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GENETIC VARIABILITY AND SELECTION CRITERIA OF SOME SESAME GENOTYPES FOR THEIR AGRONOMIC TRAITS AND SEED QUALITY

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Abstract: The identification of genetic variation, mean performance, and selection criteria for twelve sesame genotypes is required for the genetic enhancement of agronomic traits and seed quality. Thus, using a randomized complete block design with three replications, these genotypes were evaluated in a field trial at the Kafr-El-Hamam Agricultural Research Station, Agricultural Research Center, Sharkia Governorate, Egypt, and laboratory experiments at the Seed Technology Research Department, ARC, Giza, Egypt, during the two consecutive seasons of 2018 and 2019. For earliness in flowering, N.A.$_{130}$ and Shandweel$_3$ were the most promising sesame genotypes, while N.A.$_{114}$ and RH$_1$F$_3$ had the heaviest weight of seed plant^{-1} and one or more yield-related traits, and NA$_{114}$, Shandweel$_3$, and Zahar$_{12}$ had the best seed quality traits. Furthermore, Shandweel$_3$ and M$_1$A$_{12}$ had the highest proportion of seed oil, Shandweel$_3$ and Zahar$_{12}$ had the largest amount of oleic acid, N.A.$_{114}$ and RH$_1$F$_3$ had the highest content of linoleic acid, and Zahar$_{12}$ and N.A.$_{114}$ had the highest proportion of linolenic acid. Seed weight plant^{-1} can be improved through selecting genotypes having the lengthiest fruiting zone, more branches and capsules, and the high electrical values of seed conductivity, accelerated aging germination as demonstrated by selection criteria. Moreover, the oleic acid proportion had the greatest direct and indirect effect on seed oil content, demonstrating its relevance as sesame oil quality selection criteria.

Key words: direct and joint effects, fatty acid compositions, phenotypic and genotypic correlation, *Sesamum indicum* L.

Introduction

Sesame (*Sesamum indicum* L.) is one of the oldest and most significant oilseed crops worldwide, not only in Egypt (Bhattachary et al., 2014). It is a major

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industrial crop as well as a nutritious food source. There is a significant disparity between oil output and consumption in Egypt. The development of genotypes with high seed and oil yield potential is deemed required to close this significant gap. As a result, much emphasis must be placed on improving the genetic yield of sesame genotypes, which may be achieved by determining the degree of genetic diversity in breeding materials. This information will assist sesame breeders in selecting the best breeding approach for their sesame crop development program. In this regard, Fahmy et al. (2015), Abd EL-Satar et al. (2016), Teilep et al. (2018), Anbanandan (2018), Bhuiyan et al. (2019), Sultana et al. (2019), Pavani et al. (2020), and Abdelsatar et al. (2020) found that significant genetic variability had the greatest effect on improving yield and its components. Furthermore, yield components have a positive impact on seed yield. As a result, investigating the relationship between seed yield and its components, as well as identifying the direct and indirect effects of yield components on seed yield will help in improving it directly. Moreover, Sultana et al. (2019) and Abdelsatar et al. (2020) reported that yield components had a positive effect on seed yield.

Seed germination and seedling vigor are two factors that determine a seed’s ability to germinate rapidly and uniformly and develop into healthy seedlings under a wide range of conditions. Farmers’ most common difficulties are a low sesame germination rate and poor seedling establishment (Khare and Bhale, 2016). Poor seedling vigor is one of the primary causes of poor germination and irregular seedling establishment (Khan et al., 2017). As a result, seed quality parameters such as germination % and vigor index affect yield by influencing plant population density, which includes field emergence, spatial arrangements, and crop duration (Khare and Bhale, 2016).

Therefore, the current investigation was designed to study mean performance, genetic parameters and selection criteria represented in correlation and path analyses at both phenotypic and genotypic levels of some sesame genotypes for agronomic traits and seed quality.

Materials and Methods

Site description

During the two consecutive summer seasons of 2018 and 2019, a field experiment was conducted at the Experiment Farm of the Kafr-El-Hamam Research Station, Zagazig, Sharkia Governorate, Agricultural Research Center, Egypt (30° 58'N, 31° 50'E).

Experimental design

The experiment was laid out in a randomized complete block design with three replications. After harvesting wheat in both seasons, each genotype was sown in five ridges with a ridge length of 4 m spaced at 60 cm between ridges and 20 cm from hill to hill. Tested sesame genotypes, *i.e.* $N.A_{52}$, M_2A_5, $Shandweel_3$, M_1A_{12}, NA_{32}, RH_1F_3, NA_{114}, RH_6F_6, NA_{130}, $Zahar_{12}$, $H_{88}A_2$ and M_2A_{24}, were received from the Department of Oil Crops Research, Field Crop Research Institute, Agricultural Research Center, Egypt.

Agricultural practices

Sesame genotype seeds were hand-planted in 60-centimeter-wide ridges at the 20-centimeter spacing between hills. In both seasons, this was done during the first week of June. At 15 days following planting, plants of the sesame genotypes under investigation were thinned to maintain two plants $hill^{-1}$. Other cultural practices were used in accordance with the recommendations.

Data collected

Agronomic traits:

Days to 50% flowering (days) were recorded on the basis of the number of plants in the plot. Plant height (cm), length of fruiting zone (cm), number of branches $plant^{-1}$, number of capsules $plant^{-1}$, weight of 1000-seed (g), and seed weight $plant^{-1}$(g) were all measured on ten competitive plants randomly selected from the 2nd and the 4th ridges. Seed yield per m^2 was determined from plants in each plot's central ridge and converted to seed yield in kg per hectare.

Seed quality: During the 2018 and 2019 seasons, seed quality testing for several seed quality parameters was done at the Seed Technology Research Department, ARC, Giza, Egypt.

Germination test: Seedlings were counted according to ISTA (1993) international criteria based on normal seedlings. The percentage of germination was determined using the Krishnasamy and Seshu's methodology (1990). The seed vigor index (S.V.I.) was computed using Copeland's (1976) formula:

S.V.I. = (Number of germinated seeds (first count) / Days to the first count) + (Number of germinated seeds (final count) / Days to final count), with the first count made after 3 days of germination.

Seedling evaluation: According to the rules of the Association of Official Seed Analysis, normal seedlings were used for seedling evaluation (AOSA, 1983). After a six-day germination test, the seedling shoot and root lengths were measured. The shoots and roots were also dried for 72 hours at 70 degrees Celsius. Seedling vigor index was computed using ISTA's (1985) formula: Seedling vigor index = seedling length (cm) × germination percentage.

Accelerated aging: The seeds were maintained in an aging chamber for three days at 45°C and 100% relative humidity. The seeds were dried in the sun after aging, and the percentage survival of the seeds was measured using a standard germination test at 25 degrees Celsius, and the mean normal seedling percentage was computed using AOSA guidelines (1983).

Electrical conductivity test: The electrical conductivity of the leachate was determined using the techniques outlined by ISTA (1999). Fifty seeds of each cultivar were weighed to 0.001g, put in plastic cups with 250 ml of distilled water, and kept at 25°C for four sub-samples. The electrical conductivity of the leachates was measured using an EC metre after 24 hours. The average values were given in $Scm^{-1}g^{-1}$.

Seed oil content and its quality

Crude oil percentage: According to AOSA (2000), crude oil percentage was measured using the Soxhlet apparatus with hexane as the solvent. A Hewlett Packard gas chromatograph model 5890 with a cabowa × Hp 20 M column was used to examine the methyl esters of fatty acids.

Fatty acid compositions: Fatty acid compositions were determined in samples of roughly 50 g of air-dried seeds of each genotype that were picked at random from two replications and finely ground for chemical composition estimation.

Statistical analysis

For all examined traits in field and laboratory trials, an analysis of variance was performed using a randomized complete block design with three replications according to Gomez and Gomez (1984). After confirming that the error variance for the studied traits was homogeneous using the Hartley's (1950) F-max test technique, a combined analysis of variance was conducted over two seasons. Genotypic and phenotypic coefficients of variation were estimated as described by Burton and DeVane (1953). The estimate of broad-sense heritability (h^2_b) was done by the formula suggested by Hansen et al. (1956). Moreover, the genetic advance as percent of the mean was performed according to Johnson et al. (1955). For the identification of selection criteria, the phenotypic and genotypic correlation coefficient was computed according to Weber and Moorthy (1952). Moreover, phenotypic and genotypic path analysis was computed as described by Dewey and Lu (1959).

Results and Discussion

Mean performance

Agronomic traits

Significant variations were found among the twelve sesame genotypes in terms of most seed weight $plant^{-1}$ and related traits (Table 1), showing that there was enough genetic diversity to effectively select better or preferred genotypes. The earlier study by Singh et al. (2020) found similar results.

Table 1. The agronomic performance of twelve sesame genotypes across 2018 and 2019 summery seasons.

Genotypes	Days to 50% flowering (day)	Plant height (cm)	Fruiting zone length (cm)	Branch number	Capsule number	1000-seed weight (g)	Seed weight plant^{-1} (g)	Seed yield hectare^{-1} (kg)
N.A.$_{52}$	64.00	188.60	128.08	5.38	280.48	5.35	48.57	1761.67
M_2A_5	57.00	184.60	120.83	4.88	251.65	4.65	45.42	1543.52
Shandweel$_3$	53.50	163.07	68.83	1.53	227.43	3.55	37.47	1233.98
M_1A_{12}	55.67	162.55	78.83	3.57	197.98	3.60	38.52	1390.60
N.A. $_{32}$	54.00	167.67	90.23	6.00	230.58	4.53	42.78	1389.17
RH_1F_3	57.67	185.07	141.62	5.45	261.12	5.53	48.62	1562.14
N.A. $_{114}$	65.00	192.85	117.93	6.37	300.20	5.47	56.13	1569.71
RH_6F_6	56.17	177.00	108.90	4.55	219.55	4.75	44.98	1501.14
N.A.$_{130}$	53.00	180.77	111.80	5.17	286.15	4.47	46.88	1213.26
Zahar$_{12}$	58.17	175.27	143.22	6.13	307.45	4.88	47.07	1934.69
$H_{88}A_2$	57.33	190.03	124.55	5.60	258.40	5.37	46.12	1579.88
M_2A_{24}	55.83	175.45	109.08	4.65	218.63	4.50	42.67	1415.55
LSD 5%	1.27	3.04	2.85	0.22	4.28	0.47	1.42	19.38
LSD 1%	1.72	4.13	3.87	0.30	5.82	0.63	1.93	26.33

The earliness of genotypes in days to 50% flowering (Table 1) was detected in N.A.$_{130}$ (53.00 days), followed by Shandweel$_3$ (53.50 days). The shortest plant height (Table 1) was obtained by M_1A_{12} (162.55 cm), followed by Shandweel$_3$ (163.07 cm). Zahar$_{12}$ (143.22 cm) and RH_1F_3 (141.62) possessed the longest fruiting zone length (Table 1). N.A.$_{114}$ (6.37) followed by Zahar$_{12}$ (6.13) had more branches plant^{-1} (Table 1). More capsules plant^{-1} (Table 1) were generated by Zahar$_{12}$ (307.45), followed by N.A.$_{114}$ (300.20). The heaviest weight of 1000 seeds (Table 1) was achieved by RH_1F_3 (5.53 g), followed by N.A.$_{114}$ (5.47 g). Consequently, N.A.$_{114}$ (56.13 g) followed by RH_1F_3 (48.62 g) possessed the heaviest weight of seed plant^{-1}(Table 1). Moreover, the highest seed yield hectare^{-1}(Table 1) was obtained by Zahar$_{12}$ (1934.68 kg ha^{-1}) followed by N.A.$_{52}$ (1761.67 kg ha^{-1}).

Seed quality:

Germination traits:

The results revealed highly significant differences between sesame genotypes with regard to all studied traits (Table 2). Meanwhile, N.A.$_{114}$ (96.67) achieved higher standard germination %, followed by M_2A_5 (96.17), Shandweel$_3$ (96.00) and Zahar$_{12}$ (95.33) genotypes, respectively. RH_6F_6 (91.17) and N.A.$_{32}$ (92.67), on the other hand, had lower standard germination percentages. These variations in sesame genotypes might be ascribed to genetic impacts on sesame seed germination ability. The seed vigor index findings in Table 2 showed the same normal germination percent patterns, with N.A.$_{114}$ (48.33), M_2A_5 (48.03), Shandweel$_3$ (48.00), and Zahar$_{12}$ (47.89) having the highest seed vigor index. On the other hand, N.A.$_{32}$ (44.50) and RH_6F_6 (44.75) gave the lower value of this trait. These results mostly took the same trend of seed weight plant^{-1}and its attributes and seed oil content traits. Zahar$_{12}$ (80.50) had the greatest value of accelerated aging germination % in Table 2, followed by M_2A_5 (78.50) and $H_{88}A_2$ (78.00), without any significant differences between them. These results indicated that these genotypes could be tolerant to bad storage or environment conditions. Meanwhile, RH_6F_6 (62.33) and M_1A_{12} (62.33) had a lower proportion of accelerated aging germination.

Table 2. The performance of twelve sesame genotypes for seed quality traits across 2018 and 2019 summery seasons.

	Seed quality traits								
	Germination traits				Seedling traits				
Genotypes	Standard germination %	Seed vigor index	Accelerated aging germination %	Electrical conductivity µScm^{-1}g^{-1}	Root length (cm)	Shoot length (cm)	Seedling length (cm)	Seedling dry weight (mg)	Seedling vigor index
N.A.$_{52}$	93.50	45.92	64.50	122.05	5.84	2.60	8.44	4.86	787.77
M_2A_5	96.17	48.03	78.50	109.94	6.23	2.57	8.80	4.96	845.61
Shandweel$_3$	96.00	48.00	71.33	100.18	6.46	2.63	9.09	5.35	872.82
M_1A_{12}	93.67	45.94	62.33	123.96	6.84	2.66	9.50	8.46	888.42
N.A.$_{32}$	92.67	44.50	73.67	124.73	6.33	2.41	8.74	5.66	810.88
RH_1F_3	95.50	45.81	68.83	119.25	6.07	2.65	8.73	5.42	832.87
N.A.$_{114}$	96.67	48.33	75.67	103.47	6.41	2.73	9.15	5.59	883.96
RH_6F_6	91.17	44.75	62.33	114.64	6.45	2.45	8.91	6.54	811.96
N.A.$_{130}$	92.67	45.89	64.67	111.85	6.06	2.71	8.77	4.99	812.16
Zahar$_{12}$	95.33	47.89	80.50	102.75	6.22	2.89	9.12	5.86	869.14
$H_{88}A_2$	91.83	45.64	78.00	134.60	6.13	2.42	8.55	6.28	784.66
M_2A_{24}	94.33	45.72	67.33	121.98	6.26	2.57	8.83	5.85	832.88
LSD 5%	2.26	1.41	3.29	7.93	N.S	0.25	N.S	0.70	55.24
LSD 1%	3.07	1.92	4.47	10.78	N.S	0.34	N.S	0.96	75.08

The electrical conductivity (EC) is more often employed to determine seed vigor of crops because, as seed degradation advances, cell walls become less stiff and more water-permeable, enabling cell contents to escape into solution with the water and increasing electrical conductivity. Shandweel$_3$ (100.18), Zahar$_{12}$ (102.75) and N.A.$_{114}$ (103.47) recorded the lower EC values, respectively, without any differences between them (Table 2). However, the high EC values were recorded in $H_{88}A_2$ (134.60), followed by N.A.$_{32}$ (124.730). Standard germination percent, seed vigor index, and accelerated aging germination % were among the seed viability and vigor outcomes that were usually in the opposite direction of the forms provided. The results are in agreement with those reported by El Shakhess, Samar et al. (2008), Eraky, Hania et al. (2010) and Ahmed, Fadia et al. (2013).

Seedling traits:

On the one hand, the data in Table 2 revealed no significant variations between genotypes in both radical and seedling length traits. Shoot length, seedling dry weight, and seedling vigor index traits, however, showed highly significant variations among genotypes. The longest shoot length was found in Zahar$_{12}$ (2.89 cm), followed by N.A.$_{114}$ (2.73 cm), N.A.$_{130}$ (2.71 cm), Shandweel$_3$ (2.63 cm), and M_2A_5 (2.57 cm). Meanwhile, the short root length was given by N.A.$_{32}$ (2.41 cm.) and $H_{88}A_2$ (2.42 cm.). The higher seedling dry weight came from M_1A_{12} (8.46 mg), while the lower seedling dry weight came from N.A.$_{52}$ (4.86 mg). M_1A_{12} (888.42), N.A.$_{114}$ (883.96), Shandweel$_3$ (872.82), and Zahar$_{12}$ (869.14) had the highest seedling vigor index values, whilst $H_{88}A_2$ (784.66) had the lowest. Other traits such as seed weight plant^{-1} and its attributes, germination, and seedling traits followed a similar trend as these results.

Seed oil content and its quality

Again, highly significant differences in seed oil contents and fatty acid compositions were found among examined sesame genotypes (Table 3), suggesting that sesame genotypes have large genetic variability that allows for the successful selection of favorable genotypes. Mohanty et al. (2020) observed similar findings.

According to the sesame breeder, the best genotypes have low total saturated fatty acid compositions along with high total unsaturated fatty acid compositions. Shandweel$_3$ (7.53 %), followed by M_1A_{12} (7.54 %), had a low percentage of palmitic acids (C16:0), and N.A.$_{114}$ (4.22%), followed by N.A.$_{130}$ (4.23%), had a low proportion of stearic acids (C18:0). On the other hand, a high proportion of seed oil was detected in Shandweel$_3$ (60.08%), followed by M_1A_{12} (56.27%). Shandweel$_3$ (45.90%), followed by Zahar$_{12}$ (45.67%), was found to have the highest content of oleic acids (C18:1). The highest proportion of linoleic acids (C18:2) came from N.A.$_{114}$ (43.79 %), followed by RH_1F_3 (43.45%). The highest content of linolenic acids (C18:3) was achieved by Zahar$_{12}$ (0.74 %), followed by N.A.$_{114}$ (0.72 %).

Table 3. The performance of twelve sesame genotypes for seed oil content and its quality across 2018 and 2019 summery seasons.

		Fatty acid composition %							
Genotypes	Seed oil content	Saturated fatty acids		Unsaturated fatty acid			TS%	TU%	TS/TU ratio
		Palmitic C16:0	Stearic C18:0	Oleic C18:1	Linoleic C18:2	Linolenic C18:3			
N.A.$_{52}$	46.42	9.46	4.34	41.15	43.20	0.65	13.80	85.00	0.162
M_2A_5	47.92	9.28	4.62	43.77	42.87	0.53	13.89	87.17	0.159
Shandweel$_3$	60.08	7.53	5.51	45.95	41.26	0.27	13.03	87.47	0.149
M_1A_{12}	56.27	7.54	5.73	45.27	40.06	0.34	13.27	85.67	0.155
N.A.$_{32}$	54.80	8.65	5.13	44.67	41.82	0.42	13.78	86.91	0.159
RH_1F_3	46.56	9.51	4.46	43.17	43.45	0.65	13.96	87.28	0.160
N.A.$_{114}$	46.48	10.30	4.22	43.62	43.79	0.72	14.52	88.13	0.165
RH_6F_6	48.64	7.60	4.75	44.53	42.23	0.47	12.35	87.23	0.142
N.A.$_{130}$	46.30	10.53	4.23	41.59	40.56	0.32	14.76	82.47	0.179
Zahar$_{12}$	49.04	7.79	5.54	45.67	41.35	0.74	13.33	87.76	0.152
$H_{88}A_2$	47.27	9.36	4.54	43.70	42.79	0.58	13.90	87.07	0.160
M_2A_{24}	49.48	8.69	4.91	44.25	41.88	0.46	13.60	86.58	0.157
LSD 5%	1.08	0.20	0.10	1.88	1.27	0.03	0.23	2.38	0.01
LSD 1%	1.47	0.27	0.13	2.55	1.73	0.04	0.31	3.23	0.01

TS = Total saturated fatty acids TU = Total unsaturated fatty acids

Genetic parameters for agronomic traits and seed quality

The phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability in the broad sense (h^2_b), and expected genetic advance as percent mean for seed weight plant^{-1} and its related traits were computed to gain a better understanding of the extent of genetic variability for twelve sesame genotypes, as shown in Table 4. For all traits studied, PCV was slightly greater than GCV, indicating that the environment had a little effect on their expression. In the same line, Bhuiyan et al. (2019) and Abdelsatar et al. (2020) found that the differences between genotypic and phenotypic components of variance were narrow for investigated traits, indicating that phenotypic variation had a large genetic component in nature. Saravanan et al. (2020) also found that seed weight plant^{-1}, the number of branches per plant, and the number of capsules per plant had higher PCV and GCV values.

Consequently, selection for these traits would be successful in improving these breeding materials. Fruiting zone length, capsule number plant^{-1}, seedling vigor index and seed oil content had high PCV and GCV, while electrical conductivity, accelerated aging germination, plant height, branch number plant^{-1}, and seed weight plant^{-1} had moderate PCV and GCV, while the remaining traits had drastically reduced PCV and GCV.

Most studied traits have high heritability in the broad sense, indicating that a genotype can be recognized by its phenotypic performance, allowing for more effective selection to improve these traits.

As demonstrated in Table 4, heritability estimates combined with expected genetic advance as percent of the mean are usually more effective in predicting genetic gain under selection than heritability estimates alone, as validated by Johnson et al. (1955). High values of heritability coupled with high (more than 20%) values of genetic advance (as % of mean) were detected for fruiting zone length, branch number, capsule number, 1000-seed weight, seed weight plant^{-1}, palmitic, stearic and linolenic acid contents. As a result of the significance of additive gene effects in the inheritance of these traits, selection for these traits would be successful. In the same sense, Umamaheswari et al. (2019) and Abdelsatar et al. (2020) found that plant height at maturity, number of branches per plant, number of capsules per plant, length of the capsule, number of seeds per capsule, 1000-seed weight, and seed weight plant^{-1} had high heritability and high genetic advance as percent of the mean. This might be due to additive gene action influencing the expression of these traits; as a result, simple selection would likely be efficient in improving these traits. Moreover, Saravanan et al. (2020) found that the number of branches per plant and 1000-seed weight had a high heritability as well as a high genetic advance as percent of the mean. For days to 50% flowering, plant height, seedling dry weight, electrical conductivity, accelerated aging germination, seed oil content, and total saturated/total unsaturated ratio, high heritability combined with moderate (10–20%) expected genetic advance as percent of the mean were recorded, indicating that these traits appear to be controlled by both additive and non-additive gene actions. The variability study of Mohanty et al. (2020) indicated high to moderate genetic advance as percent of the mean for traits like plant height, days to first flowering, days to 50% flowering, days to maturity, number of productive branches plant^{-1}, height of the 1st capsule, number of productive capsules per plant, number of seeds per capsule, biological yield per plant, harvest index, 1000-seed weight, stearic acid, linolenic acid, linoleic acid, oleic acid, palmitic acid, oil content, oil yield per plant and seed weight plant^{-1}(g). This study indicates the preponderance of an additive gene effect, which will help to make the selection in an early segregating generation. However, high heritabilities coupled with low (less than 10%) expected genetic advance as percent of the mean were recorded for standard germination, root length, shoot length, seedling length, seed vigor index, seedling vigor index, oleic acid, linoleic, total saturated and total unsaturated fatty acids. This indicated that an increased influence of environment on these traits and thus the selection procedures involving progeny testing are recommended for these traits. Similar results were found by Mourad et al. (2019), who recorded that the expected genetic advance ranged from 2.28% for standard germination to 22.31% for seedling dry weight.

Table 4. Genetic parameters for agronomic traits and seed quality across 2018 and 2019 summery seasons.

Parameter	Agronomic traits						
	Days to 50% flowering	Plant height	Fruiting zone length	Branch number	Capsule number	1000-seed weight	Seed weight plant^{-1}
PCV	8.42	20.06	158.48	11.89	163.57	3.46	18.08
GCV	8.10	19.46	157.64	11.77	162.73	2.93	17.56
h^2_b	0.96	0.97	0.99	0.99	0.99	0.85	0.97
GA 5%	7.54	20.74	47.35	2.71	72.36	1.22	9.95
GAM%	13.17	11.62	42.28	54.89	28.57	25.87	21.90

Parameter	Seed quality traits								
	Germination traits				Seedling traits				
	Standard germination	Seed vigor index	Accelerated aging germination	Electrical conductivity	Root length	Shoot length	Seedling length	Seedling dry weight	Seedling vigor index
PCV	1.59	1.61	21.50	35.78	0.73	0.44	0.61	2.17	80.30
GCV	0.96	1.11	19.73	29.47	0.15	0.15	0.17	1.26	37.88
h^2_b	0.60	0.69	0.92	0.82	0.21	0.35	0.27	0.58	0.47
GA 5%	2.64	2.13	12.78	18.94	0.16	0.13	0.23	0.72	43.67
GAM%	2.81	4.60	18.09	16.36	2.52	5.08	2.56	12.98	5.22

Parameter	Oil quality traits								
	Fatty acid composition %								
	Seed oil content	Saturated fatty acids		Unsaturated fatty acids			TS%	TU%	TS/TU ratio
		Palmitic C16:0	Stearic C18:0	Oleic C18:1	Linoleic C18:2	Linolenic C18:3			
PCV	14.10	4.28	1.97	2.26	1.37	1.64	1.04	1.43	0.019
GCV	13.83	4.23	1.95	1.33	0.92	1.62	0.99	0.67	0.017
h^2_b	0.98	0.99	0.99	0.59	0.67	0.99	0.96	0.47	0.90
GA 5%	9.30	2.17	1.09	2.10	1.83	0.32	1.29	1.87	0.02
GAM%	18.62	24.53	22.58	4.78	4.35	63.31	9.41	2.16	11.08

TS = Total saturated fatty acids TU = Total unsaturated fatty acids

PCV: Phenotypic coefficient of variability, GCV: Genotypic coefficient of variability, h^2_b: Broad-sense heritability, GA 5%: Genetic advance, GAM% of means: Genetic advance as percent of the mean.

Selection criteria

Phenotypic and genotypic correlations

Seed weight plant^{-1} and its related traits

Phenotypic and genotypic correlations were estimated between seed weight plant^{-1} and its related traits for 12 sesame genotypes based on the average of 2018 and 2019, as presented in Table 5. Seed weight plant^{-1} was positively and significantly or highly significantly correlated with its related traits, *i.e.* days to 50% flowering, plant height, fruiting zone length, branch number, capsule number and 1000-seed weight at phenotypic and genotypic levels.

Table 5. Phenotypic (above diagonal) and genotypic (below diagonal) correlations of 12 sesame genotypes for seed weight plant^{-1} and its related traits across 2018 and 2019 summery seasons.

Traits	X_1	X_2	X_3	X_4	X_5	X_6	X_7
Days to 50% flowering (X_1)	1.000	0.796**	0.590*	0.465	0.548	0.740**	0.088
Plant height (X_2)	0.825**	1.000	0.878**	0.666*	0.759**	0.899**	0.061
Fruiting zone length (X_3)	0.608*	0.889**	1.000	0.832**	0.907**	0.891**	0.112
Branch number (X_4)	0.482	0.682*	0.838**	1.000	0.685*	0.826**	0.056
Capsule number (X_5)	0.560	0.772**	0.911**	0.687*	1.000	0.726**	0.138
1000-seed weight (X_6)	0.804**	0.952**	0.921**	0.864**	0.757**	1.000	0.063
Standard germination (X_7)	0.096	0.099	0.133	0.088	0.172	0.061	1.000
Root length (X_8)	-0.529	-0.569	-0.700*	-0.719**	-0.553	-0.619*	-0.406
Shoot length (X_9)	0.274	0.080	0.238	0.235	0.589*	0.090	-0.011
Seedling length (X_{10})	-0.408	-0.538	-0.597*	-0.617*	-0.287	-0.583*	-0.415
Seedling dry weight (X_{11})	-0.600*	-0.311	-0.148	0.073	-0.220	-0.248	0.364
Seedling vigor index (X_{12})	-0.381	-0.505	-0.539	-0.582*	-0.191	-0.571	0.186
Seed weight plant^{-1} (X_{13})	0.753**	0.911**	0.855**	0.799**	0.807**	0.935**	0.225

Traits	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}
Days to 50% flowering (X_1)	-0.233	0.157	-0.163	-0.538	-0.130	0.707*
Plant height (X_2)	-0.333	0.041	-0.308	-0.304	-0.273	0.882**
Fruiting zone length (X_3)	-0.375	0.124	-0.315	-0.140	-0.259	0.840**
Branch number (X_4)	-0.358	0.116	-0.302	0.061	-0.266	0.780**
Capsule number (X_5)	-0.295	0.336	-0.149	-0.202	-0.091	0.785**
1000-seed weight (X_6)	-0.308	0.019	-0.292	-0.236	-0.257	0.882**
Standard germination (X_7)	-0.125	0.007	-0.119	0.334	0.258	0.159
Root length (X_8)	1.000	-0.146	0.915**	-0.176	0.844**	-0.266
Shoot length (X_9)	-0.248	1.000	0.266	-0.097	0.258	0.153
Seedling length (X_{10})	0.895**	0.209	1.000	-0.211	0.928	-0.196
Seedling dry weight (X_{11})	-0.349	-0.278	-0.480	1.000	-0.079	-0.154
Seedling vigor index (X_{12})	0.726**	0.181	0.816	-0.279	1.000	-0.129
Seed weight plant^{-1} (X_{13})	-0.518	0.290	-0.390	-0.131	-0.266	1.000

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

This indicates that selection will be more successful for a long period to 50% flowering, tall height, long fruiting zone length, more branches, more capsules, and the heaviest weight of 1000 seeds.

These findings were confirmed by Roy and Pal (2019), Umamaheswari et al. (2019), and Abdelsatar et al. (2020), who found that the number of branches per plant, number of capsules per plant, number of seeds per capsule, and weight of 1000-seeds per capsule were strongly related to sesame yield.

As a result, these traits may be used to select advanced sesame lines with higher seed yields. Furthermore, these traits might be used as selection criteria for improving sesame seed yield in the future agricultural system. Similarly, Saravanan et al. (2020) indicated that yield per plant had a significant positive correlation with the number of capsules per plant followed by 1000-seed weight, plant height and the number of branches per plant. Furthermore, the positive and significant or highly significant phenotypic and genotypic correlation was detected among the studied traits, *i.e.* days to 50% flowering, plant height, fruiting zone length, branch number, capsule number and 1000-seed weight at phenotypic and genotypic levels. This demonstrated that selecting for any of the previous traits would immediately enhance the others, particularly seed weight plant^{-1}. As a result, these traits might be used as indications for achieving desired genetic improvements in sesame seed weight plant^{-1}.

Seed oil content and its quality

Phenotypic and genotypic correlations were estimated between seed oil content and its contents of fatty acid composition for 12 sesame genotypes based on the average of 2018 and 2019 summer seasons as presented in Table 6. Seed oil content was positively and significantly or highly significantly correlated at both levels with the proportion of stearic and oleic acids on the one hand. On the other hand, a negative and valuable correlation at both levels was observed between seed oil content and the proportion of palmitic acid and linoleic acid. Moreover, fatty acid composition exhibited various trends of association among them. However, a highly significant negative phenotypic and genotypic correlation of the proportion of palmitic acid was detected with stearic acid along with oleic with linoleic and linolenic acids.

While significant positive associations of the proportion of stearic acid with oleic acid content along with the proportion of linoleic acid were noticed, an unsaturated fatty acid with the proportion of linolenic acid at both phenotypic and genotypic levels was observed. In the same sense, Khayambashi and Asadi-Gharneh (2020) showed a negative correlation between saturated and unsaturated fatty acid contents. Moreover, they showed that arachidic acid was positively correlated with stearic acid ($r=0.8$; $p<0.05$). In addition, palmitic acid was negatively correlated with oleic acid ($r=-0.78$; $p<0.05$).

Table 6. Phenotypic (above diagonal) and genotypic (below diagonal) correlations of 12 sesame genotypes for seed oil content and its contents of fatty acid composition across 2018 and 2019.

Traits	Seed oil content	Palmitic	Stearic	Oleic	Linoleic	Linolenic
Seed oil content	1.000	-0.700*	0.810**	0.615*	-0.508	-0.662*
Palmitic	-0.711**	1.000	-0.874**	-0.702*	0.438	0.318
Stearic	0.824**	-0.885**	1.000	0.721**	-0.571	-0.370
Oleic	0.791**	-0.897**	0.949**	1.000	-0.265	-0.172
Linoleic	-0.638*	0.518	-0.734**	-0.478	1.000	0.646*
Linolenic	-0.674*	0.317	-0.375	-0.247	0.781**	1.000

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

Phenotypic and genotypic path analyses

Seed weight plant^{-1} and its related traits

The phenotypic and genotypic path analyses were used to separate phenotypic and genotypic correlations into direct and joint effects, with seed weight plant^{-1} as a dependent variable and yield-related traits as independent variables, as shown in Table 7 and Figure 1. A critical perusal of phenotypic and genotypic path analyses revealed that root length had the highest positive direct effects (P=3.700, G=1.866) on seed weight plant^{-1}, followed by plant height (P=1.061, G=1.642), shoot length (P=1.094, G=0.773), seedling length (P=0.905, G=0.556), capsule number (P=0.688, G=1.429) and branch number (p=0.555, G=1.171).

The high positive direct effects of the previously mentioned traits, in addition to their highly significant correlation coefficient with seed weight plant^{-1}, indicated that the direct selection through these traits would be effective for sesame improvement. Moreover, the direct impacts of fruiting zone length on seed weight plant^{-1} were negative and insignificant, despite a positive and significant phenotypic and genotypic correlation with seed weight plant^{-1}. Consequently, the indirect effect of fruiting zone length through plant height (P=0.931, G=1.460) had a positive effect on improving seed weight plant^{-1} of these materials than direct effect of fruiting zone length.

The high positive phenotypic and genotypic indirect effects on seed weight plant^{-1} were detected for days to 50% flowering through plant height (P= 0.844, G=1.354), plant height through branch number (P=0.369, G=0.798), capsule number (P=0.522, G=1.103), fruiting zone length through branch number (P=0.462, G=0.982) and capsule number (P=0.623, G=1.301), branch number via plant height (P=0.706, G=1.119) and capsule number (P=0.471, G=0.981), capsule number via plant height (P=0.805, G=1.268) and branch number (P=0.380, G=0.804), 1000-seed weight via plant height (P=0.953, G=1.563), branch number (P=0.458, G=1.012) and capsule number (P=0.499, G=1.081), root length via seedling length (P=0.508, G=3.873), shoot length through plant height (P=0.043, G=0.132), branch number (P=0.065, G=0.275) and capsule number (P=0.231, G=0.842), seedling length (P=0.422, G=1.236), seedling dry weight (P= 0.187, G=0.306) and seedling vigor index (P=0.348, G=1.115) through fruiting zone length, and seedling vigor index via seedling length (P=0.516, G=3.531). It is apparent from the above-mentioned results that the preferred improvement of seed weight plant^{-1}can be achieved through selecting genotypes having the long fruiting zone length, more branches plant^{-1}, more capsules plant^{-1}, the heaviest weight of 1000 seeds, the longest root length, shoot length and seedling length, the heaviest dry weight of seedling and the highest index of seedling vigor. These results agreed with those of Umamaheswari et al. (2019), who reported that the traits of plant height at maturity, number of capsules per plant and number of seeds per capsule directly influenced the seed weight per plant.

Table 7. Phenotypic (P) and genotypic (G) path analyses of twelve sesame genotypes for seed weight plant^{-1} and its related traits across 2018 and 2019 summery seasons.

		DF	PH	FZL	BN	CN	TSW	SG
DF	P	**-0.283**	0.844	-0.790	0.258	0.377	0.292	0.092
	G	**0.382**	1.354	-1.259	0.564	0.800	-0.946	-0.267
PH	P	-0.225	**1.061**	-1.177	0.369	0.522	0.355	0.064
	G	0.315	**1.642**	-1.841	0.798	1.103	-1.120	-0.276
FZL	P	-0.167	0.931	**-1.340**	0.462	0.623	0.352	0.117
	G	0.232	1.460	**-2.071**	0.982	1.301	-1.084	-0.369
BN	P	-0.132	0.706	-1.115	**0.555**	0.471	0.326	0.059
	G	0.184	1.119	-1.735	**1.171**	0.981	-1.017	-0.245
CN	P	-0.155	0.805	-1.215	0.380	**0.688**	0.286	0.144
	G	0.214	1.268	-1.886	0.804	**1.429**	-0.890	-0.477
TSW	P	-0.209	0.953	-1.194	0.458	0.499	**0.395**	0.066
	G	0.307	1.563	-1.907	1.012	1.081	**-1.177**	-0.168
SG	P	-0.025	0.065	-0.150	0.031	0.095	0.025	**1.048**
	G	0.037	0.163	-0.275	0.103	0.245	-0.071	**-2.776**
RL	P	0.066	-0.353	0.503	-0.199	-0.203	-0.121	-0.131
	G	-0.202	-0.935	1.449	-0.842	-0.790	0.728	1.128
SHL	P	-0.044	0.043	-0.167	0.065	0.231	0.008	0.007
	G	0.105	0.132	-0.493	0.275	0.842	-0.106	0.031
SL	P	0.046	-0.327	0.422	-0.167	-0.103	-0.115	-0.124
	G	-0.156	-0.883	1.236	-0.723	-0.410	0.686	1.153
SDW	P	0.152	-0.322	0.187	0.034	-0.139	-0.093	0.350
	G	-0.229	-0.511	0.306	0.085	-0.314	0.291	-1.010
SVI	P	0.037	-0.290	0.348	-0.147	-0.063	-0.102	0.270
	G	-0.146	-0.829	1.115	-0.681	-0.273	0.672	-0.517

Table 7. Continued.

		RL	SHL	SL	SDW	SVI	r
DF	P	-0.434	0.121	-0.090	-0.001	0.322	0.707
	G	4.814	-1.207	-1.764	-0.075	-1.643	0.753
PH	P	-0.622	0.032	-0.171	-0.001	0.675	0.882
	G	5.184	-0.354	-2.326	-0.039	-2.176	0.911
FZL	P	-0.700	0.096	-0.175	0.000	0.642	0.840
	G	6.372	-1.049	-2.583	-0.018	-2.320	0.855
BN	P	-0.669	0.090	-0.168	0.000	0.657	0.780
	G	6.545	-1.036	-2.671	0.009	-2.506	0.799
CN	P	-0.550	0.260	-0.083	-0.001	0.225	0.785
	G	5.034	-2.597	-1.242	-0.027	-0.823	0.807
TSW	P	-0.574	0.015	-0.162	-0.001	0.636	0.882
	G	5.635	-0.395	-2.524	-0.031	-2.460	0.935
SG	P	-0.233	0.005	-0.066	0.001	-0.637	0.159
	G	**3.700**	0.048	-1.796	0.045	0.802	0.225
RL	P	**1.866**	-0.113	0.508	0.000	-2.088	-0.266
	G	-9.106	**1.094**	3.873	-0.044	3.127	-0.518
SHL	P	-0.273	**0.773**	0.148	0.000	-0.638	0.153
	G	2.261	-4.408	**0.905**	-0.035	0.781	0.290
SL	P	1.707	0.206	**0.556**	-0.001	-2.296	-0.196
	G	-8.153	-0.922	4.326	**-0.060**	3.516	-0.390
SDW	P	-0.329	-0.075	-0.117	**0.003**	0.195	-0.154
	G	3.179	1.227	-2.078	0.125	**-1.202**	-0.131
SVI	P	1.576	0.200	0.516	0.000	**-2.473**	-0.129
	G	-6.611	-0.800	3.531	-0.035	4.308	-0.266
Residual effect					P		0.268
					G		0.170

DF: Days to 50% flowering, PH: Plant height, FZL: Fruiting zone length, BN: Branch number, CN: Capsule number, TSW: 1000-seed weight, SG: Standard germination, RL: Root length, SHL: Shoot length, SL: Seedling length, SDW: Seeding dry weight, SVI: Seed vigor index, r: Correlation of yield related traits with seed weight plant^{-1}

Moreover, Saravanan et al. (2020) revealed that the number of capsules per plant had a highly positive direct effect on yield per plant. So, the selection based on these traits such as the number of capsules per plant, plant height, 1000-seed weight and the number of branches per plant would be a benefit for crop improvement. The residual effect at the phenotypic and genotypic levels was 0.268 and 0.170, indicating that independent traits included in the phenotypic and genotypic path analyses explained 73.23% and 82.98% of the total variance in seed weight plant^{-1}, respectively. The largest residual effects of phenotypic and genotypic path analyses revealed that the existence of other traits not included in the current study was linked with the greatest influence on seed weight plant^{-1}.

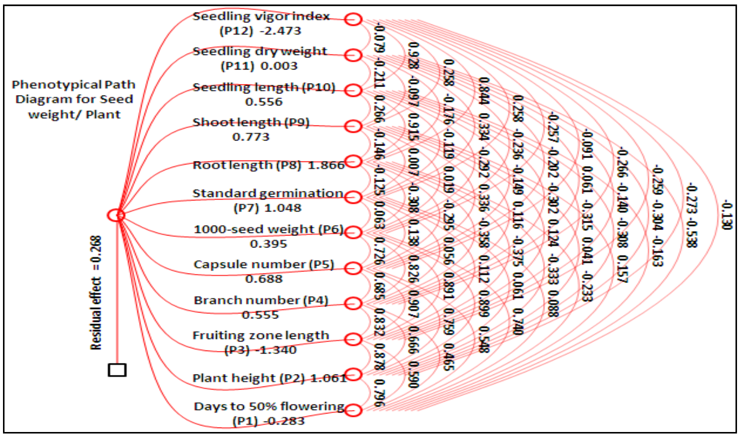

Figure 1a. The Phenotypical Path Diagram for Seed weight/plant.

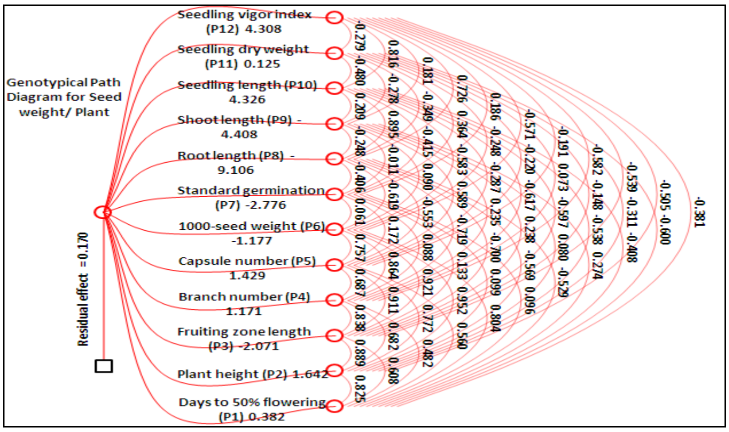

Figure 1b. The genotypical Path Diagram for Seed weight/plant.

Seed oil content and its quality

The phenotypic and genotypic path analyses were used to split phenotypic and genotypic correlations into direct and joint effects to identify interrelationships between seed oil content and its contents of the fatty acid composition. As indicated in Table 8 and Figure 2, the seed oil content was regarded as a dependent variable, whereas oil proportions of fatty acid composition were considered independent variables.

Oleic acid content had a positive direct impact (P=0.1081, G=2.0683), and there was a correlation at both levels (P=0.615*, G=0.791**). This demonstrates that seed oil content is influenced by oleic acid. Furthermore, oleic acid content has a significantly positive indirect impact via its association with linolenic acid content (P=0.0998, G=0.0649) and stearic acid content (P=0.0779, G=1.9637). These findings suggest that increasing the oleic fatty acid component of these materials effectively increases oil content. The residual effect was 0.378 and 0.426 at phenotypic and genotypic levels, respectively. This indicated that independent variables included in the phenotypic and genotypic path analyses explained 62.17 and 57.43 percent of the overall variance in seed oil content, respectively. The largest residual effects of phenotypic and genotypic path analyses revealed that the existence of other traits not included in the current study was linked with the greatest influence on seed oil content.

Table 8. Phenotypic and genotypic path analyses of twelve sesame genotypes for seed oil content and its contents of fatty acid composition across 2018 and 2019 summery seasons.

		Palmitic C16:0	Stearic C18:0	Oleic C18:1	Linoleic C18:2	Linolenic C18:3	Correlation with seed oil content
Palmitic	P	**0.1292**	-0.6982	-0.0759	0.1293	-0.1840	-0.6996
C16:0	G	**0.1680**	1.4315	-1.8552	-0.3722	-0.0834	-0.7113
Stearic	P	-0.1129	**0.7991**	0.0779	-0.1686	0.2144	0.8099
C18:0	G	-0.1487	**-1.6171**	1.9637	0.5279	0.0986	0.8245
Oleic	P	-0.0907	0.5758	**0.1081**	-0.0782	0.0998	0.6148
C18:1	G	-0.1507	-1.5353	**2.0683**	0.3436	0.0649	0.7907
Linoleic	P	0.0566	-0.4566	-0.0286	**0.2951**	-0.3743	-0.5078
C18:2	G	0.0870	1.1873	-0.9884	**-0.7190**	-0.2052	-0.6382
Linolenic	P	0.0410	-0.2958	-0.0186	0.1907	**-0.5792**	-0.6620
C18:3	G	0.0533	0.6070	-0.5106	-0.5615	**-0.2627**	-0.6745
Phenotypic residual						0.37831	
Genotypic residual						0.42568	

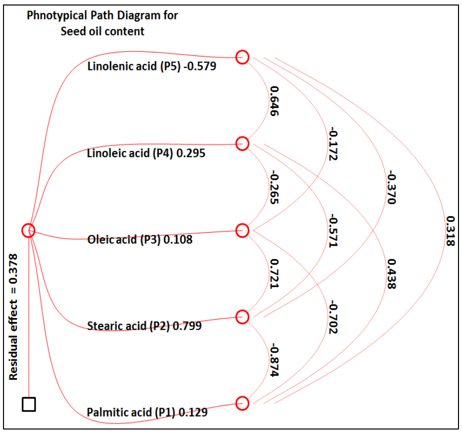

Figure 2a. The phenotypical Path Diagram for Seed oil content.

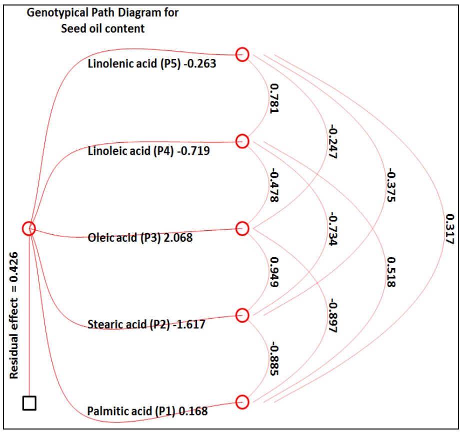

Figure 2b. The genotypical Path Diagram for Seed oil content.

Conclusion

In conclusion, all studied traits showed a significant genetic diversity among genotypes, indicating the possibility of improving sesame yield and oil quality. As a result, selection within this population or hybridization among members of this population can result in genetic improvement in seed weight plant^{-1} and oil quality for assessed genotypes.

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GENETSKA VARIJABILNOST I KRITERIJUMI ZA IZBOR NEKIH GENOTIPOVA SUSAMA U POGLEDU NJIHOVIH AGRONOMSKIH OSOBINA I KVALITETA SEMENA

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Rezime

Identifikacija genetske varijabilnosti, srednjih performansi i kriterijuma selekcije za dvanaest genotipova susama je potrebna radi genetskog poboljšanja agronomskih osobina i kvaliteta semena. Tako su, koristeći potpuno slučajni blok dizajn sa tri ponavljanja, ovi genotipovi ocenjeni u terenskom ispitivanju u Poljoprivrednoj istraživačkoj stanici Kafr-El-Hamam, Poljoprivrednog istraživačkog centra, Guvernorat Šarkija u Egiptu, i laboratorijskim eksperimentima na Odseku za istraživanje tehnologije semena, PIC, Giza, Egipat, tokom dve uzastopne sezone 2018. i 2019. U pogledu ranog cvetanja, N.A.$_{130}$ i Shandweel$_3$ su bili najperspektivniji genotipovi susama, dok su N.A.$_{114}$ i RH$_1$F$_3$ imali najveću masu semena po biljci i jednu ili više osobina povezanih sa prinosom. NA$_{114}$, Shandweel$_3$ i Zahar$_{12}$ su imali najbolji kvalitet semena. Pored toga, genotipovi Shandweel$_3$ i M$_1$A$_{12}$ su imali najveći udeo ulja u semenu, Shandweel$_3$ i Zahar$_{12}$ su imali najveću količinu oleinske kiseline, N.A.$_{114}$ i RH$_1$F$_3$ su imali najveći sadržaj linolne kiseline, a Zahar$_{12}$ i N.A.$_{114}$ su imali najveći udeo linolne kiseline. Masa semena po biljci može se poboljšati odabirom genotipova koji imaju najduži period plodonošenja, više grana i kapsula, visoke vrednosti električne provodljivosti semena i ubrzano klijanje, što je pokazano kriterijumima za odabir. Osim toga, udeo oleinske kiseline imao je najveći direktan i indirektan uticaj na sadržaj ulja semena, pokazujući njegovu relevantnost kao kriterijuma za izbor kvaliteta susamovog ulja.

Ključne reči: direktni i udruženi uticaji, sastav masnih kiselina, fenotipska i genotipska korelacija, *Sesamum indicum* L.

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