Scholars Academic Journal of Biosciences (SAJB) **ISSN 2321-6883 (Online)**
Sch. Acad. J. Biosci., 2014; 2(5): 318-325 **ISSN 2347-9515 (Print)**

(An International Publisher for Academic and Scientific Resources)
www.saspublishers.com **DOI:** 10.36347/sajb.2014.v02i05.002

Research Article

Genetic Analysis of Seed Yield Components in Sesame (*Sesamum indicum* L.) at Mora (Cameroon)

Aladji Abatchoua MMI[1*], Noubissié Tchiagam JB[1], Njintang Yanou N[1, 2]
[1]Department of Biological Sciences, Faculty of Science, University of Ngaoundéré, P.O. Box 454 Ngaoundéré, Cameroon
[2]Department of Food Sciences, Higher School of Agro-industrial Science(ENSAI), University of Ngaoundéré, P.O. Box 455 Ngaoundéré, Cameroon

***Corresponding author**
Aladji Abatchoua MMI
Email: abatchouaaladji@yahoo.fr

Abstract: Little genetic information is available for seed yield in sesame in Cameroon. In order to select varieties with high yield, 12 promising lines were genetically screened at Mora (Northern Cameroon) during 2011 crop season for eight characters viz., days to 50% flowering, days from flowering to capsule maturity, plant height, number of branches, number of capsules per plant, capsule length, number of seeds per capsule and number of days to maturity. Six divergent lines were therefore crossed in all combinations using a diallel mating scheme without their reciprocals. Progenies of F_1's along with their parents were evaluated during 2013 cropping season in a randomized complete block with three replicates. Preliminary analysis of variance indicated that the genotypes were significantly different for all yield components ($p<0.05$) indicating the probability of selection. Broad-sense heritability estimates were high for all traits (0.66 – 0.99). Narrow sense heritability and GCA/SCA ratio indicated that both dominant and additive gene effects were significant for these parameters with a predominance of non additive effects. Genetic analysis demonstrated that the parents differed for their general combining ability (GCA) and the crosses showed specific combining ability (SCA). Association between GCA effects and mean characters in most cases implied that parental sesame lines with high values of the characters have superior combining ability. For these traits, recurrent selection might be a useful breeding strategy.
Keywords: *Sesamun indicum* L., yield components, diallel analysis, breeding strategy.

INTRODUCTION

Sesame (*Sesamum indicum* L., Pedaliaceae), a self pollinated crop, is an ancient cultivated oil crop and thought to have originated to Africa [1]. *S. indicum* is an important source of food worldwide and constitutes an inexpensive source of protein, fat, minerals and vitamins in the diets of rural populations, especially for children [2, 3]. Sesame oil contains vitamin E and several important antioxidative constituents such as sesamol, sesamin and sesamolin, which are believed to promote the integrity of body tissues in the presence of oxidizing compounds [2, 3]. Sesame oil compounds have also multiple physiological functions, such as estrogenic activity, providing anti-inflammatory functions, decreasing blood lipids and arachidonic acid levels **[**4]. In addition, sesame possesses some agricultural advantages such as the ability to grow well under tropical and subtropical climates with soil moisture without rainfall or irrigation, and grow as mixed stands with diverse crops **[**4]. It is grown in tropical to the temperate zones from about 40° N latitude to 40° S latitude [4, 5, 6]. However, it thrives best on well-drained soil with a moderate fertility and a pH between 5.5 and 7.0 **[**6, 7]. In Cameroon, the crop is cultivated in all regions but his productivity remains very low due to the scarcity of improved varieties **[**8]. Despite its nutritional value and medicinal importance, sesame yields in Cameroon are very low, averaging 38.378 tons on a total production area of 26.897 hectares in 2008 **[**8]. In Africa in general, the sesame cultivation is limited by insufficiency of genetic information and breeding program [6, 9]. Indeed, a further increase in sesame productivity per unit area and unit time needs intensive research in genetics and plant breeding [6, 10].

Compared to other plants of food importance, the sesame has been modified little and standardized little by the human being, so that a very large genetic variability exists within this species [1, 6]. Genetic variation and information regarding genetic control for different agronomic traits is needed to produce improved cultivars. Menzir [7]; Mishra *et al*. [10]; Pham *et al.* [10] recorded an important variability for days to 50% flowering, plant height, number of branches per plant, days to maturity, number of capsules per plant, capsule length and number

of seeds per capsule in *S. indicum*. Selection for high yielding types with wider adaptability shall be not only very useful but shall help in increasing the production both locally and globally [6]. For efficient breeding and crop improvement, it is of utmost importance in any crop plant to ascertain the contribution of each growth related trait to yield and to select components that help maximize yield [12].

In Cameroon, research on the genetics of sesame is limited until now. Proper understanding of genetic mechanisms involving in the expression of important characters would help in planning effective breeding strategies. In general, diallel mating designs are used in plant breeding to get information on genetic effects for a fixed set of parental lines, estimate combining abilities as well as heritability [6]. Therefore, the present investigation was aimed at finding out the nature and magnitude of genetic variability of sesame for some yield components, clarifying the genetic basis of these polygenic traits through diallel cross technique.

MATERIALS AND METHODS

Experimental Site

The research was conducted from 2011 to 2013 in a private farm at Mora, Far North region (Cameroon), which is intersected by 10.32° E East longitude and 09.30° N North latitude. This region belongs to the sahelian savannah agro-ecological zone. The climate is characterized by two seasons with an average annual rainfall of 1200 mm that is fairly distributed over the rainy growing period (June to September). The soil of experiments was sandy texture.

Plant Materials

The experimental material comprised of twelve sesame local varieties including two lines from Tchad: Local 1 Djamena (L1Dj), Local 2 Djamena (L2Dj), two registered genotypes originated from Nigeria: Local 1 Banki (L1B), Local 2 Banki (L2B) and eight local landraces from northern Cameroon: Local 1 Figuil (L1F), Local 1 Doulo (L1D), Local Podoko (LP), Local Mora (LM), Local 2 Doulo (L2D), Local 2 Figuil (L2F), Local 1 Yagoua (L1Y) and Local 2 Yagoua (L2Y). Six genotypes (L1F, L1D, LP, LM, L2D and L2F) which were chosen based on their genetic variation for these traits were planted in pots from June to September 2012 for crossings. At flowering, manual crossings were made with emasculation to provide F_1 generation. At 6x6 half-diallel mating was obtained giving 21 combinations consisting of six pure lines and 15 F_1 hybrids.

Experimental Design and Agronomic Practices

A preliminary field trial was conducted during the 2011 growing season to evaluate the genetic variability for yields components. The seeds of 12 entries were sown in a randomized complete block design (RCBD) with three replications. Sowing took place on June 05, 2011, on an experimental surface of 105 m^2 (17.5m length x 6 m broad). Each plot unit consisted on one row of 2m length x 0.5 m broad, spaced 30 cm apart. Six seeds of each variety were sown at an intra-row spacing of 30 cm and thinned to two per hill, 15 days after sowing (DAS). A mineral fertilizer (7% N; 14% P_20_5; 7% K_20) was applied to the seedlings three weeks after planting at rate of 60 kg per ha. The plots were manually weeded at 20 DAS, 45 DAS and at 65 DAS. Ten representative plants per treatment in each replication were selected randomly, tagged and observations were recorded on these plants for different characters *viz*, days to 50% flowering (DF), days from flowering to maturity of 90% of capsules (DFM), plant height (PH), number of branches per plant (NB), number of capsule per plant (NCP), capsule length (CL), number of seeds per capsule (NSC) and days to maturity from sowing to full maturity (DM). These traits were assessed as described by Bedigian [4], Menzir [7], Pham *et al.* [11] and Sandipan *et al.* [12].

During the growing season 2013, all 21 genotypes obtained from diallel mating, were arranged in a duplicated randomized complete block design (RCBD) with three replications. Sowing took place on June 15, 2013, at the beginning of the rainy season on an experiment surface of 140 m^2 (20 m x 7 m). Plot unit size, spacing, weeding, treatments and recording were as previous described for variability study.

Statistical analysis

The data were subjected to analysis of variance (ANOVA) using STATGRAPHICS PLUS statistical package program. The genotypic means were compared using the Least Significant Difference at 5% level of probability (LSD).

Diallel analysis

The diallel analysis was done using Dial 98 microcomputer package [13]. The Griffing's [14] method 2 (excluding reciprocal F_1 crosses), model 1 (fixed effects) was used to analyze the general combining ability (GCA) of lines and the specific combining ability (SCA) of crosses, supplemented by the analysis of variance by Walters and Morton [15]. With this approach, the components of variation were partitioned into the additive effects (a) and the dominance effects (b) which were further sub-divided into b_1, b_2 and b_3. The genetic parameters were estimated as per Hayman [16]. Heritability in broad sense (h^2) was measured as the proportion of genetic variance (δ^2g) in the phenotypic variance between the parents (δ^2p), while heritability in narrow sense (h^2n) was calculated as the proportion of additive variance (δ^2_A) in the phenotypic variance between the parents (δ^2p) [17,18]. The correlation between parental values (Pr) and recessive factor (Wr+Vr) indicated the gene action for each trait [14].

RESULTS AND DISCUSSION

Genotypic Variation for Yield Components

Mean performance of sesame parents for all studied characters were shown in Table 1. Analysis of variance revealed significant difference among the studied

genotypes for all investigated yield components. The values of days to 50% flowering ranged from 36.15 to 57.9 days (mean = 47.29 days) with line L1Y had the lowest mean. The duration from flowering to maturity of capsules ranged from 34.3 days for LM to 45.4 days for L1D (mean = 40.70 days). The parents L2F and L2D possessed the highest values of plant height which varied from 68.15 to 127.2 cm (mean= 89.87cm). Results indicated that the number of branches ranged from 2.7 to 5 (mean= 3.83) and L2F and L1Dj were the best parents. There was high number of capsule per plant for L2D and L2F, and this trait varied from 16.29 to 56.3 (mean= 32.91). The capsule length ranged from 17.75 to 25.3 mm (mean= 21.07 mm) and varieties LM and L2D showed high values. The number of seeds per capsule ranged from 28.2 to 65 (mean= 44.74), and genotypes LM and L2D possessed highest number of seeds per capsule. The days to maturity varied from 88.95 to 112.4 days (mean= 100.97 days), and lines L1B and L2B showed lowest values.

Significant differences amongst the twelve genotypes for evaluated yield components indicated the presence of diversity in the materials. Presence of significant variability for agronomic traits in sesame was earlier reported by [7, 11, 19, 20, 21]. The extent of genotypic variability for days to 50% flowering, days from flowering to capsule maturity, plant height, number of branches, number of capsules per plant, capsule length, number of seeds per capsule and days to maturity was in agreement with other studies [10, 11, 22, 23]. The presence of sufficient variability for a character could be considered valuable for further biometrical assessments. The genetic variation can be used in breeding programs to improve the potential of seed yield and earliness.

Genetic analysis of yield related traits

The ANOVA of the 6 x 6 half-diallel mating with Walters and Morton's [15].method showed the significance of genotypic effects and their components (Table 2). Both additive (a) and dominant effects (b) were all significant ($p < 0.01$). Within (b), the mean dominance effects (b_1) were significant except for days to 50% flowering and number of branches while the additional dominance effects due to the parents (b_2) appeared not significant only for plant height and number of branches. The residual dominance effects (b_3) were also highly significant ($p < 0.01$) for the eight morphological characters.

The significance of the mean dominance deviation (b_1) for traits indicated that, there is a non-directional dominance effects [15]. The dominance effects are directional only for days to 50% flowering and number of branches per plant. The significant b_2 item illustrated an asymmetrical distribution of dominant genes among the parents, reflecting that some parents harbored considerably dominant genes than others. Dominant and recessive loci are not harmoniously distributed among the parents. The residual dominance (b_3) was significant for all characteristics confirming the presence of specific dominance or combining ability in some crosses.

Table 1: Variability of studied yield components in 12 sesame genotypes

Lines	DF(days)	DFM (days)	PH (cm)	NB	NC/P	CL (mm)	NS/C	DM (days)
L1F	53.5±0.14^{c}	41.3±0.70^{de}	78.5±5.93^{g}	2.7±0.14^{f}	20.40±1.67^{i}	20.8±0.56^{cde}	47.6±0.1^{de}	93.7±0.14^{g}
L1D	54.9±0.98^{bc}	45.4±1.41^{a}	90.9±1.55^{f}	2.9±0.70^{f}	16.4±1.69^{j}	22.3±0.70^{bc}	49.2±2.26^{d}	100.8±0.28^{e}
LP	57.9±0.42^{a}	42.4±0.1^{cd}	106.3±12.02^{de}	4.6±0.8^{abc}	32.1±0.42^{g}	21.6±1.69^{bcd}	52.6±3.67^{c}	103.7±0.14^{d}
LM	49.6±0.28^{de}	37.7±0.42^{h}	117.8±0.84^{bc}	4.3±0.42^{abc}	41.2±0.28^{d}	23.5±0.70^{ab}	61.8±0.28^{b}	107.5±0.14^{c}
L2D	55.5±0.42^{b}	34.3±1.27^{i}	124.2±0.84^{ab}	4.2±0.56^{abc}	47.3±0.14^{b}	25.3±0.42^{a}	65±0.84^{a}	112.4±0.56^{a}
L2F	50.6±1.69^{d}	39.3±0.70^{fg}	127.2±2.12^{a}	4.80±0.5^{ab}	56.3±0.42^{a}	22.25±0.07^{bc}	45.2±0.56^{ef}	111.8±1.13^{ab}
L1Y	36.15±0.35^{g}	40.35±0.63^{ef}	78.4±0.84^{g}	4.05±0.21^{cde}	25.8±1.55^{h}	18±0.42^{f}	28.2±0.42^{h}	99.1±0.84^{f}
L2Y	47.9±0.56^{e}	37.95±0.21^{gh}	99.15±0.63^{ef}	3.05±0.35^{ef}	21.7±1.69^{i}	19.42±0.42^{ef}	30.95±0.77^{h}	100.95±1.05^{e}
L1Dj	40.5±1.97^{f}	44.3±0.84^{ab}	68.15±1.06^{h}	5.00±0.14^{a}	16.29±0.84^{j}	17.75±1.62^{f}	30.75±1.76^{h}	91.25±1.06^{h}
L2Dj	37.9±0.28^{g}	42.2±0.42^{cd}	72.9±0.56^{gh}	3.85±0.49^{def}	35.25±0.63^{f}	20.5±0.49^{de}	36.15±0.77^{g}	110.8±0.28^{b}
L1B	40.95±0.49^{f}	40±0.98ef	91.03±0.19^{f}	3.05±0.21^{ef}	38.65±1.2^{e}	19.45±0.77^{ef}	43.2±0.98^{f}	88.95±0.07^{i}
L2B	42.1±0.56^{f}	43.3±0.84^{bc}	114.95±3.74^{cd}	3.20±0.56^{def}	43.6±0.56^{c}	22±1.27^{bcd}	46.3±0.56^{def}	90.75±0.35^{h}
Mean	47.29±0.61	40.70±0.71	89.87±2.52	3.83±0.42	32.91±0.92	21.07±0.76	44.74±1.08	100.97±0.50
LSD(0.05)	2.4	1.85	10.25	0.95	2.4	2.05	4.0	1.7

Local 1 Figuil (L1F), Local 1 Doulo (L1D), Local Podoko (LP), Local Mora (LM), Local 2 Doulo (L2D), Local 2 Figuil (L2F), Local 1 Yagoua (L1Y) and Local 2 Yagoua (L2Y), Local 1 Djamena (L1Dj), Local 2 Djamena (L2Dj), Local 1 Banki (L1B) and Local 2 Banki (L2B). DF: days to 50% flowering; DFM: days from flowering to capsule maturity; PH: Plant height; NB: number of branches; NC/P: number of capsules per plant, CL: capsule length; NS/C: number of seeds per capsule and DM: days to maturity. Means with the same subscript within the same column do not differ ($p > 0.05$); LSD (0.05): Least significant difference at 5% level.

Table 2: Computation of mean squares for ANOVA of 6 x 6 half diallel tables for yield components

Source	Df	DF	DFM	PH	NB	NC/P	CL	NS/C	DM
Repetition	2	0.37^{ns}	0.87^{ns}	3.40^{ns}	0.21^{ns}	2.88^{ns}	0.10^{ns}	1.92^{ns}	0.62^{ns}
a	5	20.5**	30.0**	767.28**	1.88**	487.55**	5.75*	133.2**	104.8**
b	15	14.4**	60.6**	599.86**	1.75**	975.26**	15,36**	209.1**	71.24**
b_1	1	1.15^{ns}	158.5**	537.20**	0.01^{ns}	422.00**	114.1**	1314.4**	87.77**
b_2	5	7.24**	72.3**	138.19^{ns}	0.12^{ns}	241.72**	5.88*	35.89**	21.83**
b_3	9	19.9**	43.2**	863.30**	2.85**	1444.25**	9.65*	182.5**	96.86**
Error	20	0.83	1.91	57.73	0.41	1.03	1.50	7.28	0.40

Df: Degree of freedom; DF: days to 50% flowering; DFM: days from flowering to capsule maturity; PH: Plant height; NB: number of branches; NC/P: number of capsules per plant, CL: capsule length; NS/C: number of seeds per capsule and DM: days to maturity. a = Additive effects of genes; b = dominant effects of genes; b_1 = mean dominance effects; b_2 = additional dominance deviation due to the parents, b_3 = residual dominance effects, * indicates significance at 5%, ** indicates significance at 1%.

For each morphological trait, the genetic parameters (average degree of dominance, direction of dominance, correlation between the degree of dominance and parental value) as well as the broad and narrow sense heritability values were presented in Table 3. Broad and narrow sense heritability for these characters were ranged from 0.66 (number of branches per plant) to 0.99 (number of capsule per plant) and from 0.28 (days from flowering to capsules maturity) to 0.69 (days to maturity). The direction of dominance was positive for all traits except the plant height and number of branches. The average degree of dominance $(H_1/D)^{1/2}$ was greater than one for all traits suggesting over dominance while for other traits. Globally, the parents tested had a moderate proportion of dominant genes. The correlation between parental values (Pr) and recessive factor (Wr+Vr) was positive for plant height (r = 0.90), number of branches (r=0.46), number of capsule per plant (r = 0.83) and days to maturity (r = 0.33) but negative for days to 50% flowering (r = -0.09), days from flowering to capsule maturity (r = -0.67), capsule length (r = -0.80) and number of seeds per capsule (r = -0.92).

Broad sense heritability values were high (0.66 to 0.99) indicating that, these characters are controlled mainly by genetic factors. High heritability values were also suggested for days to 50 per cent flowering, days from flowering to capsule maturity, plant height, number of capsule per plant, capsule length, number of seeds per capsule and days to maturity by Shindhe *et al*. [25]; Rani and Kumar [26]; Bisen *et al*. [27] and Sarwar *et al*. [28]. Narrow sense heritability value (0.28 to 0.60) showed remarkably that all traits are controlled additive and non additive genes with preponderance of by non additive genes except for which days to maturity, number of capsule per plant and number of seeds per capsule. For all traits, the average of degree of dominance $(H1/D)^{1/2}$ was greater than one suggesting over dominance. Globally, the parents had a high proportion of dominant genes. Significant over-dominance for days to 50% flowering was reported by Praveenkumar *et al*. [24]. Kamala [24] observed that, additive and non-additive genes implication for days to maturity. Mishra *et al*. [10] outlined that the plant height and the number of capsule per plant were governed by a preponderance of additive effects. According to Kamala [24]; Krishnaiah *et al*. [30]; Fatteh *et al*. [31], the capsule length and the number of seeds per capsule in sesame were controlled mainly by additive genes.

The positive correlation between parental values (Pr) and recessive factor (Wr+Vr) indicated that recessive genes were in favor of plant height, number of branches, number of capsule per plant and days to maturity. These results are in harmony with the findings of El-Bramawy [21], Sarwar and Haq [28]. In contrast, Kim-Dong *et al*. [32] reported that the number of branches per plant controlled by dominant genes. The association of these yield components with recessive genes might present some difficulties for selection during the early generations. For capsule length, number of seeds per capsule and days from flowering to maturity, correlation analysis of the genotypes showed highly positive dominant genes control, indicating the possibility of early selection.

Table 3: Genetic components estimates and heritability values for sesame yield components based on a 6 x 6 half diallel.

Parameters	DF	DFM	PH	NB	NC/P	CL	NS/C	DM
$(H_1/D)^{1/2}$	1.48	2.89	1.48	1.62	1.97	2.98	1.76	1.07
Kd	0.58	0.67	0.54	0.39	0.35	0.47	0.44	0.50
H	+0.61	+7.1	-13.19	-0.02	+11.69	+6.08	+20.63	+5.33
H^2	0.93	0.96	0.91	0.66	0.99	0.85	0.95	0.99
h^2_n	0.42	0.28	0.41	0.29	0.59	0.31	0.49	0.69
h^2-h_n^2	0.51	0.68	0.50	0.37	0.40	0.54	0.46	0.30
r(Pr,Wr+Vr)	- 0.09	- 0.67*	+0.90*	+0.46	+0.83*	-0.80*	-0.92*	+0.33

DF: days to 50% flowering; DFM: days from flowering to capsule maturity; PH: Plant height; NB: number of branches; NC/P: number of capsules per plant, CL: capsule length; NS/C: number of seeds per capsule and DM: days to maturity. $(H_1/D)^{1/2}$: Average degree of dominance; kd: Proportion of dominant genes; h: Direction of dominance ; h_2: Broad sense heritability; h_2n: Narrow sense heritability. r (Pr, Wr+Vr): Correlation between the degree of dominance of the parents (Wr+Vr) and the parental value (Pr); ns : not significant; * Significant at the 5% level.

The analysis of variance based on Griffing's [14] method showed that, the mean squares of GCA and SCA were significant ($p < 0.05$) for all traits (Table 4). The values of δ^2GCA/ δ^2SCA ratios showed that, SCA variance was higher than GCA variance component (0.16 to 0.80) except for number of seeds per capsule (1.05) and days to maturity (1.29). The significance of GCA and SCA for all traits showed the importance of both additive and dominance effects [16]. The SCA variance was more than GCA variance indicating the role of non-additive gene action for the inheritance of date to flowering, duration of maturation, plant height, number of branches, number of capsules per plant, capsule length. Hence, it is suggested that these characters can be possibly enhanced through exploitation of heterosis [22, 24].The values of δ^2GCA /δ^2SCA ratios and the variance components showed the preponderance of GCA for number of seeds per capsule and days to maturity, demonstrating the influence of additive gene effects [17]. In contrast, Praveenkumar *et al*. [24] observed that days to 50% flowering, days to maturity and plant height was governed mainly by additive genes while and the number of capsule per plant was controlled non-additive gene. In Egypt, El-Bramavy [21] found that GCA had major contributions in genetic variation of yield characters in sesame. However, it could be emphasized that the δ^2GCA /δ^2SCA ratio may not always project the true picture of gene action for a particular character, due to the deferential of parental ability to combine well with each other.

Table 4: Mean square for combining ability for yield components in sesame

Source	Df	DF	DFM	PH	NB	NC/P	CL	NS/C	DM
GCA	5	19.7**	85.31**	660.34**	1.09*	1777.24**	15.50**	249.41**	146.86**
SCA	9	14.3**	36.29**	575.05**	1.68*	587.51**	4.81*	58.91**	28.46**
Error	14	1.5	2.81	69.54	0.88	1.63	2.31	9.38	0.81
δ^2GCA/ δ^2SCA		0.34	0.58	0.28	0.16	0.75	0.80	1.05	1.29

Df: Degree of freedom; DF: days to 50% flowering; DFM: days from flowering to capsule maturity; PH: Plant height; NB: number of branches; NC/P: number of capsules per plant, CL: capsule length; NS/C: number of seeds per capsule and DM: days to maturity. GCA: Variation due to general combining ability; SCA: variation due to specific combining ability; Error: error variation or interaction between the replication and genotypes; δ^2GCA: variance of general combining ability; δ^2SCA: variance of specific combining ability; *and ** indicates significance at $P \leq 0.05$ and $P \leq 0.01$, respectively.

Based on GCA effects (Table 5) good combiners were genotypes LM (-1.28) and L2F (-2.44) for days to 50% flowering, L1F(-2.74) and L1D (-2.09) for days from flowering to capsule maturity, L1F (-7.92) and L1D (-1.39) for days to maturity, L1D (9.45) and L2F (6.84) for plant height, L2F for number of branches per plant and for number of capsules per plant, L1F (0.69) for capsule length and LM (1.74) for number of seeds per capsule. Genetic analysis demonstrated that the parents differed for their general combining ability effects. This result is in line with findings of Praveen kumar *et al*.[24]; Parameshwarappa and Salimath [33]; Kumar *et al*. [34], and Kumar and Kannan [35], for days to 50% flowering, plant height, number of branches per plant, days to maturity, and number of capsules per plant, capsule length and number of seeds per capsule. GCA effects provide a measure of the general potential of genetic material. It's worth to mention that aforementioned sesame genotypes in addition to possessing higher GCA have the highest mean performance of these characters. In this connection, El-Bramawy [21] detected that some parents of sesame were identified as good combiners for seed yield on the basis of their high mean. Therefore, according to the present results, it can be noted that parents L1F and L1D could be used in hybridization program for future improvement of earliness while lines L2D and LM proved the best parents for seed yield components. Considerable association between GCA effects and mean characters of parental lines imply that the value can be used to choose parents with superior combining ability.

Table 6: Predicted general combining ability effects (GCA) for yield components of six sesame cultivars on a 6 x 6 half-diallel.

Lines	DF	DFM	PH	NB	NC/P	CL	NS/C	DM
L1F	1.57**	-2.74**	-7.03**	-0.46*	-17.81**	0.69*	-2.61**	-7.92**
L1D	1.27**	-2.09**	-14.01**	-0.47*	-11.71**	0.16	-2.98**	-1.39*
LP	0.07*	-0.28	5.51**	0.16	-5.15**	-2.23**	-5.73**	1.43*
LM	-1.28**	-1.14**	-0,76**	0.16	0.72*	1.74**	6.32**	4.26**
L2D	0.81*	-0.10	9.45**	0.24*	11.81**	0.57*	7.74**	1.33*
L2F	-2.44**	6.33**	6.84**	0.38*	22.14**	-0.94**	-2.7**	2.28**
SE	0.60	0.93	2.48	0.08	0.48	0.68	3.55	0.20

*Significant at p = 0.05 and **significant at p = 0.01; SE: standard error.

Among fifteen crosses combinations (Table 6), the hybrids LM x L2F (good x moderate general combiners) for days to 50 flowering; L1F x L2F (moderate x poor general combiners) for days from flowering to capsule maturity; LP x L2D (moderate x moderate general combiners) for plant height; L2D x L2F (moderate x moderate general combiners) for number of branches per plant; LM x L2F (good x poor general combiners) for number of capsule per plant; LP x L2F (poor x poor general combiners) for capsule length; LP x LM; L1F x L1D (good x good general combiners) for number of seeds and days to maturity were identified as good specific combiners. There were also positive and negative significant differences in SCA of crosses for all characters. These observations were in agreement with the findings of other studies [35, 36, 37]. The SCA represents the dominance and epistasic, which can be related with heterobeltiosis [33, 36]. It is therefore suggested that SCA performance might be considered as a criterion for selecting the best crosses. Inclusion of F_1 hybrids showing high SCA and having parents with good GCA, into multiple crosses, could be a worthwhile approach for tangible improvement of these traits. Thus, hybrid combinations with high means, favourable SCA and involving at least one of the parents with high GCA, would tend to increase the concentration of favourable alleles. According to El- Bramawy [21] although sesame is completely self pollinated, breeding method of cross pollinated crop can be use in this species. The low x low or low x moderate general combiners exhibiting high SCA effects suggested gene dispersion and genetic interaction between favourable alleles contributed by both parents [33, 36, 37].. Cross combinations involving poor or moderate combiners might be used through intermating in segregating generations and simultaneous selection for desirable traits.

Table 6: Estimation of specific combining ability (SCA) of fifteen sesame crosses in 6 x 6 half diallel.

Crosses	DF	DFM	PH	NB	NC/P	CL	NS/C	DM
L1F x L1D	-3.00	-0.55	17.79**	0.63*	12.63**	-0.06	6.72**	0.06**
L1F x LP	3.30**	1.55*	20.46**	0.81**	16.02**	-1.67*	-3.63	5.43**
L1F x LM	-2.45**	0.50	-5.26	-0.69	-4.30	-0.74**	-5.18*	3.11*
L1F x L2D	-1.64	0.77	-12.1*	-0.04	-12.93**	1.73*	2.60*	-4.07*
L1F x L2F	-1.64	-2.27*	-20.86**	-0.72*	-11.42**	0.74**	-0.52	-4.52*
L1D x LP	-0.90	-2.00	-18.05**	-0.78*	5.17*	0.35	0.25	-4.79**
L1D x LM	1.75*	-4.15	2.42	0.22	5.91*	0.49	4.00	-1.82**
L1D x L2D	1.36	7.92**	-10.79*	-0.97**	-11.68**	0.55	-7.83**	2.61**
L1D x L2F	0.81	-1.22	8.62*	0.89*	-12,02**	-1.34*	-3.15	3.96**
LP x LM	-0.85	4.65**	-4.60	0.29	-0.16	2.48**	4.35**	-1.54**
LP x L2D	-0.04	-5.74**	14.69**	0.91*	-5.15	-1.52	-3.00	0.68*
LP x L2F	-1.49*	1.55	-12.50**	-1.23	-15.88**	0.35*	-3.00	0.23
LM x L2D	2.51**	-2.94	-4.54	-1.23	-5.51	-1.62*	-3.33*	0.36
LM x L2F	-2.17*	1.93	11.97**	0.57*	4.06*	-0.61	0.15	-0.09**
L2D x L2F	-2,44**	0.01	12.76**	0,48*	4.06	0.85**	6.53**	0.43*
SE	0.46	1.10	33.36	0.22	0.61	0.90	4.28	0.28

SE: Standard error; *significant at p = 0.05 and **significant at p = 0.01.

CONCLUSION

Sesame genotypes were highly variable for yield components. These characteristics could be genetically improved and were controlled by additive and non additive genes. Recurrent selection might be a useful breeding strategy. Improved methods to predict genetic gain and evaluate these quantitative traits without the environmental influence are also needed.

ACKNOWLEGEMENT

Authors are thankful to Prof UKAI YASUO of the University of Tokyo for providing the DIAL computer program used to carry out the present work.

REFERENCES

1. Ram R, Catlin D, Romero J, Cowley C**;** Sesame: New Approaches for Crop Improvement. Timber Press, USA, 1990: 100-115.
2. Chakraborthy GS, Sharma G, Karishik KN; *Sesamum indicum*: a review. Journal of Herbal Medicine and Toxicology, 2008; 2(2): 15-19.
3. Shahidi F, Liyana-Pathirana CM, Wall DS; Antioxidant activity of white and black sesame seeds and their hull fractions. Food Chemistry, 2006; 99: 478-483.
4. Bedigian D; Evolution of sesame revisited: domestication, diversity and prospects. Genetic Resources and Crop Evolution, 2003; 50: 779-787.
5. Attibayeba, Nsiba-Mikolo E, Nkounkou JS, Djianga JGC, Mandoukou-Yembi F; Description of different growth stages of *Sesamum indicum* L. using BBCH scale. Pakistan Journal of Nutrition, 2010; 9(3): 235-239.
6. Ashri A; Sesame breeding. Plant Breeding Review, 1998; 16: 179-228.
7. Menzir A; Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum*

indicum L.) genotypes. Nature and Science, 2012; 10(10): 117-126.
8. AGRI-STAT; Annual Statistics of 2007 and 2008 Agricultural Production, Number 16, Ministry of Agriculture and Rural Development, Yaoundé, Cameroon, 2010: 98-101.
9. Ibrahim SE, Khidir MO; Genotypic correlation and path coefficient analysis of yield and some yield components in sesame (*Sesamum indicum* L.). International Journal of Agriculture and Science, 2012; 2(8): 664-670.
10. Mishra HP, Misra RC, Sahu PK; Combining ability and nature of gene action in sesame *(Sesamum indicum* L.). Indian Journal of Agricultural Research, 2009; 43 (2): 119-123.
11. Pham TD, Thi Nguyen TD, Carlsson AS, Minh Bui T; Morphological evaluation of sesame (*Sesamum indicum* L.) varieties from different origins. Australian Journal of Crop Science, 2010; 4(7): 498-504.
12. Sandipan C, Animesh KD, Aditi S, Sonali S, Rita P, Susmita M, Ananya D; Traits influencing yield in sesame (*Sesamum indicum* L.) and multilocational trials of yield parameters in some desirable plant types. Indian Journal of Science and Technology, 2010; 3(2): 163-166.
13. Ukai Y; DIAL 98. Program for the analysis of full half diallel table. University of Tokyo, Japan, 2002: 18p. Available from http://plach.ab.a.u-tokyo.ac.jp.
14. Griffing B; A generalized treatment of the use of diallel crosses in quantitative inheritance. Heredity, 1956; 30: 31-51.
15. Walters DE, Morton JR; On the analysis of variance of a half diallel table. *Biometrics*, 1978; 34: 91-94.
16. Hayman B; The theory and analysis of diallel crosses. Genetics, 1954; 39: 789-809.
17. Mather K, Jinks JL, Biometrical Genetics. Chapman and Hall. 2nd edition, London, 1982: 179- 282.
18. Kearsey MJ, Pooni HS, The Genetical Analysis of Quantitative Traits. Chapman and Hall. 1st edition, London, 1996: 189-301.
19. Shekhawat RS, Rajput SS, Meena SK, Singh B; Variation and character association in seed yield and related traits in sesame (*Sesamum indicum Linn.*). Indian Research Journal of Genetics and Biotechnology, 2013; 5(3): 186-193.
20. El-Bramawy MAS, Shaban WI; Inheritance of yield, yield components and resistance to major diseases in *Sesamum indicum* L. Spanish Journal of Agricultural Research, 2008; 6(4): 623-628.
21. El-Bramawy MAS; Genetic analyses of yield components and disease resistance in sesame (*Sesamum indicum* L.) using two progenies of diallel crosses. Research Journal of Agronomy, 2010, 4(3): 44-56.
22. Banerjee PP, Kole PC; Combining ability analysis for seed yield and some its components characters in sesame (*Sesamum indicum* L). International Journal of Plant Breeding and Genetics, 2009; 3(1):11-21.
23. Kurdistani R, Tohidinejad E, Mohammadi-Nejad G, Zareie S; Yield potential evaluation and path analysis of different sesame genotypes under various levels of iron. African Journal of Plant Sciences, 2011; 5(15): 862-866.
24. Praveenkumar K, Madhusudan HL, Nadaf R, Patil K, Deshpande SK; Combining ability and gene action studies in inter-mutant hybrids of sesame (*Sesamum indicum* L.). Karnataka Journal of Agricultural Sciences, 2012; 25 (1): 1-4.
25. Shindhe GG, Lokesha R, Vasudevan SN, Naik MK; Phenotypic characterization of F_3 progenies in sesame (*Sesamum indicum* L.). Plant Archives, 2011; 11(2): 875-877.
26. Rani PJ, Kumar PVR; Genetic parameters of yield and yield components pooled over environments in sesame (*Sesamum indicum* L.). International Quarterly Journal of Biology and Life Sciences, 2013; 1(4): 231-234.
27. Bisen R, Tripathi A, Ahirwal RP, Paroha S, Sahu R, Ranganatha ARG; Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. International Quarterly Journal of Life Sciences, 2014; 8(4): 1387-1391.
28. Sarwar G, Haq MA, Chaudhry MB, Rabbani I; Evaluation of early and high yielding mutants of sesame (*Sesamum indicum* L.) for different genetic parameters. Journal of Agricultural. Research, 2008; 46(2): 125-133.
29. Kamala T; Gene action for seed yield and yield components in sesame (*Sesamum indicum* L.). Journal of Agricultural Sciences, 1999; 69: 73-74.
30. Krishnaiah G, Reddy KR, Reddy GLK, Sekhar MR; Combining ability in sesame**.** Crop Research, 2003; 24(1): 72-76.
31. Fatteh UG, Patel NA, Chaudhari FP, Dangaria CI, Patel PG; Heterosis and combining ability in sesame (*Sesamum indicum* L.). Journal of Oil Seeds Research, 1999; 12: 184-190.
32. Kim-Dong H, Kang-Chul W, Shim-Kang B, Park-Chang H, Lee-Sung W; Genetic analysis of shattering habit and some quantitative characters in sesame. Korean Journal of Crop Science, 2007; 52(2): 198-203.
33. Parameshwarappa SG, Salimath PM; Studies on combining ability and heterosis for yield and yield components in sesame (*Sesamum indicum* L.). Green Farming, 2010; 3(2): 91-94.
34. Kumar KB, Vivekanandan P; Studies on combining ability studies in sesame (*Sesamum indicum* L.). Electronic Journal of Plant Breeding, 2009; 1: 33-36.
35. Kumar PS, Kannan B; Studies on general and specific combining ability in sesame (*Sesamum indicum* L.). Electronic Journal of Plant Breeding, 2010; 1(6):1405-1408.
36. Vijayarajam S, Siruthaiyur KG, Mahalingam G; Generation mean analysis for quantitative traits in sesame. Genetics and Molecular Biology, 2007; 30(1):80-84.

37. Bayoumi TY, El-bramawy MAS; Genetic analyses of some quantitative characters and *Fusarium* wilt disease resistance in sesame. African Crop Science, 2007; 8: 2198-2204.