Moroccan Journal of Agricultural Sciences
Vol 1 No 5 (2020): (September 2020)
Crop Production and Environment

Genetic evaluation of some sesame genotypes for seed yield and its components

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To study genetic variation, genetic parameters and selection criteria of seventeen sesame genotypes, a field experiment was conducted across different environments represented by two summer seasons of 2018 (E1) and 2019 (E2) at Etay-El-Baroud/Behaira Agricultural Research Station and one summer season of 2019 (E3) at Kafr-El-Hamam/Sharkia Agricultural Research Station, Agricultural Research Center, Egypt using a randomized complete block design with three replications for each environment. The promising sesame genotypes were L25 for earliness in flowering at E1 and across environments, L101 for plant height and fruiting zone length when grown at E2 and L110 across environments, L35 for number of branches plant and seed yield per feddan when grown at E2 and across environments, L48 for capsules length when grown at E2 and L2 across environments, L82 for 1000-seed weight when grown at E3 and L35 across environments, L2 for seed weight per plant when grown at E1 and across environments and L101 for seed oil content when grown at E1 and across environments. Among the most effective traits in improving seed weight per plant were fruiting zone length and number of branches per plant, as verified through correlation and path analyses at phenotypic and genotypic levels.These traits had the highest broad-sense heritability and genetic advance as percent of mean.

Keywords: Correlation, Genetic variability, Heritability, Path analysis

Introduction

Sesame is one of the important oil crops in Egypt and the world due to its high nutritional value for humans. Its old presence on the agricultural map in Egypt, makes it necessary to move towards improving its yield to align with the high population increase. One of the requirements for genetic improvement is the existence of genetic variation among the members of the population. In this regard, genetic variation between sesame genotypes was found in a study of Anbanandan (2018) and Bhuiyan et al., (2019). An effective selection criterion is the highest broad-sense heritability coupled with genetic advance as percent of mean. The results of the application for this rule indicated that all studied traits in the study of Anbanandan (2018), seed yield followed by capsule plant-1 in the study of Bhuiyan et al., (2019) and hundred seed weight followed by days to 80% maturity, capsules per plant and number of branches per plant in the study of Sultana et al., (2019) are considered effective in improving seed yield per plant. Moreover, among selection criteria to improve seed yield per plant is estimation of correlation and path analyses at phenotypic and genotypic levels. In this regard, genotypic correlation of seed yield per plant with days to 50% flowering, plant height and number of capsules per plant at both the genotypic and phenotypic level was positive and significant. Abd EL-Satar et al., (2016), Teilep et al., (2018) and Pavani et al., (2020) recorded high heritability combined with high genetic advance for days to 50 per cent flowering, number of branches per plant, plant height to first capsule, plant height, number of capsules/plant and seed index. They added that high heritability combined with high genetic advance for these traits, indicated that additive gene action of high magnitude and phenotypic

selection could be effective for improving these characters.

From above-mentioned of importance of the previous studies in this field to improve sesame yield, the current study was done. This aimed to estimate genetic variation between evaluated sesame genotypes across different environments in their edaphic and climatic conditions, to identify genetic parameters of studied traits across different environments and to estimate correlation and path analysis at phenotypic and genotypic levels across different environments.

Materials and methods

Site description

A field experiment was conducted at three environments i.e. two summer season of 2018 (E1) and 2019 (E2) at Etay-El-Baroud/Behaira Agricultural Research Station and one summer season of 2019 (E3) at Kafr-El-Hamam/Sharkia Agricultural Research Station, Agricultural Research Center, Egypt (Table 1).

Table 1: Soil texture, pH, organic matter, EC, salt concentration in soil, latitude and longitude of field stations

Code	Growing season (summer)	Governorate/Research station	Soil texture	pH	Organic matter (g/kg)	EC ($ds.m^{-1}$)	Latitude	Longitude
E_1	1st June 2018	Etay-El-Baroud/Behaira	clay loam	7.8	2.93	1.48	30° 53'	30° 39'
E_2	15th June 2019	Etay-El-Baroud/Behaira	Clay loam	7.6	2.45	1.56	30° 53'	30° 39'
E_5	15th June 2019	Sharkia/ Kafr El Hamam	clay loam	7.7	2.89	1.16	30° 58'	31° 50'

Table 1:

Experimental design

The experiment was laid out in randomized block design with three replications for each environment. Each genotype was sown, after harvesting wheat in both seasons, in five ridges with a ridge length of 4 m spaced at 60 cm between ridges and 20 cm between hill to hill. Evaluated sesame genotypes as presented in Table 2 i.e. L48, L101, L110, L38, L82, L8, L94, L25, L35, L93, L12, L95, L16, L49, L2, L82 and L77 were received from Department of Oil Crops Research, Field Crop Research Institute, Agricultural Research Center, Egypt.

Table 2: Name, pedigree and origin of evaluated sesame genotypes

Genotypes	Name	Pedigree	Origin
L48	Hybrid 74	Local 2 x NA48	Egypt
L101	Hybrid 102	Giza 25 x NA 217	Egypt
L110	Introduce 304	Unknown	USA 1975
L38	Hybrid 108	NA 217 x NA130	Egypt
L82	Hybrid 516	Unknown	Indonesia 1981
L8	Hybrid 102	Giza 25 × NA 217	Egypt
L94	Hybrid 115	Giza 25 x NA432	Egypt
L25	Hybrid 117	Giza 25 x NA413	Egypt
L35	Introduce 545	Unknown	FAO 1983
L93	Introduce 588	Unknown	Mexico 1986
L12	Hybrid 102	NA217 x Giza 25	Egypt
L95	Introduce 432	Unknown	USA 1976
L16	Hybrid 107	NA 114 x NA165	Egypt
L49	Hybrid 74	Local 2 x NA48	Egypt
L2	Hybrid 59	Local 30 x S14/18	Egypt
L82	Hybrid 82	Giza 25 x Local 124	Egypt
L77	Introduce 554	Unknown	FAO 1983

Table 2:

Agricultural practices

Sesame genotypes seeds under study were hand-planted on ridges, 60 cm as well as 20 cm apart between hills. This was done on the first week of June for each environment. Plants of sesame genotypes under study were thinned at 15 days after sowing to secure two plants hill-1. All other cultural practices were applied as recommended.

Data collected

Days to 50% flowering (day), plant height (cm), length of fruiting zone (cm), number of branches/plant, capsules length, 1000-seed weight (g), seed weight per plant (g) and seed yield per feddan (kg) were determined. Crude oil percentage was determined using Soxhlet apparatus and hexane as solvent according to AOSA (2000).

Statistical analysis

Analysis of variance for each environment according to Gomez and Gomez (1984) was done using randomized block design with three replications for all studied traits. For combined analysis of variance across three environments was done after confirmation of homogenous for all studied traits using Bartlett's test according to Snedecor and Cochran (1989). Genotypic and phenotypic coefficients of variation (Burton and DeVane 1953), estimate of broad sense heritability (H2b) (Hansen et al.,1956), genetic advance as percent of the mean (Johnson et al.,1955), phenotypic and genotypic correlation coefficient (Weber and Moorthy 1952), phenotypic and genotypic path analysis (Dewey and Lu, 1959).

Results and discussion

Environmental effects

The considerable variation was detected between evaluated environments for all studied traits, as they had valuable differences in edaphic and climatic conditions (Table 3). Hence, these environments had considerable effects on performance of all evaluated sesame genotypes for all studied traits (Table 4). Across evaluated sesame genotypes (Table 4), in this regard, the earliest sesame genotypes in flowering were detected at E1 (52.6 day), the shortest plants in height at E2 (168.4 cm), the longest plants in fruiting zone at E2 (89.0 cm), more branches plant-1 at E3 (5.35 branch), the longest capsules per plant at E3 (3.20 cm), the heaviest weight of 1000-seed at E3 (4.52 g), the heaviest weight of seed per plant at E3 (42.0 g), the highest proportion of seed oil at E3 (47.7 %) and the highest seed yield per feddan at E3 (829.0 kg).

Table 3: Mean squares of environments, genotypes and their interaction for all studied traits

Sources of variation	df	Days to 50% flowering	Plant height	Fruiting zone length	Number of branches per plant	Capsules length	1000-seed weight	Seed weight per plant	Seed oil content	Seed yield per feddan
Rep.	6	2.22	42.7	12.14	1.14	0.07	0.15	7.49	0.5	1815.1
Treatment	50	165.5**	473.9**	325.6**	7.25**	0.45**	0.37**	89.9**	29.2**	16209.2**
Environment (E)	2	734.7**	508.5**	696.2**	3.07**	0.4**	0.67**	22.3*	18.9**	8265.0*
Genotypes (G)	16	252.5**	684.3**	594.5**	12.6**	1.04**	0.67**	241.1**	37.6**	33918.4**
E X G	32	86.5**	366.6**	168.0**	4.81**	0.16**	0.2**	18.5**	25.7**	7851.1**
Error	96	2.21	54.4	14.2	0.58	0.07	0.08	5.28	0.73	1715.1

, Significant at 0.05 and 0.01 probability level, respectively*

Table 3:

Table 4: Environments effects on all studied traits

Item	Days to 50% flowering	Plant height (cm)	Fruiting zone length (cm)	Number of branches per plant	Capsules length, cm	1000-seed weight (g)	Seed weight per plant (g)	Seed oil content (%)	Seed yield per feddan (kg)
E1	52.6	172.9	82.5	4.86	3.03	4.29	40.7	46.6	814.6
E2	59.0	168.4	89.0	5.12	3.07	4.44	41.4	46.8	803.6
E3	59.3	174.4	88.7	5.35	3.20	4.52	42.0	47.7	829.0
LSD 5%	0.58	2.90	1.48	0.30	0.10	0.11	0.90	0.34	16.3
LSD 1%	0.77	3.84	1.96	0.40	0.13	0.14	1.20	0.44	21.5

Table 4:

Sesame genotypes effects and their interaction with environments

Variation of evaluated sesame genotypes (Table 3) was highly significant for all studied traits, certainly due this to difference of genetic structure for each genotype for all studied traits. Moreover, the interaction of sesame genotypes with evaluated environments (Table 3) was highly significant for all studied traits. This suggests that performance of studied genotypes varied from environment to another, as these environments had considerable variation in the edaphic and climatic conditions. In this respect (Table 5 and 6), L25 required the shortest time to flowering when grown at E1 (42.0 day) and across environments (45.6 day). L101 was the shortest genotype when grown at E2 (146.9 cm), whereas L110 (156.1 cm) was the shortest one across environments. The longest fruiting zone was observed in L101 (114.7 cm) when grown at E2 and across environments (100.3 cm). More branches plant-1 was detected in L35 when grown at E2 (8.33 branch) and across environments (7.67 branch). The longest capsules was detected in L48 when grown at E2 (3.85 cm) and L2 across environments (3.72 cm). The heaviest weight of 1000-seed was detected in L82 when grown at E3 (4.49 g) and L35 across environments (4.73 g). The heaviest

seed weight plant-1 was detected in L2 when grown at E1 (55.0 g) and across environment (49.9 g). The highest proportion of seed oil was observed in L101 when grown at E1 (56.7 %) and across environment (50.6 %). L35 grown at E2 (977.2 kg) had the highest seed yield per feddan and across environments (934.1 kg). Similar results have been reported by earlier workers of Singh et al., (2020).

Table 5: Sesame genotypes effects on all studied traits

Item	Days to 50% flowering	Plant height (cm)	Fruiting zone length (cm)	Number of branches per plant	Capsules length (cm)	1000-seed weight (g)	Seed weight per plant (g)	Seed oil content (%)	Seed yield per feddan (kg)
L48	57.4	186.9	91.3	5.56	3.38	4.62	49.2	49.3	821.9
L101	64.0	166.5	100.3	5.89	3.22	4.08	43.3	50.6	872.5
L110	58.3	156.1	75.1	4.11	2.76	4.57	32.3	45.1	688.8
L38	62.4	175.8	84.3	3.89	2.34	4.36	43.3	48.3	839.4
L82	61.7	163.1	78.1	4.78	2.93	4.48	41.4	44.0	770.3
L8	58.8	173.9	85.1	5.11	3.39	4.57	40.6	45.5	828.3
L94	54.0	160.7	95.1	3.89	2.86	4.37	40.3	45.8	715.0
L25	45.6	171.5	84.4	3.78	2.92	4.34	40.3	48.8	865.4
L35	59.0	174.2	89.1	7.67	3.29	4.73	43.7	48.1	934.1
L93	46.1	172.0	76.3	3.33	2.79	3.53	28.1	44.9	758.5
L12	58.1	164.4	84.0	4.00	2.93	4.43	40.4	48.0	814.7
L95	50.6	164.6	81.3	6.78	2.91	4.43	41.1	45.8	852.5
L16	57.2	169.1	75.3	5.44	3.27	4.41	39.2	48.6	758.9
L49	57.1	183.0	99.0	6.33	3.56	4.64	42.5	49.0	873.1
L2	57.2	179.8	96.3	5.56	3.72	4.40	49.9	47.4	833.2
L82	57.8	176.2	92.5	5.11	3.27	4.60	43.7	43.5	820.9
L77	63.1	184.8	86.7	5.67	3.21	4.50	44.0	46.7	820.1
LSD 5%	1.39	6.90	3.52	0.71	0.24	0.26	2.15	0.80	38.7
LSD 1%	1.84	9.14	4.66	0.94	0.32	0.34	2.85	1.06	51.3

Table 5:

Table 6: Interaction of environments with sesame genotypes effects on all studied traits

Item		Days to 50% flowering	Plant height (cm)	Fruiting zone length (cm)	Number of branches per plant	Capsules length (cm)	1000-seed weight (g)	Seed weight per plant (g)	Seed oil content (%)	Seed yield per fedadan (kg)
E1	L48	61.0	192.2	83.7	3.67	3.16	4.21	48.1	45.5	881.6
	L101	63.0	196.7	88.7	5.00	3.78	3.35	44.2	56.7	873.2
	L110	45.0	150.9	71.1	3.33	2.58	4.21	25.3	44.0	690.9
	L38	59.3	177.8	80.0	4.33	2.19	4.52	41.8	46.2	831.1
	L82	59.0	161.4	79.9	4.33	2.87	4.28	43.0	45.5	740.0
	L8	53.0	172.4	86.8	4.67	3.27	4.51	41.0	49.0	835.2
	L94	56.0	159.6	86.2	3.67	2.78	4.18	39.3	44.6	768.0
	L25	42.0	161.0	81.5	3.00	2.82	4.31	40.0	46.6	845.6
	L35	48.0	165.7	83.6	7.00	3.34	4.68	42.7	46.7	862.2
	L93	42.0	193.1	71.4	2.33	2.57	3.32	26.4	43.6	685.6
	L12	44.3	160.8	86.6	3.67	2.85	4.33	40.2	42.7	813.6
	L95	44.3	162.3	89.6	8.00	2.88	4.32	39.5	46.8	821.3
	L16	64.0	163.7	86.3	7.33	2.93	4.20	39.5	50.2	900.7
	L49	44.3	184.5	81.4	7.00	3.49	4.85	42.4	48.5	926.3
	L2	48.0	172.6	81.8	7.00	3.78	4.70	55.0	46.6	820.7
	L82	58.0	162.1	80.2	4.33	3.17	4.51	43.3	43.3	796.5
	L77	62.7	203.1	83.1	4.00	3.11	4.44	40.5	45.2	756.3
E2	L48	57.0	182.6	96.4	5.00	3.85	4.80	51.0	50.0	756.5
	L101	62.0	146.9	114.7	7.67	2.75	4.27	42.4	43.0	870.9
	L110	65.3	153.2	75.7	4.00	2.65	4.77	34.6	45.9	686.6
	L38	63.3	176.7	86.2	4.33	2.16	4.19	43.6	50.1	820.3
	L82	64.0	160.1	76.7	5.00	2.87	4.65	39.7	42.7	782.8
	L8	63.0	172.2	86.0	5.00	3.52	4.73	39.9	43.4	819.6
	L94	53.0	155.1	101.0	4.00	2.74	4.49	39.2	47.5	691.2
	L25	47.0	178.0	84.3	3.67	2.89	4.19	37.3	45.3	879.0
	L35	63.0	173.1	85.3	8.33	3.32	4.85	44.7	49.1	977.2
	L93	47.0	159.5	77.5	4.33	2.73	3.65	28.3	44.8	722.1
	L12	65.3	160.9	81.1	4.00	2.85	4.49	40.9	49.5	800.8
	L95	53.0	156.9	76.7	6.00	2.81	4.31	42.5	45.8	845.4
	L16	53.0	165.4	68.6	3.67	3.62	4.54	38.9	46.6	665.4
	L49	64.0	182.6	111.5	7.67	3.42	4.57	43.9	49.4	842.4
	L2	62.0	186.9	108.7	3.00	3.76	3.85	49.3	49.7	828.6
	L82	58.0	187.4	97.4	5.33	3.08	4.40	43.9	43.4	808.5
	L77	63.0	165.0	85.5	6.00	3.20	4.71	43.1	49.3	864.0
E3	L48	54.3	185.9	93.9	8.00	3.14	4.84	48.5	52.2	827.6
	L101	67.0	155.7	97.7	5.00	3.13	4.63	43.4	52.2	873.5
	L110	64.7	164.3	78.7	5.00	3.04	4.74	36.9	45.4	688.8
	L38	64.7	173.0	86.7	3.00	2.66	4.36	44.4	48.5	866.8
	L82	62.0	167.6	77.6	5.00	3.05	4.53	41.5	43.8	788.2
	L8	60.3	177.0	82.4	5.67	3.39	4.48	41.1	44.1	830.1
	L94	53.0	167.6	98.0	4.00	3.05	4.44	42.5	45.4	685.8
	L25	47.7	175.7	87.2	4.67	3.06	4.52	43.5	54.5	871.5
	L35	66.0	183.7	98.4	7.67	3.21	4.66	43.7	48.5	963.0
	L93	49.3	163.4	80.0	3.33	3.07	3.61	29.6	46.3	867.8
	L12	64.7	171.5	84.3	4.33	3.10	4.46	40.1	51.9	829.6
	L95	54.3	174.7	77.6	6.33	3.03	4.65	41.4	44.9	890.9
	L16	54.7	178.3	71.1	5.33	3.26	4.48	39.3	49.0	710.5
	L49	63.0	182.1	104.1	4.33	3.76	4.49	41.3	49.2	850.6
	L2	61.7	179.7	98.4	6.67	3.61	4.64	45.5	46.0	850.4
	L82	57.3	179.0	99.9	5.67	3.56	4.89	43.8	43.7	857.7
	L77	63.7	186.2	91.6	7.00	3.32	4.36	48.4	45.5	839.9
LSD 5%		2.41	11.96	6.10	1.24	0.42	0.45	3.72	1.38	67.1
LSD 1%		3.19	15.83	8.07	1.64	0.55	0.59	4.93	1.83	88.9

Table 6:

Genetic parameters

Considerable phenotypic, genotypic variance and genotypic-environment interaction variances were detected for all studied traits (Table 7). Moreover, the phenotypic variance and phenotypic coefficient of variation (PCV) converged with genotypic variance and genotypic coefficient of variation (GCV), respectively for all studied traits (Table 7), indicating that the environmental impact on all studied traits was neglected. Moreover, the variance of genotype-environment interaction was high for all studied traits, hence this justified that selection of desired genotypes for each environment was effective. In the previous study of Bhuiyan et al., (2019), the range was narrow between genotypic and phenotypic components of variance for all studied traits, indicated the phenotypic variance had major genetic portion in nature. Moreover, Saravanan et al., (2020) showed that the magnitude of PCV and GCV values were higher for the traits yield per plant, the number of branches per plant and the number of capsules per plant.

Table 7: The pooled genetic parameters across three environments

Item	Days to 50% flowering	Plant height	Fruiting zone length	Number of branches per plant	Capsules length	1000-seed weight	Seed weight per plant	Seed oil content
Phenotypic variance	28.1	76.0	66.0	1.41	0.12	0.07	26.8	4.18
Genotypic variance	18.4	35.3	47.4	0.87	0.10	0.05	24.7	1.33
Environment-genotypes interaction variance	28.1	104.1	51.3	1.41	0.03	0.04	4.40	8.31
Genotypic coefficient of variability	7.54	3.46	7.94	18.3	10.1	5.21	12.0	2.45
Phenotypic coefficient of variability	9.30	5.07	9.37	23.2	11.0	6.19	12.5	4.35
Broad-sense heritability	65.7	46.4	71.7	62.0	84.7	70.8	92.3	31.8
Genetic advance	7.17	8.34	12.0	1.51	0.59	0.40	9.8	1.34
Genetic advance as percent of mean	12.6	4.85	13.8	29.6	19.2	9.03	23.8	2.84

Table 7:

Broad-sense heritability is an effective tool for genetic selection, but it is preferable to combine it with genetic advance as percent mean to increase accuracy selection to improve studied traits of evaluated genotypes as confirmed by Johnson et al., (1955). In this regard (Table 7), the highest broad-sense heritability (>60 %) coupled with genetic advance as percent of mean (>20) was observed in number of branches per plant and seed weight per plant, indicating the additive gene action was predominant in the inheritance of these traits, hence the selection was effective for these traits. Similarly, Umamaheswari et al., (2019) showed that high heritability coupled with high genetic advance as percent of mean was observed for 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 yield per plant indicating the influence of additive and non-additive gene action, as such simple selection would likely to be effective for improvement of these traits. Moreover, Saravananet al., (2020) observed that number of branches per plant and 1000 seed weight exhibited a high heritability along with a high genetic advance as percent of mean. The highest broad-sense heritability (> 60 %) and moderate genetic advance as percent of mean (10-20) was detected in days to 50% flowering, fruiting zone length and capsule length, indicating that additive and non-additive gene action had major role in genetic control of these traits, and consequently the selection for improving these traits was moderately effective. The variability study

of Mohanty et al., (2020) indicated high to moderate genetic advance as per cent of mean for traits like plant height, days to first flowering, days to 50% flowering, days to maturity, number of productive branches/plant, height of 1st capsule, number of productive capsules per plant, number of seeds per capsule, biological yield per plant, harvest index, 1000 seed weight, oil content and seed yield per plant. The remaining traits were governed by non-additive gene action, as broad-sense heritability and genetic advance were low, so selection was ineffective for improving these traits.

Selection criteria

To be able to determine the selection traits to improve seed weight per plant, it is necessary to identify the relationship between seed yield per plant as a dependent variable and its related traits as independent variables. In this regard (Table 8), seed weight per plant was associated with a positive and highly significant relationship with days to 50% flowering, plant height, fruiting zone length, number of branches per plant, capsules length and 1000-seed weight at phenotypic and genotypic levels. Hence, these traits can be taken as selection criteria to improve seed yield per plant of evaluated sesame genotypes. These selection criteria were positively correlated with each other and it reached the significant in many relationships. This indicates that improvement in one of these traits will be reflected in the remaining traits until it reaches seed yield per plant. These findings are confirmed by those of Roy and Pal (2019) and Umamaheswari et al. (2019) who indicated that number of branches/plant, number of capsule/plant, number of seeds/capsule and 100 seed weight were strongly related with sesame yield. Thus, selection of advance lines of sesame, that have higher seed yield, can be done on the basis of these traits. Moreover, these traits may be employed as the selection criteria for the betterment of sesame seed yield in 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.

Table 8: The pooled phenotypic (above diagonal) and genotypic (below diagonal) correlations of 17 sesame genotypes for seed weight plant^{-1} and its related traits across three environments

Traits	Days to 50% flowering	Plant height	Fruiting zone length	Number of branches per plant	Capsules length	1000-seed weight	Seed weight per plant
Days to 50% flowering	1	0.129	0.266	0.311*	0.163	0.441**	0.453**
Plant height	0.070	1	0.425**	0.336*	0.537**	0.185	0.570**
Fruiting zone length	0.315*	0.790**	1	0.371**	0.539**	0.204	0.654**
Number of branches per plant	0.555**	0.842**	0.453**	1	0.609**	0.495**	0.517**
Capsules length	0.242	0.741**	0.764**	0.962**	1	0.356*	0.543**
1000-seed weight	0.773**	0.672**	0.378**	0.561**	0.496**	1	0.559**
Seed weight per plant	0.560**	0.879**	0.815**	0.631**	0.575**	0.671**	1

, Significant at 0.05 and 0.01 probability level, respectively*

Table 8:

Path analysis

To increase certainty of the previous correlations at phenotypic and genotypic levels, it is necessary to divide phenotypic and genotypic correlation between seed yield per plant as a dependent variable and its related traits as independent variables into direct and indirect or joint effects using path coefficient analysis at the phenotypic and genotypic levels (Table 9 and Figure 1). The highest positive direct effects on seed weight per plant was detected at both levels in fruiting zone length (P= 0.4056, G= 0.6734), plant height (P= 0.3082, G= 0.8093), days to 50% flowering (P= 0.1411, G= 0.4530) and number of branches per plant (P= 0.0707, G= 0.5155). Based on the highest positive direct effects of these traits on seed weight per plant with their positive and significant association with it, hence it increased confidence in them as effective selection criteria to improve

seed weight per plant. The highest positive phenotypic and genotypic indirect effects on seed weight per plant were detected for days to flowering via fruiting zone length (P=0.1079, G=0.2123), fruiting zone length (P= 0.1309, G= 0.6394), number of branches per plant (P=0.1036, G=0.6815), capsules length (P=0.1654, G=0.5993) and 1000-seed weight (P=0.0569, G=0.5438) through plant height, number of branches per plant via fruiting zone length (P=0.1504, G=0.3053) and capsules length via fruiting zone length (P=0.2187, G=0.5147). These results agreed with those of Umamaheswari et al., (2019) revealed that the traits plant height at maturity, number of capsules per plant and number seeds per capsule were directly influencing the seed yield per plant. Moreover, Saravanan et al., (2020) revealed that the number of capsules per plant had a high positive direct effect on yield per plant. So, the selection based on these traits such as number of capsules per plant, plant height, 1000 seed weight and the number of branches per plant would be advantageous for crop improvement. From above-mentioned results, it was clearly that these traits can be played an effective role in improving seed weight per plant, as it explained 46.42 % and 71.79 % of the total phenotypic and genotypic variations, respectively. However, there are some traits that are not covered in this study, which have valuable effect on seed weight per plant at phenotypic and genotypic levels (P=0.5358, G= 0.2821).

Table 9: Pooled phenotypic and genotypic path analysis of 17 sesame genotypes for seed weight per plant and its related traits across three environments

		Days to 50% flowering	Plant height	Fruiting zone length	Number of branches per plant	Capsules length	1000-seed weight	Correlation with seed weight per plant
Days to 50% flowering	P	0.1411	0.0398	0.1079	0.0220	-0.0042	0.1462	0.4528
	G	0.4530	0.0570	0.2123	0.2862	-0.2452	-0.2038	0.5595
Plant height	P	0.0182	0.3082	0.1722	0.0238	-0.0137	0.0612	0.5699
	G	0.0319	0.8093	0.5321	0.4341	-0.7509	-0.1770	0.8794
Fruiting zone length	P	0.0375	0.1309	0.4056	0.0262	-0.0138	0.0677	0.6541
	G	0.1428	0.6394	0.6734	0.2337	-0.7749	-0.0995	0.8150
Number of branches per plant	P	0.0438	0.1036	0.1504	0.0707	-0.0156	0.1641	0.5170
	G	0.2515	0.6815	0.3053	0.5155	-0.9752	-0.1477	0.6309
Capsules length	P	0.0230	0.1654	0.2187	0.0431	-0.0256	0.1179	0.5426
	G	0.1096	0.5993	0.5147	0.4958	-1.0139	-0.1307	0.5748
1000-seed weight	P	0.0622	0.0569	0.0828	0.0350	-0.0091	0.3314	0.5593
	G	0.3504	0.5438	0.2542	0.2890	-0.5028	-0.2634	0.6711
Phenotypic residual				0.5358				
Genotypic residual				0.2821				

Table 9:

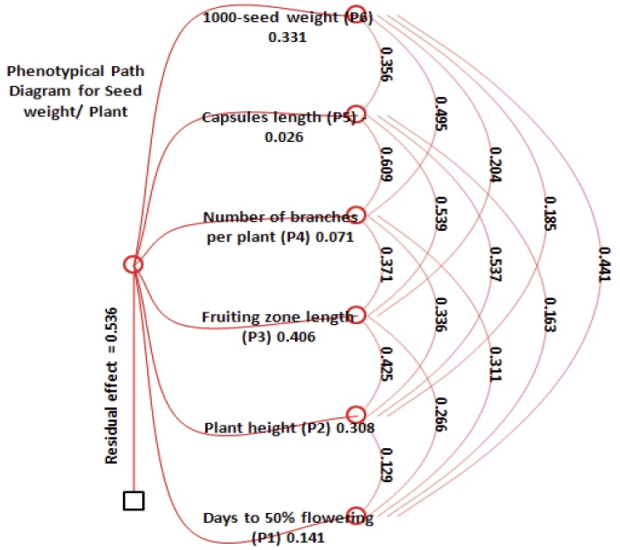


Figure 1a: Phenotypic path diagram for seed weight plant^{-1}

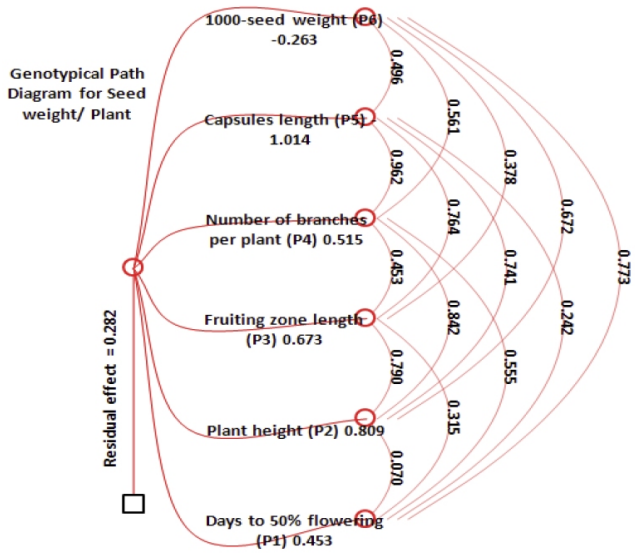


Figure 1b: Genotypic path diagram for seed weight plant^{-1}

Figure 1:

Conclusion

The study revealed, in its entirety, that these evaluated sesame genotypes have considerable genetic variation, which gives the opportunity for effective selection within these genotypes. Moreover, efficiency of some studied traits i.e. days to 50% flowering, plant height, fruiting zone length and number of branches per plant in improving seed weight per plant, as they had the highest broad-sense heritability with genetic advance as percent of mean in addition to their significant association with it and its direct and indirect positive effect on it.

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