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Estimate of Combining Ability and Heterosis for Seed Yield and Yield Component Traits in Castor (*Ricinus Communis L.*)

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Abstract

Castor (*Ricinus communis L.*) is one of the world's most important non-edible oil seed crops and is indigenous to eastern Africa. Estimates of heterosis and combining ability help identify parents with better-combining abilities, which may be hybridized to produce elite crosses. This paper aims to estimate the magnitude of heterosis and combining ability in castor for yield and yield-related traits. A total of 28 entries (twenty-one crosses generated in a half-diallel mating design and seven parents) were planted in three replications of RCBD at the Melkassa Agricultural Research Center and Negelle Arsi sub-centers. Separate mean square analysis due to total genotypes, parents, crosses, and parent vs crosses for yield and yield contributing characters indicated significant differences for all of the studied traits except 100-seed weight, number of branches per plant, and female inflorescence length for parent vs crosses contrast, suggesting there was considerable genetic variation among materials studied. Combining ability analysis for general (GCA) and specific (SCA) was very highly significant (P <0.001) for all traits, indicating the importance of both additive and non-additive gene action in controlling the expression of traits. The high yielder and dwarf genotype MD-1 was the best general combiner for most yield- and yield-related traits, followed by genotype M-5/Sel-1. Five crosses, MD-1 x M-5/Sel-1 (6.03***), Hiruy x M- 5/Se-1 (5.23***), 106552 x 21936/1 (4.54***), Hiruy x 21936/1 (3.83**) and MD-1 x 208630 (2.92*), exhibited good specific cross combinations for biological seed yield. For 100-seed weight, MD-1 x 208630 and M-5/Sel-1 x 21936/1 crosses expressed significant effects for good specific combinations. The wide range of standard heterosis recorded for seed yield varied from -45.68 to 86.13% over Hiruy and -52.81 to 61.71% over Abaro. Three hybrids, MD-1 x 208630, MD-1 x M-5/Sel-1, and Hiruy x M-5/Se-1, manifested high standard heterosis over both Hiruy and Abaro for total seed yield of commercial value. Estimated heterosis for seed yield ranged from 52.81 to 57.02% for the better parent; and - 45.05 to 65.06% for mid-parent heterosis. The information generated in this study can be used to develop castor hybrids with high seed yields.

Keywords: Additive and non-additive genes; General and specific combining ability; Mid-parent heterosis; Better parent heterosis; Standard heterosis; Ricinus communis

Introduction

Castor *(Ricinus communis L.)* with 2n = 20, belongs to the monospecific genus Ricinus of the family Euphorbiaceae, and it is one of the most important exploitable non-edible oilseed crops in the world. Castor is indigenous to both India and Africa based on its widespread cultivation, documentation, and physical pieces of evidence (Ojo and Bello, 2004) and most probably originated in East Africa, Ethiopia where it shows tremendous genetic variability (Anjani, 2012). The seeds contain about 45-56% oil (Delvadiya IR. et al, 2018), the highest among all cultivated oil crops. In Ethiopia, castor does well under dry land or moisture stress areas in East and North West Ethiopia, and in the rift valley areas; specifically, Melkassa, Arsi Negelle, and Arba Minch are most suitable [1].

Ethiopia has not benefited from the available genetic resources of castor for the development of modern varieties, though it is the center of diversity. The crop was neglected in terms of research attention until a few years ago in the country; however, many scientific investigations have been launched to improve its seed yield and other yield-contributing traits to meet the country's demand and the world market in general. The growing demand for biofuel and industrial applications stimulated the need for research on this crop. The development of high seed-yielding, semi-dwarf, and early maturing commercial varieties are the main objectives focused on by the Ethiopian Institute of Agricultural Research of the national castor improvement program [2,3].

Castor breeding involves an adequate understanding of the genetics of its economically important traits like seed yield and yield components usually inherited quantitatively. It is usually cultivated

as a local cultivar and only a few synthetic varieties are developed in Ethiopia, but hybrids give significantly higher yields than varieties (Reif et al., 2007). Crossing various parents can result in stronger heterotic effects and superior hybrids. The magnitude of heterosis on castor seed is determined by both the genetic diversity and individual combining capacity of the parents (Ramana et al., 2005; Lavanya et al., 2006) [4].

In the genetic improvement of complex quantitative characters, such as seed yield and its different attributes, the selection of appropriate parents to be incorporated in the hybridization program is a preliminary approach for breeders. Provided that, it is always essential to evaluate available promising lines in their hybrid combinations for their seed yield and yield contributing characters (Giriraj et al., 1973) [5]. The use of parents of known superior genetic worth ensures much better success. Obtaining evidence for their per se performance, proper information on the magnitude of heterosis and combining ability, and their gene action involved in the inheritance of different parents and their crosses would be more helpful to plant breeders in selecting promising parents. It is also used in formulating an efficient breeding

method for the improvement of its different attributes (Dangaria et al., 1987) and selecting desirable cross combinations for commercial exploitation of hybrid vigor [6].

The information on the variance components of GCA and SCA provides an appropriate diagnosis for the predominant role of additive or non-additive gene action. Heterosis analysis aims to find out the best combination of crosses giving a high degree of useful heterosis and characterization of hybrids for commercial exploitation (Dushyant D. et al. 2018). Thus, this study was carried out to estimate the amount of heterosis in the hybrids, combining ability of parents and gene action involved in the inheritance of seed yield and yield components, and identify superior parents for the production of hybrids [7].

Material and Methods

Planting material

Five castor genotypes (MD-1, 208630, 106552, M- 5/Sel-1, and 21936/1) and two improved varieties with many contrasting characters were selected for their yield and yield-related characters. The selected parental lines were crossed in a 7 x 7 half diallel mating design to generate 21 possible crosses, excluding the reciprocals. The crosses were made by hand emasculation and subsequent pollination 3 to 4 times for full inflorescent seed setting and covered immediately with a paper bag [8].

A total of 28 entries (7 parents and 21 crosses) were planted at the Melkassa Agricultural Research Center on-station and Negelle Arsi sub-stations. The trail was laid down in a Randomized Complete Block Design (RCBD) with three replications. The spacing between plots and blocks was 1m and 1.5m, respectively. The experimental plot area was 12m2 (4m x 3m) having five rows each of 3 m in length with 60cm intra- and 80cm inter-row spacing. At first, two seeds were planted per hill by hand for a uniform stand, and then they were thinned to one plant per hill after emergence to get 25 plants per plot. Field management and protection practices were applied based on research recommendations [9,10].

Data collection

Observations were recorded on the following agronomic traits; for the number of spikes/racemes) per plant, male inflorescence length (cm), female inflorescence length (cm), length of the main spike (cm), number of effective capsules per plant, number of seeds per plant, number of effective branches per plant, seed yield per plant (g), 100-seed weight (g), total seed yield. The data was collected on five randomly selected and tagged plants for all characters except for 100-seed weight (g) and total seed yield, where 100-seed weight data was recorded by counting a hundred seeds and weight on sensitive balance while Seed yield per plot was recorded on plot basis and converted to per hectare [11].

Data analysis

The homogeneity of error variances of the locations was tested before conducting combined ANOVA. Both locations and genotypes were considered fixed effects, while blocks within locations were considered random effects. ANOVA was conducted using the General Linear Model (PROC GLM) of SAS (SAS, 2012). The General Linear Model that was used for the combined analysis of variance across locations was given by:

The statistical model for the mean value of a cross (i ×j) is: Yij = μ + gi + gj +Sij + l/b ΣΣeij

Xijk = μ + Gi + Lj + RLk (j) + (GL) ij + Eijk

Where Xijk = observation of the ith genotypes in a jth location in the kth replication;

μ = overall mean; li = the effect of the ith location, (l = 1,2); RLk(j)= The Effect of jth Replication within location; j (r= 1,2,3); (GL)ij = the Genotype-by-location interaction; and Eijk = experimental error [12].

Estimate of Combining Ability

General combining ability (GCA) and specific combining ability (SCA) effects for the traits having a significant difference between genotypes were estimated using Model-I (Fixed model), Method-II (Half-Diallel including parental self and excluding reciprocal crosses) of Griffing (1956), using SAS software the DIALLEL- SAS05 program (Zhang et al., 2005).

Estimation of heterosis

The superiority of hybrids over the better or highest parent was estimated as better parent heterosis or heterobeltiosis, and over the average of the two parentsas Mid parent or relative heterosis, and their superiority over the best checks (Abaro and Hiruy) was estimated as standard heterosis or economic heterosis. Heterosis was estimated for the characters that showed significant differences between genotypes (crosses and parents) following the method proposed by Falconer (1996) [13].

Mid-parent heterosis (MPH) $= \dfrac{\bar{\bar{F}}1 - \bar{\bar{MP}}}{\bar{\bar{MP}}} \times 100\%$

Better-Parent Hetrosis (BPH) $= \dfrac{\bar{\bar{F}}1 - \bar{\bar{BP}}}{\bar{\bar{BP}}} \times 100\%$

Standard Heterosis (SH) $= \dfrac{\bar{\bar{F}}1 - \bar{CH}}{\bar{C}\bar{\bar{H}}} X100\%$

The significance of heterosis has been tested using the t-test against the critical difference (CD). The critical differences for testing the significance of mid-parent,

Mid-parent, better-parent, and standard heterosis were calculated as suggested by Singh and Chaudhary (1985) as follows:

The standard error difference, SE (d) of heterosis for individual locations is calculated as follows:

SE (d) for MPH = $\sqrt{3MSE/2r}$ E (d) for BPH = $\sqrt{2MSE/r}$

(d) for SCH = $\sqrt{2MSE/r}$

The standard error of difference (SE (d)) over the environment was computed according to the following formulae.

SE (d)for MPH = $\sqrt{3MSE/2re}$ SE(d)for BPH = $\sqrt{2MSE/re}$

SE (d) for SCH = $\sqrt{2MSE/re}$

The critical difference is calculated as (CD): = SE (d) x t (tabulated).

CD (MPH) =SE (d) of MPH x t

$t (MPH) = (\bar{\bar{F}}1 - \bar{\bar{MP}})/SE(d)$, CD (BPH) = SE(d) of BPH x t

$t (BPH) = (\bar{\bar{F}}1 - \bar{\bar{BP}})/SE(d)$,

CD (SH) = SE (d) of SH x t

$t (SH) = (\bar{\bar{F}}1 - \bar{\bar{SH}})/SE(d)$,

Where, $\overline{F1}$ – Mean of the F1 hybrids, $\overline{\overline{MP}}$ – Mean of mid parental value = (P1+P2)/2, $\overline{\overline{BP}}$ – Mean performance of better parent, $\overline{P1}$- Mean of performance of parent one, $\overline{P2}$- Mean of performance of the two parents, $\overline{\overline{CH}}$ - Mean performance of the standard check,

EMS-Error mean square in the analysis of Variance, r& e number of replications and environment (location) respectively [14].

Result and Discussion

Analysis of variance

Mean square analysis of variance due to genotypes revealed very highly significant (P ≤ 0.001) for all the characters, indicating the presence of sufficient amount of genetic variability in experimental material for the characters under study, which could be exploited for the improvement of traits. The mean squares due to genotypes were further partitioned into parents, crosses, and parent vs cross. Separate mean square analysis due to crosses and parents showed significant variation for all traits except seed yield per plant for parents, indicating the parents used in diallel mating and their crosses were genetically diverse [15]. The one-degree freedom contrast between parent vs crosses indicated that the diallel parents and crosses differed significantly for all the characters except for the number of effective branches, female inflorescences length, and 100-seed weight. Consequently, this result showed evidence for the possibility of the existence of heterotic effects for these yield component characters in the castor.

A similar finding was reported by different scholars that the existence of significant differences among genotypes for yield and yield components in castor. Similarly, Punewar et al., (2017) and Akpan et al., (2006) reported that total genotypes, parents, hybrids, parent vs hybrids, and check vs hybrids were significant for all the traits they studied [16]. Again, Jalu et al., (2017) evaluated 55 genotypes developed in line x tester crossing method that significant difference was observed for all the characters among all genotypes, parents, and hybrids, and in contrast to this result, seed yield per plant was not significant for the partition of mean squares due to parent. Anjani, (2010) forwarded that significant genotypic variation for most of the traits he studied, and recommended that effective selection would be effective. Mutallab Sh., (2014) also reported highly significant differences among genotypes for all the traits he studied; the number of branches, number of racemes, peduncle length, plant height, 100-seed weight, and seed yield/plant. The analysis of variance in the combining ability study revealed significant differences among the genotypes, indicating wide diversity in the material studied (Rao et al., 2010) [17].

Combining ability analysis

The analysis of variance for combining ability for yield and yield-related traits is presented. Mean square analysis showed both general combining ability (GCA) and specific combining ability (SCA) were very highly significant (P < 0.001) for all studied traits. The significant result indicates the importance of both additive and non-additive genetic variances for the inheritance of all characters under study. In line with this finding, both additive and non-additive gene actions inter-played in all agronomic characters studied by (Delvadiya IR et. Al., 2018). Similar results were also reported by several authors; Punewar et al. (2017), Patel et al. (2016), and Rajani et al. (2015) [18].

On the other hand, the estimates of variance components due to SCA were higher than the corresponding GCA variances for most of the traits. Accordingly, the ratio of GCA to SCA variances was less than unity for total seed yield, seed yield per plant, male inflorescences length, number of effective branches per plant, number of capsules per plant, and 100-seed weight, indicating the traits are predominantly under the control of non-additive gene action. There is a great opportunity for heterosis breeding to exploit the non- additive genetic variance. In contrast, the ratio was greater than unity for the number of spikes per plant, female inflorescence length, and length of primary spikes, thereby suggesting additive gene actions were playing a greater role in the inheritance of the traits. Hence, these characters can be improved through recurrent selection schemes. Both additive and non-additive gene action were equally important for the number of effective branches per plant as its variance ratio approaches the unit [19].

In line with this study, the predominance of non-additive gene action in castor for yield and agronomic characters were studied by Patel et al., (2016), Chaudhari and Patel, (2014), and Geeta and Patel (2014) and Ramesh et al., (2013). A similar finding was reported that seed yield was controlled by non-additive gene actions while apart from this finding; 100-seed weight was controlled by predominantly additive gene actions (Gila M.A. and Onovo J.C., 2015). However, the preponderance of additive gene action for the number of effective branches/plants, the effective length of primary racemes, the number of capsules on primary racemes, and oil content reported by Patel K.P. et al., (2017) and Punewar et al. (2017) [20].

Estimate of general combining ability effects (gi)

The variation in the GCA effect was estimated among parents to identify the best parent for subsequent hybrid development programs. The high value of the GCA effect is desired and parents with positive and significant effects are considered as good general combiners for yield and yield attribute traits. The parental line MD-1 showed the best combining ability for all the studied traits, except hundred seed weight, female inflorescences length, and length of primary spike. Similarly, following the MD-1, the genotype M- 5/Sel-1 was the good general combiner for the majority of the traits, seed yield per plant, number of spikes per plant, seed yield, number of seeds per plant, number of branches per plant, number of capsules per plant. Parents showing good general combiner for all the studied traits, there is the possibility of making an effective selection for the traits, which could lead to considerable genetic improvement [21].

The high value of GCA effect was recorded for seed yield per plant varying from -19.93 to 25.86. The genotype MD-1 (25.86***) found the highest score followed by M-5/Sel-1 (11.06*) exhibiting a positive and highly significant GCA effect for the seed yield per plant. In contrast, the two improved open-pollinated varieties Abaro and Hiruy, showed poor general combiner for the same trait [22]. Three parents MD-1, 208630, and M-5/Sel-1 exhibited significant positive GCA effects. For the 100-seed weight, three parents, Abaro (2.52***), 106552 (1.18**), and Hiruy (1.11**) were good general combiners having a positive and highly significant GCA effect. Three genotypes MD-1, 208630, and M-5/Sel-1 showed good general combiners for the number of spikes per plant with a very highly significant positive GCA effect. Inversely, the rest of the parents, Hiruy, Abaro, 106552, and 21936/1 exhibited poor general combiners. For the number of capsules per plant, the GCA effects varied from -14.37 to 14.17 while it varied between -43.10 to 42.51 for the number of seeds per plant. Genotypes growing with more branching habits, MD-1, and M-5/Sel-1, exhibited highly significant positive GCA effects for the associated traits; number of capsules, and number of seeds per plant [23].

The genetic basis of heterosis of seed yield is due to the factors that the improved parental lines for spike density and high female spikes/

inflorescences. It is mainly due to the high female tendency inherited from the dominant female nature and contributes to increased seed yield. The whole length of flower inflorescences recalled as of this paper, length of primary spikes/racemes having many capsules containing seeds in it. The Hiruy variety, which is tall and non-branching growth habit, is unique in its length of primary spikes and expressed very highly significant positive GCA values for both male and female inflorescence length. In addition to the Hiruy variety, one genotype 21936/1 for female inflorescence length and two genotypes 208630 and MD-1 for male inflorescence length showed good general combiners. Therefore, these genotypes could be exploited for the development of femaleness, as well as a male parental line for the crossing program. For the number of branches per plant, three genotypes MD-1, M-5/Sel-1, and 208630 exhibited good general combiners which had a direct and indirect association for seed yield.

Parents identified as good general combiners simultaneously for the majority of traits, could be considered as potential parents and should be preferred in the breeding program to combine more characters by involving fewer parents in the crossing program. Further, the lines showing the good general combining ability for particular components may also be utilized in the crossing program for effective improvement in particular components, ultimately seeking yield improvement. The highly significant positive GCA effect of parents indicates the potential advantage of the parents for developing high-yielding hybrids. Similar results were reported by various scholars (Jalu et al., 2017; Punewar et al., 2017; Aher et al., 2014) [24].

Estimate of specific combining ability (SCA) effects The estimates of the SCA effects of 21 crosses are presented in. A high range of SCA effect was recorded from the number of seeds-1 plants varying from-50.80 to 64.58 and followed by the seed yield plant-1 that extends from -28.32 to 40.12. Estimation of SCA effect for total seed yield ranged from -4.63 to 6.03, from which 52.38% of the crosses showed positive effects. Among these, five crosses; MD-1 X M-5/Sel-1 (6.03***), Hiruy X M-5/Se-1 (5.23***), 106552 X 21936/1 (4.54***), Hiruy X 21936/1 (3.83**), and MD-1 X 208630 (2.92*), were showed good specific combiners with highly significant SCA effect [25].

Among the crosses, which depicted significant and positive SCA effects for total seed yield, MD-1 x M- 5/sel-1 was a good specific combiner for seed yield per plant, 100- weight, number of spikes per plant, number of capsules per plant, female inflorescences length, length of primary spikes, number of seeds per plant. Similarly, cross Hiruy x M-5/se-1 was a good specific combiner for seed yield per plant, male inflorescences length, length of primary spikes, and average specific combiner for number of spikes per plant, number of capsules per plant, female inflorescences length, number of seeds per plant and 100- weight. Further, the cross MD-1 x 208630, is also a good specific combiner for 100- weight and number of spikes per plant whereas average specific cross combination for all the rest of the traits. For seed yield per plant, six cross combinations, Hiruy x M-5/Se-1, Hiruy x 21936/1, MD-1 x M-5/Sel-1, MD-1 x 106552, Abaro x 208630 and 106552 x 21936/1,showed best specific combining abilities with significant positive values. For the number of spikes per plant, crosses MD-1 x M-5/Sel-1, MD-1 x 208630, and Hiruy x Abaro exhibited good specific cross combinations. Crosses MD-1 x M-5/Sel-1, Hiruy x M-5/Se-1, 106552 x 21936/1, Hiruy x 21936/1 and MD-1 x 208630 exhibited good specific cross combiners for total seed yield whereas, crosses MD-1 x M-5/Sel-1 and 208630 x 21936/1 depicted good specific combiners for number of capsules per plant. Similarly, three crosses MD-1 x M- 5/Sel-1, MD-1 x 106552 and 208630 x 21936/1 for the number of seeds

per plant, and two crosses M-5/Sel-1 x 21936/1 and MD-1 x 208630 for 100-seed weight depicted good specific cross combination with highly significant positive SCA effects. For the length of primary spikes, MD-1 x M-5/Sel-1, Hiruy x M-5/Se-1, 106552 x M-5/Sel-1, and Abaro x 106552 showed a desirable SCA effect. Whereas, Crosses MD-1 x M-5/Sel-1 and 106552 x M-5/Sel-1 for female inflorescences length and crosses 208630 x 106552, Hiruy x M-5/Se-1, MD-1 x Abaro, M-5/Sel-1 x 21936/1 for male inflorescences length had desirable significant SCA effects.

Among the evaluated crosses, seven cross combinations had desirable good SCA effects, and also simultaneously had desirable effects for almost all characters. Good specific combiners for seed yield also depicted desirable SCA effects for most of the yield component attributes. Regarding the GCA effects of the parents involved in the half-diallel mating, crosses could be classified into the following six groups: GxG, GxA, AxA, AxP, and PxP. These categories represent the consequence of good, average, and bad general combiner parents. The crosses that possessed the high SCA effects generally did not always include both good general combiner parents with high GCA effects, indicating the significance of intra- and inter-allelic interactions. In general, crosses with high heterotic response generally had high SCA effects. The high SCA effect of crosses in general corresponded to their high heterotic response, but these might also be accompanied by poor and/or average GCA effect of the parents. For seed yield per plant, a total of five crosses exhibited significant positive SCA effects; and out of seven parents, six parents were involved in these crosses, of which three parents viz. MD-1, 208630, and M-5/Sel- 1 were good general combiners, and three parents viz., Hiruy, 106552 and 21936/1 were bad combiners. In line with this study, similar results were reported by various scholars (Jalu et al., 2017; Punewar et al., 2017; Aher et al., 2014). Okoh et al., (2007) noticed good general and specific combining ability effects among castor accession [26].

Estimate heterosis

Mid- and better-parent heterosis

Seed yield is a complex quantitative trait of all yield contributing characters and breeding for its improvement is the main goal of researchers. Thus, to gain the yield associated with other heterotic characteristics, hybrids with vigor and superior performance over the checks would be selected. Large and positive estimates of heterosis are desirable for all the traits under consideration. The percent estimate of heterosis for mid-parent (relative heterosis) and better parent (heterobeltosis) for traits of interest.

The result substantiated that heterosis for mid and better parent was highly magnified and significant effects were observed for the yield and its related components considered under the study. The estimate of heterosis for total seed yield ranged from -45.05% for Abaro x 21936/1 to 65.06 % for MD-1 x M-5/Sel-1 over mid- parent while it extends from -52.81% for Abaro x 21936/1 cross to 57.02% for Hiruy x M-5/ Se-1 cross over the better parent. Out of a total of 21 crosses, 66.67% and 52.38% of the crosses revealed the desired heterosis for the mid and better parent, respectively. The highest desirable and significant heterosis were recorded from crosses MD-1 x M-5/Sel-1 (65.06, 37.61), Hiruy x M-5/Se-1 (65.05, 57.02), 106552 x 21936/1 (57.38, 52.20), and M-5/Sel-1 x 21936/1 (46.62, 40.38) for both mid and better parent heterosis corresponding to their percent in the bracket. In addition, three crosses Hiruy x 21936/1 (47.19%), MD-1 x 106552 (32.00%), and MD-1 x 208630 (29.69%) showed significant mid-parent heterosis in the desired direction for the same trait. The result indicated the

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crosses showed significantly higher mean values as compared to their respective parents, confirming the existence of sufficient heterosis that can be exploited for yield improvement in the castor.

The magnitude of mid-parent heterosis varied from -36.19 for Abaro x 106552 to 66.60% for Hiruy x M- 5/Se-1 for seed yield per plant. Similarly, a greater range of better parent heterosis was recorded for the same trait from -41.79% for Abaro x 106552 to 63.32% for Hiruy x 21936/1. The highest desirable heterosis for seed yield per plant recorded from four crosses Hiruy x M-5/Se-1 (66.60**, 51.35**), Hiruy x 21936/1 (63.81**, 63.32**), MD-1 x M-5/Sel-1 (50.24**, 30.48*), and 106552 x21936/1 (44.03*, 57.38*) over both mid and better parent with their values in bracket respectively. High manifestations of heterosis for male inflorescence length are important and most likely possess high male-to- female proportions, used to develop male lines as a pollinator. For male inflorescence length, the current finding revealed that all crosses expressed the desired heterosis for mid-parent ranging from 1.51 to 32.09%, except for cross Hiruy x 21936/1 (-3.2). Whereas the heterotic values for better parent ranged from -15.81 to 26.43%, and sixteen (76.19%) of the crosses had desirable heterosis for the male inflorescence length.

A higher proportion of females to males will produce a higher seed set. In the case of female inflorescence length, eleven (52.38%) and five (23.81 %) of the crosses had a desirable mid- and better-parent heterosis, respectively. The heterotic value extends from 21.65 to 43.76% for mid-parent and -41.00 to 43.12% for better- paren. Two Crosses 106552 x M-5/Sel-1 (43.76%) and MD-1 x M-5/Sel-1 (41.75%) for mid-parent and one crosse 106552 x M-5/Sel-1 (43.12%) for better parent depicted significant and desirable estimate which could be exploited for the development of femaleness.

The estimate of the current finding showed all crosses had exhibited the desired heterosis for mid-parent heterosis for the length of primary spikes except for three crosses. However, about 12 (57.14%) of crosses had manifested heterosis in the desired direction over the better parent performances. Their magnitudes varied from 3.88 to 28.01% for a mid-parent and -22.50 to 27.82% for a better parent. Two crosses MD-1 x M- 5/Sel-1 (27.82%) and 106552 x M-5/Sel-1 (26.77%), which are associated with the estimates of seed yield, exhibited consistent desirable significant heterosis for both heteroses. Concerning the number of effective spikes per plant, the estimate of mid-parent magnified from -12.57% for Abaro x 21936/1 to 48.91% for Hiruy x Abaro. However, the heterotic values for better parents ranged from -34.78 to 39.75%. Out of the total, 76.19% and 28.57% of the crosses depicted desirable heterosis for mid and better parent respectively [27].

The magnitude of heterosis for the number of capsules and seeds per plant varied from -24.26 to 48.13% for mid-parent, while the range extends from -30.03 to 46.56% for better-parent heterosis. MD-1 x M-5/Sel-1 (40.20%) showed the highest positive significant mid- parent heterosis but none of the crosses showed a significant result for better parent for both of the traits. With regards to 100-seed weight, mid-parent heterosis ranged from -14.87 for 208630 x 106552 to 13.40% for M-5/Sel-1 x 21936/1. The lowest heterotic value for a better parent is -22.45% for Abaro x 208630, while the highest value is 10.02% for M-5/Sel-1 x 21936/1. About nine (42.86%) and seven (33.33%) of the crosses exhibited positive mid and better parent heterosis. M- 5/Sel-1 x 21936/1 (13.40%) crosse showed the desired heterosis with significant positive mid-parent heterosis, in against, three crosses showed negative significant heterosis. Six crosses showed negative significant better parent heterosis. Mid-parent and better-parent heterosis for the number of branches per plant ranged from -27.56 to 88.8% and -46.4

to 32.63%, respectively. Out of the total crosses, 12 (57.142%) and 5 (23.81%) of the crosses recorded desirable heterosis which indirectly contributes to seed yield.

Standard heterosis

The magnitude of standard heterosis varied depending on the crosses and standard checks used in the study. For total seed yield, seventeen (80.95%) and twelve (57.14%) of the crosses had higher yield improvement over the two checks, hence they exhibited desirable heterosis for the checks Hiruy and Abaro, respectively. Its heterotic value ranged from -45.68% for

Abaro x 21936/1 to 86.13% for MD-1 x M-5/Sel-1 over check Hiruy. Whereas the magnitude of the estimate extends from -52.81% for Abaro x 21936/1 to 61.71% for MD-1 x M-5/Sel-1 over check Abaro. Four crosses MD-1 x M-5/Sel-1 (86.13, 61.71%), MD-1 x 208630(64.72, 43.11%), Hiruy x M-5/Se-1 (57.02%, 36.42%)and MD-1 x 106552 (47.63%, 28.26%), showed significantly higher seed yield over both checks Hiruy and Abaro with their mean in bracket respectively. This result confirms the existence of high potential exploitable heterosis for improvement of seed yield in castor and suggests these crosses would be selected for multi-location variety evaluation trials. For seed yield per plant, 76.19% and 57.14 % of the crosses exhibited a higher yield advantage compared to the best check Hiruy and Abaro. The desirable positive economic heterosis ranged from 7.18 to 116.75% over Hiruy, while the range varied from 4.89 to 66.02% over Abaro. The highest desirable significant economic heterosis was recorded from two cross combinations MD-1 x 106552 (94.36%, 48.86%) and MD-1 x M-5/Sel-1 (116.75%, 66.02%), with the yield advantage over the two checks Hiruy and Abaro, respectively. In addition, four crosses MD-1 x 208630 (86.30%), Hiruy x M-5/Se-1 (85.28%), Hiruy x 21936/1 (64.31%), and 106552 x M-5/Sel-1 (64.01%) showed superior performance for seed yield per plant having significant heterosis for check Hiruy [28].

For the effective number of racemes/spikes per plant, all crosses had higher mean performance and exhibited large positive standard heterosis for both checks, except Abaro x 21936/1 for Abaro. The magnitude of heterosis varied from 22.69% for Abaro x 21936/1 to 205.34% for MD-1 x M-5/Sel-1 compared to Hiruy, while, the positive estimate lies between 0.62% for Hiruy x 106552 to 125.68% for MD-1 x M-5/Sel-1 over the check Abaro. 2.38 % and 80.95% of the crosses showed a significantly larger number of effective capsules per plant over the Hiruy and Abaro varieties resp. The positive heterotic values ranged from 4.87% to 48.96% compared to Hiruy while 9.14% to 100.26% compared to the Abaro variety for the number of capsules. For 100-seed weight, 28.57% of the crosses recorded positive heterosis estimate. However, the check Abaro is previously characterized by bold seeded variety, it was superior for the 100-seed weight overall crosses according to the present studies. For male inflorescence length, 52.38 % of the crosses depicted longer mean performances than the Hiruy, the positive heterotic values ranged from 1.16 % to 21.84%. In contrast, all crosses performed better for male inflorescence length compared to the check Abaro, thus, they exhibited positive standard heterosis. The heterotic value ranged from 10.80% for Abaro x 21936/1 to 68.33% for Hiruy x 208630, where most of them showed significant estimates. Concerning female inflorescence length, the check Hiruy variety was significantly superior compared to all crosses, hence, none of the crosses exhibited desirable heterosis. However, for check Abaro, 11 (52.38%) of crosses depicted desirable positive heterosis, of which four crosses had significant heterotic value. In the case of the length of the main inflorescence, the Hiruy variety was characterized by a non-branching growth habit with its unique purple color, single, and

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the longest in main inflorescence/spikes length. Based on the present study, the Hiruy variety was the top in mean performance from all genotypes included in the study. As a result, almost all crosses showed significant negative standard heterosis compared to Hiruy. Differently, all crosses depicted desirable positive heterosis ranging from 3.16% to 47.16% compared to the check Abaro, ten (47.62%) of the crosses showed positive significant heterosis for the traits.

Kanwal et al. (2006) found similar results when estimating positive and negative significant heterosis for seed yield and yield components. Najan et al., (2010) reported similar results that considerably high degree of standard heterosis in castor seed yield. Golakia et al. (2004) investigated the heterosis of yield-determining characters and discovered a significantly desired heterobeltisis ranging from 18.7 to 39.6%. Furthermore, other characters showed excellent heterosis above superior parent and standard checks. According to Patel et al. (2016), for heterosis to occur, at least one parent must have a greater GCA for yield-attributing components. These findings show that additive and non- additive components can be used to develop potential varieties and hybrids. Other scholars also reported similar results: Rajani et al., (2015); Ramesh et al., (2013); Lavanya and Chandramohan, (2003) [29].

Conclusion

This study examined to evaluate the combining ability and heterosis for agronomic parameters to identify potential castor families for further selection and breeding for seed yield and yield-related characters. The variances of GCA and SCA for all traits were significant suggesting additive and non-additive gene effects contribute to the genetic variability. Though, additive and non-additive gene effects were important, almost all characters were predominantly controlled by non- additive gene action. Parents were found to be good combiners for the characters studied. The dwarf genotype MD-1 was the best combiner for most of the characters studied, which are exploited for developing high seed yield and short plant stature. The estimation of SCA effects is an essential criterion to determine the usefulness of the hybrids. A huge range of heterosis was observed for mid and better parent and standard heterosis for all characters studied.

In general, the best-performing single crosses and parental lines with desirable heterosis, GCA, and SCA effects for seed yield and yield-related traits were successfully identified. These genotypes could be used as high-yielder hybrids in seed yield for the economic benefit of Ethiopia. The promising crosses observed in this study can be utilized for future breeding work as well as direct use in production through systematic hybridization. It is, however, advisable to evaluate the genotypes across locations and across years to confirm the promising results observed in the present study. In general, it can be concluded that the information from this study could be useful for researchers who intend to develop high seed yielding with high oil content, which is a major constraint in oil seed improvement.

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