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Estimation of Genetic Variability, Heritability and Genetic Advance for Seed Yield and Its Attributes in Sesame (*Sesamum indicum* L.)

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Abstract

The field experiment was conducted during July to October, 2018 at Castor-Mustard Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India to access genetic variability, heritability and genetic advance for seed yield and its attributing traits in 45 genotypes of sesame. Analysis of variance revealed significant difference among genotypes for all the eleven characters which indicated presence of sufficient variability among the genotypes under study, hence there is an ample scope of selection for superior and desired genotypes to plant breeder for further crop improvement. The values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for all the traits studied. The high values of genotypic coefficient of variation and phenotypic coefficient of variation were recorded for seed yield plant^{-1}, leaf area plant^{-1} and number of effective branches plant^{-1} indicated the presence of wide genetic variation for these characters. High heritability was recorded for 1000 seed weight, followed by leaf area plant^{-1}, oil content, days to flowering, capsule length plant^{-1}, number of capsules plant^{-1}, days to maturity, seed yield plant^{-1} and number of effective branches plant^{-1} indicated that heritability may be due to higher contribution of genotypic component in these traits. High heritability combined with high genetic advance as percentage of mean was recorded for leaf area plant^{-1}, seed yield plant^{-1}, number of effective branches plant^{-1}, number of capsules plant^{-1}, 1000 seed weight and days to flowering indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for genetic improvement of seed yield in sesame.

Keywords: Genetic variability, heritability, genetic advance and sesame

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. Introduction

Sesame (*Sesamum indicum* L.) is a diploid with 2n=2X=26 chromosomes; a self-pollinated crop which belongs to the family of pedaliaceae. Though its origin is believed to be in Indian subcontinent (Bedigian and Harlan, 1986); it has high genetic diversity in east Africa, Ethiopia. The presence of weedy or wild forms of sesame (*S. alatum*; 2n=26 and *S. latifolium*, 2n=32) in Ethiopia shows that it is indigenous to this country. It is one of the oldest and most important traditional oilseed crops of the world. Sesame

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is called as the "Queen of Oilseeds" because of its excellent qualities of the seed, oil and meal. Generally, the oil content in sesame ranges from 34 to 63% (Were et al., 2006). Late maturing cultivars are reported to have higher oil content than early cultivars (Yermanos et al., 1972) and the indeterminate cultivars accumulate more oil than determinate ones (Uzun et al., 2002). Sesame seeds are rich in oil and protein and two unique substances namely sesamin and sesamolin known to have a cholesterol lowering effect in human and to prevent high blood pressure (Anilakumar et al., 2010). Also, it is rich in micronutrients such as minerals, liganans, tocopherol and phytosterol (Hassan et al., 2018). Sesame is an important source of high quality oil and protein (Elleuch et al., 2007). Brown seeded genotypes records higher polyphenol content (Gadade et al., 2017). Sesame seed cake is a by-product of traditional oil processing (Plaitho et al., 2017). Sesame seed oil was found to be rich in tocopherols (Gharby et al., 2017). The substitution of sesame oil as the sole edible oil has an additive effect in further lowering BP and plasma glucose in hypertensive diabetics (Sankar et al., 2001).

The lack of high yielding varieties, poor stand establishment and poor fertilizer response are the major constraints in the cultivation of sesame (Alex et al., 2017). It offers several advantages by virtue of its faster growth, short duration and drought tolerant capacity cultivated throughout the year in sub-tropical and tropical conditions. Sesame had more preference from farmers because of low input required and high price of produce (De et al., 2013). Thus, there is a need to enhance the productivity of this crop by developing high yielding genotypes, which depends on the availability of variability for seed yield and its component traits in the populations. Therefore, the first step in any crop breeding programme is to assess genetic variability. The phenotypic and genotypic variations of the yield contributing characters are considerably high in sesame (Gangadhara et al., 2012; Sivaprasad et al., 2013 and Teklu et al., 2014), which points out the possibility of developing a variety with high yield. Heritability is the heritable portion of phenotypic variation and it is a good index of transmission of a character from parents to their off springs. Heritability determines the expressivity of genes carried by a genotype. Heritability and genetic advance when calculated together would be more useful in predicting the resultant effect of selection. Keeping in view of this fact, the present experiment was carried out to know the nature and extent of genetic variability, heritability and genetic advance in a set of 45 genotypes of sesame.

2. Materials and Methods

Forty five diverse genotypes of sesame were obtained from Agricultural Research Station, Junagadh Agricultural University, Amreli and Castor-Mustard Research Station, S. D. Agricultural University, Sardarkrushinagar (Table 1). The experiment was sown during July to October months of the year 2018 in a randomized block design with three replications

Table 1: List of 45 sesame genotypes used in study

Sl. No.	Genotypes	Source
1.	GT-1	Agricultural Research Station, JAU, Amreli
2.	GT-2	Agricultural Research Station, JAU, Amreli
3.	GT-3	Agricultural Research Station, JAU, Amreli
4.	GT-4	Agricultural Research Station, JAU, Amreli
5.	GT-10	Agricultural Research Station, JAU, Amreli
6.	TKG-22	Agricultural Research Station, JAU, Amreli
7.	MT-75	Agricultural Research Station, JAU, Amreli
8.	COS-13006	Agricultural Research Station, JAU, Amreli
9.	AT-325	Agricultural Research Station, JAU, Amreli
10.	AT-326	Agricultural Research Station, JAU, Amreli
11.	AT-328	Agricultural Research Station, JAU, Amreli
12.	AT-324	Agricultural Research Station, JAU, Amreli
13.	AT-335	Agricultural Research Station, JAU, Amreli
14.	AT-340	Agricultural Research Station, JAU, Amreli
15.	AT-378	Agricultural Research Station, JAU, Amreli
16.	AT-385	Agricultural Research Station, JAU, Amreli
17.	AT-386	Agricultural Research Station, JAU, Amreli
18.	AT-390	Agricultural Research Station, JAU, Amreli
19.	AT-420	Agricultural Research Station, JAU, Amreli
20.	AT-10-99	Agricultural Research Station, JAU, Amreli
21.	DSM 6	Agricultural Research Station, JAU, Amreli
22.	DS 35	Agricultural Research Station, JAU, Amreli
23.	DS 37	Agricultural Research Station, JAU, Amreli
24.	JLS 613-1-1	Agricultural Research Station, JAU, Amreli
25.	RAMA	Agricultural Research Station, JAU, Amreli
26.	AT-350	Agricultural Research Station, JAU, Amreli
27.	AT-352	Agricultural Research Station, JAU, Amreli
28.	AT-354	Agricultural Research Station, JAU, Amreli
29.	AT-362	Agricultural Research Station, JAU, Amreli
30.	AT-363	Agricultural Research Station, JAU, Amreli
31.	AT-364	Agricultural Research Station, JAU, Amreli
32.	AT-366	Agricultural Research Station, JAU, Amreli
33.	AT-370	Agricultural Research Station, JAU, Amreli
34.	AT-371	Agricultural Research Station, JAU, Amreli
35.	AT-372	Agricultural Research Station, JAU, Amreli
36.	SKT-12-2	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
37.	SKT-1601	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar

Table 1: Continue...

Sr. No.	Genotypes	Source
38.	SKT-1602	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
39.	SKT-1603	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
40.	SKT-1604	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
41.	SKT-1605	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
42.	SKT-1606	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
43.	SKT-1607	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
44.	SKT-1608	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar
45.	SKT-1609	Castor-Mustard Research Station, S.D.A.U., Sardarkrushinagar

at Castor-Mustard Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India. Sardarkrushinagar is situated at semi-arid region of North Gujarat. Geographically, it is situated at 20°.12' N latitude and 72°.12' E longitude with an altitude of 154.52 meters above the mean sea level. Each entry was sown in 3.0 m row length with 45 cm×15 cm spacing. The sowing was carried out by hand drilling. The recommended agronomical practices and plant protection measures were adopted for raising a good crop. The observations were recorded both as visual assessment (days to flowering and days to maturity) and measurement on randomly selected five competitive individual plants (plant height, number of effective branches plant^{-1}, number of capsules plant^{-1}, capsule length plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight, seed yield plant^{-1}, oil content and leaf area plant^{-1}). The replication wise mean values of each entry for the eleven traits were analysed using Randomized Block Design (RBD) as suggested by Sukhatme and Amble (1985). Genotypic and phenotypic variances were computed according to method suggested by Johnson et al. (1955). Genotypic and phenotypic coefficient of variation (GCV and PCV) were estimated based on formulae given by Burton (1952) and heritability and genetic advance as per cent mean were calculated according to Allard (1960).

3. Results and Discussion

The analysis of variance for the experimental design is presented in Table 2. In the present study, analysis of variance showed that mean sum squares due to genotypes were significant for all the traits indicated the presence of sufficient amount of genetic variability among the genotypes for seed yield plant^{-1} and other yield contributing traits. The

Table 2: Analysis of variance showing mean squares for 11 characters in 45 genotypes of sesame

Sr. No.	Source of variation	Mean squares		
		Replications	Genotypes	Error
	d.f.	02	44	88
1.	Days to flowering	1.42	55.96**	2.46
2.	Days to maturity	6.82	42.96**	2.92
3.	Plant height	46.66	534.59**	102.90
4.	No. of effective branches plant^{-1}	0.22	2.18**	0.16
5.	No. of capsules plant^{-1}	23.82	245.61**	16.13
6.	Capsule length plant^{-1}	0.01	0.27**	0.014
7.	No. of seeds capsule^{-1}	42.87	180.01**	43.00
8.	1000 seed weight	0.01	0.70**	0.05
9.	Seed yield plant^{-1}	5.48	43.77**	3.21
10.	Oil content	1.44	34.43**	0.51
11.	Leaf area plant^{-1}	125558.10	6637293.36**	133343.71

wide range of variation provides ample scope of selection for superior and desired genotypes to plant breeder for further crop improvement. These findings are in accordance with the findings of Parameshwarappa et al. (2009) and Jadhav and Mohrir (2012), who also observed significant variability in sesame germplasm. Hence, it can be noted that systematic crossing among selected genotypes in crops like sesame creates variability in subsequent generation.

The genotypic co-efficient of variance (GCV), phenotypic co-efficient of variance (PCV), heritability in broad sense and genetic advance as per cent of mean for 11 characters are presented in Table 3. The perusal of data revealed that phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. Genotypic coefficient of variation helps to measure the range of genetic variability present in the particular character. The high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for leaf area

Table 3: Range of variation, mean, genotypic and phenotypic coefficients of variation, heritability (Broad Sense) and genetic advance expressed as % of mean for 11 characters in 45 genotypes of sesame

Characters	Range	Mean	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (Broad Sense) (%)	Genetic advance as % of mean
Days to flowering	31.33-49.66	37.81	11.16	11.91	87.84	21.56
Days to maturity	85.33-103.66	91.62	3.98	4.40	82.01	7.43
Plant height	102.33-157.33	124.68	9.62	12.59	58.31	15.13
No. of effective branches plant^{-1}	1.63-5.90	3.24	25.25	28.10	80.73	46.74
No. of capsules plant^{-1}	31.50-67.10	48.76	17.93	19.73	82.58	33.57
Capsule length plant^{-1}	2.50-4.36	2.93	10.11	10.93	85.47	19.25
No. of seeds capsule^{-1}	51.06-92.79	74.60	9.05	12.62	51.50	13.39
1000 seed weight	3.16-5.33	3.96	12.20	12.34	97.79	24.86
Seed yield plant^{-1}	8.16-22.88	14.47	25.40	28.26	80.77	47.03
Oil content	32.09-48.16	40.69	8.26	8.44	95.67	16.64
Leaf area plant^{-1}	3185.47-8479.47	5470.33	29.70	29.82	96.21	60.92

plant^{-1} followed by seed yield plant^{-1} and number of effective branches plant^{-1}. Similar results were also obtained by Teklu et al. (2014) and Hika et al. (2015) for seed yield plant^{-1} and Rani (2014) for number of effective branches plant^{-1} in sesame as observed in the present study.

The moderate values of genotypic coefficient of variation and phenotypic coefficient of variation were observed for number of capsules plant^{-1}, 1000 seed weight, capsule length plant^{-1} and days to flowering. Similar results were also reported in sesame by Gangadhara et al. (2012) for capsule length plant^{-1} and Ganapathy et al. (2007) for number of capsules plant^{-1}. The low values of GCV and PCV was observed for days to maturity and oil content. These findings are in accordance with the earlier reports by Teklu et al. (2014) for days to maturity and oil content. High values of heritability in broad sense are helpful in identifying the appropriate character for selection and in enabling the breeder to select superior genotypes on the basis of phenotypic expression of quantitative traits (Johnson et al., 1955). In the present study, high estimates of heritability (broad sense) was observed for 1000 seed weight followed by leaf area plant^{-1}, oil content, days to flowering, capsule length plant^{-1}, number of capsules plant^{-1}, days to maturity, seed yield plant^{-1}, number of effective branches plant^{-1}. Remaining traits such as plant height and number of seeds capsule^{-1} exhibited moderate estimates of heritability. High heritability estimates indicated that the characters were least influenced by the environmental effects and high capacity of the characters for transmission to subsequent generation. This also suggested that the phenotypes were the true representative of their genotypes for these traits and selection based on phenotypic value could be reliable.

The genetic advance expressed as percentage of mean was found maximum for leaf area plant^{-1}, seed yield plant^{-1}, number of effective branches plant^{-1}, number of capsules plant^{-1}, 1000 seed weight and days to flowering. Similar results have also been reported by Parameshwarappa et al. (2009) and Toprope et al. (2009) for number of effective branches plant^{-1}, number of capsules plant^{-1}and seed yield plant^{-1}. Moderate values of genetic advance expressed as percentage of mean were recorded for capsule length plant^{-1}, oil content, plant height and number of seeds capsule^{-1}, while the value was low for days to maturity. Moderate estimates of genetic advance expressed as percentage of mean in sesame has been reported by Teklu et al. (2014) for number of seeds capsule^{-1}.

Heritability and genetic advance when considered together would be more reliable and useful in predicting the resultant effects of selection (Johnson et al., 1955). Rapid progress in selection can be achieved when high heritability is accompanied with high genetic advance, which forms the most reliable index of selection (Burton, 1952). High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for leaf area plant^{-1}, seed yield plant^{-1}, number of capsules plant^{-1}, number of effective branches plant^{-1}, days to flowering and 1000 seed weight which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on these characters for their rationale improvement. These results were in conformity with those of Parameshwarappa et al. (2009) and Toprope et al. (2009) for number of capsules plant^{-1} and seed yield plant^{-1}; Alake et al. (2010) for 1000 seed weight; Bindu et al. (2014) for number of effective branches plant^{-1} and Parameshwarappa et al. (2009) for number of seeds capsule^{-1}. High heritability accompanied with moderate genetic advance

was found for capsule length plant^{-1} and oil content which indicate involvement of both additive and non-additive gene action. High heritability with low genetic advance was noted for days to maturity, while moderate heritability along with moderate genetic advance was observed for plant height and number of seeds capsule^{-1}. Moderate heritability along with moderate genetic advance was reported by Ahadu (2012) for plant height and Teklu et al. (2014) for number of seeds capsule^{-1} as observed in the present investigation.

4. Conclusion

Seed yield plant^{-1}, number of effective branches plant^{-1}, number of capsules plant^{-1} and 1000 seed weight were governed by dominance genetic variance with the predominance of additive type of gene action. Pedigree breeding method with hybridization and selection at later generations could be followed for genetic improvement of these traits.

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