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Genetic Variability and Interrelationships of Some Traits in Six Sesame (*Sesamum indicum* L.) Genotypes under Rainfed Conditions[•]

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ABSTRACT

The objectives of this study was to estimate the genetic variability and association between yield and its components in six sesame genotypes widely grown in North Kordofan under rainfed conditions. The genotypes showed highly significant variation in agronomic performance for all of the studied traits except of plant height. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all studied traits. High PCV and GCV were recorded for biological yield and seed yield. High heritability (in a broad sense) was obtained for 1000 seed weight and the number of seeds per capsule. The highest genetic advanced (GA) was exhibited by biological

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yield and seed yield. High genetic advance as a percentage of the mean (GAM %) was recorded for a thousand seed weight and number of branches per plant. High heritability coupled with genetic advance as a percentage of the means was registered by thousand seed weight, number of branches per plant and harvest index. Number of capsules per plant showed significant negative genotypic and phenotypic correlations with a thousand seed weight indicating selection of one trait will be accompanied by low performance of the other. Highly significant positive genotypic and phenotypic correlations were revealed by the association of plant populations with a thousand seed weight, number of seed per capsule with harvest index, and thousand seeds weight with biological yield. Therefore, selection based on these traits would be effective in future sesame yield under rain fed conditions.

***Keywords**: Association character; Genetic; Heritability; Rain-fed condition; Sesame; Variability.*

1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is a member of Pedaliaceae family. It is one of the oldest oilseed crops cultivated by man. Sesame was grown in wide regions over the world, from tropical and temperate zone of Africa, Asia, Latin America and some parts of the United States (Islam *et al.*, 2016). Traditional sesame landraces and related wild species are considered as an important source of genetic diversity for breeders and farmer’s fundamental role in agriculture production. Traditional and improved cultivars are important in providing information regarding genetic variability and interrelationship of yield components. Sesame production in many countries is affected by many factors such as: climatic factors, pests and diseases, low harvest index and lack of improved cultivars. Therefore, selection based on new cultivars for high yield with wider adaptability will help in increasing the local and global production of sesame and overcome the problems associated with its productivity.

For the improvement of a crop species, a thorough knowledge of genetic variability is important for the identification of potential parents and traits of interest to be used in its improvement programs. Therefore, it is necessary to study the variability with respect to quantitative parameters such as genotypic and phenotypic variance, heritability in board sense and genetic advanced (Singh *et al.*, 2018). Moreover, yield is a complex characters and it is known to be associated with the various component, to understand the relationship between yield and its components. Correlation analysis has great importance to help plant breeders in selecting desirable genotypes (Abate, 2019). Hence, the objective of the study is to estimate genetic variability and association between yield and its components in some sesame genotypes.

2. MATERIALS AND METHODS

Experimental Sites

The field experiment was conducted during the rainy season 2018/2019at Elobied Research Station at two locations representing sandy and gardud soil (Elobied and Jabel Kordofan Demonstration Farms) in North Kordofan State, Sudan (Table1). The area is located in an arid and semiarid zone. With the total rainfall of 347.5 mm in Elobied and 261mm in Jabel Kordofan (Table 2).

Experimental Materials and Design

Four local varieties were used in this study, namely. Hereheri, Gabarouk, Elobied, and Eldaw collection which were widely grown in North Kordofan and two released varieties (Bromo and Um Shegaira) commonly used by farmers.

Randomized Complete Block Design (RCBD) with four replications was used to conduct the experiments. Each genotype was planted in a plot consisted of four rows of five meters' length. Spacing was 50 cm between rows and 30 cm between plants. Cultural package practices of sesame were done as recommended.

Table 1. General Characteristics of the Soil at the Study Locations

Property	Elobied	Jabel Kordofan
Latitude	13° 12′ 32.71″ N	13° 06 ′ 17.06 ″ N
Longitude	30° 14′ 13.35 ″ E	30° 18 ′ 48.04 ″ E
Elevation	576m	580 m
Sand (%)	97.0	94.0
Clay (%)	2.00	3.60
Silt (%)	1.00	2.40
PH (H_2O)	7.11	7.80
N (%)	0.03	0.03
P (ppm)	7.00	30.0
K (ppm)	41.0	49.0
Organic matter (ml/lit)	0.55	0.37
Organic carbon (ml/lit)	0.32	0.64
C.E.C	6.0	14.0

Source: Elobied Agriculture Research Station (Soil & Water Lab), 2018 rainy season.

Table 2. Monthly Rainfall (mm) during 2018 Rainy Season in two Locations of the Experiment.

Month	Elobied farm	Jabel Kordofan
July	145	83
August	120	178
September	82.5	109
October	0.0	17
Total	347.5	387

Data Collection

In each plot, the data was collected from the two middle rows to estimate the following parameters: Plant population per plot (PP), Days to 50%flowering (DF), Plant height (PHT) The number of primary branches per plant (NBP), number of capsules per plant (NCP), Seeds per capsule (NSC), Biomass yield per plot (BY), Seed yield per plot (SY), 1000 seed weight (TSW) and Harvest index (HI).

Data Analysis

The collected data were subjected to the individual and combined analysis of variance as the procedure described by Gomez and Gomez (1984). Genstat 18th statistical analysis system software was used to calculate the analysis of variance (ANOVA). The means were separated using the least significant differences (LSD) at 5% level.

The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and de Vane (1953). Broad sense heritability ($^2h2$) expressed as the percentage of the ratio of the genotypic variance ($\sigma\ ^2g$) to the phenotypic variance ($\sigma\ ^2p$) was estimated on genotype mean basis as described by Allard (1999). Genetic advance (GA) and AG as percentage of mean (GAM) was estimated following the methods illustrated by Johnson *et al*., (1955).

$$\text{Genetic advance (GA)} = \text{K}\times\sigma^2 g/\sigma\text{p}$$

The Genetic advance as a percentage of the mean (GAM) was estimated as follows:

$$\text{GAM} = (\text{GA}/\ x)\ \text{x}\ 100$$

Where

GAM = genetic advance as percent of the mean,

GA = expected genetic advance,

***x* =** grand mean of a character.

Phenotypic and genotypic covariance between all pairs of different traits was determined according to the procedure described by Gomez and Gomez (1984). Phenotypic and genotypic correlations between the characters estimated according to the method described by Miller *et al.* (1958) using statistical software META-R.

$$\text{Genotypic correlation coefficient (rg)} = \frac{\sigma g12}{\sqrt{}(\sigma^2 g1\times\sigma^2 g2)}$$

$$\text{Phenotypic correlation coefficient (rp)} = \frac{\sigma p12}{\sqrt{}(\sigma^2\text{p1}\times\sigma^2\text{p2})}$$

3. RESULTS AND DISCUSSION

Analyses of Variances

The combined analysis of variances for the two environments, Jabel Kordofan and El Obeid, revealed highly significant differences among locations for most of the traits studied, except for plant height, number of branches per plant and number of seeds per capsule (Table 3). Highly significant differences among the genotypes were recorded for the number of branches per plant, number of capsules per plant, seeds yield, number of seeds per capsule, thousand seeds weight and harvest index. Furthermore, significant differences were detected for plant population and biological yield per hectare. On the other hand, plant height showed non-significant differences among sesame genotypes (Table 3).

The analyses of variance revealed a highly significant difference among sesame genotypes for all traits studied except for plant height. This indicates the presence of large variation among the evaluated genotypes for the traits under the study. As reported by many researchers Teklu *et al.* (2017) and Gadisa *et al.* (2015).Non-significant difference among genotypes in plant height, was reported by Naser *et al* (2012), who showed that plant height wasn't influenced by the environment and the effect may be due to variety (genetic effect). In contrast Mohamed (2017), recorded a non-significant difference among ten sesame genotypes for, number of capsules per plant, number of seeds per capsule, thousand seed weight and harvest index.

Genetic Variability

Variance components [phenotypic (σ^2p), genotypic (σ^2g) and environmental variances (σ^2e)], genetic coefficient of variation (GCV), heritability (h2), genetic advance (GA) and genetic advance as percentage of the mean (GA as % of mean) are presented in Table 4. The estimated, phenotypic coefficients of variation (PCV %) were higher than genotypic coefficients of variation (GCV %) for all traits studied at the two locations. The biological yield, seed yield and the number of branches per plant showed high GCV and PCV estimates (Table 4).

Table 3. Mean squares from the analyses of variance for the different characters in six Sesame genotypes evaluated at combined locations in 2018 season.

Character	Source of variation			
	Replication (D. F=3)	Genotype (D. F=5)	Error (D. F=5)	CV%
Days to 50% flowering	4.01961	0.00741**	0.00983	5
Plant population/ha	14.7799	0.1014*	0.1036	18
Plant height (cm)	0.5469	0.1825^{ns}	0.1722	12
Number of primary branches/plant	0.1928	0.0044**	0.1920	19
Number of capsules /plant	33.0588	0.0113**	0.1125	25
Number of seeds/ capsule	0.03700	0.03948**	0.07859	16
Biological yield	240.693	1.391*	0.857	17
Seeds yield/ plant	128.664	0.800*	0.995	19
1000-seed weight (g)	0.325438	0.009352**	0.001661	14
Harvest index %	0.0223371	0.0001123**	0.0001373	18

*, significant at 5%; ** significant at 1% and ns not significant.

The highest (GCV %) value was observed for seed yield (32.8%) while the lowest one showed for plant height (4%). The highest (PVC %) value observed was for biological yield (53.9 %) and the lowest value recorded was for harvest index (7.8 %). The heritability in broad sense estimates was high to moderate for most of the studied traits. The highest value was obtained by thousand seeds weight (77.1%), while the lowest one was recorded for plant height (3.4%). The highest genetic advance was obtained for biological yield (1.92) and grain yield (1.76) and the highest estimate of genetic advance as a percentage of the mean (GA %) was recorded for thousand seeds weight (79.0%) (Table 4).

In the present study, the higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) for all studied traits, indicate the effect of the genetic on the expression of these traits. Similar results for high (PCV) and (GCV) were recorded for the number of branches per plant, seed yield and biomass yield by Abate *et al* (2015). High genotypic coefficients of variation (GCV) indicate the possibility of phenotypic selection. The moderate (PCV) and (GCV) obtained for plant population, number of capsules per plant and thousand seed weight also reported by Kanak and Rajani (2017). On the other hand, the low estimates of phenotypic and genotypic coefficient of variation for days to 50 %flowering and harvest index is in agreement with Kanak and Rajani (2017) who found similar results. High heritability (in board sense) observed for thousand seed weight, number of seeds per capsule, harvest index, number of branches per plant, number of capsules per plant and days to 50 % flowering. Hence, selection based on the phenotypic performance could be practiced to improve these traits. Similar results were reported by Kanak and Rajani (2017), Abate *et al* (2015), Sudhakar *et al* (2007) and Siva *et al* (2013) for the same traits. In this study, the highest genetic advance exhibited by biological yield and seed yield and highest genetic advance as a percentage of the mean (GA %) obtained for thousand seeds weight, number of branches per plant and harvest index is in agreement with the results of Gadisa (2015). Therefore, Selection based on these traits will be effective for the improvement of the performance of these genotypes. Heritability estimates would be reliable if it is coupled with high estimate of genetic advance. High values for heritability combined with high genetic advance as a percentage of the mean in this study as showed by thousand seeds weight, number of branches per plant and harvest index, indicate the importance of these traits as selection criteria for developing new sesame cultivars as reported by Kanak and Rajani (2017) and Sumathi and Muralidharan (2010).

Combined Analysis of Correlation Coefficients for Different Agronomic Traits

Based on overall means of day to 50% flowering with other characters, the phenotypic and genotypic correlations are presented in (Table 5). The plant population with thousand seeds weight significantly and positively correlated to genotypic and phenotypic levels (0.81and 0.99) respectively. Furthermore, highly significant but negative phenotypic and genotypic correlations were shown for number of seeds per capsule with a thousand seeds weight (-0.96 and -0.99) respectively. At the genotypic correlation level, positive and significant correlation was exhibited between harvest index with the number of seeds per plant (0.99), while highly significant negative correlation coefficients were exhibited by different pairs of traits; PP with NCP (-0.99), TSW with HI (-0.99), PP with NSC (-0.99) and DF with TSW (-0.96). At the phenotypic correlation level, significant positive correlations were shown for a thousand seeds weight with biological yield (0.88) and harvest index with the number of capsules/plant (0.83) while highly significant negative phenotypic correlation was revealed among different pairs of traits; PHT with NCP (-0.95), BY with DF (-0.90), and TSW with NSC (-0.96). It was also significant negative correlations between HI with PHT (-0.89), NSC with PP (-0.87), and BY with NSC (-0.83).

Table 4. Estimates of the phenotypic coefficient of variation (PCV %), genotypic coefficient of variation (GCV %), Heritability (h^2), expected genetic advance from selection (GA) and percentage genetic advance (GA %) for six sesame genotypes at two locations, 2018 season.

TRIAT	σ^2g	σ^2ph	σ^2e	H BS (%)	GM	GCV (%)	PCV (%)	GA	GA (%)
DF	0.02	0.04	0.02	53.4	5.8	5.9	8.1	0.22	3.7
PP	0.26	0.85	0.59	30.9	7.0	19.4	34.9	0.59	8.4
PHT	0.02	0.50	0.48	3.4	10.3	4.0	22.0	0.05	0.5
NBP	0.17	0.30	0.14	55.1	1.7	31.4	42.3	0.62	36.9
NCP	0.23	0.43	0.20	54.0	6.9	18.3	24.9	0.73	10.5
NSC	0.16	0.24	0.08	66.8	6.6	15.7	19.2	0.68	10.2
SY	3.00	10.35	7.35	29.0	35.7	29.0	53.9	1.92	5.4
YP	1.49	3.03	1.54	49.2	13.9	32.8	46.8	1.76	12.7
TSW	0.03	0.04	0.01	77.1	0.4	27.3	31.1	0.31	79.0
HI	0.0007	0.0011	0.0004	63.1	0.2	6.2	7.8	0.04	24.0

DF= Days to 50%flowering, PP= Plant population, PHT= Plant height, NBP= Number of braches/pant, NCP= Number of capsules/plant, NSC= Number of seed/capsule, BY= Biological yield, SY= Seeds yield/plant, TSW= 100 seed weight, HI= Harvest index.

In-depth knowledge of variability along with information on interrelationships among various traits are important for efficient selection, especially when associated with yield. Such traits could be used as a direct indicator to increase yield and improve the quality traits of a crop. In the present study, the significant positive genotypic and phenotypic correlation recorded for plant population with thousand seeds weight, number of seed per capsule with harvest index, number of seed per capsule, plant population with thousand seed weight and thousand seeds weight with biological yield could be used as direct selection criteria to improve sesame yield as reported by Gadisa (2015) for the association of the same traits. On the other hand, the significant negative association of the traits, of biological yield with days to 50% flowering, plant height with number of capsules per plant and harvest index, number of seeds per capsule with plant population, thousand seed weight with biological yield may be due to the competition for assimilates, indicating that selection for one of these trait will be accompanied by low performance of the other trait.

Table 5. Phenotypic and Genotypic Correlation Coefficients between Different Pairs of Traits in Six Sesame (*Sesamum indicum*) Genotypes evaluated at two Locations in 2018 Season.

Traits	DF	PP	PHT	NBP	NCP	NSC	BY	SP	TSW	HI
DF		-0.38	0.00	0.49	0.32	0.65	0.00	0.00	-0.96***	0.58
PP	-0.29		0.00	-0.22	-0.60	-0.99***	0.00	0.00	0.99**	-0.60
PHT	-0.29	0.74		0.00	0.00	0.00	0.00	0.00	0.00	0.00
NBP	0.60	-0.14	0.37		-0.32	0.29	0.00	0.00	-0.34	-0.77
NCP	0.29	-0.49	-0.95**	-0.50		0.49	0.00	0.00	-0.03	0.73
NSC	0.57	-0.87*	-0.63	0.42	0.43		0.00	0.00	-0.99***	0.99***
BY	-0.90*	0.64	0.62	-0.44	-0.55	-0.83*		0.00	0.00	0.00
SY	-0.46	-0.24	-0.38	-0.46	0.35	0.26	0.15		0.00	0.00
TSW	-0.70	0.81*	0.49	-0.61	-0.28	-0.96**	0.88*	0.00		-0.99***
HI	0.33	-0.70	-0.89*	-0.17	0.83*	0.78	-0.66	0.61	-0.61	

The genotypic correlations are the upper triangle and phenotypic correlations in the lower one. *, ** and ns are the level of significance at 5%, 1% and non-significant, respectively. D.F = n-2=4, r 5%=, r 1%.

4. CONCLUSION

The result of this study indicated that there was sufficient variability among the evaluated genotypes.

The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits studied.

The genotypes Promo, Elobied-1 are the best in the most studied traits exhibited the highest mean seeds yield.

The negative and positive phenotypic correlation was observed in the biological yield, days to 50% flowering, plant height, capsules per plant, harvest index, number of seeds per capsule, plant population and thousand seeds weight. Direct Selection depending on these traits might be useful to increase the seeds yield in sesame breeding programs.

According to the results of present study, it's highly recommended to repeat these experiments for 2-3 seasons to ensure reliability and adaptability of testing materials. In addition, more traits need to be included especially qualitative ones like oil and protein contents.

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Genetic Variability and Interrelationships of Some Traits in Six Sesame (*Sesamum indicum* L.) Genotypes under Rainfed Conditions•

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المستخلص

هدفت هذه الدراسة إلى قياس التباين الوراثي والإرتباط الوراثي والمظهري بين الإنتاجية ومكوناتها في ست طرز من محصول السمسم الذي يزرع على نطاق واسع في ولاية شمال كردفان تحت ظروف الامطار. تحليل التباين أظهر وجود فروقات معنوية عالية لكل الصفات المورفولوجية التي تمت دراستها ما عدا طول النبات. معامل الإختلاف المظهري كان أعلى من معامل الإختلاف الوراثي لكل الصفات، وكان أعلى معامل إختلاف وراثي ومظهري للوزن الحيوي للنبات وإنتاجية البذور. أعلى نسبة لمعامل التوريث على النطاق العريض تم رصدها لوزن الألف حبة وعدد البذور في الكبسولة. أعلي قيمة لمعدل التقدم الوراثي سجلت للوزن الحيوي وإنتاجية البذور. أعلى معدل تقدم وراثي كنسبة من المتوسط العام سجلت لوزن الألف حبة وعدد الأفرع في النبات. أعلي معدل توريث مصحوب بأعلى معدل تقدم وراثي كنسبة من المتوسط العام تم رصدها لوزن الألف حبة، عدد الأفرع في النبات ودليل الحصاد. الإرتباط المظهري كان أعلى من الإرتباط الوراثي لكل الصفات المدروسة وذلك لتأثير البيئات المختلفة. أعلى نسبة للإرتباط المظهري والوراثي الموجب كانت بين الكثافة النباتية ووزن الألف حبة. عدد الكبسولات في النبات مع وزن الألف حبة أظهرت إرتباط مظهري ووراثي سالب مما يشير إلى أن انتخاب صفة واحدة قد يكون مصحوب باداء أقل للصفات الأخري. الكثافة النباتية ووزن الألف حبة وعدد البذور في

•جزء من أطروحة تقدم بها المؤلف الأول لنيل درجة الماجستير لجامعة السودان للعلوم والتكنولوجيا.

الكبسولة ودليل الحصاد ووزن الألف حبة والوزن الحيوي أظهرت فروقات عالية في الارتباط الوراثي والمظهري الموجب لذلك فإن الانتخاب على اساس هذة الصفات سيكون مفيداً في تحسين إنتاجية السمسم تحت ظروف الامطارفي المستقبل.

كلمات مفتاحية : *سمسم، التباين الوراثى؛ التباين المظهرى؛ الزراعة المطرية؛ الصفات المشتركة.*