# Heterosis in Sesame (*Sesamum indicum L.*) Hybrids of Diverse Parental Lines for Agromorphology Characters in Ethiopia

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**Abstract:** Heterosis breeding is a technique with potential to improve sesame yield. The productivity of sesame need to be increased significantly to exploit the maximum benefit from the increasing world market demand for this crop as well as to reduce the deficit in edible oil in Ethiopia. The objective of this study was to determine the extent of heterosis for yield and yield related traits in sesame. The present investigation on sesame comprised a full-diallel set of 10 parents and their 90 $F_1$ crosses. The hybrids were produced during the main growing season of 2011. Seeds of all $F_1$ and their parents were planted in randomized complete block design, with three replications at two experimental sites viz., Uke (1383 meters above sea level) and Wama (1436 meters above sea level) of Bako Agricultural Research Center on 12 and 14 June 2012, respectively. The data was recorded for four traits viz., days to flowering, branches per plant, yield per plan (g) and oil content (%). Analysis of variance computed for each location and over locations revealed highly significant differences among the parental lines and $F_1$ hybrids for all the studied traits. The magnitude of mid and better parent heterosis for seed yield ranged from -40.0 to 31.6-% and-40.2 to 23.3%, respectively. The range of standard heterosis for yield and oil content was -41.8 to 13.6% and –5.6 to 7.8%, respectively. Seven crosses of $F_1$ and reciprocal $F_1$ displayed positive and significant standard heterosis for number of branches per plant while a total of 35 (37.6%) crosses of $F_1$and reciprocal $F_1$ had negative better parent heterosis for days to flowering of which 18 (20.0%) displayed negative and significant standard heterosis. A total of 16 crosses (of $F_1$ and reciprocal $F_1$) displayed positive better parent heterosis for seed yield per plant, of which BG006 x EW003-1, EW023-2 x Dicho and BG006 x EW002 crosses of $F_1$and rceeprocal $F_1$ exhibited positive and significant standard heterosis of 10.5, 29.4 and 13.6%, respectively. All except two crosses of $F_1$ displayed positive standard heterosis for seeds oil content of which 74 (82.22%) of crosses exhibited positive and significant standard heterosis. The different magnitude of heterosis displayed by some crosses of $F_1$ and their reciprocal $F_1$ for all characters indicated the presence of maternal inheritance, which suggested the importance of considering the use of female parents in the respective crosses and characters to maximize the exploitable heterosis in hybrids. Generally, the results of the research revealed higher chances of producing heterotic sesame hybrids that combined the highest yield, oil content, early maturity and high number of fertile branches. This suggests that heterosis breeding and/or hybridization could be one of the breeding methods in sesame in Ethiopia to produce heterotic hybrids that combine desirable traits as many as possible or to develop potential recombinant pure lines from segregating generations.

**Keywords:** Better parent heterosis, Mid parent heterosis, Oil content, Seed yield and Standard heterosis.

## 1. Introduction

Sesame (*Sesamum indicum* L.) is a source of edible oil with high nutritive value and keeping quality (Pathak *et al.*, 2014). It is the most important oil crop grown in Ethiopia having tremendous potential for export; making Ethiopia the second largest world exporter of raw sesame seed after India (Rutes *et al.*, 2015). However, domestic processing of edible oil from sesame seed in Ethiopia is low.Therefore, Ethiopia imports large quantities of edible oil, mainly palm oil (Wijnands *et al.*, 2011), to satisfy the demand of increasing human population.

The production and productivity of sesame need to be increased significantly to exploit the maximum benefit from the increasing world market demand for sesame as well as to reduce the deficit in edible oil in Ethiopia. Since 1960s, efforts have been made to improve the productivity of sesame through introduction, which have high yielding, high oil quality and disease esistant/tolerant varieties in Ethiopia (Tadele, 2005). Studies on genetic gain progress in sesame variety showed the existence of reasonable level of yield and oil quality over the last five decades (Musa *et al.*, 2011) which is advanced nearly to 1 ton $ha^{-1}$. However, its productivity is still low (0.8 ton $ha^{-1}$) (CSA, 2017) as compared its genetic potential, which is 2 ton $ha^{-1}$. Therefore, it is vatal to develop high yielding varieties with high oil quality and disease resistance than the released varieties, which are under production.

Heterosis breeding is the most important breeding method in both self and cross-pollinated crops to develop improved varieties. Parental identification and evaluation is the major technique in the development of crop varieties in which to enhance productivity (Gowda *et al.,* 2010). Estimation of heterosis provides clues to select desirable parents for future crossing in hybridization. Heterosis has been developing due to deviation from the parental means, which is expressed



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in increase vigourity and productivity (Khan *et al.,* 2009).

Heterosis breeding is a potential technique to improve yields in sesame (Nayak *et al*., 2017). Sesame, although predominantly a self-pollinated crop, its reproductive biology and making crosses offers a good scope for exploitation of heterosis (Rani *et al*., 2015). High levels of mid parent heterosis in sesame have been reported from various countries (Sundari and Kamala, 2012). In addition, the heterotic response over the standard check (Jadhav and Mohrir,2013;, Vavdiya *et al*.,2013; Rani et al.,2015) and over better parent (heterobeltiosis) for seed yield and yield components has been observed in sesame *(*Prajapati *et al.,* 2010; Padmasundari and Kamala*,*2012*,*Chaudhari *et al.,* 2017). Heterosis over better parent is relatively more important than the mid heterosis for commercial exploitation of hybrids *(*Prajapati *et al*.,2010, Padmasundari and Kamala 2012; Tripathy *et al*.,2016; Nayak *et al*.,2017).

The magnitude of heterosis provides a basis for genetic diversity and a guide to the choice of parents for developing superior $F_1$ hybrids, so as to exploit hybrid vigour and/or for building better gene pools to be employed in population, improvement (Jatothu *et al*., 2013). Information on heterosis in sesame is highly required for breeding work in Ethiopia. Therefore, the objective of this study was to determine the extent of heterosis for yield and yield related traits in sesame.

## 2. Materials and Methods

### 2.1. Planting Materials

The 10 parental genotypes *viz*., EW002, BG006, EW023-2, EW006, EW003-1, EW019, Obsa, Dicho, Wama and EW010-1 used in the study (Table 1). Parental lines, Obsa and Dicho are released varieties while others were elite breeding lines. Initially Bako Agricultural Research Center (BARC) identified the elite breeding lines among many sesame genotypes collected from western Ethiopia. For the crossing purpose, to establish the 10 parents as pure lines, seeds of a single plant from each genotype were collected during 2010 main season.

Table 1. Description of 10 sesame parental lines for selected agromorphology traits they exhibited variations.

| Genotype | Code | Collection zone | Collection altitude (masl) | Soil texture | Reaction to bacterial blight |
|---|---|---|---|---|---|
| EW002 | P1 | East Wellega | 1470 | Clay loam | R |
| BG006 | P2 | Benshangul-Gumuz | 1000 | Clay loam | R |
| EW023-2 | P3 | East Wellega | 1580 | Sandy | MR |
| EW006 | P4 | East Wellega | 1400 | Clay | R |
| EW003-1 | P5 | Horo-GuduruWellega | 1346 | Clay loam | R |
| EW019 | P6 | Benshangul Gumuz | 1095 | Clay loam | R |
| Obsa | P7 | Horo-GuduruWellega | 1395 | Clay | R |
| Dicho | P8 | East Wellega | 1460 | Clay | MR |
| Wama | P9 | East Wellega | 1430 | clay | MR |
| EW010-1 | P10 | East Wellega | 1473 | Sandy loam | R |

*Note:* masl=meters above sea level, DF=days to flowering, BP=number of branches per plant, YP= seed yield per plant (g) and OC=oil content (%), R=resistant, MR=moderately resistant.

### 2.2. Experimental Sites and Experimental Procedures

Ten parental lines were crossed in 10 x 10 diallel mating design, including reciprocals in 2011cropping season. Seeds of all 90 $F_1$s and their 10 parents was planted on 12 June 2012 at Uke (1383 meters above sea level) and on 14 June 2012 at Wama (1436 meters above sea level.) experimental sites of the BARC in a randomized complete block design with three replications. Each plot consisted of a single row of 5 m length with 50 cm and 25 cm inter and intra-row spacing, respectively. The seeds were drilled in each row at the seeding rate of five kg $ha^{-1}$. Twenty days after planting, the plants were thinned out to adjust for optimum population per hectare. Nitrogen fertilizer at the rate of 50 kg N $ha^{-1}$in the form of Urea was applied as side dressing four weeks after emergence. Hand weeding was carried out four times at a two-week interval starting 20 days after planting. Observations were made on various characters of sesame genotypes (10 parental lines and 90 $F_1$s hybrids) but only four characters of interest in sesame breeding were selected as representative of groups of characters (phenology, growth, yield and oil content) to assess the magnitude of heterosis. Data for days to flowering (50%) was registered on a plot basis. Observations were made on ten randomly selected plants for number of branches per plant, seed yield per plant, and percentage oil content. Oil content of seeds was determined at Holetta Research Center using Nuclear Magnetic Resonance Method (Robbelen *et al.,* 1989).

### 2.3. Data Analysis

Analysis of variance was performed using SAS Software to determine the existence of significant variations among parents and crosses for all the traits. The performance of the hybrids was estimated in terms of the percentage increase or decrease of their performance over the mid-parent (heterosis), better parent (heterobeltiosis) (Hochholdinger and Hoecker, 2007) and standard parent. Mid parent heterosis, better parent heterosis (heterobeltiosis) and standard heterosis were estimated following procedure developed by

Fonesca and Patterson (1968). Heterosis over mid parent value ($H_m$) was estimated as:

$$Hm = \left(\frac{F1 - m}{m}\right) x100 \quad (1)$$

Where: *Hm* is heterosis over the mid parent value; $F_1$is mean performance of $F_1$; m is mean value of the two parental lines involved in producing that particular $F_1$.

Heterosis over the better parent (also known as heterobeltiosis) was estimated as:

$$Hbp = \left(\frac{F1 - bp}{bp}\right) x100 \quad (2)$$

Where, *Hbp* is heterosis over the better parent value; $F_1$is mean performance of $F_1$; bp was mean value of the better parent value involved in producing that particular $F_1$.

Heterosis over the standard variety/check (also known as standard heterosis or commercial heterosis) was estimated as:

$$Hsv = \left(\frac{F1 - sv}{sv}\right) x100 \quad (3)$$

Where: *Hsv* is stanadard heterosis; $F_1$ is mean performance of $F_1$; sv is mean value of the standard/check variety included in the experiment. The mean of two standard checks (Obsa and Dicho) was used to estimate standard heterosis.The significance of mid parent heterosis was tested as per the method proposed by Panse and Sukhatme (1961) where critical difference was calaculated as:

CD for mid parent heterosis = $\sqrt{3xEMS/2r}$ x "t"

CD for better parent and standard heterosis= $\sqrt{2xEMS/r}$ x "t" (4)

*Where:* r = number of replications, EMS = error mean square, t = table value of "t" at error degree of freedom at 5% and 1% probability level.

## 3. Results and Discussion

### 3.1. Analysis of Varaiance and Mean Performance of Genotypes

The mean square for the parental lines, $F_1$ cross and reciprocal $F_1$ crosses for all traits at each location was significant, indicating that there was sufficient variability among the genotypes for the traits (data not presented). Parental diversity of sesame is desirable to exploit heterosis in its breeding program (Das *et al.*, 2013). The analysis of variance (ANOVA) over location for parents, $F_1$ cross and reciprocal $F_1$cross showed that there was a significant variation among genotypes for days to flowering and branches per plant (Table 2). Similar results were reported earlier for these and other traits in sesame by Aladji *et al.* (2015), Pawar and Aher (2016), Chaudhari *et al.* (2017) and Nayak *et al.* (2017).

Table 2. Mean squares from combined analysis of variance (ANOVA) over location for phenology and growth characters of three groups of sesame genotypes tested at Uke and Wama, western Ethiopia in 2012.

| | 10 parental lines | | 45 $F_1$ crosses | | 45 reciprocal $F_1$ crosses | |
|---|---|---|---|---|---|---|
| Source of variation | Days to flowering | Number of branches/plant | Days to flowering | Number of branches/plant | Days to flowering | Number of branches/plant |
| Replication (location) | $4.1^{ns}$ | 3.1ns | $59.1^{**}$ | $20.7^{**}$ | $20.1^{ns}$ | $26.4^{**}$ |
| Genotype | $17.3^{**}$ | 9.7** | $21.3^{**}$ | $6.3^{**}$ | $25.2^{**}$ | $7.8^{**}$ |
| Location | $0.1^{ns}$ | 0.8ns | $9.6^{ns}$ | $2.0^{ns}$ | $34.8^{ns}$ | $0.9^{ns}$ |
| Genotype x location | $1.2^{ns}$ | 7.8** | $10.2^{**}$ | $4.8^{**}$ | $15.8^{ns}$ | $4.2^{**}$ |
| Error | 4.9 | 3.0 | 3.7 | 1.9 | 10.9 | 2.5 |

*Note:* ns,* and ** non signficant, significant at P< 0.05 and P< 0.01, respectively.Degree of freedom for Replication (location) and location was 4 and 1, respectively, while for genotype, it was 9, 44 and 44 for parental lines, $F_1$and reciprocal $F_1$ crosses, respectively. Accordingly, degree of freedom for genotype x location and error for parental lines was 9 and 36, respectively, while it was 44 and 44 for both $F_1$and reciprocal $F_1$ crosses, respectively.

For yield per plant and oil content, the combined mean square over locations (Table 3) was significant for parents, for $F_1$ cross and $F_1$ reciprocal, demonstrating high variability among the genotypes for both traits. This is consistent with the results of studies in sesame by Sumathi and Murlidharan (2010) and Gidey *et al.*, (2013). The mean square for genotype x location was significant for all characters, indicating the importance of testing genotypes over locations. The overall combined ANOVA for all studied traits was highly significant for genotypes and genotype x locations (Table 4).This indicates that there is variation among genotypes for all studied characters. Combined ANOVA was significant for locations for all traits except branches per plant.

Table 3. Mean squares from combined ANOVA over location for seed yield and seed oil content of three groups of sesame genotypes tested at Uke and Wama, western Ethiopia in 2012.

| Source of variation | 10 parental lines | | 45 $F_1$ crosses | | 45 reciprocal $F_1$ crosses | |
|---|---|---|---|---|---|---|
| | Seed yield per plant (g) | Seed oil content (%) | Seed yield per plant(g) | Seed oil content (%) | Seed yield per plant (g) | Seed oil content (%) |
| Replication (location) | 26,2$^{ns}$ | 0.4$^{ns}$ | 95.4$^{**}$ | 10.2$^{*}$ | 83.9$^{**}$ | 2.3$^{ns}$ |
| Genotype | 77.7$^{**}$ | 7.9$^{**}$ | 44.1$^{**}$ | 7.3$^{**}$ | 55.1$^{**}$ | 3.8$^{**}$ |
| Location | 2.6$^{ns}$ | 14.0$^{**}$ | 45.8$^{**}$ | 15.6$^{**}$ | 132.5$^{**}$ | 11.2$^{**}$ |
| Genotype x location | 29.6$^{ns}$ | 1.8$^{*}$ | 50.8$^{**}$ | 2.5$^{**}$ | 52.6$^{**}$ | 2.9$^{**}$ |
| Error | 15.7 | 0.8 | 16.3 | 1.1 | 15.3 | 1.4 |

*Note:* ns,*, ** non signficant, significant at P< 0.05 and P< 0.01, respectively.Degree of freedom for Replication (location) and location was 4 and 1, respectively, while for genotype, it was 9, 44 and 44 for parental lines, $F_1$and reciprocal $F_1$ crosses, respectively. Accordingly, degree of freedom for genotype x location and error for parental lines was 9 and 36, respectively, while it was 44 and 44 for both $F_1$and reciprocal $F_1$ crosses, respectively.

Table 4. Mean squares from combined analysis of variance over locations for yield and related traits of 10 sesame parental lines and their $F_1$ crossess tested at Uke and Wama, western Ethiopiain 2012.

| Sourceof variation | Degree of freedom | Days to flowering | Number of branches per plant | Seed yield per plant (g) | Seed oil content (%) |
|---|---|---|---|---|---|
| Replication (location) | 4 | 61.3 | 44.8 | 187.1 | 9.1 |
| Genotype | 99 | 19.4** | 7.5** | 51.8** | 6.5** |
| Location | 1 | 20.5* | 3.68ns | 164.0** | 37.0** |
| Genotype x location | 99 | 7.5** | 4.5** | 48.4** | 2.6** |
| Error | 396 | 4.4 | 2.3 | 15.7 | 1.3 |

*Note:* ns, *, and ** non signficant, significant at P< 0.05 and P< 0.01, respectively.

Mean performance of sesame parents for all the studied traits are shown in Table 5. Days to flowering ranged 65 to 70, the number of branches per plant 5 to 9, seed yield per plant 12 to 17 gram, and oil content of the seed 50 to 54%. Parental genotype, EW023-2 had least number of branches per plant, however, with above average seed yield per plant. Two parents viz., EW003-1 and EW019 had maximum days to flowering, indicating that these lines are important to develop late maturing varieties. Parental line, Dicho had above average days to flowering, number of branches per plant and seed yield per plant. Parental genotype, Wama had maximum days to flowering, and above average yield per plant, average number of branches per plant but with below average oil content, indicating that it is important parent for yield per plant. Genotype, EW010-1 is a parental line that had very minimum days to flowering, showing that it could be suitable to contribute for early flowering genes. However, it has low oil content among all parental lines with above average yield per plant.

Table 5. Mean performance of 10 sesame parental lines over locations for seed yield and related characters as evaluated at Uke and Wama, western Ethiopia in 2012.

| Parental line | Code | Days to flowering | Number of branches/plant | Seed yield per plant (g) | Seed oil content (%) |
|---|---|---|---|---|---|
| EW002 | P1 | 70 | 9 | 17 | 53 |
| BG006 | P2 | 67 | 7 | 16 | 54 |
| EW023-2 | P3 | 68 | 5 | 12 | 53 |
| EW006 | P4 | 67 | 8 | 12 | 53 |
| EW003-1 | P5 | 70 | 8 | 13 | 52 |
| EW019 | P6 | 70. | 8 | 12 | 53 |
| Obsa | P7 | 68 | 7 | 14 | 52 |
| Dicho | P8 | 70 | 8 | 16 | 51 |
| Wama | P9 | 70 | 6 | 16 | 51 |
| EW010-1 | P10 | 65 | 7 | 15 | 50 |
| Mean | | 69 | 7 | 14 | 52 |

Parents generally exhibited variable mean performance and none of them had done well for all characters. They are, however, certain parents, which showed good performance for two traits or more. For instance, EW002 had maximum yield per plant, number of branches per plant, and days to flower and with above average oil content. Genotype, BG006 is the top ranking parental line for its high oil content with

average seed yield per plant. Parental line, EW006 had above number of branches and oil content. Parental genotype, Obsa possessed average number of branches per plant, yield per plant, oil content with below average days to flowering, indicating that this line is desirable for these all traits.Such parents possessing with multiple desirable characters may be of great value in sesame breeding program (Tripathy *et al*., 2016).

### 3.2. Heterosis for Phenology and Growth characters

The estimate heterosis mid parent, better parent and standard variety for days to flowering and branches per plant in $F_1$ and reciprocal $F_1$ crosses of sesame is presented in Table 6. The mid and better parent heterosis in $F_1$ and reciprocal $F_1$crosses for days to flowering ranged from –12.4 to 5.9% and -14.3 to 5.9%, respectively, while standard heterosis range from -15.0% to 4.3 %. A total 26, 35 and 22 ($F_1$s and reciprocal $F_1$) crosses exhibited negative and significant mid, and better parent and standard heterosis for days to flowering, respectvely. Prajapati *et al*., (2010), reported similar results.

Four F1 crosses *viz.,* EW002 x EW003-1, BG006 x Wama, EW019 x Wama, and Obsa x Dicho showed highly significant negative heterosis over both better and stanadard parents for days to flowering. Among which cross EW019 x Wama and Obsa x Dicho were the crosses with the maximum value for their negative standard heterosis. Eleven reciprocal $F_1$ crosses such as BG006 x EW002, EW003-1 x EW002, Obsa x EW002, Wama x BG006, Dicho x EW0023-2, EW003-1 x EW006,EW019 x EW003-1, Wama x EW003-1, EW010-1 x EW019, Wama x Obsa and EW010-1 x Dicho also demonstrated highly significant negative better and stanadard heterosis for days to flwering. Out of these Wama x BG006 was with the maximum value followed by EW003-1 x EW002. Evidently, a large number of crosses showed significant negative heterosis over both better and standard parents, indicating the chances of developing early flowering/maturing genotypes out of the cross-combinations. Jatothu *et al* (2013) reported negative heterosis for days to flowering and were of the view that earliness could be induced in sesame.

Earliness characters are of paramount importance in breeding for early maturing varieties/hybrids of oilseed crops in general and sesame in particular for better adaptation to climate change (Paroda, 2013). Selection for maturation period can be effective using flowering period for improving uniform ripening capsule (Jamie *et al*., 2002). A suitable breeding methodology and the identification of superior parents are the most important pre-requisites for the development of early maturing and high yielding genotypes.

Regarding number of branches per plant, mid, and better parent and standard heterosis ranged from --36.8 to 46.7%, -40 to 22.2% and -36 to 5.3%, respectively. Sumathi and Murlidharan (2010) reported that number of branches per plant have high association with grain yield in sesame. For number of branches 27, 11 and 7 crosses (F1 and reciprocal F1) displayed significant positive mid, better parent and standard heterosis, respectively.For the same trait, two F1 crosses viz., EW023-2 x EW003-1 and EW023-2 x Dicho showed positive and highly significant heterosis over both better and standard parents. Four reciprocal crosses such as EW019 x EW002, Wama x EW023-2, EW010-1 x EW023-2 and Dicho x EW006 also demonstrated positive and highly significant better parent and stanadard variety heterosis for the same trait. In the present study for both traits viz., days to flowering and branches per plant majority of the hybrids exhibited negative and significant mid, better and standard parent heterosis, indicating that for these traits the genes with negative effects were dominant. Jadhav and Mohrir (2013), Parimala *et al.*(2013) and Nayak *et al.* (2017) have also reported both negative and positive signficant heterosis for these and other different traits in sesam.

Table 6.Heterosis over mid, better and standard parents in 45 $F_1$ and reciprocal 45$F_1$ crosses of sesame for phenology and growth characters evaluated over two locations in western Ethiopia in 2012.

| | Days to flowering | | | Number of branches/plant | | | | Days to flowering | | | Number of branches/plant | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $F_1$ cross | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv | Reciprocal $F_1$ cross | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv |
| P1xP2 | -0.7 | -2.9 | -1.4 | 0 | -11.1** | -15.8** | P2 x P1 | -3.6* | -5.7** | -4.5** | 12.5** | 0 | -5.3** |
| P1x P3 | 0 | -1.4 | 0 | 0 | 0 | -5.3** | P3x P1 | -1.4 | -2.8 | -1.5 | 0 | 0 | -5.3** |
| P1 xP4 | 0.7 | -1.4 | 0.0 | -17.6** | -22.2** | -26.3** | P4xP1 | -2.2 | -4.3* | -3.0 | -5.9** | -11.1** | -15.8** |
| P1x P5 | -7.1** | -7.1** | -5.8** | -17.6** | -22.2** | -26.3** | P5 x P1 | -8.6** | -8.5** | -7.8** | -5.9** | -11.1** | -15.8** |
| P1xP6 | -5.7** | -5.7** | -4.3* | -29.4** | -33.3** | -36.8** | P6 X P1 | -4.3* | -4.3* | -3 | 17.7** | 11.1** | 5.3** |
| P1 xP7 | -1.4 | -2.9 | -1.4 | -15.8** | -20.0** | -15.8** | P7 X P1 | -5.8** | -7.1** | -6.1** | -26.3** | -30.0** | -26.3** |
| P1x P8 | -4.3* | -4.3* | -2.9 | -22.2** | -22.2** | -26.3** | P8 XP1 | 0 | 0 | 1.4 | -11.1** | -11.1** | -15.8** |
| P1x P9 | -4.3** | -4.3* | -2.9 | 6.7** | -11.1** | -15.8** | P9 x P1 | 0 | 0 | 1.4 | -6.7** | -22.2** | -26.3** |
| P1xP10 | -0.7 | -4.3* | -2.9 | -12.5** | -22.2** | -26.3** | P10 x P1 | -0.7 | -4.3* | -3.0 | -12.5** | -22.2** | -26.3** |
| P2xP3 | 2.2 | 1.5 | 0 | -12.5** | -22.2** | -26.3** | P3 XP2 | 2.2 | 1.5 | 0 | 12.5** | 0 | -5.3** |
| P2 xP4 | 0.0 | 0 | -2.9 | 20.0** | 12.5** | -5.3** | P4 X P2 | -1.5 | -1.5 | -4.6** | 6.7** | 0 | -15.8** |
| P2 x P5 | 2.2 | 0 | 1.4 | -6.7** | -12.5** | -26.3** | P5X P2 | -2.2 | -4.3* | -3.0 | 20.0** | 12.5** | -5.3** |
| P2 x P6 | 3.6* | 1.4 | 2.9 | -6.7** | -12.5** | -26.3** | P6 X P2 | 0.7 | -1.4 | 0.0 | -6.7** | -12.5** | -26.3** |
| P2 xP7 | -2.2 | -2.9 | -4.3* | -5.9** | -20.0** | -15.8** | P7X P2 | 2.2 | 1.5 | 0 | -17.7** | -30.0** | -26.3** |
| P2 xP8 | -0.7 | -2.9 | -1.4 | 0 | -11.1** | -15.8** | P8X P2 | -2.2 | -4.3* | -3 | 0 | -11.1** | -15.8** |
| P2x P9 | -5.1** | -7.1** | -5.8** | 23.1** | 14.3** | -15.8** | P9x P2 | -12.4** | -14.3** | -15.0** | -7.7** | -14.3** | -36.8** |
| P2x P10 | -1.5 | -3.0 | -5.8** | 0 | 0 | -26.3** | P10 x P2 | 4.6** | 3 | 0 | -14.3** | -14.3** | -36.8** |
| P3 x P4 | 0.7 | 0 | -1.4 | -5.9** | -11.1** | -15.8** | P4 X P3 | 2.2 | 1.5 | 0 | 5.9** | 0 | -5.3** |
| P3 x P5 | -2.9* | -4.3* | -2.9 | 17.6** | 11.1** | 5.3** | P5X P3 | 1.5 | 0 | 1.4 | -5.9** | -11.1** | -15.8** |
| P3 xP6 | 1.4 | 0 | 1.4 | -17.6** | -22.2** | -26.3** | P6X P3 | 0 | -1.4 | 0 | 5.9** | 0 | -5.3** |
| P3 x P7 | 5.9** | 5.9** | 4.3* | 5.3** | 0 | 5.3** | P7 X P3 | 1.5 | 1.5 | 0 | -5.3** | -10.0** | -5.3** |
| P3 xP8 | 1.4 | 0 | 1.4 | 11.1** | 11.1** | 5.3** | P8X P3 | -5.8** | -7.1** | -6.1** | 0 | 0 | -5.3** |
| P3xP9 | 4.3** | 2.9 | 4.3* | 6.7** | -11.1** | -15.8** | P9 x P3 | 2.9* | 1.4 | 2.8 | 46.7** | 22.2** | 15.8** |

*Note:* *, and ** significant at P< 0.05 and P< 0.01 level of significant, respectively.*Hmp, Hbp and Hsv* =Heterosis over mid, better and standard parents, respectively.P1=EW002, P2=BG006, P3=EW023-2, P4=EW006, P5=EW003-1, P6=EW019, P7=Obsa, P8=Dicho, P9=Wama, P10=EW010-1.

Table 6. Continued.

| $F_1$ cross | Days to flowering | | | Number of branches/plant | | | Reciprocal $F_1$ cross | Days to flowering | | | Number of branches/plant | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv | | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv |
| P3 xP10 | 3.8** | 1.5 | 0.0 | 0.0 | -11.1** | -15.8** | P10 x p3 | 2.3 | 0.0 | -1.5 | 25.0** | 11.1** | 5.3** |
| P4x P5 | 2.2 | 0.0 | 1.4 | 0.0 | 0.0 | -15.8** | P5 xP4 | -3.6* | -5.7** | -4.6** | 12.5** | 12.5** | -5.3** |
| P4 xP6 | 0.7 | -1.4 | 0.0 | 0.0 | 0.0 | -15.8** | P6 x P4 | -0.7 | -2.8 | -1.5 | 0.0 | 0.0 | -158** |
| P4 x P7 | 5.2** | 4.4* | 2.9 | -22.2** | -30.0** | -26.3** | P7x P4 | -2.2 | -2.9 | -4.5** | -22.2** | -30.0** | -26.3** |
| P4 xP8 | -0.7 | -2.9 | -1.4 | -5.9** | -11.1** | -15.8** | P8 xP4 | 0.7 | -1.4 | 0 | 17.7** | 11.1** | 5.3** |
| P4x P9 | 0.7 | -1.4 | 0.0 | 28.6** | 12.5** | -5.3** | P9 x P4 | 5.1** | 2.8 | 4.2* | 14.3** | 0.0 | -15.8** |
| P4 x P10 | 4.5** | 3.0 | 0.0 | -6.7** | -12.5** | -26.3** | P10x P4 | 1.5 | 0.0 | -3.0 | -6.7** | -12.5** | -26.3** |
| P5 xP6 | -4.3** | -4.3* | -2.9 | -25.0** | -25.0** | -36.8** | P6x P5 | -5.7** | -5.7** | -4.6** | 0.0 | 0.0 | -15.8** |
| P5x P7 | 0.0 | -1.4 | 0.0 | -11.1** | -20.0** | -15.8** | P7x P5 | -2.9* | -4.3* | -3.0 | -22.2** | -30.0** | -26.3** |
| P5 x P8 | 0.0 | 0.0 | 1.4 | -29.4** | -33.3** | -36.8** | P8 x P5 | -1.4 | -1.4 | 0.0 | -17.7** | -22.2** | -26.3** |
| P5 xP9 | 0.0 | 0.0 | 1.4 | 14.3** | 0.0 | -15.8** | P9 x P5 | -5.7** | -5.7** | -4.6** | 0.0 | -12.5** | -26.3** |
| P5 x P10 | -2.2 | -5.7** | -4.3* | 6.7** | 0.0 | -15.8** | P10x P5 | -0.7 | -4.3* | -3.0 | 6.7** | 0.0 | -15.8** |
| P6x P7 | -2.9* | -4.3* | -2.9 | -22.2** | -30.0** | -26.3** | P7 x P6 | -1.4 | -2.8 | -1.5 | -11.1** | -20.0** | -15.8** |
| P6 xP8 | -2.9* | -2.9 | -1.4 | -17.6** | -22.2** | -26.3** | P8x P6 | -4.3** | -4.3* | -3.0 | -29.4** | -33.3** | -36.8** |
| P6 x P9 | -8.6** | -8.6** | -7.2** | 0.0 | -12.5** | -26.3** | P9 xP6 | -2.8 | -2.8 | -1.5 | 14.3** | 0.0 | -15.8** |
| P6X P10 | 2.2 | -1.4 | 0.0 | -20.0** | -25.0** | -36.8** | P10xP6 | -3.7* | -7.1** | -6.2** | -6.7** | -12.5** | -26.3** |
| P7x P8 | -7.2** | -8.6** | -7.2** | -36.8** | -40.0** | -36.8** | P8 xP7 | -2.9* | -4.3* | -3.0 | -26.3** | -30.0** | -26.3** |
| P7 x P9 | -1.4 | -2.9 | -1.4 | -25.0** | -40.0** | -36.8** | P9 x P7 | -4.4** | -5.7** | -4.6** | -25.0** | -40.0** | -36.8** |
| P7xP10 | 3.8** | 1.5 | 0.0 | -17.6** | -30.0** | -26.3** | P10xP7 | 2.3 | 0.0 | -1.5 | -5.9** | -20.0** | -15.8** |
| P8 x P9 | -5.7** | -5.7** | -4.3* | -20.0** | -33.3** | -36.8** | P9x P8 | -2.8 | -2.8 | -1.5 | 20.0** | 0.0 | -5.3** |
| P8 x P10 | 2.2 | -1.4 | 0.0 | 0.0 | -11.1** | -15.8** | P10xP8 | -2.2 | -5.7** | -4.6** | -12.5** | -22.2** | -26.3** |
| P9x P10 | 0.7 | -2.9 | -1.4 | 7.7** | 0.0 | -26.3** | P10x P9 | 3.7* | 0.0 | 1.4 | 7.7** | 0.0 | -26.3** |

*Note:* *, and ** significant at P< 0.05 and P< 0.01 level of significant, respectively.*Hmp, Hbp and Hsv* =Heterosis over mid, better and standard parents, respectively.P1=EW002, P2=BG006, P3=EW023-2, P4=EW006, P5=EW003-1, P6=EW019, P7=Obsa, P8=Dicho, P9=Wama, P10=EW010-1.

**3.3. Heterosis for Seed Yield and Seed Oil Content**

To achieve higher yields in sesame, exploitation of heterosis is the most practical and achievable option. For yield per plant, mid, better and standard parent heterosis was ranged from -40 t0 31.6, -46.2 to 23.3 and -41.8 to 13.6 %, respectively (Table 7). The total of 32 ($F_1$ and reciprocal $F_1$) crosses revealed positive and significant mid heterosis for seed yield per plant. Eight $F_1$ crosses viz., BG006 x EW023-2, BG006 x EW003-1, BG006 x EW010-1, EW023-2 x Dicho, EW023-2 x Wama EW023-2 x EW010-1 EW019 x Dicho and Dicho x Wama were desirable crosses for their better parent heterosis for seed yield per plant. Chaudhari *et al.*( 2015) and Das *et al.* (2013) noted desirable heterosis for seed yield and other yield contributing characters.

Eight reciprocal $F_1$ crosses such as BG006 x EW002, EW23-2 x BG006, EW019 x BG006, Dicho x BG006, EW019 x EW023-2, Wama x EW023-2 and Wama x Dicho were exhibited positive and significant better parent heterosis. Similar findings were reported by Jadhav and Mohrir (2013), Vavdiya *et al* (2013),Subashini *et al* (2014) and Chaudhari *et al*(2017) for seed yield per plant.The best promising crosses for their both better and standard heterosis were $F_1$ cross BG006 x EW03-1 and EW023-2 x Dicho and reciprocal $F_1$ cross BG006 x EW002. Parents of these crosses are good combiners and could be used for increasing yield per plant in future breeding program. Therefore, more emphasis should be given to these crosses for development of varieties with high seed yield per plant. Georgiev *et al.* (2011) and Parimala *et al.* (2013) also reported significant positive heterosis over both mid and better parents for this trait.In this study, the percentage of hybrids significantly superior to the standard check was low, indicating the necessity to make a large number of crosses to obtain heterotic hybrids for economic exploitation of yield per plant (g).

On the other hand, for seed yield per plant, 15 $F_1$ cross and 22 reciprocal $F_1$ crosses showed negative and highly significant mid parent heterosis. For the same trait large number of crosses exhibited significant negative better and standard heterisis as compared to mid parent for yield per plant. According to Ilker *et al.* (2010), large negative values of mid parent heterosis and heterobeltiosis were observed for certain hybrids for seed yield per plant that may have accumulated deleterious genes which causes difficulties for selection in breeding program. Generally, positive heterosis is desired in the selection for seed yield and its components, whereas negative heterosis is important for early maturty and low plant height (Lamkey and Edwards, 1999). This shows that both positive and negative heteroses are useful, depending on the breeding objectives.

To exploit commercially viable heterosis the new crosses are usually compared with released varieties, so that the crosses with high heterotic potential could be commercialized. From the perspective of the breeder, better parent heterosis (heterobeltiosis) is more effective than mid parent heterosis (relative heterosis), particularly in the breeding of self-pollinating crops where the objective is to identify superior hybrids (Lamkey and Edwards, 1999). However, in some cases, the yields of $F_1$ hybrids being considerably higher than those of the better parents have been reported (Azeez and Morakinyo, 2014).

The single economic trait in sesame is its oil content. For oil content, a total of 24 $F_1$ crosses for mid, 17 for better and 33 for standard parents showed positive and significant heterosis. Among these 12 $F_1$ crosses viz., EW002 x Obsa, EW006 xEW019, EW003-1x EW019, EW003-1 x Obsa, EW003-1 x Dicho, EW003-1 x Wama, EW003-1 x EW010-1, EW019 x Dicho, Obsa x Dicho, Obsa x EW010-1,Dicho x Wama and Wama x EW010-1 exhibited positive and highly significant heterosis over both better and standard parents. $F_1$ cross EW006 x EW019 was the best for its high degree of standard heterosis for oil content, demonstrating that this cross can be used in breeding for high seed oil content.

For mid 28, for better 7, and for standard parent 41 reciprocal $F_1$ crosses showed highly positive and significant heterosis for oil content. For oil content, mid, better and standard heterosis was ranged from -3.8 to 8.9, -5.6 to 7.8 and -1 to 8.7, respectively. Reciprocal $F_1$ cross EW010-1 x Wama was the best for its high better parent and standard heterosis followed by EW023-2 x EW002 and EW006 x EW023-2. The parents of these all crosses have the potential to be used in breeding program. In agreement with this finding, Banerjee and Kole (2011), Salunke and Lokesha, 2013) and Subashini *et al* (2014) reported positive and highly significant heterosis for sesame. As compared to other studied traits large number of crosses, showed appreciable advantage over the parents for oil content.

Generally, heterosis is associated with the non-additive effects (over-dominance and epistasis) (Beche *et al*., 2013). Critical choice of parents is the most crucial step in any breeding program and particularly in heterosis breeding (Salunke and Lokesha, 2013). In the present study, large number of crosses showed mid parent heterosis than better and standard heterosis for all studied traits except for oil content. On the contrary, Sunduri and Kumala (2012) reported high number of crosses having standard heterosis than heterosis over mid parent for yield and related traits in sesame.

Heterotic behavior of crosses with respect to yield and yield related traits differ trait to trait. However, a few crosses such as cross EW023-2 x Dicho possessed positive and significant standard heterosis for three traits viz., branches per plant, yield per plant and oil content. Cross BG006 x EW003-1 also showed an appreciable level of promising hybrid vigour for yield per plant and oil content.

Table 7. Heterosis over mid, better and standard parents in 90 $F_1$ and reciprocal $F_1$ crosses of sesame for seed yield and seed oil content evaluated over two locations in western Ethiopia in 2012.

| | Seed yield (g) | | | Seed oil content (%) | | | Reciprocal $F_1$ cross | Seed yield (g) | | | Seed oil content (%) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $F_1$ cross | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv | | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv |
| P1xP2 | -4.2 | -13.3** | -17.3** | 0.9 | 0.0 | 4.9** | P2 x P1 | 31.6** | 19.1** | 13.6** | 2.8** | 1.9 | 6.8** |
| P1x P3 | 0.5 | -11.4** | -15.5** | 0.0 | 0.0 | 2.9** | P3x P1 | 8.1** | -4.8 | -9.1** | 3.8** | 3.8** | 6.8** |
| P1 xP4 | -13.5** | -15.5** | -15.5** | -3.8** | -5.6** | -1.0 | P4xP1 | -2.3 | -4.6 | -4.6 | 1.9* | 1.9 | 4.9** |
| P1x P5 | -40.5** | -41.8** | -41.8** | -1.0 | -1.9* | 1.0 | P5 x P1 | -20.9** | -22.7** | -22.7** | 1.0 | 0.0 | 2.9** |
| P1xP6 | -12.2** | -24.8** | -28.2** | -1.9* | -1.9* | 1.0 | P6 X P1 | 22.2** | 4.8 | 0.0 | 0.0 | 0.0 | 2.9** |
| P1 xP7 | -8.1** | -16.9** | -1.8 | 4.8** | 3.8** | 6.8** | P7 X P1 | -23.4** | -30.8** | -18.2** | 2.9** | 1.9 | 4.9** |
| P1x P8 | -14.9** | -21.0** | -24.5** | 0.0 | -1.9* | 1.0 | P8 XP1 | 12.8** | 4.8 | 0.0 | 0.0 | -1.9 | 1.0 |
| P1x P9 | 11.0** | 5.7 | 0.9 | 1.9* | 0.0 | 2.9* | P9 x P1 | -10.0** | -14.3** | -18.2** | 0.0 | -1.9* | 1.0 |
| P1xP10 | 22.8** | 5.2 | 0.5 | 1.0 | -1.9* | 1.0 | P10 x P1 | -11.1** | -23.8** | -27.3** | 4.9** | 1.9 | 4.9** |
| P2xP3 | 19.4** | 15.9** | -10.5** | -0.9 | -1.9* | 2.9** | P3 XP2 | 15.2** | 11.8** | -13.6** | 0.9 | 0.0 | 4.9** |
| P2 xP4 | 11.3** | -1.4 | -1.4 | -2.8** | -3.7** | 1.0 | P4 X P2 | -33.3** | -40.9** | -40.9** | 0.9 | 0.0 | 4.9** |
| P2 x P5 | 24.6** | 10.5** | 10.5** | 0.0 | -1.9* | 2.9** | P5X P2 | 18.0** | 4.6 | 4.6 | 3.8** | 1.9 | 6.8** |
| P2 x P6 | 5 | -1.2 | -23.6** | -2.8** | -3.7** | 1.0 | P6 X P2 | 25.0** | 17.7** | -9.1** | 2.8** | 1.9 | 6.8** |
| P2 xP7 | -21.9** | -35.4** | -23.6** | -1.9* | -3.7** | 1.0 | P7X P2 | -2.3 | -19.2** | -4.6 | 0.0 | -1.9 | 2.9** |
| P2 xP8 | 3.4 | 0.6 | -17.7** | 4.8** | 1.9* | 6.8** | P8X P2 | 20.0** | 16.7** | -4.6 | 2.9** | 0.0 | 4.9** |
| P2x P9 | -5.6* | -10.5** | -22.7** | 2.9** | 0.0 | 4.9** | P9x P2 | -11.1** | -15.8** | -27.3** | 2.9** | 0.0 | 4.9** |
| P2x P10 | 15.0** | 8.2* | -16.4** | 3.8** | 0.0 | 4.9** | P10 x P2 | -6.3* | -11.8** | -31.8** | 1.9* | -1.9 | 2.9** |
| P3 x P4 | 1.6 | -12.3** | -12.3** | 0.0 | -1.9* | 2.9** | P4 X P3 | -15.8** | -27.3** | -27.3** | 3.8** | 3.8** | 6.8** |
| P3 x P5 | 12.1** | -3.2 | -3.2 | -1.0 | -1.9* | 1.0 | P5X P3 | -21.1** | -31.8** | -31.8** | 2.9** | 1.9 | 4.9** |
| P3 xP6 | 14.2** | 4.1 | -19.5** | 0.0 | 0.0 | 2.9** | P6X P3 | 16.1** | 12.5** | -18.2** | 1.9* | 1.9 | 4.9** |
| P3 x P7 | -4.3 | -22.7** | -8.6** | 1.0 | 0.0 | 2.9** | P7 X P3 | -19.1** | -34.6** | -22.7** | 1.0 | 0.0 | 2.9** |
| P3 xP8 | 30.6** | 27.8** | 29.4** | 1.9* | 0.0 | 2.9** | P8X P3 | 11.8** | 5.6* | -13.6** | 0.0 | -1.9 | 1.0 |
| P3xP9 | 27.4** | 17.4** | 1.4 | 1.9* | 0.0 | 2.9** | P9 x P3 | 27.8** | 21.1** | 4.6 | 1.9* | 0.0 | 2.9** |

*, and ** significant at P< 0.05 and P< 0.01 level of significant, respectively.*Hmp, Hbp and Hsv* =Heterosis over mid, better and standard parents, respectively.P1=EW002, P2=BG006, P3=EW023-2, P4=EW006, P5=EW003-1, P6=EW019, P7=Obsa, P8=Dicho,P9=Wama, P10=EW010-1.

Table 7. Continued.

| | Seed yield (g) | | | Seed oil content (%) | | | Reciprocal | Seed yield (g) | | | Seed oil content (%) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| $F_1$ cross | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv | $F_1$ cross | Hmp | Hbp | Hsv | Hmp | Hbp | Hsv |
| P3 xP10 | 23.2** | 12.4** | -13.2** | 4.9** | 1.9* | 4.9** | P10 x p3 | 3.2 | 0.0 | -27.3** | 2.9** | 0.0 | 2.9** |
| P4x P5 | -1.4 | -1.4 | -1.4 | 1.0 | -1.9* | 2.9** | P5 xP4 | -4.6 | -4.6 | -4.6 | 2.9** | 1.9 | 4.9** |
| P4 xP6 | 3.2 | -13.2** | -13.2** | 5.7** | 3.7** | 8.7** | P6 x P4 | -13.5** | -27.3** | -27.3** | 1.9* | 1.9 | 4.9** |
| P4 x P7 | -37.9** | -42.7** | -32.3** | 4.8** | 1.9* | 6.8** | P7x P4 | -16.7** | -23.1** | -9.1** | 2.9** | 1.9 | 4.9** |
| P4 xP8 | 15.5** | 5.0 | 5.0 | 3.8** | 0.0 | 4.9** | P8 xP4 | -20.0** | -27.3** | -27.3** | 1.9* | 0.0 | 2.9** |
| P4x P9 | 0.5 | -6.4* | -6.4* | 0.0 | -3.7** | 1.0 | P9 x P4 | -22.0** | -27.3** | -27.3** | 3.9** | 1.9 | 4.9** |
| P4 x P10 | -20.5** | -33.2** | -33.2** | 4.9** | 0.0 | 4.9** | P10x P4 | -2.7 | -18.2** | -18.2** | 4.9** | 1.9 | 4.9** |
| P5 xP6 | -1.1 | -16.8** | -16.8** | 4.8** | 3.8** | 6.8** | P6x P5 | 24.3** | 4.6 | 4.6 | 2.9** | 1.9 | 4.9** |
| P5x P7 | -36.3** | -41.2** | -30.5** | 3.8** | 3.8** | 4.9** | P7x P5 | -41.7** | -46.2** | -36.4** | 3.9** | 3.9** | 4.9** |
| P5 x P8 | -24.5** | -31.4** | -31.4** | 4.9** | 3.8** | 4.9** | P8 x P5 | -5.0 | -13.6** | -13.6** | 2.9** | 1.9 | 2.9** |
| P5 xP9 | -11.2** | -17.3** | -17.3** | 6.8** | 5.8** | 6.8** | P9 x P5 | -7.3** | -13.6** | -13.6** | 2.9** | 1.9 | 2.9** |
| P5 x P10 | 14.6** | -3.6 | -3.6 | 7.8** | 5.8** | 6.8** | P10x P5 | 13.5** | -4.6 | -4.6 | 5.9** | 3.9** | 4.9** |
| P6x P7 | 3.4 | -18.5** | -3.6 | 1.0 | 0.0 | 2.9** | P7 x P6 | -12.2** | -30.8** | -18.2** | 1.0 | 0.0 | 2.9** |
| P6 xP8 | 16.4** | 6.7* | -12.7** | 5.8** | 3.8** | 6.8** | P8x P6 | -9.1** | -16.7** | -31.8** | 3.9** | 1.9 | 4.9** |
| P6 x P9 | -15.3** | -24.2** | -34.5** | 3.8** | 1.9* | 4.9** | P9 xP6 | -5.9* | -15.8** | -27.3** | 0.0 | -1.9 | 1.0 |
| P6X P10 | 6.0 | 6.0 | -27.7** | 4.9** | 1.9* | 4.9** | P10xP6 | -6.7* | -6.7* | -36.4** | 4.9** | 1.9 | 4.9** |
| P7x P8 | -23.2** | -35.0** | -23.2** | 6.8** | 5.8** | 6.8** | P8 xP7 | 4.6 | -11.5** | 4.6 | 2.9** | 1.9* | 2.9** |
| P7 x P9 | -27.6** | -37.3** | -25.9** | 1.0 | 0.0 | 1.0 | P9 x P7 | -28.9** | -38.5** | -27.3** | 4.9** | 3.9** | 4.9** |
| P7xP10 | -9.8** | -28.8** | -15.9** | 5.9** | 3.8** | 4.9** | P10xP7 | -17.1** | -34.6** | -22.7** | 3.9** | 1.9* | 2.9** |
| P8 x P9 | 21.6** | 18.4** | 2.3 | 5.9** | 5.9** | 4.9** | P9x P8 | 24.3** | 21.1** | 4.6 | 5.9** | 5.9** | 4.9** |
| P8 x P10 | 9.1** | 0.0 | -18.2** | 1.0 | 0.0 | -1.0 | P10xP8 | 15.2** | 5.6 | -13.6** | 5.0** | 3.9** | 2.9** |
| P9x P10 | 7.1* | -4.2 | -17.3** | 5.0** | 3.9** | 2.9** | P10x P9 | -23.5** | -31.6** | -40.9** | 8.9** | 7.8** | 6.8** |

*Note:* *, and ** significant at P< 0.05 and P< 0.01 level of significant, respectively.*Hmp, Hbp and Hsv* =Heterosis over mid, better and standard parents, respectively.P1=EW002, P2=BG006, P3=EW023-2, P4=EW006, P5=EW003-1, P6=EW019, P7=Obsa, P8=Dicho,P9=Wama, P10=EW010-1.

Heterosis is a complex phenomenon depending upon the balance of additive, dominance and their interacting components as well as distribution of genes in parental lines.The extent of heterosis relies upon the extent of diversity among parental lines, gene frequency difference between parents and degree of dominance for the particular trait (Parimala *et al*., 2013). Like many other crops, the magnitude of heterosis in sesame has been related to the degree of divergence of the parents (Yadav *et al*., 2005). High genetic diversity for Ethiopian sesame has been reported earlier by Daniel and Parzies (2011) and Ahadu, (2012).

In the present study, for almost all the characters, varying number of crosses depicted heterosis in both positive and negative directions indicating that genes with negative and positive effects or a complementary type of gene interaction or simply correlated gene distribution may seriously inflate the mean degree of dominance and convert partial dominance into apparent over dominance (Hayman, 1954). Sesame is the most suitable crop for exploiting heterosis on a commercial scale because of low seed rate, high seed multiplication ratio (1:50), epipetalous floral structure enabling easy emasculation and natural out crossing to an extent of 5 to 50 per cent (Chaudhari *et al*.,2017).

## 4. Conclusion

From the present study, it can be concluded that cross EW019 x Wama, Obsa x Dicho, Wama x BG006 and EW03-1 x EW002 were the top ranking hybrids among eighteen promising crosses for early maturity to better adaptation to climate change. Out of seven crosses with high standard heterosis, cross Wama x EW023-2 was the best for its maximum value for number of branches. For seed yield per plant, sixteen crosses had high standard heterosis of which BG006 x EW03-1, EW023-2 x Dicho and BG006 x EW002 were the best promising. Large number of crosses had showed high standard heterosis of which cross EW010-1 x Wama, EW023-2 x EW002 and EW006 x EW023-2 were the top ranking for their high value for oil content.The selected crosses for each trait have high potential to be used for recombination breeding to develop high potential pure lines. All parents in the selected crosses can be used for future breeding program of this crop.

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