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Per se performance, genetic variability, heritability and genetic advance in sesame (*Sesamum indicum* L.) genotypes

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Abstract
Sesame (*Sesamum indicum* L.) is one of the oldest oilseed crops and is widely cultivated in India and Worldwide. The present investigation was carried out to evaluate the sesame genotypes using 11 traits to provide the indication of the degree of variability in yield and with yield attributing traits. Based on the variability parameters such as ANOVA (Analysis of variance), phenotypic and genotypic coefficient of variations (PCV, GCV) and analysis of variance indicated the existence of significant genotypic differences for yield and yield contributing components for all characters, the genotypic coefficients for all characters under question were lesser than the phenotypic coefficient of variation indicating the effect of the environment. The high GCV and PCV values were observed for traits number of capsules per plant and seed yield per plant. High heritability with high genetic advance as % mean was observed for number of capsules per plant, number of seeds per capsule, 1000-seed weight, and seed yield per plant indicating the influence of additive gene action, as such simple selection would likely to be effective for improvement of these traits.

Keywords: Sesame, ANOVA, GCV, PCV, Heritability

Introduction
Sesame, an annual herb belongs to *Pedaliaceae* family (Sugano & Akimoto, 1993) [30], and it is the largest genus, pollen grain morphology of this family was 5–13 colpate and oblate-subprolate (van Haaster, 1990) [32]. The *Sesamum indicum* being widely adopted as oil crop and said to be originated from Africa from its progenitor Sesamum latifolium, and it is anciently known crop for the mankind, recent archeological findings suggests that Sesame cultivation derived from South Asian native populations, its cultivation began in times of Harappan civiliazation (2000 B.C.) and spread west towards the Mesopotamia (Fuller, 2003) [16]. Archeological findings strongly suggests that from early dates Indus valley civilization been familiar with the Sesamum cultivation (Alegbejo *et al*., 2003; Purseglove, 1969) [3, 26] and been a major source of edible oil in Indus valley Civilization and from here, in later dates was likely transferred to Mesopotamian civilizations around 2500 B.C. (Tunde-Akintunde *et al*. 2012) [31].

Possessing the highest oil content among all oilseeds, it is one of most common ingredient in world cuisines (Oplinger *et al*., 1990; Hansen, 2011) [28, 19]. They were used in sweets such as sesame bars and halva (dessert), widely used in bakery products or milled to get high-grade edible oil (Bedigian, 2004; Chen *et al*., 2005) [7, 12]. Sesame oil has significant resistance against oxidation due to the presence of antioxidants including lignins (sesamin and sesamolin) and tocopherols (Elleuch *et al*., 2007; Lee *et al*., 2008) [14, 22]. Sesamum oil is a rich source of UFAs (Elleuch *et al.*, 2007) [14]; Seeds were chemically composed of 44–57% oil, 18–25% protein, 13–14% carbohydrates (Borchani *et al*., 2010) [11]. Sesame oil is famous for its stability as a result of its resistance to oxidative rancidity after long exposure to air (Global Agri Systems, 2010) [18]. Generally, the oil contains 35% monounsaturated fatty acids and 44% polyunsaturated fatty acids (Hansen, 2011) [19]. Recent research into sesame showed that it contains immunoglobulin E (IgE)–mediated food allergens when they used in baked and fast food products (Agne *et al*., 2003; Dalal *et al*., 2002; Pastorello *et al*., 2001) [2, 13, 25]. Though it was cosmopolitan crop a very little research was undertaken in this crop by any crop research institute (Bedigian and Harlan, 1986; Bhat *et al*., 1999) [6, 10], left this crop as an orphan crop in research scenario, reminds the need and scope for further research in sesame.

Materials and Methods

During the *kharif* of 2016, the current study's field experiment was conducted at the Oil Seeds Research Station in Latur (18°24'53.2"N, 76°36'50.2"E). During July of 2016, 65 accessions (Table 1) were grown in a randomized block design (RBD) with two replications. The 65 sesame genotypes were sowed in a Randomized Block Design with two replications on July 1, 2016. Each genotype in each replication was seeded by dibbling the seeds in a single row plot of 9.0 m length, with 45 cm row spacing and 10 cm hill spacing. After 10 days of seeding, seedlings were thinned, with one seedling per hill remaining. In terms of irrigation, weeding, and fertilizing, the prescribed cultural practices were followed. As and when necessary, plant protection measures were employed. When the genotypes had reached physiological maturity, they were harvested.

Statistical analysis

For statistical analysis, the mean values were used. The software SPSS version 17.0 and AGRES were used to analyze per se performance, genetic variability, heritability, and genetic progress.

Table 1: Details of sixty-five genotypes of sesame.

S. No	Genotype	Source	S. No	Genotype	Source
1	SI-413-A	P.C. Unit, Jabalpur.	34	IC-42200	P.C. Unit, Jabalpur.
2	SI-205-61	P.C. Unit, Jabalpur.	35	IC-23233	P.C. Unit, Jabalpur.
3	SI-199-2-84	P.C. Unit, Jabalpur.	36	NIC-16220	P.C. Unit, Jabalpur.
4	SI-1147	P.C. Unit, Jabalpur.	37	EC-231-2-84	P.C. Unit, Jabalpur.
5	IS-299A	P.C. Unit, Jabalpur.	38	EC-370840	P.C. Unit, Jabalpur.
6	ES-44	P.C. Unit, Jabalpur.	39	EC-209	P.C. Unit, Jabalpur.
7	ES-146-1-84	P.C. Unit, Jabalpur.	40	EC-89111	P.C. Unit, Jabalpur.
8	ES-113-18-84	P.C. Unit, Jabalpur.	41	EC-377015	P.C. Unit, Jabalpur.
9	EC-370936	P.C. Unit, Jabalpur.	42	SI-983	P.C. Unit, Jabalpur.
10	IC-204001	P.C. Unit, Jabalpur.	43	OSC-3209	P.C. Unit, Jabalpur.
11	GM-NIC- 7909	P.C. Unit, Jabalpur.	44	DS-21	P.C. Unit, Jabalpur.
12	GM-NIC- 7913	P.C. Unit, Jabalpur.	45	EC-101396	P.C. Unit, Jabalpur.
13	GM-NIC- 8202	P.C. Unit, Jabalpur.	46	SI-5354	P.C. Unit, Jabalpur.
14	GM-NIC- 8631	P.C. Unit, Jabalpur.	47	IS-424	ORS, Latur.
15	GM-NIC- 8934	P.C. Unit, Jabalpur.	48	SI-3168	ORS, Latur.
16	GM-NIC- 16146	P.C. Unit, Jabalpur.	49	KMR-69	ORS, Latur.
17	GM-NIC- 16226	P.C. Unit, Jabalpur.	50	KMR-114	ORS, Latur.
18	GM-NIC- 16330	P.C. Unit, Jabalpur.	51	GT-3	ORS, Latur.
19	GM-NIC- 16332	P.C. Unit, Jabalpur.	52	SI-1003	ORS, Latur.
20	GM-NIC- 8254	P.C. Unit, Jabalpur.	53	YLM-17	ORS, Latur.
21	NIC-7855	P.C. Unit, Jabalpur.	54	EC-303423	ORS, Latur.
22	NIC-7903	P.C. Unit, Jabalpur.	55	PKDS-8	ORS, Latur.
23	NIC-10621	P.C. Unit, Jabalpur.	56	JLT-07	ORS, Latur.
24	NIC-16114	P.C. Unit, Jabalpur.	57	TKG-22	ORS, Latur.
25	NIC-16324	P.C. Unit, Jabalpur.	58	EC-S-0523A	ORS, Latur.
26	NIC-16104	P.C. Unit, Jabalpur.	59	EC-S-0223	ORS, Latur.
27	NIC-8263	P.C. Unit, Jabalpur.	60	TKG-306	ORS, Latur.
28	EC-310439	P.C. Unit, Jabalpur.	61	IS-207	ORS, Latur.
29	ES-42-2-84	P.C. Unit, Jabalpur.	62	JLT-408	ORS, Latur.
30	K-5170	P.C. Unit, Jabalpur.	63	MADURI	ORS, Latur.
31	UKNM-1067	P.C. Unit, Jabalpur.	64	G-1	ORS, Latur.
32	UKNM-2386	P.C. Unit, Jabalpur.	65	SWETA	Local selection from Telangana
33	IC-41962	P.C. Unit, Jabalpur.			

Table 2: Analysis of variance for eleven characters in 65 genotypes of sesame

S. No.	Character	Mean sum of squares		
		Replications (df=1)	Treatments (df=64)	Error (df=64)
1	Days to 50% flowering	0.0076	26.5900**	1.9100
2	Days to maturity	3.3920	51.4200**	1.3100
3	Capsule length (cm)	0.0180	0.0690**	0.0027
4	Capsule width (cm)	0.0015	0.0056**	0.0009
5	Plant height (cm)	13.3300	242.2400**	20.6100
6	No. of branches plant^{-1}	0.1350	0.9740**	0.0460
7	No. of capsules plant^{-1}	29.380	330.9700**	20.8600
8	No. of seeds capsule^{-1}	86.7500**	210.7500**	11.6100
9	Seed yield plant^{-1} (g)	0.6030	27.2600**	0.9100
10	1000-seed weight (g)	0.0028	0.2150**	0.0062
11	Oil content (%)	9.8100	15.0900**	0.5720

Table 3: Mean, range, variability, heritability (broad sense), genetic advance and genetic advance as % mean for eleven characters in 65 sesame genotypes

Character	Mean	Range		Coefficient of Variation		Heritability (%) (Broad sense)	Genetic advance at 5%	Genetic advance as % of mean at 5%
		Min	Max	Genotypic	Phenotypic			
Days to 50% flowering	37.2	32	48	9.43	10.14	0.86	6.73	18.08
Days to maturity	82.7	73	94	6.04	6.2	0.95	10.05	12.14
Plant height (cm)	95.8	74	126	11.01	11.9	0.84	19.91	20.83
Number of branches $plant^{-1}$	3.56	1.6	4.9	19.09	20.02	0.90	1.338	37.49
Number of capsules $plant^{-1}$	48.3	25.5	85.25	25.75	27.43	0.88	24.08	27.11
Capsule length (cm)	2.44	2.02	2.76	7.49	7.80	0.92	0.36	14.84
Capsule width (cm)	0.64	0.46	0.78	7.45	8.90	0.70	0.08	12.85
Number of seeds $capsule^{-1}$	71.7	58	101.8	13.9	14.69	0.89	24.08	49.81
1000 seed weight (g)	9.4	2.09	3.78	12.06	12.42	0.94	0.64	24.14
Oil content (%)	42.7	36.3	49.3	6.31	6.55	0.92	5.34	12.51
Seed yield $plant^{-1}$ (g)	2.68	4.04	26	38.60	39.92	0.93	7.22	76.88

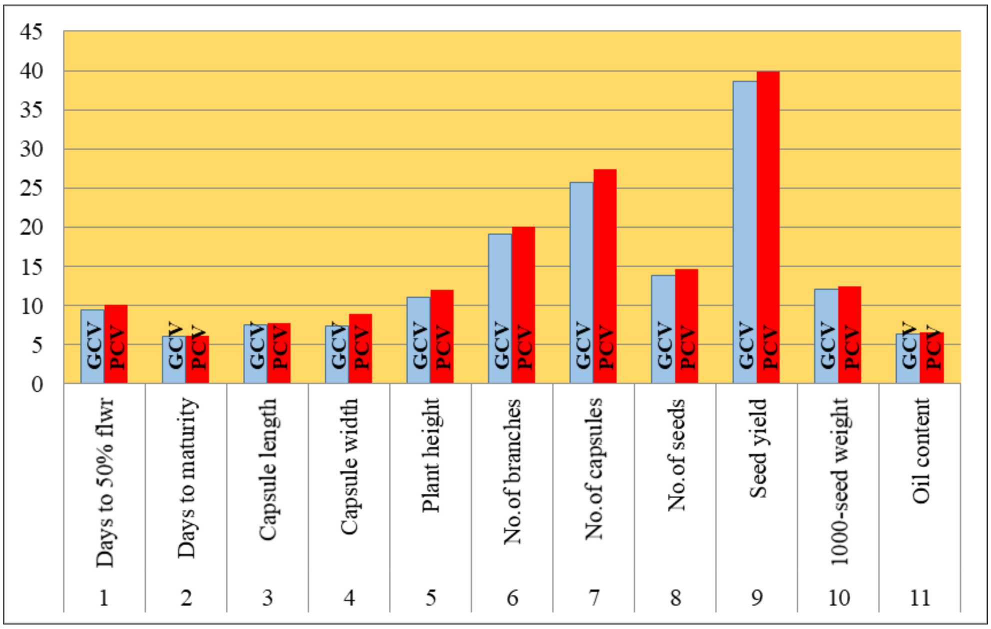

Fig 1: Graphic representation of genotypic and phenotypic coefficients of variation for various characters in 65 sesame genotypes

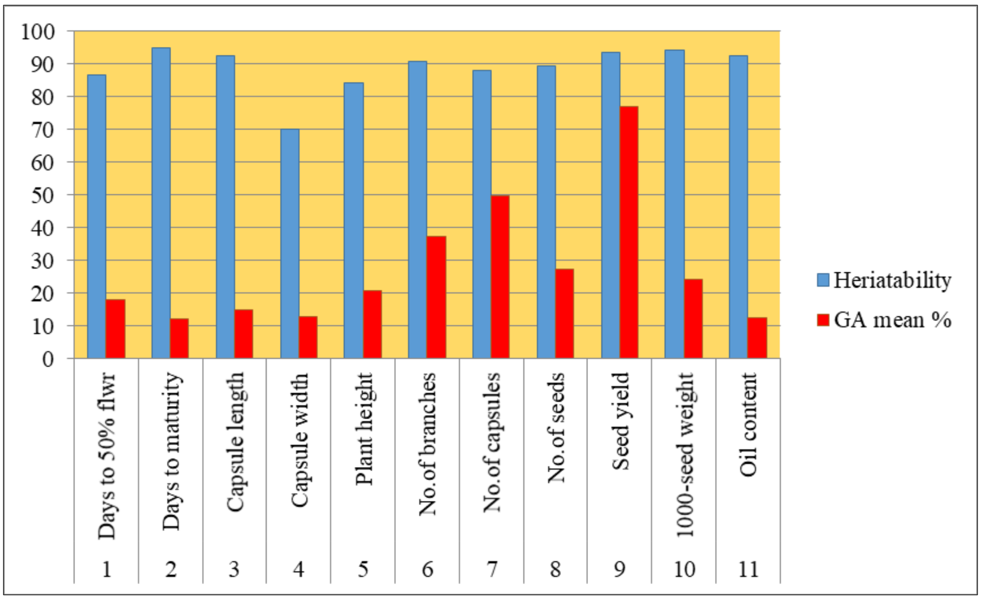

Fig 2: Graphic representation of heritability and Genetic advance as mean % of various characters of 65 sesame genotypes

Results and Discussion

Analysis of variance for 11 yield contributing characters was presented in Table 2 and revealed that the presence of significant differences among the genotypes for all the characters studied, these significant differences could also be attributed to the composition of the population.

Various variability parameters of 65 genotypes for 11 traits were presented in Table 3 and Fig. 1. The Present investigation revealed that PCV ranged from 6.20% to 39.92% to for days to maturity and seed yield per plant respectively. The maximum GCV was observed to be 38.60% for seed yield per plant. Days to maturity, on the other hand exhibited the lowest genotypic coefficient of variation (6.04%). Out of 11 traits, genotypic coefficient of variation was high in seed yield per plant (39.92%), number of capsules per plant (25.75%) for the plant characters with respect to yield attributes.

Low mean Values were obtained for the traits days to 50% flowering (9.43), capsule width (7.45), capsule length (7.49), oil content (6.31) followed by days to maturity (6.04).

The maximum GCV was observed for seed yield per plant, whereas days to maturity recorded for low GCV values, High GCV estimates for one or more of these traits were reported earlier by Vanishree *et al.* (2013) [33], Bharathi *et al*. (2014) [8] and Mohan (2014) [24].

Low mean values were recorded for the traits days to 50% flowering, capsule width, capsule length, oil content followed by days to maturity. Low GCV values for these reported by Gidey *et al*. (2012), Tripathi *et al*. (2013), Shekawat *et al*. (2013a), Bharathi *et al*. (2015) [8], Bamrotiya *et al*. (2016) [5] and Saxena *et al*. (2016). The simple measures of variability like mean and coefficient of variation reveal the extent of variability but not the heritable portion of the total variation. To have the knowledge of heritable portion of variability, it is necessary to estimate the heritability of each character. The broad sense heritability gives an idea about the portion of observed variability attributable to genetic difference. The estimated values for heritability (broad sense) and genetic advance as % of mean for 65 sesame genotypes were tabulated in Table 3 & Fig. 2. All the characters studied in this research invariably showed high heritability (more than 80%) except for capsule width (70%). Days to maturity was observed to be the most heritable trait with the highest heritability (95%) followed by 1000-seed weight (94%). The least heritability was recorded for capsule width (70%) among the 65 genotypes studied.

The heritability (broad sense) was found maximum in all characters under study except for the capsule width and days to maturity found with the highest heritability followed by 1000-seed weight, similar findings were reported by Tripathi *et al.* (2013), Vanishree *et al.* (2013) [33], Bharathi *et al.* (2014) [8], Mohan (2014) [24] and high heritability for trait oil content and capsule width were reported by Saxena *et al.* (2016) and Bamrotiya *et al.* (2016) [5] respectively.

The genetic advance expressed as percent of the mean is a useful indicator of the progress that may be foreseen as a result of selecting the relevant population. The traits with high heritability and high genetic advance indicate the control of additive gene action and selection may be effective for those characters. The traits Seed yield showed a substantial high heritability and high genetic advance as % mean (76.88) followed by number of seeds per capsule (49.81) and number of branches (37.49) and moderate genetic advance as % mean were recorded for the traits *viz.*, 1000-seed weight (24.14), plant height (20.83) and days to 50% flowering (18.08). Whereas low genetic advance as % mean recorded for the traits days to maturity (12.14), capsule length (14.84), capsule width (12.85) and oil content (12.51).

The genetic advance as % of mean found high found high in traits seed yield and similar results were reported Velu and Shunmugavalli (2005) [34] and Saxena *et al.* (2016) followed by number of branches and number of seeds per capsule were in conformity with reports of Vanishree *et al.* (2013) [33] and Mahmoud *et al.* (2015) [23], whereas moderate genetic advance as percent mean were recorded for the traits *viz.*, 1000-seed weight, plant height and days to 50% flowering and similar track of results were reported by Vanishree *et al.* (2013) [33] for plant height and 1000-seed weight and by Abate and Mekbib (2015) [1] for days to 50% flowering. Low genetic advance as percent mean was recorded in traits days to maturity, capsule length, capsule width and oil content these results were in harmony with Ismaila and Usman (2014) [20] for capsule length, Bamrotiya *et al.* (2016) [5] for capsule width and Saxena *et al.* (2016) for oil content.

Conclusion

In the present study, wide variability was observed for the traits plant height (cm), number of seeds per capsule, number of capsules per plant, oil content (%) and seed yield per plant (g) in terms of mean values and range. When coefficients of variation (PCV and GCV) were considered, high mean was observed in cases of seed yield per plant and number of capsules per plant. Other features with a large range of variability had PCV and GCV values that were modest. The traits *viz.*, days to 50% flowering, days to maturity, capsule length and capsule width recorded narrow range of variability as well as low PCV and GCV values.

All of the traits recorded high heritability values, number of branches per plant, number of seeds per capsule and seed yield per plant and registered high heritability coupled with high genetic advance as % of mean indicating the influence of additive gene action in the direction of desired improvement. High heritability with moderate genetic advance was recorded for 1000-seed weight (g), days to 50% flowering, and plant height suggesting the role of both additive and non-additive gene actions and direct selection for these traits may yield moderate genetic gains.

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