



ASSESSMENT OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN ETHIOPIAN LOW-ALTITUDE SESAME (*SESAMUM INDICUM* L.) GENOTYPES

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ABSTRACT

Forty nine sesame genotypes collected from low-altitude areas of Ethiopia were evaluated at Werer Agricultural Research Centre, during the 2011/12 growing season for genetic variability and character association. Morphological data recorded on 14 quantitative traits were analyzed for analysis of variance, phenotypic and genotypic variability, heritability, genetic advance, correlation and path coefficient analysis. Analysis of variance revealed significant difference among the genotypes for each character except for primary branches, suggesting the existence of considerable genetic variation in the studied germplasm with regard to seed yield and its component traits. There is a high variation in mean performance of genotypes for the studied traits. Am-NG-15 is a high yielding genotype but with lowest oil content, whereas Tigray-13 is a low yielding genotype but with highest oil content. Hence, a crossing program between these genotypes can result in desirable hybrid that can be used for the ongoing sesame improvement program. Moderate heritability with moderate genetic advance was observed for most of the yield related traits, signifying that these attributes are governed by both additive and non-additive genes action. The traits Biomass/plant, harvest index and 1000 seed weight exhibited highly significant positive correlation with seed yield/plant. These characters also had the highest positive direct effect on seed yield/plant. Hence these three traits can be considered as the principal yield components while selecting for yield improvement of lowland sesame genotypes in Ethiopia.

Keywords: Genetic advance; heritability; path coefficient analysis; lowland sesame; yield related traits.

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1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is a very ancient oilseed crop [1] and especially grows well and gives high yields in both tropical and temperate climates [2]. Sesame is cultivated on 7 million ha worldwide; India and China are the world's largest producers followed by the areas found in developing countries Myanmar, Sudan, Ethiopia, Uganda, Nigeria, Tanzania, Pakistan and Paraguay [3]. It is a small farmers' crop in the developing countries [4], and its center of origin is thought to be in Africa, Ethiopia [5].

Sesame is often referred to "the queen of oil seeds" because of its high nutritive quality and quantity of oil ranging from 40 to 63% [6]. This oil is rich in antioxidants and has a significant amount of oleic and linoleic acids. Despite its long history and nutritional value, the crop has low yielding capacity compared to other oilseed crops, mainly due to its low harvest index, susceptibility to diseases, seed shattering and indeterminate growth habit [7].

Seed yield in sesame like other field crops, is a multifacet character and direct selection for this trait may often be misleading. The components that determine the yield are best indices for selection. Therefore, knowledge of relationship between important yield traits and seed yield may help the researcher to identify suitable donors for a potential and successful breeding program [8]. The estimation of character associations could identify the relative importance of independent characters contributing to dependent ones and suggest upon the character(s) that may be useful as indicator for one or more of other characters. In other words, character associations between yield components can be used as the best guide for successful yield improvement by indirect selection. Achievement of such success depends upon sort and accuracy of correlation coefficient estimated as well as plant materials, environmental conditions and their interaction [9]. Thus, the analysis of genetic variation within and among elite breeding materials is of fundamental interest to plant breeders.

In Ethiopia, to date, study on genetic diversity of sesame population is very limited. Hence, the lack of information on variability of the local germplasm has been limiting the use of breeding materials in sesame improvement program of the country. Therefore, the present study was aimed to generate scientific knowledge on the genetic variation and character association of low-altitude sesame genotypes in Ethiopia.

2. MATERIALS AND METHODS

2.1 Description of the study site

The experiment was conducted at Werer Agricultural Research Center (WARC) during the 2011/12 main crop season. WARC is located along the Middle Awash valley between 9° 60' N and 40° 9' E with altitude of 740 m.a.s.l. The mean annual temperature during the study season ranged from 19.5 to 32.5 °C and the mean annual rain fall was 450 mm with Fluvisol and Vertisol soil.

2.2 Genotypes and field layout

The material for the study comprised 49 low-altitude sesame genotypes (Table 1) received from the Ethiopian Biodiversity Institute (EBI). The experiment was laid out in 7 x 7 Simple Lattice Design with two replications where each genotype was planted in a plot consisting of two rows of 2.5 m long at a distance of 40 cm between rows and 10 cm between plants. All agronomical practices were carried out throughout the season as required.

2.3 Data collection

Data were collected from net plot size. Five plants in each plot were selected at random and the data were recorded on the following parameters: days to emergence (DE), days to 50% flowering (DF), days to 75% maturity (DM), number of primary branch/plant (PBPL), number of capsules/plant (CPPL), number of seeds/capsule (SDPC), capsule length (CL), plant height (PH), biomass/plant (BMPL), harvest index/plant (HIPL), 1000 seed weight (TSW), seed yield/plant (SYPL), seed yield/plot (SYP) and oil content (OC). Oil content (%)

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was determined for each genotype from five gram of seeds using nuclear magnetic resonance spectroscope (NMRS).

Table 1. List of 49 sesame genotypes with areas (regions) of collection used in the study

No.	Genotypes	Region	Altitude	No.	Genotypes	Region	Altitude
1	Oromia-28	E. Wellega	1200	25	Tigray-14	Mirabawi	820
2	Gambella-1	Gambella	500	26	Tigray-15	"	710
3	Gambella-2	"	500	27	Am-NG-18	Amhara N. G	1110
4	SNNP-5	N.Omo	770	28	Tigray-16	Mirabawi	710
5	SNNP-6	Bench Maji	850	29	Tigray-17	"	710
6	Tigray-6	Mirabawi	600	30	Tigray-18	"	820
7	Tigray-7	"	650	31	Tigray-19	"	820
8	Tigray-8	"	650	32	Tigray-20	"	900
9	Oromia-29	Jimma	1200	33	Oromia-32	Jimma	1110
10	Oromia-30	"	1210	34	Oromia-33	"	1100
11	Tigray-9	Mirabawi	1090	35	Am-NG-19	Amhara N. G	600
12	Tigray-10	"	1140	36	Am-NG-20	"	600
13	Tigray-11	"	1130	37	Am-NG-21	"	650
14	Tigray-12	"	1200	38	Am-NG-22	"	650
15	Am-NG-13	Amhara N. G	900	39	Am-NG-23	"	700
16	Am-NG-14	"	900	40	Am-NG-24	"	650
17	Am-NG-15	"	980	41	Am-NG-25	"	780
18	Am-NG-16	"	830	42	Am-NG-26	"	760
19	Am-NG-17	"	810	43	Am-NG-27	"	750
20	SNNP-7	N. Omo	1050	44	Klf-74	Check variety	
21	SNNP-8	Gurage	1135	45	Abasena	"	
22	Gambella-3	Gambella	500	46	Serkamo	"	
23	Gambella-4	"	600	47	Adi	"	
24	Tigray-13	Mirabawi	700	48	Mehado-80	"	
				49	S	"	

Key: Amhara N. G = Amhara North Gonder, E. Wellega = East Wellega, N. Omo = North Omo, SNNP = Southern Nation & Nationality People.

2.4 Data analysis

Analysis of variance and correlation were carried out for the data with SAS statistical software (9.2), to test for significant differences among the genotypes according to the standard statistical procedure described by Gomez and Gomez [10].

The phenotypic and genotypic variances and their coefficients of variation for each character were estimated by the formula suggested by Singh and Chaudary [11] as follows:

Genotypic variance (σ^2_g) = $\frac{MSg - MSe}{r}$ and Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$. Where; MSg = mean square genotype

MSe= mean square error, r = number of replications and σ^2_e = error variance.

Genotypic coefficient of variation (GCV) = $(\sigma_g / \bar{x}) \times 100$ and phenotypic coefficient of variation (PCV) = $(\sigma_p / \bar{x}) \times 100$. Where; σ_g and σ_p = genotypic and phenotypic standard deviations, and \bar{x} = grand mean.

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Heritability in broad sense (H) and genetic advance (GA) for all traits were computed using the formula adopted by Allard [12] as follows:

$$H = (\sigma^2_g / \sigma^2_p) \times 100 \text{ and } GA = (k * \sigma_p * H)$$

$$\text{Genetic advance as \% of the mean (GA \%)} = (GA / \bar{x}) \times 100.$$

Where; k is selection differential at 5% selection intensity ($k=2.06$), and \bar{x} is grand mean.

Phenotypic and genotypic correlations between quantitative traits were estimated using the method described by Miller *et al.* [13]. And direct and indirect effect of various traits on seed yield was estimated by path coefficient analysis using the formula suggested by Dewey and Lu [14]. Seed yield per plant was used as dependent character and the remaining characters were used as independent variables as required.

3. RESULTS AND DISCUSSION

3.1 Analysis of variance and mean performance of genotypes

The analysis of variance revealed significant difference among the genotypes for each character except for number of primary branches/plant, indicating the presence of considerable variability among the genotypes for the characters studied (Table 2). Previous studies from Ethiopia [15 and 16] also reported the existence of enormous amount of genetic variability in the evaluation of 64 and 36 sesame accessions respectively, for several characters. Mean performance of 49 sesame genotypes (data not shown) revealed high variation for the studied morphological traits.

Generally, a high variation in seed yield/plant, days to flowering, plant height, number of capsules/plant, harvest index and oil content was found among the studied genotypes. The maximum mean performance for most yield components such as harvest index (84.55%), biomass/plant (8.7g), seed yield/plant (7.3g) and yield/plot (367g) was recorded for Am-NG-15. Although, this genotype was found to be superior even as compared to the check varieties, it had the lowest oil content (38.15) of all genotypes. In the contrary, genotype Tigray-13 generally showed the lowest means for seed yield (3.15g) and its component traits viz., number of seed/capsule (30.05), biomass/plant (4.5g), harvest index (69.75%) and 1000 seed weight (1.25g); though it had highest mean oil content (53.7%). One of the important goals in sesame breeding is to improve varieties with high oil content and high seed yield. While the low yielding type Tigray-13 was the highest in oil content, the best high-yielding type Am-NG-15 was the lowest in oil content. Hence, it is important to combine high-yield potential with high oil content to create novel recombinant [17].

Generally, 50% of the genotypes (24 of 49) expressed greater mean seed yield and mean number of capsules over the grand mean. Hence, there is an opportunity to find genotypes among the tested material that perform better than the existing varieties in moisture stressed areas and/or to use them as parents for hybridization program.

Table 2. Mean squares from analysis of variance for 14 morphological traits of 49 sesame genotypes

Trait	Rep (1)	Block (6)	Gen (42)	Error (42)	CV (%)	SE
Days to Emergence	0.37	0.30	0.46**	0.21	9.30	0.46
Days to Flowering	0.26	0.28	17.17**	0.37	0.88	0.61
Days to Maturity	0.01	55.44	195.87*	126.00	10.30	11.22
No. of Pr. Branches	13.30	1.39	4.09	3.61	34.64	2.02
No. of Capsules/plant	1116.62	347.30	376.42**	192.20	14.16	13.86
No. of Seeds/capsule	32.92	29.85	16.42*	12.49	11.70	4.05
Capsule Length (cm)	0.05	0.03	0.21**	0.10	11.34	0.31
Plant Height (cm)	9392.33	369.95	730.46*	498.57	17.86	22.33
Biomass/plant	0.85	0.60	1.52*	0.78	12.49	0.88

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Harvest Index (%)	0.05	7.76	13.01**	5.33	2.86	2.31
1000 Seed weight (g)	0.02	0.06	0.11*	0.07	15.71	0.27
Seed Yield/plant (g)	0.61	0.61	1.49*	0.76	15.16	0.87
Seed Yield/plot (g)	1466.50	1571.97	3695.97*	1847.17	14.96	42.98
Oil Content (%)	0.36	1.17	32.34**	3.31	3.88	1.82

**, * significant at 0.01 and 0.05 probability level; figures in parenthesis refer to degrees of freedom. CV= coefficient of variation, Gen= genotypes, SE= standard error.

3.2 Phenotypic and genotypic variability

Variability estimates revealed considerable variations for all the studied traits (Table 3). The phenotypic coefficient of variance (PCV) was greater than the genotypic coefficient of variance (GCV) for all the traits. According to Deshmukh *et al.* [18] phenotypic and genotypic coefficients of variability values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Based on this delineation, moderate PCV and low GCV values were observed for most of the yield related traits, indicating the low prevalence of additive gene action and the higher influence of environment in the expression of most of the traits.

Maximum value of PCV but low GCV was noted in number of primary branches/plant, while moderate PCV and GCV values were estimated for seed yield/plant and seed yield/plot. However most of the traits *viz.*, days to emergence, days to maturity, capsules/plant, seeds/capsule, capsules length, plant height, and biomass/plant exhibited moderate PCV with low GCV values indicating that most of the traits are sensitive to changing environments. Similar result was reported by Thangavel *et al.* [19], where most of the traits *i.e.* number of branches/plant, number of capsules/plant, plant height, number of seeds per capsule and seed yield/plant showed medium PCV and low GCV values. Ahadu [15] also reported low PCV and GCV value for days to 50% flowering, days to maturity, harvest index, thousand seed weight and oil content. Gidey *et al.* [16] and Sumathi and Murlidharan [20] also reported more or less similar results in sesame.

Lower GCV suggested that the traits are rendered to high environmental influences and hence lower opportunity exists for improvement of these traits in the tested genotypes. However, the high or low GCV recorded alone is not sufficient for the determination of the extent of genetic advance to be expected by selection. Burton [21] suggested that GCV together with heritability estimates would give the best picture of the extent of the advance to be expected by selection.

3.3 Heritability and genetic advance

Low to high estimates of heritability, in the range between (6.02 – 95.77%) were observed for the studied traits (Table 3). The highest heritability was recorded for days to flowering followed by oil content (81.44%), whereas the lowest heritability was scored for number of primary branches/plant (6.02). Estimates of genetic advance as percent of mean at 5% selection intensity ranged from 3.07% for number of seeds/capsule to 15.13% for oil content. Generally, low to medium genetic advance as percent of the mean were observed for all traits considered. Johnson *et al.* [22] generally classified heritability estimates as low (0-30%), moderate (30-60%) and high (60% and above) and the genetic advance (as % mean) as low (0-10%), moderate (10-20%) and high (20% and above). Based on this classification, high estimates of heritability coupled with moderate genetic advance for days to flowering and oil content; moderate heritability along with moderate genetic advance for capsules per plant, capsules length, biomass/plant, seed yield/plant and seed yield/plot were observed, signifying that these attributes were governed by both additive and non-additive type of genes and simple selection in favor of these traits may not be beneficial to improve seed yield. Seed yield is a complex trait, polygenic and highly influenced by environmental conditions, hence there is a need for methods other than simple selection to improve yield in sesame. This result was in accordance with Krishnaiah

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et al. [23]. Bhombe *et al.* [24], Bishwas *et al.* [25] and Khan *et al.* [26] also reported more or less similar results. On the other hand, moderate to low heritability coupled with low genetic advance for number of branches/plant, number of seeds/capsule, plant height, 1000 seed weight and harvest index exhibited render them unsuitable for improvement through conventional selection as non-additive type of genes operating in controlling these traits. These results are in the contrary with some of the previous findings [27, 28, 29] who observed high heritability and high genetic advance for number of branches, number of capsules, plant height, 1000 seed weight and seed yield in sesame.

High heritability indicates that a character is controlled by those genes which are less influenced by environment and vice versa. Johnson *et al.* [22], Panse [30] and Sarwar *et al.* [31] discussing the significance of additive type of gene action, pointed out that high values of genetic advance accompanied with high degree of heritability estimates offered a more effective criterion of direct selection due to its base on additive types of genes. They further stated that high heritability values combined with low genetic advance may be mainly due to non-additive type of genes effect (dominant or epistasis).

Table 3. Genotypic and phenotypic coefficient of variances, heritability and genetic advance in 49 sesame genotypes for 14 morphological traits.

Trait	Mean	σ^2_g	σ^2_p	GCV	PCV	H (%)	GA (%)
Days to Emergence	4.94	0.12	0.33	7.09	11.69	36.73	8.85
Days to Flowering	68.93	8.40	8.77	4.20	4.30	95.77	8.48
Days to Maturity	108.97	34.94	160.94	5.42	11.64	21.71	5.21
No. of pr. Branches	5.84	0.24	3.85	8.37	33.61	6.20	4.29
No. of Capsules/plant	97.89	92.11	284.31	9.80	17.22	32.40	11.50
No. of Seeds/capsule	34.64	1.96	14.46	4.05	10.98	13.59	3.07
Capsule length (cm)	2.76	0.06	0.15	8.66	14.27	36.85	10.83
Plant Height (cm)	125.02	115.94	614.52	8.61	19.83	18.87	7.71
Biomass/plant	7.08	0.37	1.15	8.59	15.16	32.08	10.02
Harvest index (%)	80.75	3.84	9.17	2.43	3.75	41.87	3.24
1000 Seed weight (g)	1.73	0.02	0.09	7.91	17.59	20.20	7.32
Seed yield/plant (g)	5.75	0.36	1.12	10.50	18.44	32.41	12.31
Seed yield/plot (g)	287.34	924.40	2771.57	10.58	18.32	33.35	12.59
Oil content (%)	46.82	14.51	17.82	8.14	9.02	81.44	15.13

σ^2_g = genotypic variance, σ^2_p = phenotypic variance, GA (%) = genetic advance as % of mean at 5% selection intensity, GCV & PCV= genotypic and phenotypic coefficient of variances, respectively.

3.4 Correlation and path coefficient analysis

The results of correlation coefficient (Table 4) revealed that biomass/plant, harvest index and 1000 seed weight exhibited highly significant ($P<0.001$) and very high positive association with seed yield/plant and seed yield/plot at both genotypic and phenotypic levels, which indicates that these characters are reliable yield components. Mishra *et al.* [31] and Pawar *et al.* [32] also found similar observations. Number of capsules/plant showed highly significant ($P<0.001$) and positive genotypic association with plant height, biomass/plant, harvest index, seed yield/plant, and seed yield/plot. Hence, seed yield can be increased to a substantial level through direct selection of plants bearing more number of capsules. Positive significant correlation of number

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of capsules/plant with seed yield/plant has been reported [9, 33, 34 and 35]. Chaudhary *et al.* [36] noted that total capsule per plant is predicted to be the most important selection criterion for breeding in sesame. 1000 seed weight showed highly significant ($P<0.001$) and moderately positive phenotypic association with seed yield/plant, biomass/plant, and harvest index. Thus, indirect selection in favor of this trait can improve seed yield in sesame. Days to maturity showed significant ($P<0.01$) positive correlation with number of primary branch/plant but it showed significant negative correlation ($P<0.05$) with seed yield, biomass/plant, harvest index and capsule length, indicating that indirect selection in favor of this trait would reduce the seed yield. These results were in accordance with the findings of Johnson *et al.* [22] and Padmavathi [27], in a study of mutant lines of sesame in Pakistan. Seeds/capsule showed significant negative correlation with capsules/plant and plant height. Negative correlations may occur due to competition between two developing structures of a plant for limited resources [37]. Oil content showed insignificant negative genotypic correlation with most of the yield components (Table 3) indicating that selection for high oil content would not bring change to seed yield/plant. This was inconsistent to the results of Thiyagu *et al.* [38], who reported highly significant positive genotypic association of oil content with seed yield, number of capsules and plant height. On the other hand, Onginjo and Ayiecho [39] reported insignificant moderate positive correlation with seed yield and suggested that selection for oil content had no adverse effects on seed yield.

Generally, both phenotypic and genotypic correlation results of the present investigation revealed the presence of highly significant positive correlation between seed yield and its components except with few morphological traits; namely days to emergence, days to flowering, and capsule length, which had insignificant positive correlation with seed yield at phenotypic level. Similar results were observed in previous studies [26, 40, 41, and 42].

Character association between yield components can be used as the best guide for successful yield improvement through indirect selection [43]. However, as the number of independent variables influencing a particular dependent variable increases, correlation may be insufficient to explain the associations in a manner that will enable one to decide on either a direct or an indirect selection strategy [44].

Path coefficient analysis provides a more effective means of separating direct and indirect factors, permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors. The results of both phenotypic and genotypic path analyses are presented in Table 5 and 6, respectively. The highest positive direct effect on seed at both phenotypic and genotypic level was exerted by biomass/plant followed by harvest index and 1000 seed weight. These traits are therefore considered as the principal traits while selecting for seed yield. Number of capsules/plant showed high direct effect to seed yield at genotypic level, but it showed low negative direct effect at phenotypic level showing that direct selection for this trait may not be useful to improve yield in low altitude genotypes. The highest positive indirect effect via biomass/plant at both phenotypic and genotypic level was expressed by harvest index, followed by capsules/plant at phenotypic level and 1000 seed weight at genotypic level. Biomass/plant via harvest index and plant height via biomass/plant also showed high positive indirect effects at phenotypic level. Similar results had been observed by Khan *et al.* [26], Subramanian and Subramanian [42], Abebe [45] in Ethiopian mustard and Anjay *et al.* [46].

Singh and Chaudhry [11] explained that if direct effect value is almost equal to correlation coefficient, the direct selection for that particular trait will be effective. If correlation is positive but direct effect is negative or negligible, the character may be selected indirectly based on high indirect effects.



Table 4. Genotypic correlation above diagonal and phenotypic correlation below diagonal among 14 traits in 49 sesame genotypes

Trait	DE	DF	DM	PBPL	CPPL	SDCP	CL	PH	BMPL	HIPL	TSW	SYPL	SYP	OC
DE		0.33***	-0.04	-0.07	0.06	0.03	-0.05	-0.01	-0.02	-0.01	-0.08	-0.01	-0.01	0.07
DF	0.39**		-0.15*	0.09	-0.08	0.18	0.23*	-0.12	-0.02	-0.01	-0.02	-0.02	-0.01	0.09
DM	0.25	0.15		0.38***	-0.15	-0.13	-0.68***	0.00	-0.25**	-0.24**	-0.07	-0.25**	-0.25**	-0.01
PBPL	-0.04	0.24	0.46**		0.05	-0.14	-0.29***	0.18	-0.04	0.01	-0.02	-0.04	-0.04	0.11
CPPL	0.17	0.05	-0.14	0.18		-0.5***	0.02	0.39***	0.31***	0.25**	-0.40***	0.30***	0.30***	-0.12
SDCP	0.06	0.29*	-0.12	-0.06	-0.45**		0.24**	-0.16	0.23**	0.32***	0.10	0.25**	0.25**	0.05
CL	-0.05	0.26	-0.46**	-0.12**	0.17	0.25		0.03	0.06	0.09	-0.08	0.06	0.06	0.00
PH	0.18	0.04	0.15	0.19	0.53*	-0.06	0.30		0.24**	0.13	-0.07	0.22**	0.22*	0.14
BMPL	0.06	0.00	-0.16*	-0.02	0.44**	0.33	0.07	0.27		0.93***	0.58***	1.00***	1.00***	-0.02
HIPL	0.05	0.00	-0.09*	0.08	0.37*	0.44	0.12	0.14	0.95***		0.56***	0.94***	0.94***	-0.07
TSW	-0.08	0.00	0.09	0.02	-0.35*	0.16	0.06	-0.02	0.58***	0.59***		0.58***	0.58***	0.05
SYPL	0.07	0.01	-0.15*	-0.01	0.43**	0.35	0.08	0.24	1.00***	0.95***	0.59***		1.00***	-0.04
SYP	0.06	0.01	-0.15*	-0.01	0.43**	0.36	0.08	0.23	1.00***	0.95***	0.59***	1.00***		-0.03
OC	0.24	0.12	0.05	0.20	-0.02	0.16	0.07	0.30*	-0.02	-0.06	0.10	-0.04	-0.03	

***, **, * = significant at $P < 0.001$, < 0.01 and < 0.05 respectively. DF= Days to flowering, DM= Days to maturity, PBPL= Number of primary branches/plant, CPPL= Number of capsules/plant, SDPC= Number of seeds/capsule, CL= Capsules length, PH= Plant height, BMPL= Biomass/plant, HIPL= Harvest index/plant, TSW= 1000 seed weight, SYPL= Seed yield/plant and OC= Oil content.

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Table 5. Direct (diagonal) and indirect (off diagonal) effects of quantitative traits on seed yield/plant at phenotypic level in 49 sesame genotypes

Trait	DF	DM	PBPL	CPPL	SDCP	CL	PH	BMPL	HIPL	TSW	OC	R
DF	-0.02	0.01	0.01	0.00	-0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.01
DM	0.00	0.07	0.01	0.01	0.00	-0.04	-0.01	-0.19	0.01	-0.01	0.00	-0.15
PBPL	0.00	0.03	0.03	-0.01	0.00	-0.01	-0.02	-0.02	-0.01	0.00	0.00	-0.01
CPPL	0.00	-0.01	0.01	-0.06	0.01	0.02	-0.04	0.52*	-0.04	0.02	0.00	0.43
SDCP	-0.01	-0.01	0.00	0.03	-0.02	0.02	0.00	0.39*	-0.04	-0.01	0.00	0.35
CL	-0.01	-0.03	0.00	-0.01	-0.01	0.10	-0.02	0.08	-0.01	0.00	0.00	0.08
PH	0.00	0.01	0.01	-0.03	0.00	0.03	-0.08	0.32	-0.01	0.00	0.00	0.24
BMPL	0.00	-0.01	0.00	-0.03	-0.01	0.05	-0.02	1.10*	-0.07	-0.02	0.00	0.99
HIPL	0.00	-0.02	0.00	-0.04	-0.02	0.01	-0.21	0.75*	0.52*	-0.04	0.00	0.95
TSW	0.00	0.01	0.00	0.02	0.00	0.01	0.00	0.27	-0.06	0.35*	0.00	0.59
OC	0.00	0.00	0.01	0.00	0.00	0.01	-0.02	-0.02	0.01	-0.01	0.00	-0.04

Note: * = high direct effect and indirect effects. DF= Days to flowering, DM= Days to maturity, PBPL= Number of primary branches/plant, CPPL= Number of capsules/plant, SDPC= Number of seeds/capsule, CL= Capsules length, PH= Plant height, BMPL= Biomass/plant, HIPL= Harvest index/plant, TSW= 1000 seed weight, SYPL= Seed yield/plant and OC= Oil content. Residual = **0.15**

Table 6. Direct (diagonal) and indirect (off diagonal) effects of quantitative traits on seed yield/plant at genotypic level in 49 sesame genotypes

Trait	DF	DM	PBPL	CPPL	SDCP	CL	PH	BMPL	HIPL	TSW	OC	R
DF	0.02	0.00	0.00	0.03	-0.05	0.00	0.00	-0.02	0.00	0.01	0.00	-0.02
DM	0.00	-0.03	-0.01	0.06	0.04	0.01	0.00	-0.27	-0.08	0.03	0.00	-0.25
PBPL	0.00	-0.01	-0.02	-0.02	0.04	0.01	0.00	-0.04	0.00	0.01	0.00	-0.04
CPPL	0.00	0.00	0.00	0.59*	0.11	0.00	0.00	-0.55	-0.01	0.15	0.00	0.30
SDCP	0.00	0.00	0.00	0.21	-0.28	0.00	0.00	0.25	0.11	-0.04	0.00	0.25
CL	0.00	0.02	0.01	-0.01	-0.07	-0.02	0.00	0.07	0.03	0.03	0.00	0.06
PH	0.00	0.00	0.00	-0.16	0.04	0.00	0.01	0.26*	0.04	0.03	0.00	0.22
BMPL	0.00	0.01	0.00	-0.13	-0.06	0.00	0.00	0.91*	0.48	-0.22	0.00	0.99
HIPL	0.00	0.01	0.00	-0.10	-0.09	0.00	0.00	0.71*	0.63*	-0.21	0.00	0.94
TSW	0.00	0.00	-0.08	0.17	-0.33	0.00	0.00	0.63*	0.19	0.38	0.00	0.58
OC	0.00	0.00	0.00	0.01	-0.01	0.00	0.00	-0.02	-0.02	-0.02	0.03	-0.04

Note: DF= Days to flowering, DM= Days to maturity, PBPL= Number of primary branches/plant, CPPL= Number of capsules/plant, SDPC= Number of seeds/capsule, CL= Capsules length, PH= Plant height, BMPL= Biomass/plant, HIPL= Harvest index/plant, TSW= 1000 seed weight, SYPL= Seed yield/plant and OC= Oil content. Residual = **0.14**

4. CONCLUSION

The study showed that there is high level of genetic variability with regard to seed yield and its component characters in the studied germplasm. It indicates the presence of a huge scope for selection of promising genotypes with different agronomic traits from the present collection pool. A high variation was observed in seed yield/plant, days to flowering, plant height, number of capsules/plant, harvest index and oil

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content among the studied genotypes. A crossing program between the high yielding genotype (AmNG-15) and the high oil content genotype (Tigry-13) can likely result in novel recombinant. The phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all the observed traits, indicating that genotypic expression was superimposed by environmental influences. Most of the traits in low-altitude genotypes showed moderate heritability with minimum genetic advance, which makes the yield improvement programme through important traits difficult. Biomass/plant, harvest index and 1000 seed weight exerted the highest positive direct effect on seed yield. Improving these traits may increase seed yield in sesame.

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