set percentage (22.10%) and number of nodes to pick first fruit (21.58%), moderate in magnitude (>10-20%) for number of branches / plant (19.68%); total number of fruits / plant (18.52%); total number of nodes / plant (16.09%); total yield / plant (KG) (15.93%); average fruit weight (KG) (15.57%); flesh thickness % (11.5%); plant length (M) (11.26%) and netting degree (1-10) (10.47%), and low in magnitude (<10.00%) for placenta hardness (1-10) (9.16%); fruit shape index (7.61%) and maturity duration (days) (4.87%). The estimates of GCV were high in magnitude (>20%) for total soluble solids (TSS) (25.70%) and dray matter (25.31%), moderate in magnitude (>10-20%) for fruit set percentage% (17.64%); total number of fruits / plant (16.87%); number of nodes to pick first fruit (16.03%); number of branches / plant (13.84%); total yield / plant (KG) (13.5%); total number of nodes / plant (12.34%); average fruit weight (KG) (11.02%) and flesh thickness% (10.05%) and low in magnitude (<10.00%) for plant length (M) (9.04%); netting degree (1-10) (8.62%); placenta hardness (1-10) (8.05%); fruit shape index (4.18%) and maturity duration (days) (3.13%).

Traits, dray matter (25.31-26.21); total soluble solids % (TSS) (25.7-26.99); total number of fruits / plant (16.87-18.52); placenta hardness (1-10) (8.05-9.16) and flesh thickness (10.05-11.50) explained close estimates between values of genotypic and phenotypic coefficient of variance (GCV and PCV), while differences between values were moderate for traits, total yield / plant (kg) (13.5-15.93), netting degree (1-10) (8.62-10.47), plant length (M) (9.04-11.26), fruit set percentage% (17.64-22.10), total number of nodes / plant (12.34-16.09), number of nodes to pick first fruit (16.03-21.58) and average fruit weight (KG) (11.02-15.57) same trend of these results were found by Potekar *et al.*, (2014) and Janghel *et al.*, (2018), Abd Rabou *et al.*, (2021), who reported that these results makes selection for quantitative characters more effective because these characters have large dependent on ratio between the levels of the genotypic and phenotypic variability within the population, so the characters which have equal or approximate ratio for GCV and PCV values, selection would be effective. But the gap between the values of the genotypic and

phenotypic coefficient of variance was quite large in traits such as number of branches / plant (13.84-19.68), maturity duration (days) (3.13-4.87) and fruit shape index (4.18-7.61) same trend of these results were found by Singh *et al.*, (2023) and showed that these traits interacted to some extent with the environment. The differences between PCV and GCV were wide indicating an increased environmental influence in the expression of these traits.

Heritability in broad sense is very important and should be recognized as a first step before starting any breeding program. Heritability measures are the portion of the total genetic variance that are due to hereditary factors. Heritability in broad sense includes all types of genetic variances, consequently. Metwally *et al.*, (2015). Singh *et al.*, (2023) classified the estimates of heritability in broad sense (h^2_{bs}) as, high (> 75%); moderate (> 50 to 75%) and low (< 50%), according to these classification high estimates of heritability in broad sense (> 75%) were observed for dray matter % (93.28%); total soluble solids % (90.67%); total number of fruits / plant (82.94%); placenta hardness (1-10) (77.26%) and flesh thickness % (76.34%), moderate values were observed in traits, total yield / plant (KG) (71.86%); netting degree (1-10) (67.74%); plant length (M) (64.46%); fruit set percentage % (63.67%); total number of nodes / plant (58.86 %); number of nodes to pick first fruits (nodes) (55.17%) average fruit weight (KG) (50.07). Similar results were found by Mohammdai *et al.*, (2014), Reddy *et al.*, (2013), Selim (2019) Khomphet *et al.*, (2022) and Naroui Rad *et al.*, (2023) who showed that the most important object of the analysis of variance is to break total (phenotypic) variance into two portions: the variance among genotypes due to heredity and the remaining variance, this portioning of total variance enables us to predict the degree to which the variability of a quantitative character is transmitted to the progeny of the selected individuals, this is called heritability. Heritability provides a measure of the effectiveness with which selection can be expected to exploit existing genetic variability of the population. low heritability estimates (< 50%) were observed in traits, number of branches / plant (49.44%); maturity duration (days) 43.03%) and fruit shape index (30.19).

The highest values of Genetic advance (GA) were observed in traits, flesh thickness % (9.37); total number of nodes / plant (nodes)(4.26) and total soluble solids (TSS) (4.23), this was in line with the high and moderate values of heritability for same traits (76.34%; 58.86% and 90.67% respectively) Reddy *et al.*, (2013) found similar results and reported that the high values of heritability associated with high genetic advance this mean high additive gene effects and consequently the scope for improving yield through selection is more. Concerning genetic advance as percentage of mean of S1 and S2, the highest values (>20) were in traits, dray matter (36.83 and 34.66 % for mean of S1 and S2

respectively); total soluble solids (TSS %) (34.16 and 31.22 % for mean of S1 and S2 respectively); total number of fruits / plant (24.24 and 27.53 % for mean of S1 and S2 respectively) and fruit set percentage % (23.73 and 25.37 % for mean of S1 and S2 respectively). Moderate values (>10 -<20) were in total yield / plant (KG) (19.59 and 19.91% for mean of S1 and S2 respectively); total number of nodes / plant 15.45 and 17.44 % for mean of S1 and S2 respectively); number of branches / plant (16.88 and 15.59 % for mean of S1 and S2 respectively); flesh thickness % (14.94 and 13.87 % for mean of S1 and S2 respectively); plant length (M) (11.64 and 12.54 % for mean of S1 and S2 respectively); average fruit weight (KG) (13.82 and 12.31 % for mean of S1 and S2 respectively); netting degree (1-10) (10.56 and 10.66 % for mean of S1 and S2 respectively) and placenta hardness (1-10) (11.23 and 10.55 % for mean of S1 and S2 respectively). Values of genetic advance, as percentage of mean of S1 were larger than percentage of mean of S2, in traits, number of branches / plant (16.88 and 15.59 % for mean of S1 and S2 respectively); average fruit weight (KG) (13.82 and 12.31 % for mean of S1 and S2 respectively); flesh thickness % (14.94 and 13.87 % for mean of S1 and S2 respectively); placenta hardness (1-10) (11.23 and 10.55 % for mean of S1 and S2 respectively); total soluble solids (TSS) (34.16 and 31.22 % for mean of S1 and S2 respectively) and dray matter % (36.83 and 34.66 % for mean of S1 and S2 respectively), these results are consistent with Anburani *et al.*, (2019) Naroui Rad (2022) Khomphet *et al.*, (2022) and Singh *et al.*, (2023) and reported that values are as large in the early selection generations and then gradually decrease with increasing cycles of selection generations, until the selection becomes useless as the level of improvement stabilizes.

Reduction in performance of the selection generation due to inbreeding called "inbreeding depression" (Cardoso, 2004). Estimation of inbreeding depression was positive in traits, plant length (11.01%), total number of nodes / plant (16.11%), fruit set percentage % (18.13%), total number of fruits / plant (19.91%), total yield / plant (KG) (10.89%) and fruit shape index (5.95%). The largest values were in traits total number of fruits / plant and fruit set percentages % (were 19.91 and 18.13 % respectively). These results were consistent with these of Tawinchawdoi *et al.*, (2015) who reported that the decreased fruit yield and its components, accompanied by negative effect in pollen quality and performance which will have a bad effect on the percentage of fruit set by self-pollination, lines of cucumber, zucchini, watermelon, and cantaloupe. Results were partially in disagreement with those found by Pornsuriya *et al.*, (2022) who showed that the lack of growth in the Cucurbitaceae family by inbreeding is almost intangible sometimes inbred lines can be used directly as improved commercial varieties.

Table (7). Mean performances, ranges and standard deviation of all selection cycles of cantaloupe genotypes under study for all traits under study.

SELECTION CYCLE	Measurements	Vegetative measurements			Earliness		
		Plant length (m)	Number of branches / plant	Total number of nodes / plant	Maturity duration (days)	Number of nodes to pick first fruit	
S0	Mean	2.59 _a	3.78 _b	29.14 _a	102.56 _a	3.61 _b	
	Range	1.74-3.42	2.48-5.25	20.07-39.31	71.04-134.32	2.38-5.07	
	SE	±0.53	±0.90	±5.99	±20.27	±0.84	
S1	Mean	2.48 _a	4 _{ab}	27.58 _a	103.5 _a	3.89 _{ab}	
	Range	1.71-3.20	2.63-5.48	17.97-36.6	72.22-136.02	2.59-5.38	
	SE	±0.47	±0.92	±5.68	±20.25	±0.89	
S2	Mean	2.30 _b	4.33 _a	24.44 _b	105.06 _a	4.11 _a	
	Range	1.62-2.83	2.99-5.36	16.38-30.21	72.68-128.03	2.63-5.05	
	SE	±0.399	±0.78	±4.60	±17.39	±0.78	
Yield and its components							
SELECTION CYCLE	Measurements	Fruit set percentage %	Average fruit weight (KG)	Total number of fruits / plant	Total yield / plant (KG)		
S0	Mean	3.15 _a	0.940 _b	3.63 _a	3.40 _a		
	Range	2.04-4.41	0.61-1.27	2.51-4.87	2.24-4.56		
	SE	±0.71	±0.20	±0.74	±0.71		
S1	Mean	2.76 _b	0.950 _b	3.3 _b	3.10 _b		
	Range	1.80-3.53	0.660-1.23	2.25-4.31	2.15-3.94		
	SE	±0.56	±0.19	±0.66	±0.59		
S2	Mean	2.58 _b	1.060 _a	2.91 _c	3.03 _b		
	Range	2.24-3.54	0.720-1.45	1.98-3.43	2.15-3.86		
	SE	±0.56	±0.22	±0.50	±0.55		
Fruit characteristics							
SELECTION CYCLE	Measurements	Fruit Shape Index	Flesh Thickness %	Netting degree 1- 10	Placenta Hardness (1-10)	TSS %	Dray matter %
S0	Mean	1.03 _a	31.03 _b	7.52 _b	7.70 _c	8.38 _c	5.70 _c
	Range	0.71-1.37	42.54-	5.26-	5.41-9.28	5.75-11.39	4.09-8.66
	SE	±0.21	±10.00	±1.33	±1.26	±1.81	±1.39
S1	Mean	1.00 _{ab}	31.82 _b	8.75 _a	8.32 _b	12.39 _b	7.38 _b
	Range	0.70-1.31	43.72-	6.08-	5.75-9.37	8.51-	5.11-9.52
	SE	±0.19	±9.55	±1.27	±1.21	±2.02	±1.39
S2	Mean	0.98 _b	35.08 _a	8.67 _a	8.86 _a	13.56 _a	7.84 _a
	Range	0.87-1.10	46.32-	6.99-	6.63-9.57	9.55-	5.59-9.63
	SE	±0.08	±9.05	±0.90	±1.07	±1.90	±1.28

Means with the same alphabetical litter are not significantly different from each other, using Duncan's Multiple Range Test at 5% probability

Table (8). Genotypic variance (VG), Genotypic and phenotypic coefficient of variance(GCV and PCV), heritability in broad sense (H²bs), genetic advance (GA) and inbreeding depression (ID) of characteristics under study over all genotypes.

Characteristics	(Vg)	GCV	PCV	(H ² bs) %	(GA)	Genetic advance as percentage of mean of S1	Genetic advance as percentage of mean of S2	Inbreeding depression (ID)
Plant length (m)	0.05	9.04	11.26	64.46	0.28	11.64	12.54	11.01
Number of branches / plant	0.31	13.84	19.68	49.44	0.68	16.88	15.59	-14.71
Total number of nodes / plant	11.15	12.34	16.09	58.86	4.26	15.45	17.44	16.11
Maturity duration (days)	10.96	3.13	4.87	43.03	3.66	3.54	3.48	-2.44
Number of nodes to pick first fruit	0.39	16.03	21.58	55.17	0.78	20.02	18.94	-13.85
Fruit set percentage %	0.25	17.64	22.10	63.67	0.65	23.73	25.37	18.13
Average fruit weight (KG)	0.01	11.02	15.57	50.07	0.13	13.82	12.31	-13.33
Total number of fruits / plant	0.31	16.87	18.52	82.94	0.80	24.24	27.53	19.91
Total yield / plant (KG)	0.18	13.50	15.93	71.86	0.60	19.51	19.91	10.89
Fruit shape index	0.002	4.18	7.61	30.19	0.04	3.94	4.05	5.95
Flesh thickness %	41.27	10.05	11.50	76.34	9.37	14.94	13.87	-9.73
Netting degree 1- 10	0.51	8.62	10.47	67.74	0.92	10.56	10.66	-15.21
Placenta hardness 1-10	0.45	8.05	9.16	77.26	0.94	11.23	10.55	-14.99
TSS	8.64	25.70	26.99	90.67	4.23	34.16	31.22	-61.80
Dray matter %	3.12	25.31	26.21	93.28	2.72	36.83	34.66	-37.72

CONCLUSION:

There were significant and highly significant differences between all genotypes in most traits and significant differences between the strains at the beginning of the breeding program, considered good for the breeder. The effectiveness of a plant breeding programs depends on the ability of a breeder to select superior individuals or families for many traits of interest. Differences between original population and selection cycles, were significant and highly significant for all traits under study, so it can be reported that Selection index was an effective method to achieve aggregate genetic progress for selection of more than one trait at the same time. There are isolates that are present in the population and are superior to the test variety, and these are targeted by selection to increase their genetic replication in the advanced selective generations.

The highest estimates of heritability in broad sense (> 75%) were observed for dray matter % (93.28%); total soluble solids % (90.67%); total number of fruits / plant (82.94%); placenta hardness (1-10) (77.26%) and flesh thickness % (76.34%), for this reason, selection will be more effective in these traits than in other traits that are less heritable. Genetic advance values were large in the early selection generations and then gradually decreased with increasing cycles of selection generations, until the selection becomes useless as the level of improvement stabilizes. Decreased fruit yield and its components, accompanied by negative effect in pollen quality and performance will have a bad effect on the percentage of fruit set, by self-pollination,

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الملخص العربي

كفاءة الانتخاب الإجمالي ودلائل الانتخاب لتحسين النمو والمحصول وصفات الجودة للكتالوب.

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أجريت الدراسة الحالية خلال ثلاثة مواسم متتالية خلال العامين الميلاديين 2021 و 2022. وكانت المواقع التجريبية هي البيوت المحمية والحقل التجريبي الخاص بمحطه بحوث البساتين الصبيحة بالإسكندرية ومزرعة خاصة بمنطقة المحمودية بمحافظة البحيرة. تم تطبيق دورتين من التربية الداخلية والانتخاب الإجمالي على 6 سلالات من في الموسم الصيفوالخريفي لعام 2021 تحت ظروف البيوت المحمية الخاصة بالمحطة البحثية. الانتخاب تم إجراؤه بطريقه دلائل الانتخاب للحصول على بذور الجيل الانتخابي الأول والجيل الانتخابي الثاني. بذور العشيرة الأصلية وبذور الجيل الانتخابي الأول والثاني بالإضافة لصنف مقارنه (بشرى 411) تم زراعتهم في تجربه تقييم منفصله في الموسم الصيفي لعام 2022. تم زراعه البذور في المشتل في أول مارس ثم تم نقل الشتلات في أول أبريل لمزرعة خاصه بمنطقة المحمودية بمحافظة البحيرة لاختبار التقدم في الصفات قيد الدراسة في تجربة عاملية بتصميم القطاعات العشوائية الكاملة بثلاث مكررات. تم تقدير تحليل التباين على جميع متوسطات الأداء للسلالات بالإضافة لبعض المقاييس الوراثية الهامه مثل مكونات التباين معاملي التباين الوراثيوالمظهري ودرجه التوريث % والاستجابة للانتخاب كنسبه مئوية من المتوسط العام والانخفاض في النمو الراجع للتربية الداخلية لصفات النمو الخضري والزهري والثمري والمحصول ومكوناته.

تتلخص أهم النتائج في النقاط التالية: - كانت هناك فروق معنويه وعالية المعنوية بين جميع التراكيب الوراثية في جميع الصفات باستثناء صفه دليل شكل الثمرة. كانت الفروق بين العشيرة الأصلية والأجيال الانتخابية معنويه وعالية المعنوية لجميع الصفات قيد الدراسة. بمقارنة السلالات تحت الدراسة ببعضها البعض (G, M, Q, S, W and X) يمكن ملاحظة أن السلالة S تتفوق على السلالات الأخرى في معظم الصفات، من خلال مقارنة نفس السلالات مع صنف المقارنة (بشرى 411) يلاحظ أنه كان هناك تفوق واضح للصنف في جميع الصفات قيد الدراسة. الأجيال الانتخابية الأول والثاني سجلوا أعلى قيم لصفات مثل سمك اللحم % ودرجة الشبكية (10-1) وتماسك المشيمة (10-1) والمادة الجافة %. أعلى قيم لدرجة التوريث بالمعنى الواسع (< 75%) كانت في صفات, المادة الجافة % (93.28%) و نسبة المواد الصلبة الذائبة الكلية (90.67%) و إجمالي عدد الثمار / نبات (82.94%) و تماسك المشيمة (10-1) (77.26%) وسمك اللحم % (76.34%) ، وهذا كان متوافقا مع القيم المتقاربة لمعاملي التباين الوراثي والمظهري لنفس الصفات. بالنسبة لتأثر الصفات وخاصه صفات النمو والمحصول بالتربية الداخلية كان إيجابيا في صفات طول النبات والعدد الإجمالي للعقد / النبات ؛ نسبة عقد الثمار % و عدد الثمار الكلي / نبات و والمحصول الكلي / نبات (كجم) و دليل شكل الثمرة. وكان أشد ما يكون في صفات عدد الثمار / نبات ونسبه عقد الثمار % كانت نسبه الانخفاض 19.91 % و 18.13 % على التوالي.