Advances in Crop Science and Technology

Open Access

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

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Abstract

Castor (.) 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 th

Reviewed: 18-March-2023, QC

No: acst-24-129617, **teviewed:**

Where, $\overline{F1}$ – Mean of the F1 hybrids, $\overline{MP}$ – Mean of mid parental value = (P1+P2)/2, $\overline{BP}$ – Mean performance of better parent, $\overline{P1}$- Mean of performance of parent one, $\overline{P2}$- Mean of performance of the two parents, $\overline{CH}$ - 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 ($P \leq 0.001$) 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 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 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 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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