Combing Ability for Seed Yield and Agronomic Traits of Sesame Genotypes (*Sesamum indicum* L.) from Western Ethiopia

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Abstract

Knowledge of the genetic control of characters is essential for breeders to decide on the breeding procedure to follow. The aim of this study was to determine the nature of gene action in the inheritance of major quantitative traits in sesame. Ten parents of sesame were crossed in year 2011 in a 10 x 10 full diallel mating system. Data were collected for major agronomic traits, grain yield and oil content. F_1 progenies along with their parents were evaluated during 2012 cropping season in a randomized complete block design with three replicates at Uke and Wama trial sites of Bako Agricultural Research Center. For all traits, general (GCA) and specific (SCA) combining abilities were highly significant. Mean square for reciprocal effects were significant for all traits except plant height. Inbred lines Dicho, EW002, BG006, Obsa and EW003-1 had positive GCA effects for seed yield per plant. Parental line BG006 had high GCA for oil content. For seed yield per plant, direct crosses BG006 x EW003-1, EW023-2 x Wama, EW003-1 x EW019 and EW003-1 x EW010-1 had high SCA effects, while EW019 x Dicho and Obsa x Dicho had high SCA for oil content. For seed yield per plant, reciprocal crosses EW010-1 x EW002, EW006 x BG006, EW003-1 x EW023-2 and Dicho x EW006 were good combiners. Reciprocal cross Wama x EW019 was the best for its high SCA for oil content. The predominance of non-additive gene actions in all traits considered in this study suggested the exploitation of hybrid vigor as the best approach in sesame breeding. The result of this experiment indicated that maternal effects were important in sesame breeding for high seed yield.

Key words: Gene action; General combining ability; Reciprocal effects; Specific combining ability

Introduction

Sesame (*Sesamum indicum* L.) a self-pollinated crop, is an ancient cultivated oil crop and thought to have originated from Africa, most probably in Ethiopia (Weiss, 2000). It is the leading oil crop for export in Ethiopia (Geremew, 2012). Sesame 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 (Chakraborthy *et al*., 2008). Sesame oil contains vitamin E and several important anti-oxidative constituents such as sesamol, sesamin and sesamolin, which are believed to promote the integrity of body tissues in the presence of oxidizing compounds (Shahidi *et al*., 2006). Compounds in sesame oil have multiple physiological functions, such as estrogenic activity, providing anti-inflammatory functions that are helpful to decrease blood lipids and arachidonic acid levels (Bedigian, 2003).

The genetic diversity of Ethiopian sesame landraces and cultivars showed the existence of great genetic variability between the landraces (Daniel and Parzies, 2011; Ahadu, 2012; Mohammed, 2015).This suggests that effective utilization of the available sesame genetic resources will create a better chance for sesame crop improvement in Ethiopia. In addition, reports indicate that the availability of potential arable land in different parts of the country suitable to grow the crop (Sorsa, 2009).

In the past few years, the area under sesame production in Ethiopia was increased by 45%, resulting 54% increase in production (Zerihun, 2012). The increase in the sesame area of coverage and production is mainly attributed to an increasing demand for Ethiopian sesame seed in the international market. But the productivity of the crop was stagnated and the national estimated average seed yield was less than one tone. The potential to increase the production of sesame in Ethiopia is high and production per hectare can be doubled with the use of improved seeds and management practices (Wijnands *et al.*, 2009).

Cognizing the economic importance of sesame, research has been making utmost breeding effort for the last five decades in Ethiopia (Musa *et al*., 2011). The main objective was to improve productivity of the crop through breeding of high yielding and disease tolerant cultivars. As a result, 21 varieties of sesame were released so far in Ethiopia (MoA, 2016). Despite the efforts over the past many decades, the maximum yield potential of sesame in Ethiopia has not been achieved mainly due to shortage of improved varieties. Therefore, there is an urgent need to augment sesame productivity through the incorporation of genes for high yield, disease tolerance and wide adaptability.

The identification of superior parents and designing suitable breeding methodology are the most important pre-requisites for the development of high yielding genotypes. Knowledge of the genetic control of characters is essential to the breeder when choosing parental lines and deciding the type of selection method and breeding procedure to follow (Esmail, 2007). Diallel analysis is one of the mating designs that enable to generate useful genetic information for quantitative traits (Viana *et al.*, 2001). From diallel analysis, plant breeders are able to gather information on heterosis and the effects due to reciprocal, maternal, general combining ability (GCA) and the specific combining ability (SCA) of parents in crosses (Murray *et al.*, 2003; Glover *et al.*, 2005), enabling knowledge based selection methods and parental choice.

Several types of diallel analyses have been used for various combining ability studies (Jinks and Hayman, 1953; Hayman, 1954a; Dickinson and Jinks, 1956; Griffing, 1956a; Gardner and Eberhart, 1966). Griffing's methods have commonly been used among plant breeders to determine GCA and SCA effects in crops like maize (Velu *et al*., 2011; Berger *et al*., 2012). The GCA and SCA effects have been further used for genetic diversity evaluation, inbred line selection, heterotic pattern classification, heterosis estimation, and selecting the best combiner (Melani and Carena, 2005; Barata and Carena, 2006). Genetic analysis based on a large number of progenies from diverse parents is essential for formulating an efficient strategy for varietal development. Such analysis enables broad inferences to be drawn about the nature of gene effects and estimate combining abilities of different genotypes using diallel analysis. To obtain more reliable genetic information, multi-environment data are generally needed (Alphonse, 2011).

Several studies on combining ability of sesame have been reported elsewhere on yield and its components (Preveenkumar *et al*, 2012; Salunke and Lokesha, 2013; Abatchoua *et al.*, 2014; Ahmed and Adam, 2014; Azeez and Morakinyo, 2014). However, such type of information is scanty in Ethiopia. The objective of this study was, therefore, to determine the combining abilities in the inheritance of important quantitative characters in sesame.

Materials and Methods

Planting materials

The experimental material comprised ten morphologically diverse sesame genotypes viz., EW002, BG006, EW023-2, EW006, EW003-1, EW019, Obsa, Dicho, Wama and EW010-1.Obsa and Dicho are released cultivars while EW002, BG006, EW023-2, EW006, EW003-1, EW019 and Wama were elite breeding lines.

All these genotypes were collected from Western Ethiopia. During 2010, main season a single plant from each genotype was selected and multiplied in 2010 off-season to get a pure line. These ten genotypes were crossed in 10 x 10 diallel mating design, including reciprocals in 2011cropping season.

Field design and management

Seeds of all F_1s and their parents were planted at Uke (1383 meters above sea level) and at Wama (1436 meters above sea level) testing sites of the Bako Agricultural Research Center (BARC) on June 2012. A randomized complete block design with 3 replications was used. Each plot consisted of a single row of 5 m long with 50 cm and 25 cm inter and intra row spacing, respectively. The seeds were drilled in each row at seeding rate of 5 kg ha^{-1}. Twenty days after planting, the plants were thinned out to adjust for required population per hectare. Nitrogen fertilizer in the form of Urea was applied as side dressing four weeks after emergence at the rate of 50 kg ha^{-1}. Hand weeding was carried out four times at three weeks interval starting twenty days after planting. Data for days to flowering and maturity were recorded on a plot basis. Observations were made on ten randomly selected plants for branches per plant, plant height, capsules per plant, 1000 seed weight, seed yield per plant and percentage oil content.

Statistical analysis

Analysis of variance (ANOVA) was conducted with the PROC MIXED procedure (SAS, 2002) considering genotypes as fixed effects and replication as random. General combining ability (GCA) effects of the parents, specific combining ability (SCA) and reciprocal effects (REC) were estimated from the means obtained for each character following Griffing's Method I and Model I (fixed) of diallel analysis (Griffing, 1956a) using a modification of the DIALLEL-SAS program (Zhang and Kang, 1997). The significance of mean squares for GCA, SCA and REC was tested using the corresponding interaction with the locations (L) as the error terms. The significance of GCA x L, SCA x L and REC x L was determined using the pooled error. The relative importance of GCA and SCA was estimated according to Baker (1978) as the ratio of $2\sigma^2$GCA/($2\sigma^2$GCA + $2\sigma^2$SCA), where $2\sigma^2$GCA and $2\sigma^2$SCA are the variance components for GCA and SCA, respectively.

Results and Discussion

The mean squares from the combined analyses of variances for all characters are given in Table 1. Significant differences were observed among the genotypes for all characters demonstrating the presence of genetic variability among the genotypes.

Table 1. Combined analysis of variance for eight traits in sesame

S.V.	df	DF	DM	PH	BP	CP	TSW	YP	OC
Location (L)	1	20.5*	1064.0**	5815.7**	3.68	349209.3	5.5**	164.0**	37.0**
Reps (L)	4	61.3**	11.7*	733.7**	44.8**	17464.1**	0.1*	187.1**	9.1**
Genotypes	99	19.4**	14.1**	376.6**	7.5**	5530.9**	0.2*	51.8**	6.5**
Genotypes x L	99	7.5**	7.2**	255.2**	4.5**	5189.8**	0.1*	48.4**	2.6**
Error	396	4.4	3.9	166.9	2.3	1621.4	0.04	15.7	1.3

S.V.= source of variation; *, ** significant at 0.05 and 0.01 probability level, respectively; DF=days to flowering, DM=days to maturity, PH=plant height (cm), CP=capsules per plant, TSW= 1000-seed weight (g), YP= yields per plant (g) and OC= oil content (%)

The mean squares due to GCA, SCA and REC and their interaction with locations for all traits is presented in Table 2. The mean square due to GCA was highly significant for all traits, indicating that these parents were different for frequencies of additive favorable alleles. The mean squares for GCA x L was also significant for capsules per plant and thousand seed weight, suggesting that GCA effects associated with these traits were not consistent over locations. The larger magnitude of GCA mean squares compared to GCA x L mean squares for all traits, demonstrated that interaction effects might be of relatively minor importance for these traits. General combining ability (GCA) and SCA can interact with the environment and cause changes in expected parental combining abilities over the environments (Singh *et al*., 1992). Therefore, to obtain precise combining ability estimates, it may be necessary to evaluate parents in more than one location. The SCA x L were significant for days to flowering, days to maturity, branches per plant, capsules per plant, thousand seed weight and yield per plant, showed that the SCA effects were varied over the two locations.

The overall reciprocal effect was significant for all traits except for plant height, signifying that reciprocal crosses are important for these traits. This may be due to the influence of the maternal effect or cytoplasmic influence, which could be well ascertained in the later segregating generations. For days to flowering, capsules per plant, yield per plant and oil content REC x L was significant, demonstrating that the effect of REC was affected by location effects for these traits. The reciprocal effect, if significant, may create operational difficulty in arranging controlled pollination for seed production (i.e. male and female are not inter-changeable in the mating) and in genetic analysis if it was not accounted for (Wu and Matheson, 2001).

Table 2. GCA, SCA, REC, and their interaction with environment in a 10 x10 diallel crosses and GCA to SCA ratio

Source	df	Mean squares							
		DF	DM	PH	BP	CP	TSW	YP	OC
GCA	9	26.30**	80.86**	1128.29 **	26.75**	7172.64 **	0.28**	64.5**	7.79**
SCA	45	19.12**	7.31 *	371.59**	5.42 **	6435.92 **	0.18**	59.7**	3.78**
REC	45	18.44**	7.47 *	204.69 ns	5.71 **	4651.47 **	0.09*	43.5**	4.02**
GCA x L	9	2.79ns	5.87 ns	270.68 ns	2.75 ns	3774.85**	0.20**	34.02ns	2.30ns
SCA x L	45	6.65*	7.81 *	285.54 ns	5.21 *	5931.76**	0.1**	55.5**	2.17ns
REC x L	45	9.50**	7.05 ns	223.01 ns	4.49 ns	4716.70**	0.08 ns	45.3**	4.58**
Error	396	4.45	5.38	214.2	3.30	188.96	0.06	26.7	2.32
GCA:SCA		0.73	0.96	0.86	0.91	0.69	0.76	0.68	0.80

*, ** significant at P≤ 0.05 and P≤ 0.01 probability level; GCA= general combing ability, SCA=specific combing ability, REC=reciprocal effects, and L=Location

Estimates of GCA effects for F_1 generation in eight traits of sesame were shown in Table 3. For days to flowering and days to maturity, EW010-1 was the best combiner for earliness for its high negative GCA effect. Praveenkumar *et al*. (2012) also reported significant and negative GCA effect for these two traits in sesame. On the other hand, two parental line viz., Wama for days to flowering and EW023-2 for both days to flowering and days to maturity exhibited significant and positive GCA effect, indicating that these parents are important in breeding for lateness. Inbred line EW023-2 exhibited highly significant positive GCA effect for plant height, suggesting that it is a good combiner for tallness. For this trait Preveenkumar *et al.* (2012), reported additive gene action earlier in sesame. Conversely, EW019 and EW010-1 exhibited highly significant negative GCA effect for plant height, implying that these parents are good combiners for reducing plant height. For thousand seed weight, inbred lines EW002, BG006 and Wama exhibited significant positive GCA effect, suggesting that these they are good combiners for this trait. This trait was reported to be governed by additive gene effects in sesame (Singh, 2007).

For seed yield per plant and capsules per plant Dicho, EW002, BG006, Obsa and EW003-1, demonstrated positive GCA effect, indicating that these parents exhibited above average combiners for these traits. In contrast, EW019 and EW010-1, illustrated significant negative GCA effect for seed yield per plant, showing that these parents are poor combiners for this trait. A parent with a GCA estimate of 0 (zero) has an average combining ability and depending on the index used, parents with positive or negative GCA values perform above or below average (Alphonse, 2011). Kumar and Kannan (2010) also reported high GCA effect for seed yield per plant in sesame. Inbred line BG006 showed highly significant positive GCA effect for oil content, implying that it is good combiner for this trait whereas EW002 is poor combiner.

Among all the genotype, no parent was with good GCA effect for all traits. Nevertheless, EW023-2 is good general combiner for four traits viz., days to flowering, days to maturity, for plant height and branches per plant. Since none of the parents showed desirable combining ability for majority of the traits multiple crosses involving more than two parents would be an appropriate technique to be employed in the development of cross-combinations and or selection of superior recombinants in the segregating generation (Banerjee *et al.,* 2009).

Table 3. Estimates of GCA effects among 10 parents of sesame in for eight traits

Inbred line	DF	DM	PH	BP	CP	TSW	YP	OC
EW002	-0.33	-0.34	-1.62	0.05	6.57	0.07**	0.56	-0.54**
BG006	-0.38	-0.30	0.24	-0.15	6.56	0.03*	0.47	0.35**
EW023-2	0.98**	2.20 **	6.8**	1.21**	-0.11	0.01	0.05	-0.24
EW006	0.24	0.10	0.01	0.14	-0.05	-0.08**	0.04	-0.13
EW003-1	-0.18	-0.11	1.11	0.09	3.96	-0.05*	0.4	0.10
EW019	-0.10	-0.30	-4.44**	-0.35*	-11.97*	0.00	-1.15*	-0.07
Obsa	-0.12	-0.41	-0.54	-0.07	4.51	-0.03	0.43	0.18
Dicho	-0.07	-0.26	1.14	-0.14	6.81	0.03	0.64	0.10
Wama	0.53*	0.21	0.83	-0.31 *	-1.32	0.05*	-0.01	0.13
EW010-1	-0.56**	-0.77**	-3.52**	-0.47 **	-14.96**	-0.03	-1.47**	0.10
SE(gi)	0.20	0.22	1.22	0.14	4.82	0.02	0.41	0.12
SE (gi-gj)	0.22	0.31	2.12	0.21	7.93	0.5	0.75	0.19

*, ** significant at $P \leq 0.05$ and $P \leq 0.01$ probability level, respectively; DF=days to flowering, DM=days to maturity, PH= plant height, BP=branches per plant, CP= capsules per plant, TSW=Thousand seed weight, YP=yield per plant, and OC= oils content (%)

The estimate of SCA effect for 45 cross combinations for eight traits in F_1 generation are presented in Table 4. Use of specific combining ability is considered the best method for selection of superior hybrid in a given crop. The mean squares due to SCA for all studied traits were highly significant, implying that non-additive gene is important to control the studied traits. This result is in line with the findings by Parameshwarappa and Salimath (2010), Kumar and Kannan (2010) and Ahmed and Adam (2014) in sesame.

For days to flowering, crosses such as EW002 x EW003-1, BG006 x Wama, EW023-2 x Dicho, EW0019 x Wama, Obsa x Dicho and Obsa x Wama were good combiners for earliness. These were similar with the results obtained by Praveenkumar *et al*. (2012) in crosses of sesame. Two crosses such as EW002 x EW019 and BG006 x EW006 showed significant and negative SCA effect for days to maturity, indicating that they are good combiners for earliness. For plant height, EW003-1 x Obsa and EW003-1x Wama elucidated significant negative SCA effect, suggesting that these crosses are good combiners for reduced plant height. Conversely, EW006 x EW003-1, EW006 x EW019 and Dicho x Wama, demonstrated significant positive SCA effect for the same trait. Mothilal and Manoharan (2014) also reported high SCA effect for plant height in sesame.

For capsules per plant BG006 x EW003 -1, EW023-2 x Wama , EW003-1 x EW019 and Dicho x Wama showed highly significant positive SCA effects, implying that these crosses are important for high number of capsules per plant. Salunke and Lokesha (2013) also reported high SCA for capsules per plant in sesame. For thousand seed weight crosses viz., BG006 x EW019, EW006 x EW003-1, EW003-1x Wama and Wama x EW010-1 are good combiners. The respective parents of these four crosses possessed high x low, low x low, low x high and high x high combination of GCA effects. Furthermore, the result of this study showed that parents crossed with low x low GCA effects could produce hybrids with superior SCA effect. This type of hybrids is known to have non- additive x non-additive gene action, which can be improved by intermating. On the other hand, Diwakar and Singh (1993) and Amarath and Subramaniam (1992) suggested that the crosses with high GCA effects generally gave high SCA effects.

According to Sprague and Tatum (1942), the general combining ability is due to the additive factors and specific combining ability is due to the non-additive effects including dominance and epitasis. Hence, in these cases high seed yielding ability of the cross is due to both additive as well as non-additive gene effects. For yield per plant, BG006 x EW003 -1, EW023-2 x Wama, EW003-1 x EW019 and EW003-1 x EW010-1showed superior SCA effects, suggests that these crosses are good combiners for this trait. Kumar and Kannan (2010) also reported superior hybrid for seed yield per plant in sesame. On the other hand, BG006 x EW003-1 showed significant negative SCA effect, indicating this cross is poor combiners for seed yield per plant. Uniquely both parents of this cross possess medium GCA effect. The immediate hybrid may not perform well despite both the parents possessing high GCA effects for a trait, due to interaction of the parental GCA effects, which may cause distortions on expectations (Kumar and Bharathi, 2009).

Besides seed yield, oil content is an important economic trait for sesame which breeders aim to improve. For oil content, BG006 x Dicho, EW023-2 x

EW010-1, EW006 x EW003-1, EW006 x EW019, EW003-1 x EW010-1, EW019 x Dicho and Obsa x Dicho showed positive significant SCA effect, implying that these crosses are good combiners for this trait. The parents of these all crosses had high x medium, low x medium, low x low and medium x medium GCA effects, indicating that there is inconsistent relationship between GCA and SCA effects. This inconsistent relationship between GCA and SCA effects might be due to complex interaction of genes as suggested by Matzinger and Kempthorne (1956) and Hayman (1958).

None of all the crosses showed combination of SCA effects for all the traits simultaneously. However, EW023-2 x Wama was good general combiner for four traits viz., days to flowering (for lateness), branches per plant, and capsules per plant and yield per plant. For three traits such as branches, capsules per plant and yield per plant, BG006 x EW003 -1 was good combiner and for plant height, thousand seed weight and oil content EW006 x EW003-1 was a good combiner.

For all the studied traits, the GCA ratio to SCA was less than one, indicating that non-additive effects were more important than additive effects. Ragiba and Reddy (2001) reported similar result for oil content in sesame. On the other hand, Rajaravindram *et al*. (2000), Devasena *et al*. (2001) and Rajput *et al.* (2005) reported higher GCA than SCA for days to flowering, days to maturity, plant height, capsules per plant, yield per plant and thousand seed weight in sesame.

Table 4. Estimates of SCA effects in F_1 generations for eight traits in sesame in a 10x10 diallel crosses

Direct Cross	DF	DM	PH	BP	CP	TSW	YP	OC
EW002 x BG006	-0.23	-0.16	-4.04	0.47	19.72	0.01	1.9	0.38
EW002 x EW023-2	-0.19	1.16	5.51	0.27	-3.42	-0.12	-0.12	0.3
EW002 x EW006	0.12	-0.23	-0.46	-0.83	5.76	-0.03	0.39	-0.05
EW002 x EW003-1	-2.93**	-0.35	-6.82	-0.11	-60.3**	-0.09	-5.93**	-0.79*
EW002 x EW019	-0.52	-1.41*	-3.69	0.33	12.68	0	0.96	-0.52
EW002 x Obsa	-0.91	-0.38	1.99	-0.36	2.85	-0.09	0.01	0.21
EW002 x Dicho	0.94	-0.78	-1.11	-0.62	-4.18	-0.06	-0.62	-0.37
EW002 x Wama	0.75	0.73	-1.13	-0.04	8.28	-0.06	1.12	0.6
EW002 x EW010-1	0.52	0.3	2.3	-0.28	8.09	-0.04	1.05	0.12
BG006 x EW023-2	0.52	-0.71	6.61	-0.77	0.74	0.01	0.15	-0.58
BG006 x EW006	-0.98	-1.52 *	-6.33	-0.71	-20.06	-0.05	-1.69	-0.44
BG006 x EW003 -1	0.77	0.6	5.8	0.92 *	47.42**	-0.14*	4.13**	0.23
BG006 x EW019	2.36**	1.46*	-1.47	-0.37	5.69	0.27**	0.47	-0.58
BG006 x Obsa	0.05	1.07	0.79	0.26	19.78	-0.07	2.07	0.32
BG006 x Dicho	-0.17	-1.24	0.01	0.33	-8.59	0.03	-0.5	1.06**
BG006 x Wama	-2.28**	0.36	-1.58	-0.49	-24.04	-0.08	-2.55*	0.12
BG006 x EW010-1	0.23	0.43	-5.64	-0.33	-11.56	-0.15*	-1.08	0.35
EW023-2 x EW006	-0.86	-0.03	1.85	-0.4	-10.12	0.04	-1.2	-0.18
EW023-2 x EW003-1	-0.01	-0.82	6.05	0.22	-14.7	0.02	-1.2	0.32
EW023-2 x EW019	0.07	-0.37	-5.7	-0.4	3.62	-0.11	0.11	-0.4
EW023-2 x Obsa	1.57*	0.31	5.57	0.22	-1.11	-0.05	-0.41	0.5
EW023-2 x Dicho	-1.29*	0.91	-5.61	0.38	14.5	-0.15*	1.35	-0.42
EW023-2 x Wama	1.84**	-0.47	-1.06	0.97 *	38.80**	0.07	3.99**	-0.28
EW023-2 x EW010-1	-0.22	-0.66	4.13	0.3	0.44	0.04	0.01	0.74*
EW006 x EW003-1	-0.35	-0.63	11.70**	0.21	21.54	0.35**	2.08	0.80*
EW006 x EW019	0.14	0.88	9.26*	0.24	-1.01	0	-0.06	0.81*
EW006 x Obsa	0.67	-0.5	-3.79	-1.12 *	-18.09	0	-1.52	0.55
EW006 x Dicho	0.11	1.34 *	-1.06	0.78	2.61	-0.11	0.14	0.05
EW006 x Wama	1.83**	0.12	-1.59	0.62	-0.41	-0.14*	-0.19	-0.22
EW006 x EW010-1	-0.52	0.18	-5.98	-0.21	-10.36	-0.07	-1.04	-0.28
EW003-1 x EW019	-1.17	-0.81	4.74	-0.37	29.29*	0	2.75*	0.24
EW003-1 x Obsa	0.6	0.63	-10.1**	-0.4	-50.6**	-0.07	-4.73**	-0.6
EW003-1 x Dicho	1.62**	1.06	-3.76	-1.33**	-27.56	-0.05	-2.68	-0.1
EW003-1x Wama	-0.31	0.58	-10.4**	-0.08	-3.26	0.14*	-0.54	0.03
EW003-1 x EW010-1	-0.71	-0.09	-1.34	0.5	31.95	0.09	3.22*	0.89*
EW019 x Obsa	-0.14	0.32	3.98	0.37	-1.42	-0.08	-0.1	-0.25
EW019 x Dicho	-0.53	-0.74	4.87	-0.79	-8.88	0.03	-0.89	0.74*
EW0019 x Wama	-2.06**	-0.05	-1.65	0.53	-21.5	0.1	-1.26	-0.86*
EW019 x EW010-1	0.71	0.68	-6.62	-0.38	-6.44	-0.02	-0.98	0.15
Obsa x Dicho	-2.01**	-0.3	-2.76	-0.83	10.04	0.09	1.22	0.90*
Obsa x Wama	-1.62**	-0.11	3.87	-1.08*	-28.99*	0.03	-3.06*	-0.12
Obs x EW010- 1	1.14	-1.12	3.89	0.5	-1.93	-0.03	0.1	-0.35
Dicho x Wama	-0.43	0.32	8.43*	0.24	39.21**	-0.08	3.72	0.03
EW010 -1 x Wama	-0.43	0.47	2.79	0.24	6.44	-0.01	0.63	-0.85
Wama x EW010-1	1.06	-1	2.34	-0.08	-11.09	0.19**	-1.39	0.28
0.6	0.68	3.7	0.45	14.55	0.06	1.26	0.37	
1.24	1.35	8.16	1.1	37.2	0.15	3.6	0.71	

*, ** significant at P≤ 0.05 and P≤ 0.01 probability level, respectively; DF=days to flowering, DM=days to maturity, PH=plant height (cm), CP=capsules per plant, TSW= 1000-seed weight (g), YP= yields per plant (g) and OC= oil content

Reciprocal effects

The estimates of reciprocal effects for 45 cross combinations for different traits are shown in Table 5. Reciprocal crosses such as Dicho x EW002, Obsa xBG006, EW010-1 x BG006, EW003-1 x EW023-2, Wama x EW006, Wama x EW019 and Dicho x Obsa are good combiners for early flowering. Reciprocal cross Wama x Dicho was good combiner for early maturity. Crosses such as EW010-1 x EW002, EW006 x BG006, EW003-1 x EW023-2 and Dicho x EW006 demonstrated significant positive reciprocal effect for capsules per plant, indicating that these crosses are good combiners for this character.

Reciprocal cross Dicho x EW002, EW006 x EW023-2 and EW010-1 x Obsa were good combiners for thousand seed weight. For seed yield per plant cross such as EW010-1 x EW002, EW006 x BG006, EW003-1 x EW023-2 and Dicho x EW006 exhibited significant positive REC effect, revealing that they were good combiners for this trait. Reciprocal cross Wama x EW019 was good combiner for oil content. The studies by Yao *et al*. (2013) have reported that RECs strongly influenced estimates of SCA effects. The SCA effects were different when a line was used as female from those when the same line was used as male (Mahgoub, 2011). The RECs have been shown to have a major impact on determination of hybrid yield (Yao *et al*., 2013). Fan *et al.* (2014) reported that inclusion of reciprocal crosses in a diallel greatly affected grain yield and estimates of GCA and SCA effects.

According to Cockerham and Weir (1977), reciprocal effects can be further partitioned into maternal (general reciprocal) and non-maternal (specific reciprocal) effects. This further partition may allow the genetic causes of the reciprocal effects to be inferred: e.g., whether it is a true maternal effect caused by cytoplasmic DNA or due to an interaction between nuclear and cytoplasmic DNA or due to purely environmental effects associated with the particular parent crosses. If true genetic maternal effects cause the reciprocal effect, it may persist with the age and may be exploited in the production population. If it is due to environment and interaction between environment and genetic factors, it would increase the bias of the genetic analysis.

Table 6. Estimates of REC effects in 45 reciprocal crosses

	Reciprocal cross	DF	DM	PH	BP	CP	TSW	YP	OC
1	BG006 xEW002	0.58	0.08	-5.5	-58	-33.83*	-0.08	-3.40*	-0.5
2	EW023-2 x EW002	0.66	1.58*	2.75	0.08	-5.83	-0.04	-0.51	-0.16
3	EW006 x EW002	0.91	1.25	-0.83	-0.58	-7.41	-0.03	-1.23	-0.91*
4	EW003-1 x EW002	0.58	0.08	-6.25	-0.58	-35.16*	-0.1	-3.5*	-0.91*
5	EW019 x EW002	-1.25	1.66*	-3.8	-1.91**	-31.41	-0.17*	-3.12*	-1
6	Obsa x EW002	1.33	-0.75	1.41	0.16	20.08	0.06	1.95	-0.16
7	Dicho x EW002	-1.41*	-0.33	-3.83	-0.5	-26.83	0.18*	-2.51	-0.16
8	Wama x EW002	-1.16	-0.33	1.83	0.75	20	0.06	1.9	0.83
9	EW010-1 x EW002	0.16	0.25	-0.08	0.16	31.83*	-0.04	3.22*	0
10	EW023-2 xBG006	0	0.75	-4.75	-0.66	3	0.03	0.4	-0.16
11	EW006 xBG006	0.58	-0.33	6.33	0.08	44.58**	-0.12	4.22**	-0.41
12	EW003-1 xBG006	1.58*	-0.08	-12.08**	-0.75	3.58	-0.03	0.7	-1.33*
13	EW019 xBG006	0.91	0.41	6.41	-0.33	-17.75	0.02	-1.6	-1.16*
14	Obsa xBG006	-1.75**	-0.41	-0.75	0.41	4.66	-0.17*	1.03	-0.33
15	Dicho xBG006	0.58	0.25	1.91	0.25	-13.41	0.01	-1.28	0
16	Wama xBG006	-0.75	0.66	0.91	0.75	3.66	-0.07	0.38	-0.58
17	EW010-1 xBG006	-2.16**	0.08	4.83	0.58	19.66	-0.01	1.85	-0.25
18	EW006 x EW023-2	-0.25	-0.66	5.58	-0.66	15.66	0.14*	1.64	0.08
19	EW003-1 x EW023-2	-1.50*	0.16	11.75**	1.08*	34.25*	-0.09	3.45*	-0.66
20	EW019 x EW023-2	1	-0.58	2.58	-0.83	-3.83	0.01	0.05	0.08
21	Obsa x EW023-2	1.25	-1.33	-1.91	0.41	13.91	-0.02	1.49	-0.75
22	Dicho x EW023-2	2.83**	0.08	4.25	0.5	14.83	-0.05	1.38	0.41
23	Wama x EW023-2	0.75	0.16	1	-1.58**	-4.83	0.04	-0.49	0.41
24	EW010-1 x EW023-2	0.41	-0.5	7.16	-1.08*	19.5	0.11	1.85	0.75
25	EW003-1 x EW006	2.08**	-0.41	-1.58	-0.66	6.08	0.01	0.58	0.58
26	EW019 x EW006	0.33	1.58*	-0.25	-0.25	16.41	-0.09	1.68	0.25
27	Obsa x EW006	2.33**	-1.08	0.08	-0.16	-25	-0.07	-2.65	-0.41
28	Dicho x EW006	-0.33	-0.25	-0.83	-0.83	37.33*	-0.04	3.70**	0.33
29	Wama x EW006	-1.66*	-1	-2.33	0.5	25.83	0.11	2.04	-0.91*
30	EW010-1 x EW006	0.75	0.41	-4.25	0	-17.58	-0.08	-1.42	-0.16
31	EW019 x EW003-1	0.58	0.83	-3	-0.75	-27.08	0.07	-2.38	0.75
32	Obsa x EW003-1	1	-0.66	-0.08	0.16	5	-0.09	0.56	0
33	Dicho x EW003-1	0.75	1.25	-4.75	-0.66	-23.33	0.01	-1.9	-0.5
34	Wama x EW003-1	2.25**	-0.58	1.33	0.58	-4.66	0.02	-0.38	0.25
35	EW010-1 x EW003-1	-0.41	-0.08	2	0.16	0.41	-0.11	0.4	0.08
36	Obsa x EW019	-0.16	-0.66	0.08	-0.33	5.08	0.01	0.23	0.33
37	Dicho x EW019	0.33	-0.08	-1.33	0.08	18.25	-0.02	1.87	0.25
38	Wama x EW019	-2.25**	0.91	-1.33	-0.58	-10	0.13	-0.11	0.83*
39	EW010-1 x EW019	2.08**	0.83	-4.83	-0.16	10.41	0.02	0.84	0.16
40	Dicho x Obsa	-1.66*	-0.91	3.41	-0.33	-15.5	-0.07	-1.6	0.66
41	Wama x Obsa	1	0.08	-3.75	-0.08	1.83	-0.01	0.15	-1.16*
42	EW010-1 x Obsa	0.5	-0.08	2.75	-0.66	10.25	0.17*	0.77	0.41
43	Wama x Dicho	0.08	-2.16 **	-0.5	-1.66**	-8.16	-0.04	-0.4	-0.25
44	EW010-1 x Dicho	0.25	-0.33	1.33	0.66	-5.75	-0.08	-0.51	0.16
45	EW010-1 x Wama	-0.58	0.33	0.75	-0.16	25.08	-0.15*	2.42	-0.33
SE(r)		0.67	0.75	4.09	0.49	16.07	0.07	1.39	0.47

*, ** significant at P≤ 0.05 and P≤ 0.01 probability level, respectively; DF=days to flowering, DM=days to maturity, PH=plant height (cm), CP=capsules per plant, TSW= 1000-seed weight (g), YP= yields per plant (g) and OC= oil content (%),

Conclusions

The overall ANOVA of GCA and SCA were significant for all the traits and for REC it was significant for all traits except plant height. Inbred lines such as Dicho, EW002, BG006, Obsa and EW003-1 had positive GCA effect for seed yield per plant. For oil content, BG006 was the best parent for its high GCA. For yield per plant, direct cross BG006 x EW003-1, EW023-2 x Wama, EW003-1 x EW019 and EW003-1 x EW010-1 while for oil content EW019 x Dicho and Obsa x Dicho had high SCA. For all traits the ratio of GCA to SCA was less than one indicating the predominance of non-additive gene actions. This study showed that exploiting hybrids by using F_1 was the best breeding approach. The relation between GCA and SCA was inconsistent for all the traits. Reciprocal crosses EW010-1 x EW002, EW006 x BG006, EW003-1 x EW023-2 and Dicho x EW006 were good combiners for seed yield per plant while Wama x EW019 was superior for oil content. The study of REC showed that the use of separate male and female lines in cross breeding program of sesame could have high advantage. It would also be desirable to have multi crosses involving different parents and select in the segregating generations to isolate superior genotypes.

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