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GENERATION MEAN ANALYSIS FOR YIELD AND YIELD COMPONENTS IN SESAME (*Sesamumindicum* L.)

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Abstract

Two parents with contrasting characters were used, *viz*; Gd2002SPSN.29 and Ziraa-9 described as (P1) and (P2) respectively. They were selected from the sesame breeding program, Gedarif Research Station, ARC, Sudan. In season 2004 the two parents were crossed to produce F1 hybrid. In season 2005 parents and their F1 were grown. Part of the F1 was selfed to produce F2 and the other part was back crossed to both parents to produce Bc1 and Bc2 progenies. In season 2006 the parents (P1, P2), and their F1and F2 and back crosses (Bc1, Bc2) populations were evaluated in a randomized complete block design with three replicates. A wide range of variability was exhibited for most of the characters. The highest seed yield was obtained by the BC2 (714 $Kg.ha^{-1}$), while the lowest was obtained by the BC1 (286 $Kg.ha^{-1}$). Considering the nature and magnitude of gene action, improvement of days to 50% flowering, days to maturity, plant height, number of branches $plant^{-1}$, height to first branch, height to first capsule, capsule length and 1000-seed weight could be achieved through simple pedigree method while hybrid breeding would be most effective for seed yield $plant^{-1}$ and seed $yield.ha^{-1}$.

Keywords: Sesame, Generation mean, Yield and yield components

Introduction

Sesame *(Sesamumindicum* L.*),* is a member of the family Pedaliaceae (Weiss, 1983). Several historical records indicate that sesame probably originated in Ethiopia, and from there it was introduced into India and China (Yermanos, 1980). In 2010, the world production amounted to 4.32 million metric tons, obtained from 7.87 million hectares, with an average productivity of 549 $Kg.ha^{-1}$. Sudan contributed 6% and 16% of production and producing area, respectively. The major producers are India, China, Myanmar and Sudan (FAO, 2011). Averaged from 2002 to 2009, Sudan production was 295250 tons $year^{-1}$ obtained from 1404586 hectares, with a mean yield of 210 $Kg.ha^{-1.}$ Among the Arab countries, Sudan contribution was 90% to the sesame area and 71% to the production (AOAD, 2010).

In Sudan, sesame is one of the most important oil crops and may be the main cash crop from the rainfed sector and is considered as the main agricultural exported commodity. An estimated area of 1.26-2.1 million hectares are cropped annually; but the area and production vary greatly from year to year (Ahmed, 2008). The main objective of the sesame breeding program in Sudan is the development of high yielding but dehiscent varieties. The shattering problem could be partially solved by breeding for uniform maturity (Khidir, 1969).

Plant breeding, as an evolution process, depends on genetic variation. Although Sudan has a tremendous wealth of sesame genetic variability, still there is a great need for large and diverse gene pools to meet ever-changing demands, opportunities and challenges of the future (Frankel and Bennett, 1970).

Hybridization is the most potent technique to enrich the genetic variation and for breaking yield barriers for producing varieties having built-in high yield potential. Yield is a polygenic character, the knowledge of gene action (additive, dominance, epistasis) for yield and yield attributes in sesame are of valuable importance for the breeder to choose appropriate breeding methods. The selection of suitable parents for hybridization is one of the most important steps in breeding programs. Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may yield poor recombinants in the segregating generations. It is therefore, essential that the parents should be chosen on the basis of their genetic value. Diallel analysis is used to select the parents based on their combining ability but fail to detect the epistasis, which remains the most complex problem and on which it is extremely difficult to obtain reliable results. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately. The objectives of this study were to obtain information on the nature and magnitude of genetic variability and gene action in sesame to provide a basis for an evaluation of selection methods for the improvement of the sesame population.

Materials and methods

Genetic material

Two parents with contrasting characters were used, viz; Gd2002SPSN.29 and Ziraa-9 described as (P1) and (P2) respectively. They were selected from the sesame breeding program, Gedarif Research Station, ARC, Sudan. These parents were obtained from selfed plants in the previous season to ensure their varietal purity (pure lines). Ziraa-9 is a variety

that resulted from a systematic purification and selection on basis of seed color from a local material. It is characterized by profuse branching, late flowering and maturity and white small seeds. Gd2002SPSN.29 is advanced line which is promising and adapted to the environment (Ali *et al*., 2010).

General

In season 2004 the two parents were grown in rows 10 m long and 0.8 m apart for each genotype to ensure maximum potentiality of the genotypes. The area was weeded and irrigated when necessary to increase duration of flowering. In the same season the parents were crossed to produce F1 hybrid. Some flowers in each parent were selfed to maintain the parents.

Flowers were emasculated by removing the entire corolla in the evening while still greenish and closed. The emasculated flowers were protected by insertion of soda straw over the style to avoid contamination with foreign pollen. The next day fresh pollen were collected from the predetermined male parent and rubbed gently on the stigma and covered. Each crossed female flower, was identified by tags on which parentage and date of the cross was recorded.

In season 2005 parents and their F1 were grown. Part of the F1 was selfed to produce F2 and the other part was back crossed to both parents to produce Bc1 and Bc2 progenies.

In season 2006 the parents (P1, P2), and their (F1, F2) and back crosses (Bc1, Bc2) populations were evaluated.

A randomized complete block design with three replications was used for executing the experiment. Each entry was grown on a row of 2m long and 0.6 m apart. The seeds were sown in holes 0.2 m along the rows and 3 weeks after emergence, seedling were thinned to 3 plants hole^{-1}.

In season (2006), the experiment was sown on 19th July; first rain after sowing was on the same day and seedlings emerged on 22^{ed} July. The experiment was weeded before thinning and then whenever necessary. The data were recorded on: days to 50% flowering (DFPF), days to maturity (DTM), plant height (cm) (PHT), number of branches.plant^{-1} (NBPP), number of capsules.plant^{-1} (NCPP), height to first capsule (HTFC), height to first branch (HTFB), capsule length (cm) (CL), 1000 seeds weight (g) (1000-SW), seed yield.plant^{-1} (g) (SYPP) and seed yield (Kg.ha^{-1}) (SYHa^{-1}).

Biometrical analysis for generation mean

Analysis of variance was carried out for all parameters measured to test for differences among the generation. Least significance difference test was applied to compare the means of the different generations for each character. The generation mean analysis consists of two main steps, i.e., testing for epistasis and estimation of gene effects and variances. The scaling test was carried out to determine the presence or absence of non-allelic interactions and their types. The four scaling test performed as suggested by Mather (1949) and Hayman and Mather (1955).

$$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1}$$

$$B = 2\overline{B_2} - \overline{P_2} - \overline{F_1}$$

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$$

$$D = 2\overline{F_2} - \overline{B_1} - \overline{B_2}$$

The variance for each scaling test was estimated as follows:

$$V(A) = 4V\left(\overline{B_1}\right) + V\left(\overline{P_1}\right) + V\left(\overline{F_1}\right)$$

$$V(B) = 4V\left(\overline{B_2}\right) + V\left(\overline{P_2}\right) + V\left(\overline{F_1}\right)$$

$$V(C) = 16V\left(\overline{F_2}\right) + 4V\left(\overline{F_1}\right) + V\left(\overline{P_1}\right) + V\left(\overline{P_2}\right)$$

$$V(D) = 4V\left(\overline{F_2}\right) + V\left(\overline{B_1}\right) + V\left(\overline{B_2}\right)$$

The standard error (S.E) of A, B, C and D is worked out by taking the square root of respective variances. The t values are calculated by dividing the effect of A, B, C and D by their respective standard error. The calculated t values of these four tests are compared against the tabulated values of t at 5% level of significance. Significance of any of these four scales indicates the presence of epistasis. The type of epistasis is revealed by the significance of specific scale as given bellow:

The significance of A and B scales indicates the presence of all the three types of non-allelic gene interaction, viz., additive × additive (i); additive × dominance (j) and dominance × dominance (l).

The significance of C scale suggests dominance × dominance (l) type of non-allelic gene interaction.

The significance of D scale reveals additive × additive (i) type of gene interaction, and significance of both C and D scales indicates additive × additive (i) and dominance × dominance (l) type of gene interactions (Singh and Narayanan, 2000).

The joint scaling test suggested by Hayman (1958) (six parameters model) was used to estimate gene effects and variances as follows:

m = mean effect = $\overline{F_2}$

d = additive effect = $\overline{B_1} - \overline{B_2}$

h = dominance effect = $\overline{F_1} - 4\overline{F_2} - ½\overline{P_1} - ½\overline{P_2} + 2\overline{B_1} + 2\overline{B_2}$

i = additive × additive gene interaction = $2\overline{B_1} - 2\overline{B_2} - 4\overline{F_2}$

j = additive × dominance gene interaction = $\overline{B_1} - ½\overline{P_1} - \overline{B_2} + ½\overline{P_2}$

l = dominance × dominance gene interaction = $\overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{B_1} - 4\overline{B_2}$

Where, $\overline{P_1}, \overline{P_2}, \overline{F_1}, \overline{F_2}, \overline{B_1} and \overline{B_2}$ are the mean values over replications for the character in P1, P2, F1, F2, B1, and B2 populations, respectively.

The variances for these gene effects are obtained as follows:

$$V_m = V\overline{F_2}$$

$$V_h = V\overline{F_1} - 16V\overline{F_2} +$$

$$V_h = V\overline{F_1} + 16\mathrm{V}\overline{\mathrm{F}_2} + ¼\mathrm{V}\overline{\mathrm{P}_1} + ¼\mathrm{V}\overline{\mathrm{P}_2} + 4V\overline{B_1} + 4V\overline{B_2}$$

$$V_i = 4V\overline{B_1} + ¼\mathrm{V}\overline{\mathrm{B}_2} + 16V\overline{F_2}$$

$$V_j = V\overline{B_1} + ¼\mathrm{V}\overline{\mathrm{P}_1} + \mathrm{V}\overline{\mathrm{B}_2} + ¼V\overline{P_2}$$

$$V_l = \mathrm{V}\overline{\mathrm{P}_1} + V\overline{P_2} + 4V\overline{F_1} + 16V\overline{F_2} + 16V\overline{B_1} + 16V\overline{B_2}$$

Where V is variance.

$$Variance = \frac{\left[\sum x_i^2 - \frac{\left(\sum x_i\right)^2}{n}\right]}{n-1}$$

The standard error (S.E) is worked out for each component separately by taking the square root of the variance of respective component. The t value is calculated for each component by dividing the gene effect of respective component by their standard error and then the calculated value of t compared with the tabulated value of t at 5% level of significance.

Results and discussion

Variability

The data showed significant differences among the parents and their generations for most of the measured traits (Table 1). Very highly significant differences ($P \leq 0.001$) were recorded for plant height, number of branches plant^{-1} and height to first branch, whereas highly significant differences ($P \leq 0.01$) were recorded for days to 50 % flowering, 1000-seed weight and seed yield ha^{-1}. These results indicated adequate variability in these materials. Similar results were reported by Solanki and Gupta (2001), Kumaresan and Nadarajan (2002) and Banerjee and Kole (2006).

Days to 50% flowering ranged from 33 to 45 days. The parent Gd2002SPSN29 exhibited a shorter period to 50% flowering (33 day), while the parent Ziraa-9 exhibited a longer period to 50% flowering (45 day). Their generations did not exhibit significant differences among themselves and the F1 performed as intermediate between the two parents.

For plant height, the tallest and shortest genotypes were the two parents i.e., Ziraa-9 and Gd2002SPSN29, respectively. None of their generations exceeded the tallest one.

A higher number of branches plant^{-1} was exhibited by Ziraa-9 (2.93), but no significant differences were exhibited among the generations and their parents. Gd2002SPSN29 is characterized by a low branching habit.

High significant differences were recorded among the parents and their generations in terms of the height to the first capsule. The parent Ziraa-9 recorded the highest height to the first capsule (62.1 cm) while the Bc1 recorded the lowest height to the first capsule.

For the 1000-seed weight, the parent Gd2002SPSN29 recorded significantly higher 1000-seed weight (3.2 g) compared to the generations and the parent Ziraa-9 recorded the lowest 1000-seed weight (2.37 g).

In terms of seed yield ha^{-1}., the parents, F1 and Bc2 recorded the highest seed yield ha^{-1} with non-significant differences among themselves. High seed yield ha^{-1}., was exhibited by the Bc2 (714 $Kg.ha^{-1}$) followed by F1 (610 $Kg.ha^{-1}$), P1 (553 $Kg.ha^{-1}$) and P2 (549 $Kg.ha^{-1}$).

As the two parents are characterized with contrasting characters, for most of the measured characters, one parent recorded the highest level while the other recorded the lowest. F1 generation performed as intermediate between the two parents for most of the characters. The result indicates incomplete or partial dominance for these traits *i.e.* days to 50% flowering, days to maturity, plant height, number of branches.$plant^{-1}$, number of capsules.$plant^{-1}$, height to first capsule, height to first branch and 1000 seeds weight.

Scaling test

Table (2) presents the estimates of scaling test and their level of significance for sesame yield and its components. A simple additive-dominance model was adequate as inferred from the non-significance of all the scales for days to maturity and number of capsules $plant^{-1}$ while for the remaining characters an epistaticdigenic interaction model was assumed by one, two or three of the scales being significant.

The significance of C scale for days to 50% flowering and seed yield $plant^{-1}$ reveals dominance × dominance type of non allelic interaction. Anbanandan et al. (2006) reported that, for days to 50% flowering both allelic and non-allelic interaction effects were significant in both crosses and the dominance was predominant in controlling days to 50% flowering. Significance of C scale for seed yield $plant^{-1}$ was reported by Ganesh and Sakila (1999).

The significance of A and B scales were exhibited for number of branches $plant^{-1}$, height to first branch and height to first capsule, suggesting the presence of all the three types of non allelic gene interaction i.e., additive × additive (i); additive × dominance (j) and dominance × dominance (L).

The estimates of genetic parameters *viz*., m, d, h, I, j and L of the different traits are presented in Table (3).

Simple effects are significant for days to maturity and the dominance gene effect (h) was of greater magnitude than the additive gene effect (d). The (h) and (L) components showed opposite signs indicating a duplicate dominant type of epistasis, and this result was in agreement with Ganesh and Sakila (1999) who reported a duplicate dominant type of epsitasis.

The additive effect, dominance and additive × dominance type of gene interactions were significant for branches $plant^{-1}$. Similar result was reported by Sharmila et al. (2007). The height to first capsule exhibited that only the additive effect was significant indicating the role of additive gene action in the inheritance of this character.

In terms of height to first branch, the additive, dominance and additive × dominance type of gene interactions were significant, and (h) and (L) types of gene interaction showed the same sign indicating a complementary dominant type of epistasis.

The characters vary in type of gene action involved (additive, dominance and non-allelic gene action).

Table (1) Generation means for sesame yield and its components

	DT 50% flowering	DTM	PHT	NBPP	NCPP	HTFB	HTFC	CL	1000SW	SYP^{-1}	$SYha^{-1}$
P1	33.0c	81.3	85.0b	0.27b	33.1	3.5c	31.7d	2.85	3.20a	4.3	553a
P2	45.0a	84.0	114.0a	2.93a	41.1	46.9a	62.1a	2.75	2.37c	4.9	549a
F1	38.0b	79.0	99.7ab	1.67ab	36.3	27.7b	43.8bc	3.05	2.70bc	4.1	610a
F2	35.bc	82.7	91.0b	0.13b	30.4	3.3c	34.8cd	2.95	2.78b	3.4	360b
BC1	36.0bc	80.0	84.3b	0.20b	30.5	5.7c	28.3d	2.83	2.82b	4.1	286b
BC2	38.0b	83.0	109.3a	1.33b	38.9	28.0b	46.7b	2.97	2.87ab	5.1	714a
Mean	37.7	18.7	97.3	1.1	35.0	19.2	40.6	2.90	2.79	4.3	512.0
Level of sig.	**	N.S	***	***	N.S	***	***	N.S	**	N.S	**
C.V %	7	3	7	50	33	31	14	6	7	30	19
S.E±	1.43	1.58	3.81	0.32	6.59	3.40	3.19	0.097	0.11	0.75	57.6
LSD	4.5	4.98	17.08	1.43	29.55	10.22	14.30	0.31	0.34	2.36	181.5

**, ***Means within the same column followed by the same letter(s) are not significantly different at probability level of 0.01% and 0.001

Table (2) A, B, C and D scales for sesame yield and its components

Character	A	B	C	D
Days to 50% flowering	1.0	-5.6	-11.2**	-3.3
Days to maturity	-0.3	3.0	7.5	2.4
Plant height (cm)	-17.07*	5.41	-34.88*	-11.61
Number of branches plant^{-1}	-1.534**	-1.937**	-6.011**	-1.27
Number of capsules plant^{-1}	-8.397	0.34	-25.137	-8.54
Height to first branch (cm)	-30.29**	-31.54**	-103.15**	-20.66
Height to first capsule **(**cm**)**	-18.86**	-12.44**	-42.1**	-5.4
Capsule length (cm)	-0.266*	0.137	0.091	0.11
1000-Seed weight (g)	-0.26	0.67**	0.15	-0.13
Seed yield plant^{-1} (Kg. ha^{-1})	-0.2	1.2	-3.8*	-2.4

*, **, Significant at 0.05 and 0.01 probability levels, respectively.

1. The significance of A and B scales indicate the presence of all the three types of non-allelic gene interaction, viz., additive × additive (i); additive × dominance (j) and dominance × dominance (l).
2. The significance of C scale suggests dominance × dominance (l) type of non-allelic gene interaction.
3. The significance of D scale reveals additive × additive (i) type of gene interaction, and significance of both C and D scales indicate additive × additive (i) and dominance × dominance (l) type of gene interactions.

Table (3) Estimates of gene effects (m, d, h, I, j and l) on six parameters genetic model for the different traits measured

Character	M	d	h	i	j	L
Days to 50% flowering	35.7**	-2.7	5.6	6.6	3.3	-2.0
Days to maturity	82.7**	-3.0*	-8.45*	-4.8	-1.65	2.1
Plant height (cm)	90.93**	-25.47**	23.12	23.22	-11.24*	-11.56
Number of branches plant^{-1}	0.13	-1.13**	2.6085**	2.54**	-0.2015**	0.931
Number of capsules plant^{-1}	30.4**	-8.4**	16.2515	17.08	-4.3685	-9.023
Height to first branch (cm)	0.67	-21.06**	43.805**	41.32**	0.625	20.51
Height to first capsule(cm)	34.8**	-18.46**	7.75	10.8	-3.21	20.5
Capsule length	2.95**	-0.15*	0.0315	-0.22	-0.2015	0.349
1000-Seed weight (g)	2.78**	-0.05	0.175	0.26	-0.465**	-0.67
Seed yield plant^{-1} (Kg.ha^{-1})	3.4**	-1.0	4.3	4.8	-0.7	-5.8

*, ** = Significant at 5% and 1% level of probability, respectively.

M= mean effect, d= additive gene effect, h= dominance gene effect, i= additive × additive gene effect, j= dominance × dominance gene effect and L= additive × dominance gene effect.

Conclusion

In spite of the limited number of parents used this study revealed a considerable amount of genetic variation and more opportunities for further improvement.

Considering the nature and magnitude of gene action, improvement of days to 50% flowering, days to maturity, plant height, number of branches plant^{-1}, height to first branch, height to first capsule, capsule length and 1000-seed weight could be achieved through simple pedigree method while hybrid breeding would be most effective for seed yield plant^{-1} and seed yield ha^{-1}.

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