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Validity of conventional and restricted selection indices in selecting promising lines of sesame

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ABSTRACT

To determine potential traits and selection criteria for yield improvement, twenty seven sesame lines and two checks were grown in two successive seasons of 2011 and 2012 to assess the presence of variability for desired traits and amount of variation for different parameters. The two experiments were grown in the Agricultural Production and Research Station of National Research Center, El Nubaria Province, El-Behera Governorate, Egypt, respectively. The data collected on 10 characters were subjected to three different analyses. Variability among the lines were determined with respect to the studied parameters. The results showed significant genetic variances and covariances among lines for all studied traits for all characters except, days to maturity in F_6 and fruiting zone length in F_7 , indicating the existence of variability and the potential for selection and improvement within characters. A considerable amount of variability among lines for the traits studied also indicated the usefulness of selection for these traits in the genetic material used for future improvement in sesame. In variability analysis, high heritability was accompanied by a high genetic advance and a high genotypic coefficient of variation (GCV) for number of branches plant⁻¹, stem height to 1st capsule, number of capsules plant⁻¹ and seed yield plot⁻¹. In correlation analysis, the genotypic correlation coefficient was generally higher than the corresponding phenotypic correlation coefficient which indicated that the apparent association might be due to genetic reason. In selection indices analysis, twelve conventional selection indices (I_i) and two restricted selection indices with different number of traits were evaluated. Selection index was constructed to help selecting for several important traits simultaneously. Judicious use of conventional and restricted selection indices is of a great importance to the breeder. Selection of F_6 line (s) that combine high seed yield with one or more desired agronomic or seed yield component trait in a new cultivar was practiced via 12 conventional and two restricted selection indices. These lines were evaluated in the next generation in an evaluation experiment. Heritability values ranged from 23.2 % for days to maturity to 92.2% for stem height to 1st capsule in F_6 and from 45.3% for fruiting zone length to 93.9% for oil % in F_7 . There are no discrepancies between expected (G_E) and actual (G_A) genetic advances reported for four traits viz., fruiting zone length, branches plant⁻¹, capsules plant⁻¹ and seed yield plot⁻¹ when direct selection for individual traits was applied. Seed yield plot⁻¹ was significantly and positively correlated with plant height, stem height to 1st capsule, branches plant⁻¹, capsules plant⁻¹ and yield plant⁻¹. Contradictory, seed yield plot⁻¹ was significantly and negatively correlated with both seed index and oil%. Besides, the highest relative efficiency (591) was calculated in the conventional selection experiment that contained four traits viz., plant height, branches plant⁻¹, capsules plant⁻¹ and seed yield plot⁻¹. Two restricted indices were applied for the characters that showed negative association with seed yield plot⁻¹. Holding seed index and/or oil content of selected sesame plants to the means of unselected plants in a restricted selection index increased the seed yield plot⁻¹ by 3.0 and 1.3% of lines mean while conventional selection index decreased seed yield plot⁻¹ by 5.0 and 3.0% of lines mean, respectively in the selection experiment. A rank correlation between F_6 either for direct selection for seed yield or among all selection indices used (conventional and restricted) and rank of seed yield plot⁻¹ in F_7 was positive and significant or highly significant. The line C3.8 recorded the highest seed yield plot⁻¹ and higher resistance for foliar disease amongst the 27 elite lines in F_6 and F_7 . It was higher than the mean of the

population of lines by 28.4 and 44% and than the two checks cultivar by 48 and 100 % in 2011 and 2012, respectively

Keywords: *Sesame, Phenotypic variances and covariances, Genotypic variances and covariances, Heritability, Correlations, Direct selection, Expected and actual genetic gains, Conventional selection index, Restricted selection index, Rank correlation.*

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INTRODUCTION

Sesame (*Sesamum indicum* L), is probably the most ancient oil seed crop. It is known under different names in different countries viz: simsim, benniseed, til, gingelly and a jonjoli (Khidir, 1997). Because of its high oil quality and a wide use in raw foods, confectioneries and bakery industries, the demand of sesame seed is increasing in the global market (Ashri, 1989). It is a self pollinated crop, under the family of pedaliacea. The importance of sesame lies in its high quality oil which is often referred to as the “queen” of vegetable oil. The outstanding characteristic of sesame oil is its stability and keeping quality as well as resistance to rancidity.

Plant breeders use biometrical techniques to assess genetic variability among and within genotypes, to develop selection criteria, heterotic parents for hybridization, effective breeding procedures and varietal stability (Singh, 1990). Variability plays an important key role in plant breeding program and observed the limit of selection for different plant properties. Hence, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV) and heritability.

The mathematical genetic theory, in the form of selection index, developed by Smith (1936) is the basis for simultaneous selection of several traits. A selection index most often aims at giving appropriate weight to the components maximizing gains from selection (Falconer, 1983).

The selection index technique can theoretically determine the genotypic worth of individuals or families in an objective manner (Subandi and Empig, 1973). First, Smith (1936) developed the conventional index to improve several quantitative characters simultaneously. These characters may not be equally important or may not be independent from each other, but all affect the real value of any line in different levels. This method has shown to be efficient for maximum aggregate genetic progress but has some limitations. Of these limitations; 1) the difficult in obtaining reliable estimates of phenotypic and genotypic variances and covariances; 2) assigning the appropriate economic importance to each trait; and 3) the need to wait until measurements are made for all traits. Besides, several time consuming computations are needed for the construction of the index. Unfortunately, the use of the conventional method did not produce simultaneous improvement. Some traits may be changed in the desired direction whereas others may be changed in undesired directions. This problem was recognized by Kempthorne and Nordskog (1959). They developed the theory of restricted selection indices. The objective of restricted selection is to maximize one (or more) trait while holding one or more correlated traits at the level of the population mean or at some pre-chosen optimum level.

In that context, Rosielle . (1977) revealed that direct selection in oat lines derived from a bulk population, for either seed yield or straw yield (economic traits) resulted in lines with high seed yield or straw but, selected lines were tall and late due to the high correlations between heading date and /or plant height with the economic traits. They tested 4 unrestricted and 8 restricted methods by holding heading date and height to the means of the unselected population to remove correlated responses in heading date and height. Severe restriction on unfavorable traits reduced the advance in economic value to near zero. This prevented them from selecting short, early cultivars with high economic seed yield. They added that it is difficult to select an ideal cultivar in most crop species when acceptance is conditioned by several traits.

In general, selection indices provide a useful method for quantifying selection potential as well as providing a good chance for more efficient selection. For more accurate calculations and explanation of the results, correlated response between a primary and a secondary trait can be exploited to increase the expression of the primary trait when the selection of the secondary trait produces greater genetic gain than the direct selection of the primary trait (Hallauer ., 2010). Consequently, direct selection for a primary trait, such as seed yield or oil in sesame, is not sufficient to generate sesame genotypes useful as commercial cultivars.

The application of the selection index to improve the lines of sesame was rare. Although most researcher in the developed world made benefit from the restricted selection index, research on sesame in developing countries like Korea and Egypt used only the conventional selection index.

Lee and Chang (1986) in Korea, practiced conventional selection index to 14 traits including yield plant⁻¹ using 82 cultivars. He stated that the highest genetic advance was for index that included all traits. However, for reasons of expensive and time consumed. He suggested only 3 characters to be included in the index (days to maturity, length of stem with capsules and capsules plant⁻¹) for future selection indices.

In Egypt, El-Shimy (1995) used 9 conventional selection indices and reported that after two cycles of selection improved yield plant⁻¹ by 46.34% of the overall mean of the selected families from the better parent. Samar . (2002) applied only one conventional index and compared it to direct selection for yield plant⁻¹. They found that the selection index improved seed yield by 16.1% of F₅-derived families.

Most recently, Hidalgo-Contreras (2014) in Nebraska, USA used a multi-trait genomic selection index. He used the principle component analysis via 250 principle components which, in his opinion, explained approximately 99% of the total variability. His method could represent a new era in the use of selection indices to increase selection efficiency in self – pollinated crops.

In view of the above, the objectives of the present study were: i) To generate new forms of sesame cultivars having high seed yield potential and one or more desired by using either conventional or restricted selection indices in advanced breeding generations ; ii) Estimation of variances and covariances analysis for each variable and /or each pair of variables to calculate phenotypic (r_p) and genotypic (r_g) correlation coefficients and efficiency of each selection index compared to direct selection for yield; iii) Estimation of heritability percentages, expected and actual genetic advances when selecting for a single trait and expected advance from conventional and restricted selection indices to detect the optimum selection procedures.

MATERIALS AND METHODS

Description of experimental area

The two experiments were grown at Agricultural Production and Research Station at National Research Center, El-Nubaria Province, El-Behera Governorate, Egypt, during the two successive summer seasons of 2011 and 2012 (latitude 30° 30' N, and longitude 30°19' E, and mean altitude 21 m above sea level) as shown in Fig. (1).



Figure 1. Location of the Experimental Farm in EL-Nubaria Region, Egypt

Physical and chemical characters of soil (0-30 depth) in the experimental site were as follows: sand 91.2%, silt 3.7%, clay 5.1%, PH 7.3, organic matter 0.3 %, CaCO₃ ,1.4%, EC 0.3 ds/m, soluble N 8.1 ppm and available P 3.2 ppm. The experimental area has an arid climate with cool winters and hot dry summers prevailing in the experimental area. There was not rainfall can be take in to consideration through the two seasons, because the amount was very small and the duration wasn't exceed a few minutes. Means of temperature and relative humidity through the growing seasons are presented in Table (1).

Table 1. Means of temperature and relative humidity through period from April to August in the selection and the evaluation experiments

Month	Selection Experiment (2011)		Evaluation Experiment (2012)	
	Temperature (C ^o) means	Relative humidity%	Temperature (C ^o) means	Relative humidity.%
April	18.3	62.1	19.5	61.6
May	21.1	62.8	23.1	60.7
June	23.4	66.0	26.0	66.0
August	25.6	67.2	27.2	72.0

Source: The Climate Lab National Research Centre, Giza, Egypt

Experimental materials:

Breeding materials used in this investigation were 27 elite derived lines of sesame in F₆ - and F₇, obtained via pedigree selection from a continuous breeding program that was initiated at the Agronomy Department, Faculty of Agriculture, Cairo University (Dalia 2001). The program compromised a half diallel mating among six diverse parents (Table 2). In addition, two check cultivars of sesame (Giza 32 and Shandaweel 3) were obtained from the Agric. Res. Center, Ministry of Agriculture, Egypt.

The selection in segregating generations (F₂-F₅) was for adaptive traits of ideal lines as suggested in sesame by (Baydar, 2005). These traits were tri capsules per axil, extra capsule setting, a branching type and segregates with high seed yield. Thus, the traits contributing to high sesame lines were developed sequentially from F₂, whether the same alleles (gene or groups of genes) influenced each trait independently, or whether the same alleles influenced one component directly and another indirectly is conjectural.

Table 2 . The origin breeding status and description for parents

Genotypes	Breeding status	Seed source*	Specific characters
P1(HM19)	F8- hybrid pop.	Cairo Univ.*	Early maturity, non branching first capsule set low, 3 capsules/axil.
P2 (EUL90)	Mutant line	Cairo Univ.*	Early maturity, non-branching, first capsule set low, 3 capsule/axil.
P3 (Mutant 48)	Mutant line	Cairo Univ.*	Branching, 3 capsules/axil. capsules/axil.
P4 (Giza 32)	Local cultivar	Ministry of Agric.& Land Reclamation, Egypt	Heavy seed weight, medium branching, one capsule/axil, long capsule, late maturity
P5 (NM59)	Exotic line	India through IAEA**	Stiff stem, late maturity, one capsule/axil.
P6 (Babil)	Exotic variety	Iraq through IAEA**	Low branching, 1-3 capsules/axil, semi- shattering capsules.

* Advanced breeding materials resulted from the breeding program conducted at Agronomy Department, Faculty of Agriculture, Cairo University. ** Inter. Atomic Energy Agency.

Treatments and experimental design

The lines were grown in two categories: selection and evaluation experiments in two successive seasons of 2011 and 2012. In the selection experiment, two types of selection indices were practiced (i.e., conventional and restricted selection indices) and compared to direct selection for seed yield plot⁻¹ using F₆ lines in 2011 summer season. In next generation the F_{6:7} selected lines together with the unselected lines and two check cultivars (Shandaweel 3 and Giza 32) were grown for evaluation in the evaluation experiment (2012). Both (selection and evaluation) experiments were grown in a randomized complete blocks design (RCBD) with four replications. Each block contained 27 sesame lines plus two check cultivars. Each plot was consisted of a single- ridge for each line or a check cultivar to minimize environmental variations associated with large plots. Each ridge was 3 m long and 50 cm width and seeds were sown in hills 10 cm apart.

Agricultural practices:

The land was ploughed, harrowed and later marked out into blocks and plots according to the design of the experiment. Organic fertilizer was added at the rate of 20 m³/feddan (one feddan =4200 m² = 0.42 hectare), before planting. Calcium super phosphate (15.5 % P₂O₅) was applied during soil preparation at the rate of 100 kg/feddan. The two season experiments were sown at April, 12 and April, 17 during 2011 and 2012 seasons, respectively. Sesame seeds were hand sown 3-5 seeds/hill using dry sowing method on one side of the ridge in hills 10 cm apart during the aforementioned dates in the first and second seasons, respectively. The plots were irrigated immediately after sowing directly. Sprinkler irrigation was applied every week. Potassium fertilizer was added as potassium sulfate (48% K₂O) at 200 kg/feddan after 45 days from sowing. Nitrogen fertilizer was added as ammonium nitrate (33.5% N) in three equal doses at 15, 30 and 45 days after sowing. Plants were kept free from weeds, which were manually controlled by hand hoeing at two times. Sprinkler irrigation was applied every week. Thinning was done after appearing three leaves on main stem to secure two plants per hill. The common agricultural practices for growing sesame according to the recommendations of Ministry of Agriculture were followed. All other agronomic practices were kept normal and uniform for all the treatments.

No foliar disease was observed during the two growth seasons under natural field conditions. Therefore, no spraying with fungicide was applied. However, a separate experiment was done in Field Crops Department, Biology and Agricultural Science Division, National Research Center, Giza, Egypt in July 2012 to quantify the artificial resistance or susceptibility of lines cope with the selection and evaluation experiments before any recommendation was done (Shabana . 2014).

Observations and Data Collection

At maturity when the pods turned from green to golden yellow, the capsules were harvested. The observations were recorded on 10 quantitative characters. Ten randomly selected plants were tagged in each row and used for recording the observations of characters. Biometrical data were collected on days to maturity; plant height (cm); stem height to the 1st capsule (cm); fruiting zone length (cm); number of branches plant⁻¹; number of capsules plant⁻¹; seed index (g); seed yield plant⁻¹ (g); seed yield plot⁻¹ (kg) and oil percentage: oil content (%) was determined for individual plants, on dried seeds, by a Soxhlet extraction method according to AOAC (2002) by using the following formula:

$$\text{Oil content (percent)} = \frac{\text{Weight oil extracted (g)}}{\text{Weight of sample}} \cdot 100$$

Statistical procedures

Keeping in view the objectives set out for the study, the following statistical tools and methods have been deployed.

Analysis of variance (ANOVA)

The mean values of each lines in each replication for all the traits were subjected to statistical analysis. Data were analyzed statistically using analysis of variance according to Gomez and Gomez (1984) procedure for a randomized complete block design (RCBD), using the computer program MSTAT-C (MSTAT-C, 1991). The differences among genotypes, was considered significant if the P-values were ≤ 0.05 .

Estimation of variance components and estimation of magnitude of variation

Variance and covariance analyses were computed for each variable and each pair of variables, respectively, in all experiments. The variance component expectations (Table 3) for mean squares and mean cross -products from these analyses are as follows:

Table 3. The analysis of variance (ANOVA) showing expected mean squares

Source of variation	Degree of Freedom	Mean Squares (MS)	Expected Mean Squares (EMS)
Replications	r-1		
Among lines	l-1	$M\ell_{ij}$	$\sigma^2 e_{ij} + r\sigma^2 g_{ij}$
Error	(r-1) (l-1)	Me_{ij}	$\sigma^2 e_{ij}$

Where:

- $\sigma^2 e_{ij}$ = experimental error variance when $i=j$ and covariance when $i \neq j$
- $\sigma^2 g_{ij}$ = genotypic variance when $i=j$ and covariance when $i \neq j$
- $M\ell_{ij}$ = phenotypic variance among lines when $i=j$ and covariance when $i \neq j$
- $Me_{ij} = \sigma^2 e_{ij}$, l and r are the number of lines and replicates, respectively.

To estimate the extent of magnitude of variation among all traits, all data were subjected to analysis of variance for two separate years. Hence, variance components (genotypic, phenotypic and error variance) were estimated using the formula of Wricke and Weber (1986) and Prasad . (1981) as follows:

$$V_g = [MSG - MSE / r] , V_p = [MSG / r] , V_e = [MSE / r]$$

Where MSG, MSE and r are the mean squares of genotypes, mean squares of error and number of replications, respectively.

Estimation of genotypic and phenotypic coefficient of variability

Phenotypic (PCV) and genotypic (GCV) coefficient of variation were evaluated according to the methods of Burton (1952), Johnson . (1955) and Kumar . (1985) as:

$$PCV = \frac{\sqrt{V_p}}{\bar{x}} . 100 , GCV = \frac{\sqrt{V_g}}{\bar{x}} . 100$$

Where V_p , V_g and \bar{x} are the phenotypic variances, genotypic variances and grand mean of lines per season, respectively for the characters under consideration. GCV and PCV values were categorized as low (0–10%), moderate (10–20%), and high (20% and above) as indicated by (Shivasubramanian and Menon, 1973).

Estimation of heritability in broad sense

The broad sense heritability (h^2b) was calculated as the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p) (Allard, 1960).

$$Heritability (h^2b) = \frac{\sigma_g^2}{\sigma_p^2} . 100$$

Where h^2b = % Broad sense heritability. The heritability percentage was categorized as low (0–30%), moderate (30–60%), and high $\geq 60\%$ as given by (Johnson ., 1955). Heritability percentages ($h^2\%$) were calculated by using the method of moment as described by Lunch and Walsh (1998). Because sesame lines in this study were essentially homozygous, the primary genetic effects being expressed in the various traits would be additive in nature and additive x additive (the inbreeding coefficient of $F_{5,6}$ lines is theoretically 0.968).

Estimation of genetic advance

Expected genetic (G_E) and actual genetic (G_A) advances under 10% direct selection for individual traits were calculated as applied by Shabana . (1980) by using the following formula:

$$G_E = (\bar{x}_s - \bar{x}_p) h^2 / \bar{x}_p \times 100, \quad G_A = (\bar{x}_s - \bar{x}_p) / \bar{x}_p \times 100, \quad \text{Where } \bar{x}_s \text{ is mean of selected lines, } \bar{x}_p \text{ is overall for lines and } h^2 \text{ is heritability.}$$

Estimation of phenotypic and genotypic correlation coefficients

For calculating the phenotypic (r_p) and genotypic (r_g) correlation coefficients for all possible combinations the formula suggested by Miller . (1958), Hanson . (1956) and Johnson . (1955) were adopted. The genotypic co-variance components between two traits and the phenotypic co-variance component were derived in the same way as for the corresponding variance components. These co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

Phenotypic correlation coefficient

$$r_p = \frac{Cov_{p,x,y}}{\sqrt{\sigma_p^2 x \sigma_p^2 y}}$$

r_p = Phenotypic correlation coefficient

$Cov_{p,x,y}$ = Phenotypic covariance of traits (x & y)

$\sigma_p^2 x$ = Phenotypic variance of trait (x).

$\sigma_p^2 y$ = Phenotypic variance of traits (y).

Genotypic correlation coefficient

$$r_g = \frac{Cov_{g,x,y}}{\sqrt{\sigma_g^2 x \sigma_g^2 y}}$$

r_g = Genotypic correlation coefficient

$Cov_{g,x,y}$ = Genotypic covariance of traits (x & y)

$\sigma_g^2 x$ = Genotypic variance of trait (x).

$\sigma_g^2 y$ = Genotypic variance of traits (y).

The coefficients of genotypic correlation were tested using ‘r’ tabulated value at n-2 degrees of freedom at 5 and 1 % probability level, where n denote as number of lines studied.

Selection index procedures

The 27 elite lines were dissected for the adaptive traits contributing to seed yield per plot. The means of traits across the four replicates in an experiment were used for the calculation of various selection indices. The equation of the these indices were of the form:

$I = b_1 \times_1 + b_2 \times_2 \dots \dots \dots + b_n \times_n$, Where: b_i represents the regression coefficient (index weight) for trait i , \times_i is the phenotypic value for the individual trait and $i = 1 \dots \dots n$, respectively, are number of traits that are used in formulating the index (I).The theoretical procedures used were: the conventional for selection index of Smith (1936) and the restricted index as suggested by Kempthorne and Nordskog (1959) and construction of both indices were as follows:

1. Conventional selection index:

Smith (1936) defined the genetic worth (H) of an individual as : $H= a_1G_1+a_2G_2+\dots+ a_nG_n$, Where, G_1, G_2,\dots,G_n are the genotypic values of individual characters and a_1,a_2,\dots,a_n signify their relative economic importance. Another function (I), based on the phenotypic performance of various characters, is defined as: $I=b_1 p_1+b_2 p_2+\dots+b_n p_n$, Where, b_1, b_2,\dots,b_n are to be estimated such that the correlation between H and I, i.e, $r (H, I)$,becomes maximum. The maximization of $r (H, I)$ leads to a set of simultaneous equations which upon solving give the desired estimate of b_i values. The simultaneous equations look like as follows:

$$\begin{aligned} b_1 x_{11} + b_2 x_{12} + \dots + b_n x_{1n} &= a_1 G_{11} + a_2 G_{12} + \dots + a_n G_{1n} \\ b_1 x_{21} + b_2 x_{22} + \dots + b_n x_{2n} &= a_1 G_{21} + a_2 G_{22} + \dots + a_n G_{2n} \\ b_1 x_{n1} + b_2 x_{n2} + \dots + b_n x_{nn} &= a_1 G_{n1} + a_2 G_{n2} + \dots + a_n G_{nn} \end{aligned}$$

Which in matrix form become:

$$\begin{pmatrix} x_{11} & x_{12} & \dots & x_{1n} \\ x_{21} & x_{22} & \dots & x_{2n} \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ x_{n1} & x_{n2} & \cdot & x_{nn} \end{pmatrix} \cdot \begin{pmatrix} b_1 \\ b_2 \\ \cdot \\ \cdot \\ \cdot \\ b_n \end{pmatrix} = \begin{pmatrix} G_{11} & G_{12} & \dots & G_{1n} \\ G_{21} & G_{22} & \dots & G_{2n} \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ G_{n1} & G_{n2} & \cdot & G_{nn} \end{pmatrix} \cdot \begin{pmatrix} a_1 \\ a_2 \\ \cdot \\ \cdot \\ \cdot \\ a_n \end{pmatrix}$$

The solution of these equations gave the estimates of b_i values in the following manner: $b= x^{-1}Ga$, where b is the column vector, x^{-1} is the inverse of phenotypic variance and covariance matrix, G is the genotypic variance and covariance matrix and a is the column vector for economic weights. The following traits used to compute of twelve conventional selection indices (Table 4).

Table 4. The traits used to compute of twelve conventional selection indices

Index No.	Content of the index
	Direct selection for seed yield plot
1	Days to maturity + Seed yield plot ⁻¹
2	Plant height + Seed yield plot ⁻¹
3	Stem height to 1 st capsule + Seed yield plot ⁻¹
4	Fruiting zone length+ Seed yield plot ⁻¹
5	Branches plant ⁻¹ + Seed yield plot ⁻¹
6	Capsules plant ⁻¹ + Seed yield plot ⁻¹
7	Yield plant ⁻¹ + Seed yield plot ⁻¹
8	Plant height + Stem height to 1 st capsule + Seed yield plot ⁻¹
9	Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹
10	Plant height +Stem height to 1 st capsule + Number of branches plant ⁻¹ + Seed yield plot ⁻¹
11	Plant height+ Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹
12	Stem height to 1 st capsule + Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹

2. Restricted selection indices:

Under certain situations (such as oil % and seed index of sesame that showed negative association with seed yield plot⁻¹ such that a zero advance of any of them has no effect on the price of seed used in food processing) the breeder might like to effect change in means of several favorable traits while keeping the means of one or two traits unchanged. This is restricted selection index where the coefficients were estimated according to Kempthorne and Nordskog (1959). The equation of this index was of form:

$b= [I_{nn} - P^{-1}GC (C' GP^{-1}GC)^{-1} C' G] P^{-1}Ga$, where: I_{nn} is the $n \times n$ unit matrix, P^{-1} is the inverse of phenotypic variance and covariance matrix. G is the genotypic variance and covariance matrix. C is coefficient vector matrix.

C' is transposed coefficient vector, which is defined as follows:

$$C' = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \end{pmatrix}$$

The traits used to compute of two restricted

selection indices were as follows:

Index	No.	Traits inc	Traits included
1		Seed index +Seed yield plot ⁻¹	
2		Oil % + Seed yield plot ⁻¹	

Restriction in the two above selection indices aimed to maximize seed yield plot⁻¹ while holding seed index in the first one and oil% in the second at level of the mean of the 27 F₆ lines or less such that no advance in both characters might happen. The expected genetic advance from straight selection for seed yield plot⁻¹ was obtained from the formula given by Falconer (1960). $A_E = i \times V_G/\sigma_p$, Where: σ_p is the phenotypic standard deviation of the selected character.

The expected genetic advance for each index was obtained from the formula given by Brim . (1959). $A_E = i (\sum b_i G_{iy})^{1/2}$, Where: A_E is the expected gain for an index, b_i represents the regression coefficient (index weight) for trait i and G_{iy} are genotypic covariance of the various characters with seed yield plot⁻¹. Selection indices were statistically analyzed using excel software (2010).

Spearman's Rank Correlation Coefficient

Rank correlation was calculated according to Spearman (1904) as follows:

$$r_s = 1 - \frac{6 \sum D^2}{n(n^2 - 1)}$$

Where D is rank x – rank y (i.e. the difference in the ranks) and n is the number of data pairs.

RESULTS AND DISCUSSION

The knowledge of genetic variation and association between agronomic traits is regarded to support considerable help to maintain genetic improved to breeding programme. This will assist plant breeders in choosing which agronomic traits should be used in their breeding programme. In the programme, high range of variability, heritability, genetic advance and positive correlation coefficient among traits could be an excellent tool for improving or selection genotype (Akbar ., 2003).

Sesame is the crop of small holders and devoted to soils that are not suitable for main summer crops such as maize or rice. Having this in mind (consciously or unconsciously) we had an idoetype in mind that is suitable to the conditions of growing sesame in Egypt. When the 27 elite sesame lines were selected in the segregating generations (from F₂-F₅), and as described by Baydar (2005), the traits contributing to high sesame lines were developed sequentially from F₂. But, whether the same alleles (gene or groups of genes) influenced each trait independently or whether the same alleles influenced one component directly and a subsequent indirectly in each trait selected was conjectural.

1. Analysis of Variance (ANOVA)

The results of analysis of variance for the studied traits under investigation are presented in Table (5). The result of the analysis of variance showed that there was significant (p<0.05) or highly significant (p<0.01) difference among the characteristics of lines in F₆ and F₇ generations, except for days to maturity and fruiting zone length in F₆ and F₇ generations, respectively (Table 5), indicating the presence of adequate variability among the lines which can be exploited through selection. Therefore, means of lines could be compared and the genotypic variability and the heritabilities could be estimated. The differences found in two consecutive generations are due to different environmental conditions. The differences in yield and yield components obtained in this study are in agreement with those obtained by Patil and Sherif (1996) and Reddy . (2001).

Table 5. Mean squares from ANOVA for studied traits of 27 elite sesame lines in the selection (F₆) and the evaluation (F₇) experiments

S.V.	D.F	DM	PH	Selection experiment (F ₆ : generation)				SI	SYP	Oil %	SYPL
				HTC	FZL	NB	NC				
Mean squares											
Replications	3	14.0	228.0**	193.0**	360.0**	1.8.0**	1250.0**	0.7**	30.0**	10.0**	10235.2**
Among lines	26	21.1	428.7**	207.3**	402.0**	1.3**	2997.8**	0.6**	26.1**	22.7**	5886.3**
Error	78	16.2	92.2	18.6	112.6	0.2	393.6	0.14	9.9	2.4	2233.1
S.V.	D.F	DM	PH	Evaluation experiment (F ₇ : generation)				SI	SYP	Oil %	SYPL
				HTC	FZL	NB	NC				
Mean squares											
Replications	3	0.09	0.61	0.98	198.0	0.20	2589.0**	0.22**	195.0**	150.0**	46550.3**
Among lines	26	17.4**	455.5*	198.2*	392.9	3.9**	3020.8**	0.4**	210.6**	123.0**	47394.2**
Error	78	4.5	213.1	76.8	215.2	1.4	695.3	0.04	41.1	6.5	9044.2

DM=days to maturity, PH=plant height, HFC= stem height to 1st capsule, FZL=fruiting zone length, NB= number of branches plant⁻¹, NC= number of capsules plant⁻¹, SI=seed index, SYP= seed yield plant⁻¹, Oil%=oil percentage and SYPL=seed yield plot⁻¹.

* and ** significant level at 0.05 and 0.01 of probability, respectively.

2. Statistics and genetic parameters

2.1. Mean performance and range for ten characters of 27 elite sesame lines compared with two check cultivars

Means and ranges for the performance of all traits for the experimental lines and the two check cultivars tested in the selection and the evaluation experiments are shown in Tables 6 and 7). The range and mean performance showed the presence of considerable amount of variability among the lines for most of the characters.

Comparisons between the lines and the two check cultivars revealed that, in general, the lines were higher than check cultivars for most traits except for plant height in F₆ and seed index in both experiments. Also, the lines were earlier in maturity than the two check cultivars by 6 and 9 days in the two experiments, respectively.

The results indicated that the selected lines mean (top 10%), (Ca.3 lines) were higher for seed yield plot⁻¹ than check cultivars mean by 38 and 89 % in the two experiments, respectively. Meanwhile, the top 10% lines showed superiority in mean seed yield plot⁻¹ over the population mean of the 27 lines by 20% in the selection experiment and also by 36% in the evaluation experiment. Meanwhile, the three selected lines mean were higher seed yield plot⁻¹ than the best check (Shandaweel 3) mean by 30 and 46%, in the two experiments, respectively (not presented in Tables). The line C3.8 recorded the highest seed yield plot⁻¹ amongst the 27 elite lines in F₆ and F₇ generations. It was higher than the mean of the population of lines by 29 and 44% and than the two checks cultivars by 48 and 100 % in 2011 and 2012, respectively. In addition, the ranges of means for lines tended to transgress the ranges for the check cultivars for most traits in both experiments except for days to maturity in F₆ generation. Similar results for sesame were reported by Samar . (2002).

Selection is an integral part of breeding program by which genotypes with high productivity in a given environment are selected. However, selection for high yield is made difficult by the complex nature of trait in sesame. Yield per unit area is the end product of components of several yield contributing characters (Singh and Singh, 1973 and Sastri, 1974). The polygenic inheritance of yield components makes selection more difficult. Moreover, these complex traits are highly influenced by environment, which reduces the progress to be achieved through direct selection. In such cases, there is another option to hasten the genetic improvement which is known as indirect selection for yield. So the phenotypic and genotypic variability study play of sesame crop characteristics was quite important for the improvement of the crop.

2.2. Phenotypic (VP) and genotypic (VG) variances and phenotypic (PCV) and genotypic (GCV) coefficients of variability:

Estimates of the phenotypic and genotypic variance, phenotypic and genotypic coefficient of variability and the difference between them are shown in Tables 6 and 7. The results revealed considerable phenotypic and genotypic variances among the lines for the traits under consideration. Phenotypic variances were generally higher than their respective genotypic variances thus revealing the role of environmental factors.

It is difficult to compare the variance among the range of various characters because they are not unit free (Baye, 1996). Thus estimates of phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability (in broad sense) and expected and actual genetic advance as a percentage of mean were evaluated and compared (Table 6 and 7). Results of phenotypic and genotypic coefficients of variation are presented in Tables 6 and 7. The magnitude of response which was measured by the phenotypic coefficient of variation was quite different. As stated by Shivasubramanian and Menon (1973) the PCV and GCV values are ranked as low, medium and high with 0 to 10%, 10 to 20% and >20% respectively. Based on this delineation, phenotypic coefficients of variability (PCV) ranged from 2.00 to 41.80% and genotypic coefficients of variability (GCV) ranged between 0.97% for days to maturity and 32.9.0% for number of branches plant⁻¹. All the characters showed moderate to high phenotypic and genotypic coefficient of variation except days to maturity, plant height, fruiting zone length, seed index, and seed yield plant⁻¹.

Data in (Tables 6 and 7) showed that highest values of PCV and GCV recorded for number of branches plant⁻¹, stem height to 1st capsule, number of capsules plant⁻¹ and seed yield plant⁻¹. High GCV and PCV indicated that selection may be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential (Singh ., 1994). These results are in confirmatory with these of Laurentin and Montilla (2002), Babu . (2005), Ganesan (2005), Kumar and Sasivannan (2006) and El-Shakhess . (2008).

The comparison of characters as regards to the extent of genetic variation could be better judged by the estimation of genotypic coefficient of variation (GCV) in relation to their respective phenotypic coefficient of variation (PCV). The difference between PCV and GCV values was high for stem height to 1st capsule, plant height, number of branches plant⁻¹, fruiting zone length and seed yield plant⁻¹; which indicated how much the environment influenced these characters. However, this difference was low for number of capsules plant⁻¹, seed index, seed yield plot⁻¹ and oil % in F₇ generation (Table 7). It indicates that the observed variations for the traits were mostly due to genetic factors. However, the environment played a little role on the expression of these traits.

However, El-Shimy (1995) claimed that his genetic variance was completely depleted due to the masking effect of the genotypes x locations interaction. Both PCV% and GCV% were estimated to compare the phenotypic and genotypic variances of lines for different characters and /or years in standard units. In that context, Shabana and Abo-Hagaza (1984) observed that PCV% was high for seed yield and seed yield contributing traits, but low for morphological traits. PCV values were

magnitudinally higher than GCV for all the characters studied in F₆ and F₇. The least difference recorded for oil%, seed index and number of capsules plant⁻¹ indicating little influence of environment in the expression of these traits. Abd El- Mohsen . (2008) and Siva . (2013) reported similar results.

Table 6. Means (\bar{x}), ranges (R), coefficient of variability (C.V.%), phenotypic (PV) and genotypic (GV) variances, phenotypic (PCV%) and genotypic (GCV%) coefficient of variability, heritability (h²%) and expected genetic advance (G_E) as % of lines mean from selection (top 10%) for studied traits of 27 elite sesame lines in the selection experiment and the actual genetic advance (G_A) in the evaluation experiment and check cultivars (Shandaweel 3 and Giza 32)

Elite sesame lines Statistics and Parameters	Selection experiment Characters				
	DM	PH	HFC	FZL	NB
Mean (\bar{x})	112.9	119.6	28.54	97.1	2.3
Range (R)	106.3 - 119.3	119.3 - 143.2	10.4 - 41.8	78.5 - 120.5	0 - 6.3
Phenotypic Variance (PV)	5.23	107.0	51.0	100.5	0.32
Genotypic Variance (GV)	1.22	84.0	47.0	72.5	0.27
PCV%	2.0	8.6	25.2	10.3	24.9
GCV%	0.97	7.6	24.0	8.7	22.8
PCV - GCV	1.03	1.0	1.2	1.6	2.1
h ² %	23.2	78.5	92.2	72.1	84.3
G _E %	-4.0	16.2	-47.3	13.2	84.3
Check cultivars					
Mean (\bar{x})	118.6	129.2	45.1	98.1	98.1
Range (R)	105.1-121.2	123.2-140.3	30.2-60.4	90.2-110.3	90.2-110.3
C.V.%	8.9	4.1	11.1	14.3	14.3
Elite sesame lines Statistics and Parameters	Evaluation experiment Characters				
	DM	PH	HFC	FZL	NB
Mean (\bar{x})	96.7	165.3	35.7	130.7	2.4
Range (R)	91.3 - 100.5	143.2 - 185.3	22.5- 52.3	112.6 - 152.3	0.0 - 5.1
Phenotypic Variance (PV)	4.3	113.0	49.5	98.0	0.97
Genotypic Variance (GV)	3.2	61.0	30.2	44.5	0.62
PCV%	2.14	6.4	19.7	7.6	41.8
GCV%	1.84	4.7	15.4	5.1	32.9
PCV - GCV	0.30	1.7	4.8	2.5	8.9
h ² %	74.3	54.7	61.6	45.3	64.4
G _A %	-2.1	12.0	-32.1	13.0	83.7
Check cultivars					
Mean (\bar{x})	105.6	150.3	40.1	113.3	0.3
Range (R)	105.2-120.3	130.2-155.1	35.6-55.2	100.2-130.5	0 - 3.0
C.V.%	5.7	6.6	11.4	11.1	27.5

DM=days to maturity, PH=plant height, HFC= stem height to 1st capsule, FZL=fruiting zone length, NB=number of branches plant⁻¹
- Negative values for earliness and lower stem height to 1st capsule.

Table 7. Means (\bar{x}), ranges (R), coefficient of variability (C.V.%), phenotypic (PV) and genotypic (GV) variances, phenotypic (PCV%) and genotypic (GCV%) coefficient of variability, heritability (h²%) and expected genetic advance (G_E) as % of lines mean from selection (top 10%) for studied traits of 27 elite sesame lines in the selection experiment and the actual genetic advance (G_A) in the evaluation experiment and check cultivars (Shandaweel 3 and Giza 32)

Elite sesame lines Statistics and Parameters	Selection experiment Characters				
	NC	SI	SYP	SYPL	Oil%
Mean (\bar{x})	194.3	3.7	32.7	459.5	53.8
Range (R)	150.1 - 240.3	3.1- 4.3	28.3- 38.2	400.8-573.6	50.3-58.4
Phenotypic Variance (PV)	749.0	0.15	7.0	1472.0	5.6
Genotypic Variance (GV)	651.0	0.12	4.0	913.3	5.0
PCV%	14.1	10.4	8.4	9.2	4.3
GCV%	13.2	9.6	6.1	7.2	4.1
PCV - GCV	0.9	0.8	2.3	2.0	0.2
h ² %	86.9	80.1	62.0	61.0	89.3
G _E %	17.0	13.2	8.1	12.8	8.2
Check cultivars					
Mean (\bar{x})	185.2	3.9	23.0	360	47.3
Range (R)	170.1-200.3	3.6-4.3	20.4-26.5	290.5-400.5	44.3-50.2
C.V.%	7.1	5.2	8.11	11.5	4.3

Elite sesame lines Statistics and Parameters	Evaluation experiment Characters				
	NC	SI	SYP	SYPL	Oil%
Mean (\bar{x})	228.3	3.6	38.3	543.5	53.4
Range (R)	180.6-297.6	3.0-4.2	28.6-54.2	412.8-780.3	45.8- 68.0
Phenotypic Variance (PV)	755.0	0.10	53.0	11848.5	31.0
Genotypic Variance (GV)	581.0	0.09	42.6	9587.0	29.0
PCV%	12.0	9.0	19.0	20.0	10.4
GCV%	10.5	8.3	16.9	18.0	10.0
PCV – GCV	1.5	0.7	2.1	2.0	0.4
h ² %	77.0	90.0	80.0	81.0	93.9
G _A %	16.8	17.1	23.2	13.1	36.2
Check cultivars					
Mean (\bar{x})	203.3	3.9	30.1	390	49.3
Range (R)	170.2-240.2	3.7-4.1	25.2-45.1	320.2-450.2	43.1-51.3
C.V.%	7.5	1.4	7.1	40.1	4.6

NC= number of capsules plant⁻¹, SI=seed index, SYP= seed yield plant⁻¹, SYPL=seed yield plot⁻¹ and Oil%=oil percentage.

2.3. Estimation of heritability in broad sense and expected and actual genetic advance

Estimates of heritability, genetic coefficient of variation and genetic advance would be helpful to the breeder during the application of selection in the breeding programmes. The heritabilities estimated by the variance components method would be useful in making these decisions. Mishra . (2006) also concluded that high heritability and high genetic advance would be valuable in selection programmes.

The broad sense heritability, the proportion of genotypic variance to the phenotypic variance, is an important parameter in breeding and genetics, because knowledge of numerical magnitude of heritability is of special importance for planning in breeding programmes and for the examination of experimental results. Broad sense heritability values for the ten traits are presented in Tables 6 and 7. Heritability values are categorized as low (0-30%), moderate (30-60%) and high (60% and above) as given by Johnson ., (1955). Based on this delineation, the range of heritability estimates in broad sense varied from to 23.2 % for days to maturity to 93.9 % for oil%.

According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. Although, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of environment.

Taking a closer look at the obtained results and considering the previous benchmark, highest heritability 93.9% was recorded for oil percentage and heritability estimates were very high for seed index (90.0%) followed by seed yield plot⁻¹ (81.0%), seed yield plant⁻¹ (80.0%), number of capsules plant⁻¹ (77.0%) and days to maturity (74.4%) and moderate for number of branches plant⁻¹ (64.4%), stem height to 1st capsule (61.6%), plant height (54.7%) and fruiting zone length (45.3%) and. These results are in accordance with Krishnaiah . (2002). The heritable variation with heritability (broad sense) estimates would give reliable indication of the expected improvement through selection (Johnson ., 1955). It is worth to mention here that less difference between GCV and PCV and corresponding high heritability were observed for most the characters in the present study (Tables 6 and 7), indicating that selection would be effective for these characters.

An obvious discrepancy was recorded in heritability estimates of studied characters. In general, the h² estimates in the selection experiment was lower for two traits viz., days to maturity and seed yield plot⁻¹ than in the evaluation experiment. By contrast, h² was middle to very high for other traits in the selection experiment. The reason for this discrepancy may be due to the nature of the Nubaria soil, and/or the difference between the two seasons in the temperature and relative humidity (Table 1) and the experimental error due the limited resources available for increasing the sample size. Besides, the higher homogeneity in F₇ (0.984) compared to F₆ (0.968) was reflected in higher heritability for seed index, seed yield plant⁻¹, seed yield plot⁻¹ and oil%. Shabana and Abo-Hagaza (1983) found that h² was high (90%) for days to flowering but medium to high for other traits. The expected genetic advance values for 10 characters of the lines evaluated is presented in Tables 6 and 7. These values are also expressed as percentage of the lines mean for each character so that comparison could be made among various characters, which had different units of measurement. High heritability along with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals.

Estimates of the expected genetic advance are the result of the tentative selection applied in the population based on the heritability estimates. According to Johnson . (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. This study showed that moderate heritability coupled with high expected genetic advance as percent of mean for number of branches per plant, seed yield per plant and oil % alone, indicating that the presence of more additive gene effects for potential crop improvement and so these characters could

be improved through selection. Therefore, these characters could be improved more easily than other characters measured. Most of the characters in these lines showed moderate heritability and very minimum/low genetic advance as percent of the mean, which makes the improvement program of important traits or characters of sesame, is difficult.

As shown in the results (Tables 6 and 7) there are no discrepancies between expected and actual genetic advances reported for four traits viz., fruiting zone length, number of branches plant⁻¹, number of capsules plant⁻¹ and seed yield plot⁻¹ while other traits showed discrepancies between expected and actual genetic gains. The discrepancies between expected and actual genetic advances are within the limits of random environmental variability (Pesek and Baker, 1970). Actual advances from selection should be used rather than expected advances may be biased upward considerably by genotype x environmental interaction effects which to a considerable degree are not fixable by selection (Shabana ., 1980).

2.4. Genotypic and Phenotypic Correlations among Characters

Correlation analysis is a useful technique, which provides information about the degree of relationship between important plant traits and is also a good index to predict the yield response in relation to the change of a particular character (Muhammad ., 2007). In sesame, seed yield as in other crops, is a complex character that is dependent on a number of variables.

The genotypic and phenotypic correlations between yield and the evaluated variables are presented in (Table 8). Correlation studies (Table 8) showed that for all characters genotypic and phenotypic associations were in the same direction and genotypic estimates were relatively higher than the phenotypic ones indicating an inherited association between the traits.

With regards to, the values of genotypic correlation coefficient in F₇ generation, results showed that plant height, stem height to the first capsule, number of branches plant⁻¹ and number of capsules plant⁻¹ had a significant positive correlation with seed yield plant⁻¹ (r=0.41**, r=0.28**, r=0.73** and r=0.95**, respectively), but the correlation between days to maturity and seed yield per plant was significantly negative (r=-0.29**) (Table 8). Tomar . (1999) also found similar observations.

From the result in Table 8, seed yield plot⁻¹ was significantly and positively correlated with plant height, stem height to 1st capsule, number of branches plant⁻¹, number capsules plant⁻¹ and seed yield plant⁻¹ in F₆ and F₇, respectively. The significant and positive correlation recorded between sesame seed yield per unit area and the previous characters, indicated inter-dependency between these characters. It also indicated that these parameters are important yield determinants because the higher the numbers of branches, which increase the canopy cover and hence greater interception of light energy and higher rates of photosynthesis, which translates to increase yield. Contradictory, seed yield plot⁻¹ was significantly and negatively correlated with both seed index and oil percentage in both generations. In the literature, there have been unanimously agreements about the negative association between seed yield plot⁻¹ and oil percentage in sesame.

It should be emphasized that all associations reported here were valid in the phenotypic and genotypic levels. In general, the genotypic correlation coefficients were slightly higher than the phenotypic correlation coefficients, indicating the masking effect of the environment was limited and did not mask the expression of the genotypes. Similar results were reported in Egypt by Shabana and Abu-Hagaza (1984) HobAllah (2002) Saber (2010) and Abd El- Mohsen (2013).

Table 8. Phenotypic (r_{ph}) and genotypic (r_g) correlation coefficients for seed yield and its components in F₆ and F₇-27 elite sesame lines

Char ac.	Gen er.	PH		HFC		F		NB		NC		SI		Oil %		SYP		SYPL	
		r _{ph}	r _g	r _{ph}	r _g	r _{ph}	r _g	r _{ph}	r _g	r _{ph}	r _g	r _{ph}	r _g	r _{ph}	r _g	r _{ph}	r _g	r _{ph}	r _g
		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
DM	F ₆	0.28**	0.29**	0.01	0.03	0.13	0.14	0.23*	0.29**	0.03	0.19	0.03	0.04	0.10	0.12	0.34**	0.35**	0.02	0.04
	F ₇	0.27*	0.29**	0.03	0.02	0.10	0.11	0.10	0.02	0.36**	0.38**	0.04	0.06	0.16	0.20	0.28**	0.29**	0.12	0.14
PH	F ₆	-	-	0.27*	0.34**	0.54**	0.81**	0.18	0.19	0.30**	0.34**	0.16	0.15	0.04	0.13	0.26*	0.28**	0.25*	0.27*
	F ₇	-	-	0.33**	0.57**	0.38**	0.97**	0.06	0.02	0.27*	0.37**	0.15	0.17	0.04	0.10	0.34**	0.41**	0.36**	0.50**
HFC	F ₆	-	-	-	-	0.38**	0.45**	0.23*	0.33**	0.57**	0.60**	0.16	0.20	0.21*	0.22*	0.25*	0.26*	0.24*	0.32**
	F ₇	-	-	-	-	0.48**	0.55**	0.59**	0.61**	0.25*	0.28**	0.15	0.16	0.19	0.20	0.36**	0.28**	0.34**	0.42**
F ZL	F ₆	-	-	-	-	-	-	0.04	0.11	0.17	0.20	0.12	0.07	0.17	0.11	0.04	0.03	0.03	0.05
	F ₇	-	-	-	-	-	-	0.23*	0.39**	0.08	0.02	0.02	0.05	0.16	0.17	0.19	0.20	0.15	0.19
NB	F ₆	-	-	-	-	-	-	0.42**	0.48**	0.26*	0.27*	0.19	0.20	0.35**	0.36**	0.34**	0.42**	-	-
	F ₇	-	-	-	-	-	-	0.42**	0.48**	0.26*	0.27*	0.19	0.20	0.35**	0.36**	0.34**	0.42**	-	-

	F ₇	0.43 **	0.85 **	0.54 **	0.55 **	- 0.10	- 0.11	0.46 **	0.73 **	0.70 **	0.53 **
NC	F ₆			- 0.01	- 0.02	0.46 **	0.48 **	0.64 **	0.80 **	0.70 **	0.80 **
	F ₇			- 0.10	- 0.17	0.26 *	0.29 **	0.75 **	0.95 **	0.87 **	0.89 **
SI	F ₆					0.33 **	0.27 *	0.42 **	0.48 **	0.31 **	0.51 **
	F ₇					- 0.11	- 0.12	0.32 **	0.38 **	0.33 **	0.41 **
Oil %	F ₆							0.43 **	0.44 **	0.65 **	0.83 **
	F ₇							0.26 *	0.29 **	0.27 *	0.29 **
SYP	F ₆									0.61 **	0.73 **
	F ₇									0.70 **	0.76 **

DM=days to maturity, PH=plant height, HFC= stem height to 1st capsule, FZL=fruiting zone length, NB= number of branches plant⁻¹, NC= number of capsules plant⁻¹, SI=seed index, Oil%=oil percentage, SYP= seed yield plant⁻¹ and SYPL=seed yield plot⁻¹.

*. ** Significant level at 0.05 and 0.01 of probability, respectively.

3. Efficiency of selection indices

In plant breeding, selection is applied to the populations having genetic variability for the desired characters. The genetic variability is generated by crossing different individuals or mutating genes of interest by induced mutagenesis. Main purpose of a selection program is to increase the mean of the selected portion of the population and thus to select individuals with high genotypic value. Selection in practice depends on the phenotypes of the individuals and in the absence of genotypic portion of the variance the genetic advance from selection cannot be estimated.

Many multiple trait selection protocols utilize an aggregate score, or an index, as means of differentiating genotypes possessing superior trait combination. Index selection protocols utilize simultaneous selection on a series of traits as opposed to a sequential selection (Henning and Teuber, 1996). Some indices require the estimation of genetic variances, covariance, and the economic value for all traits undergoing selection. One of these is called the Smith-Hazel, or optimum index (Smith, 1936; Hazel, 1943). Efficiency of a selection index depends not only on the kind of crop plant and considered traits, but also on the base population used for the estimation of coefficients in selection indices.

3.1. Conventional selection indices:

Selection indices for selection of two or more traits simultaneously were done in twelve indices (Table 9) via the conventional method (Smith 1936) and we applied restricted selection for seed index and/or oil percentage in two restricted indices (Table 10). Oil percentage showed a significant negative relation with seed yield plot⁻¹ (Table 8). Thus, selection with high seed yield plot⁻¹ was accompanied by decreased oil yield.

Table 9. Conventional selection indices and expected genetic advance (G_E) in the selection experiment and relative efficiency (R.E. %) over direct selection for 27 sesame lines

Index No.	Content of the index	G _E	R.E. (%)
	Direct selection for seed yield plot ⁻¹	1.11	100
1	Days to maturity + Seed yield plot ⁻¹	0.57	63
2	Plant height + Seed yield plot ⁻¹	1.28	115
3	Stem height to 1 st capsule + Seed yield plot ⁻¹	1.30	117
4	Fruiting zone length+ Seed yield plot ⁻¹	1.29	116
5	Number of branches plant ⁻¹ + Seed yield plot ⁻¹	3.52	317
6	Number of capsules plant ⁻¹ + Seed yield plot ⁻¹	2.53	227
7	Seed yield plant ⁻¹ + Seed yield plot ⁻¹	3.72	334
8	Plant height + Stem height to 1 st capsule + Seed yield plot ⁻¹	2.68	241
9	Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹	4.29	385
10	Plant height + Stem height to 1 st capsule + Number of branches plant ⁻¹ + Seed yield plot ⁻¹	2.55	229
11	Plant height + Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹	6.56	591
12	Stem height to 1 st capsule + Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹	5.74	517

In that context, Rosielle . (1977) reported that a high correlation between late flowering date and each of seed yield or straw yield was found in oats. Holding heading date to the mean of unselected population removed correlated responses in heading date, but decreased advance from selection.

Besides, selection for high oil% in sesame decreased seed yield per unit area, and vice versa (El-Shimy, 1995). All selection indices that compromised a single trait beside seed yield plot⁻¹ were efficient over direct selection for seed yield plot⁻¹ except selection index number 1 (Table 9). The highest relative efficiency (591%) among conventional indices was observed for the index number 11 that contained four traits simultaneously viz., plant height, number of branches plant⁻¹, number of capsules plant⁻¹ and seed yield plot⁻¹. This result is not in full agreement with that of Rosielle . (1977) in another self-pollinated crop. They mentioned that it is difficult to select an ideal cultivar with all desired traits when acceptance of the new cultivars (s) is conditioned by several traits. Hidalgo-Contreras (2014) used a modern technique for selection and found that highest efficiency in his data was 317%.

3.2. Restricted selection index:

Dissociation of traits that increased efficiency of selection for seed yield plot⁻¹ via conventional selection indices are for traits that have no negative or repulsion association with high yield. Restricted selection indices were developed to circumvent, insofar as possible, undesirable correlations that exist among traits. A restricted selection index might be helpful to obtain more desired gains would involve negative correlations between seed yield plot⁻¹ with other traits such as seed index and/or oil percentage (Table 10). With a restricted selection index it might be possible to restrict seed index and/or oil percentage by keeping them at the lines mean and at the same time increase seed yield plot⁻¹ appreciably. When restrictions were applied for seed index and/or oil percentage in the selection experiment the seed yield plot⁻¹ increased by 3.0 and 1.3 % of lines mean, respectively, (Table 10) while conventional selection indices decreased seed yield plot⁻¹ by 22.16 and by 13.26 % of lines mean, respectively when seed index and oil% were included without restriction.

Table 10. Expected genetic gain achieved by conventional versus restricted selection indices for either seed index or oil percentage

Character	b _i	Conventional selection	Restricted selection	
		Δ G%	b _i	Δ G%
Seed index				
Seed index	-5.5		-4.9	0
Seed yield plot ⁻¹	0.13	-22.16	0.60	12.8 g
Oil %				
Oil %	-0.73		-0.92	0
Seed yield plot ⁻¹	0.32	-13.26	0.15	6.8 g

b_i represents the index weight, Δ G% is expected genetic gain

In Egypt, Radwan and Momtaz (1974) reported that high seed yield lines in seed yield or straw of flax took more days to the onset of the first flower. However, they used the conventional selection index to improve either seed yield or straw yield with days to flowering instead of the use of restricted index. In that context, other authors, Rosielle . (1977) reported a high correlation between late flowering and each of seed yield or straw yield. They used the restriction selection method by holding heading date to the mean of unselected population which removed the correlated response in heading data with seed yield or straw yield in oats.

4. Rank correlation between selection and evaluation experiments:

Data in Table (11) showed rank correlation among ranks of the 27 elite sesame lines in each selection procedure in F₆ as well as rank of these lines after practicing selection methods and one generation of selfing in the evaluation experiment. The highest rank correlation was achieved via selection index (6) that included two traits simultaneously (number of capsules plant⁻¹ and seed yield plot⁻¹) followed by selection index (11) that included four traits simultaneously (plant height, number of branches plant⁻¹, number of capsules plant⁻¹ and seed yield plot⁻¹). It is obvious that selection to more capsules per plant was definitely better than selection for seed yield only. Thus, selection index is a very useful tool in this breeding stage and has direct output on the resulting cultivar (s).

Table 11. The rank correlation between direct selection and ranks conventional and restricted selection indices of the 27 elite sesame lines

F ₆	F ₇	Traits in index
	0.61**	Direct selection for seed yield plot ⁻¹
Index No.		
Index 1	0.50*	Days to maturity + Seed yield plot ⁻¹
Index 2	0.35*	Plant height + Seed yield plot ⁻¹
Index 3	0.51*	Stem height to 1 st capsule + Seed yield plot ⁻¹
Index 4	0.34*	Fruiting zone length+ Seed yield plot ⁻¹
Index 5	0.35*	Number of branches plant ⁻¹ + Seed yield plot ⁻¹

Index 6	0.76**	Number of capsules plant ⁻¹ + Seed yield plot ⁻¹
Index 7	0.55**	Seed yield plant ⁻¹ + Seed yield plot ⁻¹
Index 8	0.48*	Plant height + Stem height to 1 st capsule + Seed yield plot ⁻¹
Index 9	0.48**	Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹
Index 10	0.45*	Plant height + Stem height to 1 st capsule + Number of branches plant ⁻¹ + Seed yield plot ⁻¹
Index 11	0.71**	Plant height + Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹
Index 12	0.45**	Stem height to 1 st capsule + Number of branches plant ⁻¹ + Number of capsules plant ⁻¹ + Seed yield plot ⁻¹
Index 13	-0.12	Seed index + Seed yield plot ⁻¹
Index 14	0.20	Oil percentage + Seed yield plot ⁻¹

*. ** Significant level at 0.05 and 0.01 of probability, respectively.

5. Characterization of sesame lines that was common among the top 10% in several ranks:

The line C3.8 resulted from the cross (P₁ X P₄) ranked as first line in F₆ and F₇ based on selection for seed yield plot⁻¹ and in the selection experiment based on 9 conventional selection indices, out of the 12 indices constructed, (not presented in Tables). It is earlier in maturity than lines mean by ca.2 days and than the two check cultivars by ca.10 days. It is characterized by taller plants (ca.185 cm) and longest fruiting zone length (ca.152 cm) amongst the 27 elite lines. It also showed higher number of capsules plant⁻¹ (ca.268 capsule), seed yield plant⁻¹ (54 g) and seed yield plot⁻¹ (780 g), (not presented in Tables). In addition, a separate experiment for the reaction of the 27 lines against artificial infection with *Fusarium* diseases showed that this line was highly resistant.

The line C1.6 resulted from the cross (P₁ X P₂) ranked as fifth in F₇ and as first in conventional selection index No. 2 and as second in 8 conventional selection indices. Besides, this line was resistant against artificial infection with *Fusarium* diseases (Shabana ., 2014).

The line C1.8 resulted from the cross (P₁ X P₂) ranked as third line in F₆ and F₇ and as second in 2 conventional selection indices and as third in 8 conventional selection indices. It is earlier than check cultivars by about ca.8 days. It recorded the highest branches plant⁻¹ (ca.5 branches) and the highest capsules plant⁻¹ (ca.297 capsule) amongst the 27 elite lines and check cultivars. Unfortunately, this line was not resistant to artificial infection with *Fusarium* disease (Shabana ., 2014).

It is of special interest that there is a common parent (P₁) for the three lines as described before. This parent (HM19) characterized by early maturity, non branching, first capsule set low, 3 capsules/axil, the second parent (P₂) have same characters and third parent (P₄) was characterized by late maturity, medium branching, one capsule/axil, long capsule, heavy seed weight.

The ranking of selected lines revealed the validity of using the right selection index technique in the production a new high yielding sesame cultivar that combine also one or more useful traits. In that context, Pesek and Bakar (1970) reported that selection index help in selection of traits that are higher than the average of other lines plus high seed yield per se. Most recently, Hidalgo-Coutreras (2014) in Nebraska, USA used a multi-trait genomic selection index. He used the principle component analysis via 250 principle components which, in his opinion, explained approximately 99% of the total variability. His method could represent a new era in the use of selection indices to increase selection efficiency in self-pollinated crops.

Resistance of lines to foliar disease during growing seasons depends upon its reaching a minimum threshold before any line is considered as a new cultivar. Disease reaction of a line, however, cannot be involved in any selection index. To avoid repulsion linkages between the selected line (s) that affect their high quantitative traits with genes that might cause seed yield less due to natural disease epidemics in certain years, a separate experiment for artificial infection of the 27 F₆ lines was conducted in a disease nursery but not presented here (see Shabana ., 2014).

CONCLUSIONS

In general, the following major findings can be summarized from this study:

- Information on the extent of genetic variability and heritability as well as correlation among agronomically important traits is a requirement to design a suitable plant breeding method. Our results obtained from F₆ and F₇ generations showed that a good genetic variation (high GCV) was observed in the studied material for stem height to the first capsule, number of branches per plant, number capsules per plant and seed yield per plant, which shows that they were utilizable for specific traits required in the development of cultivars. Number of capsules per plant, seed index, seed yield per plot and oil % in F₇ generation, close estimates of GCV and PCV and high broad sense heritability for the most characters indicated that differences among the genotypes were mostly genetic. The genotypic correlation coefficient was generally higher than the corresponding phenotypic correlation coefficient which indicated that the apparent association might be due to genetic reason.
- Among the 27 F₆ and F₇ lines, two sesame lines (C3.8 and C1.6) showed the highest seed yield rank and were also characterized by superiority in other favorable agronomic traits. Besides, they were also resistant to artificial infection with two *Fusarium* diseases. Presumably, genes for the expression of favorable traits including disease resistant were dragged along with gene (s) for high seed yield through segregating generations. These superior lines were also higher than the best cultivars used as checks herein. Therefore, it seems necessary to continue evaluating new sesame lines by growing them at several locations over an

adequate number of years before recommending any variety for a certain location and could be recommended as new cultivars after tests and approval by the Egyptian National Seed Committee for cultivars certifications.

- The results of this research could be implemented for improving productivity of sesame crop. Last but not least the present investigation provided considerable information that could be useful for sesame breeders, statisticians and agronomists to understand the nature of the relationship between the most important factors affecting the yield of sesame.

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