Genetic Variability and Path Coefficient Analysis of some Sesame (*Sesamum indicum* L.) Genotypes for Seed Yield and Their Components

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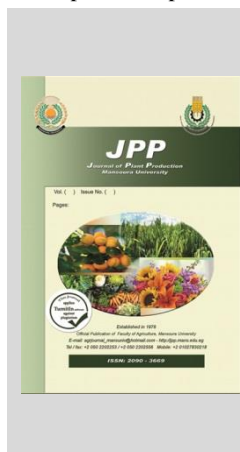
ABSTRACT

The present investigation was conducted to determine the genetic behavior of 14 genetically diverse genotypes of sesame in Shandaweel Research Station (ARC), during the two summer seasons of 2017 and 2018, for seed yield and their components using a randomized complete block design with 3 replications. Significant differences among evaluated sesame genotypes for all studied traits were observed. The highest mean values of 1000-seed weight and seed yield/plant were obtained from the genotype M_2A_{23}, while the lowest mean value was obtained from the genotype B-42. Number of branches per plant, number of capsules per plant, and seed yield per plant had the highest estimates of PCV and GCV. High heritability combined with the high genetic advance (as a percent of mean) was observed in length of fruiting zone, number of branches/ plants, number of capsules/ plants, and seed yield/ plant, showed that these traits were controlled by additive genetic influences. Seed yield /plant had positive and highly significant correlated with the length of fruiting zone in both branched genotypes and non- branched genotypes. Moreover, length of fruiting zone, number of capsules /plant and 1000- seed weight had great positive direct effects on seed yield/plant. Hence, these characteristics could be helpful in increasing sesame seed yield.

Keywords: Sesame, Performance, Selection criteria, Genetic advance and Heritability

INTRODUCTION

Sesame (*Sesamum indicum* L.) is a common and word's oldest oil seed crops. Sesame seed, which is rich in nutrients (% oil and 25% protein), has long been used for immediate use and as a supply of high-quality oil due to antioxidants such as sesamin, sesaminol, sesamol, sesamolinal, and squalene, as well as a high concentration of polyunsaturated fatty acids. (Davidson, 1999). Crop plant genetic diversity is important for sustaining high productivity levels. The knowledge of genetic variability in germplasm will aid in the selection and breeding of high yielding plants, thereby increasing production.

Thirumala Rao. *et al.* (2013) stated that seed yield per plant has a high heritability and genetic advance as a proportion of the mean. Seed yield, number of capsules per plant, number of branches per plant, test weight, and plant height all showed high genetic advance as a proportion of the mean. Seed yield is a complicated feature that is influenced by a number of factors. Hence, understanding the relationship between different characters and seed yield is critical for improving the utility of selection criteria to be used when developing varieties reported by Parameshwarappa *et al.* (2009), Toprope *et al.* (2009) and Chowdhury *et al.* (2010).

Sesame is grown the tropics regions with temperate regions from about 40° N to 40° S in well-drained soil and moderate fertility. Seed yield is a complicated feature that is said to be linked to a number of other characteristics. These traits are linked to each other. The desired level of genetic variability must be existing in a genetic stock for seed yield selection to be successful. Since effective seed selection is dependent on genetic variability details and the correlation of yield component traits with seed yield, direct selection for yield may be misleading. Correlation studies, in conjunction with route analysis, help to better comprehend the interrelationships of different characters and seed yield. By partitioning the correlation coefficient, path coefficient analysis distinguishes direct effects from indirect effects via other similar characters. (Dixit and Dubey, 1984). A breeder who wants to recognize key traits that can be profitably utilized in order to achieve the desired level of seed yield improvement needs to know the degree and direction of this relationship between different attributes and yield. Path analysis has been used in sesame to classify traits that have a direct impact on seed yield. (Mothilal 2005, Azeez and Morakinyo 2011, Goudappagoudra *et al.,* 2011 and Kurdistani *et al.,* 2011).

The current research aims to examine genotypic and phenotypic variability, heritability, and genetic advancement in sesame yield and yield components. It was also conduced to study the correlation and path coefficient which are useful in selection the desirable traits

MATERIALS AND METHODS

Fourteen sesame genotypes included the commercial Shandaweel-3 and 13 promising lines, namely: M_2A_{24}, line h 117-5, line B42, local 131, line H108-1, line H102-4, M_2A_{23}, M_2A_2, line H133-4, line B36, line B 31, local 127 and Sohag 1, The origin and main descriptions of these genotypes is showed in Table **(1),** the field experiment were carried out at Shandaweel Research Station, (ARC), Egypt during the two successive summer seasons of 2017 and 2018.

The experiment was performed using a randomized complete block design (RCBD) with three replicates. Each replication was divided into 14 plots, to which the genotypes were assigned randomly. The plot area was 10.5 m^2. Each genotype was represented by 14 rows, 5^m long and 0.6^m apart. The sowing date was May 22th and May 26th in 2017

and 2018, respectively. Each genotype was harvested at maturity. Throughout the season, all plots were irrigated as needed.

During the growing season, plots were also kept free of rodents, diseases, and weeds. Fertilizer was used at a rate of 120 kg N /fed and 50 kg P_2O_5 /fed. The traits that were recorded were: days to 50% flowering, plant height (cm), length of fruiting zone (cm), length of capsule (cm), number of branches /plant, number of capsules/plant, 1000-seed weight (g), seed yield/plant (g), seed yield (ard/fed) and seed oil content (%).

Statistical analysis

Standard statistical analysis of variance was run using randomized complete block design (RCBD) with three replications according to Gomez and Gomez (1984). Combined analysis was performed all studied traits after confirmed from homogeneity of error variance for evaluated seasons using Bartlett test according to Snedecor and Cochrane (1989). In this study were divided fourteen sesame genotypes into two groups (branched and non-branched) , The branched group includes the genetic makeup from (1 - 6) in addition to Genotype 13 (local variety) group I, and a non-branching group that includes genotypes from (7-12) in addition to genotype 14 (local variety) group II to conduct genotype and phenotype coefficient of variation described by Burton and DeVane (1953), estimate of genetics in a broad sense (H^2_b) (Hansen et al.,1956), genotypic progression as a percentage of the mean (Johnson et al.,1955), phenotypic and genotypic

correlation coefficient Weber and Moorthy 1952), Phenotype and genotypic path analysis Dewey and Lu, (1959).

Table 1. Genotype's name, origin and main descriptions of the studied.

No.	Genotypes	Origin	No. of capsules / leaf axel	Branching habit
			Main description	
1	Line M_2A_{24}	Egypt	Three	Branched
2	Line Cross 117 Family5	Egypt	Single	Branched
3	Line B-42	Egypt	Single	Branched
4	Line local 131	Egypt	Single	Branched
5	Line Cross 108 Family 1	Egypt	Three	Branched
6	Line Cross 102 Family 4	Egypt	Three	Branched
7	Line M_2A_{23}	Egypt	Three	Non branched
8	Line M_2A_2	Egypt	Three	Non branched
9	Line Cross 133 Family 4	Egypt	Single	Non branched
10	Line B 36	Egypt	Single	Non branched
11	Line B 21	Egypt	Single	Non branched
12	line local127	Egypt	Three	Non branched
13	Sohag – 1	Egypt	Three	Branched
14	Shandaweel -3	Egypt	Three	Non branched

RESULTS AND DISCUSSIONS

Analysis of variance:

The analysis of variance for yield and its attributes Table (2) confirmed that genotype variations were highly significant (p0.01) for all traits studied.

Table 2. Analysis of variation for some of the traits studied in fourteen sesame genotypes from 2017 to 2018.

S.O.V	df	50% Flowering	Plant height (cm)	Length of fruiting zone (cm)	Length of capsule (cm)	Number of branches /plant	Number of capsules /plant	1000- seed weight (g)	Seed yield /plant (g)	Seed yield (ard /fed)	Oil content (%)
Year	1	0.012	6589.7*	1.714	1.547**	0.023	2574.1**	0.0001	250.3	10.88*	7.210
Error a	4	1.762	629.5	70.85	0.059	0.029	73.00	0.611	63.41	1.167	1.458
Genotypes	13	28.31**	1116.8**	2780.2**	0.271**	29.32**	6928.7**	1.618**	141.3**	1.745**	27.47**
Year x genotypes	13	4.935**	441.9**	195.5	0.245*	0.184*	661.6**	0.103*	45.14**	0.399*	1.651**
Error b	52	0.967	140.9	124.6	0.109	0.079	97.35	0.047	16.79	0.159	0.540

* and ** Significant at 5% and 1% level of probabilities, respectively

Over the course of two years, data on seed yield /fed and other genotype characteristics are expressed in Table (3) that focused the significant (p≤00.05) variation between sesame genotypes in all of the examined traits. The ranges were registered with regard to number of days to 50% flowering (44.17 - 50.67 day), plant height (195.3 - 236.5 cm), length of fruiting zone (73.33 - 133.3 cm), length of capsule (3.617 - 4.033 cm), number of branches /plant (5.983 – 1.000), number of capsule /plant (216.2 - 148.2), 1000- seed weight (5.658 - 3.863 g), seed yield /plant (47.83

- 37.17 g), seed yield (4.272 - 6.725 ard /fed) and oil seed content (41.58 - 48.36 %). This variation among genotypes in all studied traits It's possible that this is due to a mixture of inherited traits and beneficial environmental conditions. one genotype more than other. These finding are in accept with these obtained by Pavani et al. (2020), Singh et al. (2020) and Mohanty et al. (2020). Furthermore, data in Table (2) showed that except for the length of the fruiting zone, there was a clear interaction between years and genotypes in the traits studied.

Table 3. Means of seed yield and other characters over the two years.

Genotype	50% Flowering	Plant height (cm)	Length of fruiting zone (cm)	Length of capsule (cm)	Number of branches /Plant	Number of capsules /Plant	1000- seed weight (g)	Seed yield /Plant (g)	Seed yield (ard /fed)	Oil content (%)
1	50.67	223.7	119.0	3.617	4.783	163.3	4.213	38.50	4.947	43.73
2	48.00	227.2	119.2	3.645	5.283	185.1	4.650	39.33	5.537	44.12
3	42.83	224.0	105.0	3.751	4.733	169.0	3.863	37.23	4.272	41.58
4	47.83	236.5	122.2	3.862	5.267	195.7	4.650	40.83	5.705	44.92
5	45.67	218.3	133.3	3.683	5.983	216.2	4.333	41.67	6.178	45.70
6	44.17	224.0	114.2	3.951	5.433	172.2	4.798	38.83	5.127	43.84
7	44.83	195.3	85.2	3.883	1.000	161.2	5.658	46.50	6.362	47.65
8	46.00	197.5	103.2	4.033	1.000	179.2	5.440	47.83	6.725	48.36
9	45.50	205.3	73.33	3.883	1.000	148.2	3.957	37.17	4.522	42.95
10	44.83	197.5	77.33	3.783	1.000	164.7	4.483	39.50	5.683	44.26
11	49.50	213.7	74.83	3.767	1.000	167.0	4.297	39.25	5.343	43.74
12	44.67	203.2	80.5	3.617	1.000	160.7	4.700	40.83	4.552	43.09
13	47.17	226.5	118.7	3.317	5.117	167.2	4.245	38.80	6.018	45.21
14	47.50	200.3	74.5	3.733	1.000	157.0	4.000	37.33	5.860	45.02
L.S.D 0.05	1.14	13.76	12.95	0.383	0.326	11.44	0.253	5.99	0.786	0.852

Heritability

The estimates of genetics obtained Table (4) was high in all cases studied traits except for capsule width, which scored very low inheritance for these hybrids and their parents. Estimates of heritability and genetic progression together are more important for selection than heritability alone. High heritability combined with the high genetic progression (as a percentage of average) observed in length of fruiting zone, number of branches, number of capsules, and seed yield per plant showed that these traits were controlled by additive genetic influences and the phenotypic effect of these characters was likely to be effective. Similar results have been published by Reddy *et al.* (2001) and Krishnaiah *et al.* (2002).

It is also possible to improve the characters from days to fifty percent of the flower, plant height, seed yield per fed and weight of 1000 seeds since these traits have high genetic potential and moderate genetic progression as a percentage of the average. Capsule length and oil content showed high genetic susceptibility with low gene progression. These results are consistent with those of Reddy *et al.,* 2001 and Sudhakar *et al.,* 2007. Capsule length showed low heritability and low genetic advance which may be due to non addi-tive gene action.

Table 4. Estimates of genetic variability for yield and its components

Characters	Genetic variability			Components of variance		h^2b	GA%
	σ^2P	σ^2G	σ^2E	PCV%	GCV%		
50% Flowering	10.1	9.1	2.12	6.85	6.51	90.41	10.90
Plant height (cm)	466.2	325.3	5.55	10.10	8.44	69.78	12.40
Length of fruiting zone (cm)	1009.8	885.2	11.16	31.76	29.74	87.66	49.01
Length of capsule (cm)	0.163	0.054	8.89	10.88	6.26	33.13	6.34
Number of branches /plant	9.8	9.7	9.02	100.57	100.16	99.20	175.57
Number of capsules /plant	2374.47	2277.12	6.42	31.72	31.07	95.90	53.55
1000- seed weight (g)	0.57	0.52	4.80	16.71	16.01	91.76	26.99
Seed yield /Plant (g)	64.960	38.17	13.50	21.02	16.11	58.76	21.74
Sees yield /fed	0.888	0.429	11.85	61.48	11.45	48.29	14.01
Oil content (%)	9.517	8.977`2	1.70	7.16	6.95	94.33	11.88

Phenotypic correlation among traits

Phenotypic correlations affect the characteristics of the crop triangle that give significant results in correlation. The phenotypic correlations using the total genotypes under study gave conflicting values as a result of the characteristic of the number of branches, as we have in this study branched and non-branched genotypes, and therefore the genotypes under study were divided into two groups, a branched group that includes the genetic makeup from (1 - 6) in addition to Genotype 13 (local variety) Table (5) group I, and a non-branching group that includes genotypes from (7-12) in addition to genotype 14 (local variety) Table (6) group II. The phenotypic correlations preferred to be performed in genotypes that are similar in the general direction of the traits affecting the crop.

Therefore, phenotypic correlation is presented in Table (5) group I showed significant (p≤ 0.05) and positive association of1000- seed weight with length of fruiting zone and plant height, whereas length of capsule was negative and non-significant association with days of 50% flowering. Seed weight / plant was associated with a positive and highly significant (p≤0.01) relationship with length of fruiting zone, number of branches /plant, number of capsules /plant and 1000- seed weight, 1000- seed weight with length of capsule and number of branches /plants, number of capsules /plant with length of fruiting zone and number of branches /plant, number of branches /Plant with both of fruiting zone and length of fruiting zone with days of 50% flowering.

Table 5. Phenotypic correlations for yield and yield contributing characters in group I (1-6+13 genotypes).

Characters	50% Flowering	Plant height (cm)	Length of fruiting zone (cm)	Length of capsule (cm)	Number of branches /Plant	Number of capsules /Plant	1000- seed weight (g)	Seed yield /Plant (g)
50% Flowering	--	0.288	0.412**	-0.381*	-0.163	-0.074	0.181	0.218
Plant height (cm)		--	-0.139	0.169	-0.270	-0.056	0.375*	0.092
Length of fruiting zone (cm)			--	-0.150	0.784**	0.785**	0.334*	0.923**
Length of capsule (cm)				---	0.187	0.236	0.441**	0.133
Number of branches /Plant					--	0.843**	0.510**	0.843**
Number of capsules /Plant						--	0.288	0.911**
1000- seed weight (g)							--	0.475**
Seed yield /plant (g)								--

* and ** Significant at 5% and 1% level of probabilities, respectively

While phenotypic correlation is presented in Table (6) group II showed significant (p≤ 0.05) and negative association of seed yield /plant with days of 50% flowering, and length of capsule with plant height. The correlation of seed yield /plant positive and highly significant (p≤0.01) with length of fruiting zone, length of capsule, number of capsules /plant and 1000- seed weight, 1000- seed weight with length of fruiting zone, length of capsule and number of capsules /plants, number of capsules /plant with length of fruiting zone and length of capsule, length of capsule with length of fruiting zone and plant height with days of 50% flowering.

Table 6. Phenotypic correlations for yield and yield contributing characters in group II (7-12+14 genotypes).

Characters	50% Flowering	Plant height (cm)	Length of fruiting zone (cm)	Length of capsule (cm)	Number of branches /Plant	Number of capsules /Plant	1000- seed weight (g)	Seed yield /Plant (g)
50% Flowering	--	0.7188**	-0.246	-0.072	a	0.156	-0.405**	-0.312*
Plant height (cm)		--	-0.500**	-0.345*	a	-0.177	-0.585**	-0.542**
Length of fruiting zone (cm)			--	0.674**	a	0.792**	0.806**	0.903**
Length of capsule (cm)				--	a	0.408**	0.485**	0.606**
Number of branches /Plant					--	A	A	A
Number of capsules /Plant						--	0.609**	0.699**
1000- seed weight (g)							--	0.977**
Seed yield /Plant (g)								--

* and ** Significant at 5% and 1% level of probabilities, respectively
a Cannot be computed because at least one of the variables is constant (Number of branches /plant)

As a result, these traits can be taken as selection criteria to improve seed yield per plant for 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 Umamaheswari *et al.* (2019) who discovered that the number of branches/plants, capsules/plant, seeds/capsule, and 100 seed weight were all linked to sesame yield. As a result, these traits can be used to pick advanced sesame lines with higher seed yield. Furthermore, these characteristics may be used as selection criteria for improving sesame seed yield in the future agricultural system. Similarly, Saravanan *et al.* (2020) The number of capsules per plant, 1000 seed weight, plant height, and the number of branches per plant all had a strong positive association with yield per plant.

Path coefficient analysis

Like other crops, sesame seed yield is a complicated trait. Path coefficient analysis, which considers both direct and indirect effects of the various yield components, may provide a more accurate image of relationships between these traits. Plant breeders can quickly identify selected traits that contribute the most to yield by determining interrelationships between yield components and between them and seed yield. The phenotypic correlation coefficients of seed yield/plant with length of fruiting zone, number of branches /plants, number of capsules /plant, and 1000- seed weight in Table (7) group I were separated using a path coefficient analysis in this study. Table (8) group II shows seed yield/plant with length of fruiting zone, length of capsules, number of capsules /plant, and 1000-seed weight.

The path analysis in group I the length of the fruiting zone (0.534), followed by the number of capsules per plant (0.570), and 1000-seed weight, both had a positive and direct effect on seed yield per plant (0.218). In all of these, there were significant genotypic associations with seed yield.The value of these traits as seed yield components is reflected in their greater impact. Similar results were reported by Mothilal (2005) and Goudappagoudra *et al.* (2011). While Kurdistani *et al.* (2011) found that the number of capsules per plant had the greatest positive direct effect on seed yield; the negative indirect effects of this trait through the number of branches per plant were also observed in this research (-0.085).

The number of branches per plant had a negative and direct effect on seed yield per plant (-0.167). However, through the duration of the fruiting zone (0.419), the number of capsules per plant (0.481), and the 1000-seed weight, this

trait had an indirect positive impact on seed yield/plant (0.073).

The indirect negative implications demonstrated by the other traits decreased these positive indirect effects. Over the length of the fruiting region, the trait of number of capsules/ plant had the greatest negative indirect effect (0.141) on seed yield /plant. The inverse relationship between the length of the fruiting zone and the number of capsules per plant caused this negative indirect effect.

Table 7. Direct and indirect effects of length of fruiting zone, number of branches /Plant, number of capsules /plant and 1000- seed weight on seed yield/plant in group I.

Path way association	Direct effect P	Indirect effect PX	R
1-Length of fruiting zone			
(a). Direct effect (P1Y)	0.534		
(b). Indirect effect via			
Number of branches /plantr12Py2		-0.131	
Number of capsules /plant. r13Py3		0.447	
1000- seed weightr14Py4		0.073	
(c). Total effect			0.923**
2-Number of branches /plant			
(a). Direct effect (P2Y)	-0.167		
(b). Indirect effect via			
Length of fruiting zoner12Py1		0.419	
Number of capsules /plant. r23Py3		0.481	
1000- seed weightr14Py4		0.073	
(c). Total effect			0.843**
3-Number of capsules /plant			
(a). Direct effect (P3Y)	0.570		
(b). Indirect effect via			
Length of fruiting zoner13Py1		0.419	
Number of branches /plant r23Py2		-0.141	
1000- seed weightr34Py4		0.063	
(c). Total effect			0.911**
4- 1000- seed weight			
(a). Direct effect (P4Y)	0.218		
(b). Indirect effect via			
Length of fruiting zone r14Py1		0.178	
Number of branches /Plant r24Py2		-0.085	
Number of capsules /Plant. r34Py4		0.063	
(c). Total effect			0.475**
5. Residual effect (Pxy)		-0.159	

P= Path Coefficient; (P x r)= Path coefficient; (r)= Correlation coefficient

On the other hand, the path coefficient analysis (group II) revealed that the length of the fruiting zone (0.227), the length of capsules (0.083), the number of capsules /plant (0.042), and the 1000-seed weight all had a

positive and direct effect on seed yield/plant (0.728). Similar results were reported by Azeez and Morakinyo (2011) reporting that the seed weight of 1000 seeds had the greatest direct impact on seed yield per plant. This trait also had a positive indirect impact on seed yield/plant and the relationship between them.

Table 8. Direct and indirect effects of length of fruiting zone, length of capsules, number of capsules /plant and 1000- seed weight on seed yield /plant in group II.

Path way association	Direct effect P	Indirect effect PX	R
1-Length of fruiting zone			
(a). Direct effect (P1Y)	0.227		
(b). Indirect effect via			
length of capsules r12Py2		0.056	
Number of capsules /plant. r13Py3		0.033	
1000- seed weight r14Py4		0.587	
(c). Total effect			0.903**
2-Length of capsules			
(a). Direct effect (P2Y)	0.083		
(b). Indirect effect via			
Length of fruiting zone r12Py1		0.153	
Number of capsules /plant. r23Py3		0.017	
1000- seed weight r14Py4		0.587	
(c). Total effect			0.606**
3-Number of capsules /plant			
(a). Direct effect (P3Y)	0.042		
(b). Indirect effect via			
Length of fruiting zone r13Py1		0.180	
Length of capsulesr23Py2		0.034	
1000- seed weight r34Py4		0.443	
(c). Total effect			0.699**
4-1000- seed weight			
(a). Direct effect (P4Y)	0.728		
(b). Indirect effect via			
Length of fruiting zone r14Py1		0.183	
Length of capsulesr24Py2		0.040	
Number of capsules /plant. r34Py4		0.443	
(c). Total effect			0.977**
5. Residual effect (Pxy)		-0.063	

P= Path Coefficient; (P x r)= Path coefficient; (r)= Correlation coefficient

The only traits that had significant positive direct effects on seed yield/plant and were positively associated with it in this study were length of fruiting region, number of capsules/plant, and 1000-seed weight. As a result, these traits were determined to be the most important yield components, and selection based on them would increase seed yield/plant. Furthermore, although the number of branches trait had a negative direct effect (-0.167) on seed yield/plant, it had a strong positive phenotypic association (r=0.843) with seed yield/plant. As a result, the number of branches had the greatest positive indirect effect (0.841) on seed yield / plant through the number of capsules / plant. As a result, the number of branches /plant can be used as a selection criterion, with the number of capsules/plant gaining more weight. In this study the residual impact in groups I and II (-0.159, -0.063) in this study was very small, suggesting that all essential yield contributing traits were included in the path analysis. This was in accordance with Sumathi *et al.* (2007) and Goudappagoudra *et al.* (2011).

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, the number of branches per plant, number of capsules per plant, and seed yield per plant showed high estimates of PCV and GCV. High heritability combined with the high genetic advance (as a percentage of average) observed in length of fruiting zone, number of branches, number of capsules, and seed yield per plant showed that these traits were controlled by additive genetic influences and the phenotypic effect of these characters was likely to be effective, showed that these genotypes were controlled by the effects of additive genes, and phenotype selection for these adjectives like me to be effective. The traits length of fruiting zone, length of capsules, number of capsules/plants, number of branches /plant, and 1000-seed weight ought to be given top priority based on the above findings, when compared to other traits, they demonstrated a strong positive for correlation coefficient and direct effect.

REFERENCES

Azeez M.A. and Morakinyo J.A. (2011). Path analysis of the relationships between single seed yield and some morphological traits in sesame (genera *Sesamum* and *Ceratotheca*). Int J. Plant Breed Genet., 5:358–368.

Brar, G.S. and Ahuja, K.L. (1979). Sesame: its culture, genetics, breeding and biochemistry p. 245-313. In: Malik, C.P. (ed.). Annu. Rev. of plant Sci. Kalyani publishers, New Delhi.

Burton G.W. , De Vane E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal, 45: 478-481.

Chowdhury, S., Datta, A. K., Saha, A., Sengupta, S., Paul, R., Maity, S. and Das, A. (2010). Traits influencing yield in sesame (*Sesamum indicum* L.) and multi locational trials of yield parameters in some desirable plant types. Indian J. Sci. Technol. 3: 163-166.

Davidson, A. (1999). The Oxford Companion to Food. Oxford University Press, London.

Dewey D.R., R.H. Lu (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J., 51: 515-518.

Dixit P, Dubey DK (1984). Path Analysis in Lentil (Lens culinaris Medic.). Lens Newsletter 11(2): 1517.

FAO (2018).Http://appsl.fao.org/servlet/xte.servlet.jrun.

Gomez K.A., and Gomez A.A. (1984). Statistical Procedures for Agricultural Research. 2nd Edition, John Wiley and sons Inc., USA Hoboken, p. 680.

Goudappagoudra R, Lokesha R, and Ranganatha ARG (2011). Trait association and path coefficient analysis for yield and yield attributing traits in sesame (*Sesamum indicum* L.). Electronic Journal of Plant Breeding 2:448–452.

Hansen C.H., Robinson H.F., and Comstock R.E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. Agronomy Journal, 48: 268-272.

Johnson H.W., Robinson H.F., and Comstock R.E. (1955). Estimates of genetic and environmental variability in soybean. Agronomy Journal, 47: 314-318.

Krishnaiah G, Reddy KR and Sekar MR (2002). Variability studies in sesame. Crop Research, 24: 3, 501-504

Kurdistani R, Tohidinejad E, Mohammadi- Nejad G, Zareie S (2011). Yield potential evaluation and path analysis of different sesame genotypes under various levels of iron. Afr J Plant Sci 5:862–866.

Mohanty T.A., Singh U.K., Singh S.K., Kushwaha N., and Singh D. (2020). Study of genetic variability, heritability and genetic advance in sesame (*Sesamum indicum* L.) genotypes. *Int.* J. Curr. Microbiol. App. Sci., 9: 347-356.

Mothilal A (2005). Correlation and path analysis in sesame (*Sesamum indicum* L.). Environ Eco. 233: 478–480.

Parameshwarappa, G., Palakshappa, M. G., Salimath, P. M. and Parameshwarappa, K. G. (2009). Studies on genetic variability and character association in germplasm collection of sesame (*Sesamum indicum* L.). Karnataka J. Agric. Sci. 22: 252-54.

Pavani K., Lal Ahamed M., Ramana J.V., and Sirisha A.B.M. (2020). Studies on genetic variability parameters in sesame (*Sesamum indicum* L.). International Journal of Chemical Studies, 8: 101-104.

Reddy PAV, Sekar MR, Ranganatha ARG and Dhanraj A 2001. Genetic variability and herita-bility for seed yield and its components in sesame (*Sesamum indicum* L.). Journal of Oilseeds Research, 18 : 2, 173-175

Saravanan M., Kalaiyarasi R., and Viswanathan P.L. (2020). Assessment of genetic variability, character association and path analysis in F2 population of sesame (*Sesamum indicum* L.). Electronic Journal of Plant Breeding, 111:447-450.

Singh D. (2020). Study of genetic variability, heritability and genetic advance in sesame (*Sesamum indicum* L.) genotypes. Int. J. Curr. Microbiol. App. Sci., 9: 347-356.

Snedecor, G.W., and Cochran, W.G. (1989). Statistical Methods. 8th Edition, Iowa State University Press, Ames.

Sudhakar N, Sridevi O and Salimath 2007. Variability and character association analysis in sesame, *Sesamum indicum* L. Journal of Oilseeds Research, 24: 1, 56-58.

Sumathi P, Muralidharan V, and Manivannan N (2007). Trait association and path analysis for yield and yield attributing traits in sesame (*Sesamum indicum* L.). Madras Agric J., 94:174–178.

Thirumala Rao.V., D. Bharathi, Y. Chandra Mohan, V. Venkanna and D. Bhadru. (2013). Genetic variability and association analysis in sesame (*Sesamum indicum* L.). Crop Res. 46 (1, 2 & 3): 122-125.

Toprope, V. N., Chavan, M. H., Ghodke, M. K. and Gir, S. N. (2009). Genetic variability and character association analysis in F1, F2 and F3 generations of sesame (*Sesamum indicum* L.). J. Oilseeds Res. 26: 43-45.

Umamaheswari S., Suganthi S., Sathiskumar P., and Kama-raj A. (2019). Genetic variability, correlation and path analysis in sesame (*Sesamum indicum* L.). Plant Archives, 19: 4543-4548.

Weber C.R., and Moorthy B.R. (1952). Heritable and non-heritable relationship and variability of oil content and agronomic traits in the F2 generations of soybean crosses. Agron. J., 44:202-209.

التباين الوراثي و معامل المرور لبعض التراكيب الوراثية من السمسم لمحصول البذور و مكوناته

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تم إجراء هذا البحث لتحديد السلوك الوراثي لـ 14 تركيب وراثي متنوعًا من السمسم في محطة البحوث الزراعية بشندويل في الموسمين الصيفيين (2017 و 2018) للمقارنة بينها في الصفات المحصولية باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات. لوحظت فروق معنوية بين الطرز الوراثية للسمسم المقيمة لجميع الصفات المدروسة. تم الحصول على أعلى متوسط قيم لوزن الألف بذرة ومحصول البذور / نبات من التركيب الوراثي M₂A₂₃، بينما تم الحصول على أقل متوسط قيمة من التركيب الوراثي B-42. كان عدد الأفرع لكل نبات ، وعدد الكبسولات لكل نبات ، ومحصول البذور لكل نبات تقديرات عالية للتباين المظهري والتباين الوراثي. لوحظ ارتفاع معدل التوريث مع التقدم الوراثي العالي (كنسبة مئوية من المتوسط) في طول منطقة الثمار ، وعدد الفروع / النبات ، وعدد الكبسولات / النبات ، ومحصول البذور / النبات ، مما أظهر أن هذه الصفات تم التحكم فيها عن طريق تأثير الجينات المضافة. كان لمحصول البذور / نبات علاقة موجبة ومعنوية عالية مع طول منطقة الثمار في كل من الطرز الوراثية المتفرعة وغير المتفرعة. علاوة على ذلك ، كان لطول منطقة الإثمار وعدد الكبسولات / نبات ووزن الألف بذرة تأثيرات مباشرة إيجابية كبيرة على محصول البذور / نبات. وبالتالي ، يمكن أن تكون هذه الصفات مفيدة في تحسين محصول بذور السمسم.