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Choice of Traits for Seed Yield Improvement based on Association Analysis Studies in Sesame (*Sesamum indicum* L.)

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ABSTRACT

Background: Sesame is an ancient oilseed crop of India popular for its drought resistance and stable healthy oil which is easy to extract. Information regarding the genetic association of plant traits with grain yield is of great importance to breeders in selecting suitable genotypes. Hence, the present study is based on simple measures of variability and genetic variance to identify suitable genotypes for further improvement.

Methods: The experiment was carried out at Student's Farm, Department of Agriculture, Loyola Academy, Secunderabad during *Kharif* 2021. Sixty genotypes of the Sesamum crop were studied for 13 quantitative and qualitative traits.

Result: Analysis of variance revealed that the genotypes were significant (P 0.05 and P 0.01) for all of the traits studied. A positive significant correlation at the genotypic level was observed for the character 1000 seed weight (0.222) with grain yield. A positive correlation between desirable traits is encouraging to the plant breeder as it helps in the simultaneous improvement of both traits. Positive direct effects were highest for the character 1000 seed weight (0.866) followed by the number of capsules per axil (0.660) on grain yield. This study would help to select the genotypes that have a strong association among traits.

Key words: Correlation, Genetic variance, Genotypes, Yield.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the ancient cultivated oilseed crops of the world. Sesamum belongs to the Tubiflorae order and Pedaliaceae family (Shrikanth and Ghodake, 2022). It is also popular as til and gingelly and famously known as "Queen of Oilseeds". Sesame is diploid (2n=26) and dicotyledonous. The genus Sesame has about 36 species (Esmaeil and Reza, 2019), of which *Sesamum indicum* L. is the most principal cultivated species. The plant yields rich edible oil due to the presence of powerful antioxidants Sesaminol and Sesamol. Sesame seeds are acknowledged as "the seeds of immortality". Although the crop originated in Africa, India is considered to be the major Centre of genetic diversity (Maiti *et al*., 2018).

The global production of Sesame seeds was 6.2 million tonnes, led by Tanzania, India and Sudan (FAOSTAT, 2016). More than 6 million tons of sesame seeds have been produced under nearly 11 million ha categorizing sesame at the ninth rank among the major oil crops (FAOSTAT, 2017). The distribution of most of the species takes place in three regions *viz*., Africa, India and the Far East (Kehie *et al*., 2020). The composition of sesame concerning 100 g of seed is lipid contents- 48 g, carbohydrates-25.7 g, proteins-17 g, fibre-14 g and ash-6 g approximately. Sesame seeds contain 40 to 63 per cent oil rich in antioxidants and a substantial amount of Poly unsaturated fatty acids (Abate and Mekbib, 2015). Sesame seeds are rich in minerals such as calcium, phosphorous, magnesium and potassium in large quantities and similarly have vitamins such as Niacin, Thiamin, Riboflavin and vitamin B-6 (USDA Nutrient Database, 2015). Besides, it is used in the pharmaceutical and cosmetic industries as well (Kehie *et al*., 2020). Around 70 per cent of the World's Sesame seed is processed into oil and meal. Sesame contains bactericidal and insecticidal activities and its antioxidants inhibit the absorption and production of cholesterol in the liver.

The understanding of the nature and magnitude of genetic variability is of immense value to the plant breeder for planning an efficient breeding programme to improve the yield potential of crops. Similarly, information on the genetic association of plant traits with seed yield has great significance to breeders in selecting desirable genotypes (Kehie *et al*., 2020). The phenotypic selection of parents based on their performance alone may not always be a dependable procedure since the phenotypic expression is highly influenced by environmental factors, which are non-heritable. It is thus, essential to select genotypes based on their genetic worth. Accordingly, correlation studies help in the selection of superior genotypes from diverse genetic

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populations (Jogdhande *et al*., 2017). In crop breeding, correlation coefficient measures the mutual relationship between various traits and determines the component character on which selection can be relied upon for genetic improvement of yield potential of crop plants (Kumar and Paul, 2016).However, in correlation studies, indirect associations become more complex and puzzling. Path analysis can avoid this complication by measuring the direct influence of one trait on the other as well as partitioning a given correlation coefficient into its components of direct and indirect effects (Manisha *et al*., 2018; Jogdhande *et al*., 2017). Path coefficient analysis is an effective means of analyzing direct and indirect causes of association and permits critical examination of specific traits that produce a given correlation. It provides information on the magnitude and direction of direct and indirect effects of the yield components (Chaudhary and Joshi, 2016).

However, the lack of information on the character association of yield and its contributing traits is believed to limit the genetic improvement of sesame in India. Hence, the present investigation was focused on gathering adequate information on the genetic association of yield and yield-related traits in sesame accessions collected from various areas of India.

MATERIALS AND METHODS

Study area

The experimental study was performed at Student's Farm, Department of Agriculture, Loyola Academy, Secunderabad during *Kharif* 2021.

Experimental material and design

The experimental material comprised of 60 genotypes (Table 1) seeded in a randomized full block design (RBD) with three replications. Each genotype was grown in a 5 m long row with 30 × 10 cm spacing. To ensure a successful yield, recommended agronomic practices were followed. Observations for thirteen quantitative characters like plant height (cm), number of branches per plant, seed yield per plant (g), 1000 seed weight (g), number of capsules per axil, capsule length (cm), number of capsules per plant, number of seeds per capsule, seed length (mm), seed width (mm), seed thickness (mm) and oil content were noted. Five randomly chosen plants in each entry of each replication were used for collecting the data.

Statistical analysis

Analysis of variance was carried out for the data using R software; to test for significant differences among the genotypes according to the standard statistical procedure described by Gomez and Gomez (1984).

Phenotypic and genotypic correlations between the quantitative traits were estimated using the method described by Miller *et al*. (1958). The correlation coefficient was analyzed on the tabulated data using META-R Version-6.01 (Alvarado *et al*., 2017).

The proportion of direct and indirect contributions of various characteristics with seed yield was estimated through path coefficient analysis as suggested and elaborated by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance

Table 2 depicts the ANOVA findings for 13 features of 60 sesame genotypes. According to ANOVA, the mean sum of squares for the genotypes was extremely significant (P 0.05 and P 0.01) for all characters. This indicates that the material under research showed no significant changes in replication, proving that environmental error (genotype x environment) was less widespread. The material displayed considerable variation among genotypes.These findings demonstrated that substantial differences exist among genotypes for all parameters studied, which may provide breeders with a good chance to identify high-performing accessions for desired

Table 1: List of genotypes.

Sr. no.	Genotype	Sr. no.	Genotype	Sr. no.	Genotype	Sr. no.	Genotype
1	EC 304231	16	CUMS-17	31	IC 204785	46	GT-10
2	AKT-101	17	ES-21086-2	32	IC 511141	47	JLT-408
3	Agra Balik	18	Chagatam Local	33	EC 346665	48	DORG-3052
4	EVC-122	19	ANAMIDI 74	34	EC 346829	49	DORG-60KRDS
5	CT-50	20	B-67	35	EC 346370	50	DORG-B7-11
6	TMV-4	21	RT-125	36	IC 500448	51	DORG-135-011
7	TMV-6	22	JLT-7	37	IC 500463	52	DORG-37-11
8	RT-372	23	VINAYAK	38	IC 500393	53	TKG-22
9	YLM-66	24	CT-44	39	VRI-1	54	DORG-BLSG-9
10	Phule TIL-1	25	T-78	40	Madhavi	55	IC 204550
11	EC-208652	26	TMV-7	41	Chandana	56	EC 370712
12	CT-51	27	VRI-2	42	YLM-17	57	IC 204248
13	EC 301961	28	IC 127622	43	YLM-4	58	IC 500506
14	CT-35	29	YLM-11	44	Swetha	59	IC 132828
15	RT-351	30	IC 511151	45	KIS-304	60	IC 129908

features to enhance crop breeding programmes. Shrikanth and Ghodake, 2022 and Esmaeil and Reza, 2019 discovered that the quantitative features of sesame genotypes differed significantly.

Correlation coefficient

The correlation coefficients between seed yield and yield contributing characters were worked out at the genotypic and phenotypic levels (Table 3).

Direct correlation

Positive significant correlation at genotypic and phenotypic levels was observed for 1000 seed weight (0.222, 0.170) with grain yield. A strong positive correlation between desirable traits like these is favourable to the plant breeder because it helps in the concurrent improvement of both the characters. Comparable findings were reported by Takele *et al*. (2021), Esmaeil and Reza (2019) and Shrikanth and Ghodake, (2022). A significant negative correlation was observed for days to 50% flowering (-0.262, -0.192) and seed yield. Similar findings were stated by Abate *et al*. (2018), Teklu *et al*. (2017) and Shrikanth and Ghodake, (2022).

Indirect correlation

Days to 50% flowering showed a positive and high significant correlation (genotypic and phenotypic) with capsules per plant (0.148, 0.137), while it was negatively associated with seed length (-0.203, -0.145) and seed width (-0.224, -0.205). Plant height exhibited positive and high significant correlation (genotypic and phenotypic) with number of branches (0.487, 0.446), capsule length (0.327, 0.282) and capsules per plant (0.420, 0.395). The number of branches executed a positive and high significant correlation (genotypic and phenotypic) with the number of capsules per axil (0.318, 0.301) and capsules per plant (0.702, 0.680) while negatively associated with seed thickness (-0.150, -0.129). 1000 seed weight exhibited positive and high significant correlation (genotypic and phenotypic) with number of capsules per axil (0.197, 0.165), capsule length (0.254, 0.201), seed length (0.418, 0.195), seed thickness (0.185, 0.111) and oil content (0.239, 0.216). The number of capsules per axil presented a positive and high significant correlation (genotypic and phenotypic) with capsules per plant (0.393, 0.389), but exhibited a negative association with seed width (-0.312, -0.273) and seed thickness (-0.169, -0.153). Capsule length presented positive and high significant correlation (genotypic and phenotypic) with number of seeds per capsule (0.434, 0.399), seed length (0.275, 0.197), seed width (0.299, 0.229) and seed thickness (0.221, 0.208). Capsules per plant displayed negative and high significant correlation (genotypic and phenotypic) with seed length (-0.187,-0.115), seed width (-0.282, -0.238) and seed thickness (-0.288, -0.267). The number of seeds per capsule displayed a positive and high significant correlation (genotypic and phenotypic) with seed length (0.183, 0.144), seed width (0.220, 0.195) and seed thickness (0.247, 0.199). Seed length exhibited a positive and high significant correlation (genotypic and phenotypic) with seed width (0.850, 0.577) and seed thickness (0.418, 0.308). Seed width presented a positive and high significant correlation (genotypic and phenotypic) with seed thickness (0.738, 0.605). Seed thickness displayed a positive and high significant correlation (genotypic and phenotypic) with oil content (0.212, 0.185). Shrikanth and Ghodake, (2022) reported a high, positive and significant association of days to 50% flowering, plant height, 1000 seed weight, number of capsules per axil, capsule length, capsule per plant, number of seeds per capsule, seed length and oil content. Esmaeil and Reza, (2019) and Kumar and Vivekanandan, (2019) also reported the same for plant height, 1000 seed weight, capsules per plant, seed length, seed width and seed thickness. Similar findings were reported by Teklu *et al*., 2017 for days to 50% flowering, plant height, number of

Table 2: MSQ from ANOVA for sesame yield and its components for 60 genotypes.

Source	Replication	Treatment	Error	Sem	CD (5%)	CD (1%)	CV %
Days to 50% flowering	1.37	14.67**	0.50	0.41	1.14	1.51	1.74
Plant height	70.43	952.92**	50.08	4.09	11.44	15.13	7.14
No. of branches	0.28	4.63**	0.10	0.18	0.50	0.67	9.73
1000 seed weight	0.02	0.52**	0.05	0.13	0.38	0.50	8.04
No. of capsules/axil	0.00	1.24**	0.00	0.04	0.10	0.14	5.36
Capsule length	0.04	0.31**	0.02	0.07	0.20	0.26	5.00
Capsules per plant	11.10	1697.75**	7.37	1.57	4.39	5.80	5.56
No. of seeds per capsule	4.63	751.75**	14.11	2.17	6.07	8.03	5.07
Seed length	0.00	0.14**	0.04	0.12	0.34	0.45	6.55
Seed width	0.01	0.12**	0.01	0.06	0.17	0.23	5.76
Seed thickness	0.00	0.05**	0.00	0.03	0.09	0.11	5.85
Oil content	0.14	70.80**	1.58	0.72	2.03	2.68	5.27
Grain yield	0.83	3.46**	0.32	0.33	0.91	1.21	8.14

*, **Significant at 5% and 1% level of significance.

Table 3: Genotypic (G) and phenotypic (P) coefficient of correlation among different characters in sesame genotypes.

Characters		Days to 50% flowering	Plant height	No. of branches	1000 seed weight	No. of capsules axil	Capsule length	Capsules per plant	No. of seeds per capsule	Seed length	Seed width	Seed thicknes	Soil content	Grain yield
Days to 50% flowering	G	1.000	0.397**	0.129	-0.128	-0.137	0.044	0.148*	-0.110	-0.203*	-0.224*	-0.048	-0.108	-0.262**
	P	1.000	0.325**	0.110	-0.071	-0.130	0.036	0.137	-0.102	-0.145	-0.205*	-0.051	-0.096	-0.192*
Plant height	G		1.000	0.487**	0.094	0.012	0.327**	0.420**	-0.032	-0.112	-0.103	-0.090	-0.014	-0.014
	P		1.000	0.446**	0.067	0.010	0.282**	0.395**	-0.013	-0.058	-0.087	-0.075	-0.015	-0.043
No. of branches	G			1.000	-0.034	0.318**	0.004	0.702**	-0.015	0.035	-0.039	-0.150*	0.062	0.092
	P			1.000	-0.052	0.301**	0.032	0.680**	-0.011	0.017	-0.037	-0.129	0.064	0.064
1000 seed weight	G				1.000	0.197*	0.254**	0.078	0.032	0.418**	0.125	0.185*	0.239*	0.222*
	P				1.000	0.165*	0.201*	0.074	0.042	0.195*	0.110	0.111	0.216*	0.170*
No. of capsules/axil	G					1.000	-0.090	0.393**	0.021S	0.031	-0.312**	-0.169*	0.023	0.104
	P					1.000	-0.077	0.389**	0.022	0.019	-0.273**	-0.153*	0.022	0.086
Capsule length	G						1.000	-0.052	0.434**	0.275**	0.299**	0.221*	0.130	0.049
	P						1.000	-0.048	0.399**	0.197*	0.229*	0.208*	0.116	0.041
Capsules per plant	G							1.000	-0.083	-0.187*	-0.282**	-0.288**	0.013	0.039
	P							1.000	-0.077	-0.115	-0.238*	-0.267**	0.013	0.023
No. of seeds per capsule	G								1.000	0.183*	0.220*	0.247**	-0.143	-0.026
	P								1.000	0.144	0.195*	0.199*	-0.141	-0.044
Seed length	G									1.000	0.850**	0.418**	0.124	0.119
	P									1.000	0.577**	0.308**	0.057	0.087
Seed width	G										1.000	0.738**	0.063	-0.091
	P										1.000	0.605**	0.066	-0.052
Seed thickness	G											1.000	0.212*	-0.028
	P											1.000	0.185*	-0.022
Oil content	G												1.000	0.066
	P												1.000	0.060

branches, capsule length, capsules per plant, number of seeds per capsule and oil content.

If correlation bears a negative sign, it means that increase in the value of one character will lead to a decrease in the value of the second character and vice versa. Similarly, if correlation bears a positive sign, it means that increase in the value of one variable will lead to an increase in the second character. The magnitude of all genotypic correlations is higher than that of phenotypic correlations except for the number of branches and number of capsules per axil. It means that there is a strong association between these two characters genetically, but the phenotypic value is diminished by a significant interaction with the environment. Similar findings were reported by Abate *et al*. (2018).

Path coefficient

Path coefficient analysis splits the correlation coefficient into direct and indirect effects.

Genotypic path coefficient

In Table 4, the highest positive direct effects were exhibited by seed width (2.459) on the dependent character. High positive direct effects were expressed by 1000 seed weight (0.866) followed by the number of capsules per axil (0.660) on the dependent character. Moderate positive direct effects were exhibited by oil content (0.232) followed by the number of branches (0.226) on the dependent character. Low positive direct effects were expressed by days to 50% flowering (0.167) followed by the number of seeds per capsule on dependent traits. Shrikanth and Ghodake (2022) and Takele *et al*. (2021) reported high positive direct effects on grain yield. The highest negative direct effects were observed for seed length (-1.925) followed by seed thickness (-1.236) on dependent characters. High negative direct effects were observed for capsules per plant (-0.442) on dependent character. Low negative direct effects were observed for plant height (-0.122) followed by capsule length (-0.119) on dependent character. Similar findings have been reported by Teklu *et al*. (2017) and Kumar and Vivekanandan, (2019) for seed length, seed thickness, capsules per plant, plant height and capsule length.

Phenotypic path coefficient

In Table 5, low positive direct effects were identified for the number of branches (0.191), 1000 seed weight (0.174) and seed length (0.139) on the dependent character. Moderate negative direct effects were detected for days to 50% flowering (-0.222) and seed width (-0.265) on the dependent character. Similar findings were reported by Shrikanth and Ghodake, (2022); Esmaeil and Reza, (2019) and Teklu *et al*. (2017) for 1000 seed weight, capsule length, seed length, seed width and seed thickness.

The residual effect R=0.409 (P) and 0.343 (G) indicates that the component characters under study were responsible for about 96% and 97% of variability in seed yield per plant.

Table 4: Genotypic path coefficient showing direct and indirect effect of different characters on grain yield/plant.

Characters	Days to 50% flowering	Plant height	No. of branches	1000 seed weight	No. of capsules/axil	Capsule length	Capsules per plant	No. of seeds per capsule	Seed length	Seed width	Seed thickness	Oil content	Grain yield
Days to 50% flowering	0.167	0.066	0.021	-0.021	-0.023	0.007	0.025	-0.018	-0.034	-0.037	-0.008	-0.018	-0.262**
Plant height	-0.049	-0.122	-0.060	-0.012	-0.002	-0.040	-0.051	0.004	0.014	0.013	0.011	0.002	-0.014
No. of branches	0.029	0.110	0.226	-0.008	0.072	0.001	0.159	-0.003	0.008	-0.009	-0.034	0.014	0.092
1000 seed weight	-0.111	0.081	-0.029	0.866	0.170	0.220	0.068	0.028	0.362	0.108	0.160	0.207	0.222*
No. of capsules/axil	-0.090	0.008	0.210	0.130	0.660	-0.059	0.260	0.014	0.021	-0.206	-0.111	0.015	0.104
Capsule length	-0.005	-0.039	-0.001	-0.030	0.011	-0.119	0.006	-0.051	-0.033	-0.036	-0.026	-0.015	0.049
Capsules per plant	-0.065	-0.186	-0.311	-0.035	-0.174	0.023	-0.442	0.037	0.083	0.125	0.127	-0.006	0.039
No. of seeds per capsule	-0.013	-0.004	-0.002	0.004	0.003	0.050	-0.010	0.116	0.021	0.026	0.029	-0.017	-0.026
Seed length	0.391	0.215	-0.067	-0.805	-0.060	-0.528	0.360	-0.353	-1.925	-1.635	-0.803	-0.239	0.119
Seed width	-0.550	-0.253	-0.096	0.307	-0.767	0.736	-0.693	0.540	2.089	2.459	1.815	0.154	-0.091
Seed thickness	0.059	0.111	0.185	-0.229	0.209	-0.273	0.355	-0.306	-0.516	-0.913	-1.236	-0.262	-0.028
Oil content	-0.025	-0.003	0.014	0.055	0.005	0.030	0.003	-0.033	0.029	0.015	0.049	0.232	0.066
Partial R^2	-0.044	0.002	0.021	0.192	0.068	-0.006	-0.018	-0.003	-0.228	-0.223	0.034	0.015	

Residual effect = 0.409; *,**Significant at 5% and 1% level.

Table 5: Phenotypic path coefficient showing direct and indirect effect of different characters on grain yield/plant.

	Days to 50% flowering	Plant height	No. of branches	1000 seed weight	No. of capsules axil	Capsule length	Capsules per plant	No. of seeds per capsule	Seed length	Seed width	Seed thickness	Oil content	Grain yield
Days to 50% flowering	-0.222	-0.072	-0.024	0.016	0.029	-0.008	-0.030	0.023	0.032	0.045	0.011	0.021	-0.192*
Plant height	-0.024	-0.075	-0.033	-0.005	-0.001	-0.021	-0.030	0.001	0.004	0.007	0.006	0.001	-0.043
No. of branches	0.021	0.085	0.191	-0.010	0.058	0.006	0.130	-0.002	0.003	-0.007	-0.025	0.012	0.064
1000 seed weight	-0.012	0.012	-0.009	0.174	0.029	0.035	0.013	0.007	0.034	0.019	0.019	0.038	0.170*
No. of capsules/axil	0.007	-0.001	-0.017	-0.009	-0.057	0.004	-0.022	-0.001	-0.001	0.015	0.009	-0.001	0.086
Capsule length	0.003	0.024	0.003	0.017	-0.006	0.084	-0.004	0.033	0.017	0.019	0.017	0.010	0.041
Capsules per plant	-0.010	-0.028	-0.048	-0.005	-0.027	0.003	-0.070	0.005	0.008	0.017	0.019	-0.001	0.023
No. of seeds per capsule	0.010	0.001	0.001	-0.004	-0.002	-0.038	0.007	-0.096	-0.014	-0.019	-0.019	0.014	-0.044
Seed length	-0.020	-0.008	0.002	0.027	0.003	0.027	-0.016	0.020	0.139	0.080	0.043	0.008	0.087
Seed width	0.054	0.023	0.010	-0.029	0.072	-0.061	0.063	-0.052	-0.153	-0.265	-0.160	-0.018	-0.052
Seed thickness	-0.003	-0.005	-0.008	0.007	-0.010	0.013	-0.017	0.013	0.020	0.039	0.065	0.012	-0.022
Oil content	0.003	0.001	-0.002	-0.008	-0.001	-0.004	-0.001	0.005	-0.002	-0.002	-0.007	-0.035	0.060
Partial R^2	0.043	0.003	0.012	0.030	-0.005	0.003	-0.002	0.004	0.012	0.014	-0.001	-0.002	

Residual effect = 0.343; *,**Significant at 5% and 1% level of significance.

CONCLUSION

The mean sum of square (MSS) due to genotypes was highly significant (P<0.05 and P<0.01) for all the characters under study, indicating that there is a substantial amount of variability in the genotypes, according to the analysis of variance. A positive significant correlation at the genotypic level has been observed for 1000 seed weight (0.222) with grain yield. This type of positive correlation between desirable traits is constructive to the plant breeder as it helps in the concurrent improvement of both the characters. The highest positive direct effects were noted for 1000 seed weight (0.866) followed by the number of capsules per axil (0.660) on grain yield. Low positive direct effects were observed for the number of branches (0.191), 1000 seed weight (0.174) and seed length (0.139) on the dependent character. Moderate negative direct effects were detected for days to 50% flowering (-0.222) and seed width (-0.265) on the dependent character.

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