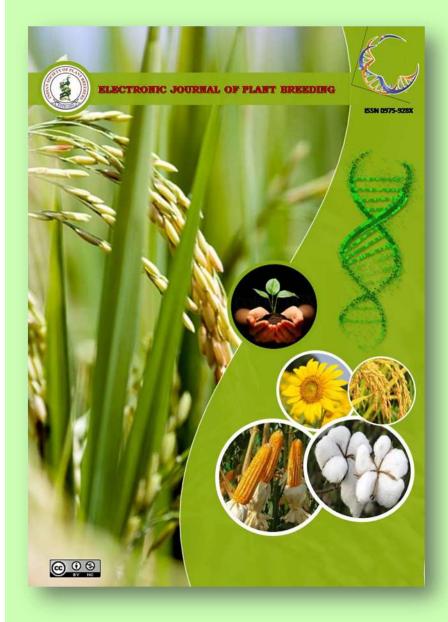# Study on the combining ability and gene action in sunflower through line x tester matting design

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Research Article

Study on the combining ability and gene action in sunflower through line x tester matting design

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Abstract

This study was conducted to evaluate gene action and combining ability for yield, agronomic traits through line X tester analysis with 36 hybrids, developed from nine testers and four lines. The experiment was conducted in randomized complete block design with three replicates for two years 2015-16 and 2016-17 at AICRP-Sunflower, Nimpith Centre. Gene action and combining ability for seed yield and other yield attributing agronomic traits were studied in the sunflower hybrids. The cytoplasmic male sterile lines were used as female lines while some new male inbreds were introduced as testers in the form of fertility restorers. The inbred lines and their F_1hybrids differed significantly in their mean values of the traits under the present study. For each of the traits, highly significant positive and negative GCA values were recorded which was reflected from the hybrid combinations. Highly significant positive effects of the GCA for seed oil content were observed in the Rf-lines R-138-2, R-104 and EC-601978 and in Pet-89-1A. On the basis of analysis, SCA: GCA ratio variances indicated that the most of the total genetic variation for head diameter, oil content (%), seed yield per plant or seed yield in kg per hectare, volume weight (g/100 cc), 100 seed weight(g), 100 seed kernel weight, hull content and oil yield in kg per hectare were governed by the non-additive gene action or non-additive component of genetic variance had a more significant role in the inheritance of the above mentioned traits in the F1 hybrid combinations in sunflower. The study's results indicate that the additive as well as non-additive components had a more or less equal role for the inheritance of plant height trait in sunflower. Highly significant positive effects of the GCA for seed yield (kg/ha) were observed in the Rf-lines R-12-96, R-104, EC-601978 and R-630 and in Pet-2-7-1A and CMS-107A. For early maturity and semi-dwarfness, the best general combiners were CMS P-2-7-1A and CMS-10A and EC-601958 (restorer line). Five parents, R-104, R-12-96, EC-601978, EC-601958 and P-2-7-1A exhibited positive high *gca effect* for seed yield and some other yield components like head diameter, 100 seed weight, volume weight (g/100cc) and oil %, therefore, these five parents could be adjudged good general combiners for high seed oil content as well as the high oil yielder sunflower hybrids in near future. It also depicted that the above genotypes appeared to possess high concentration of non-additive genes for seed yield and component traits. The results of this study may be used for the identification of new high yielding sunflower hybrids based on the hybridization between the best combiners.

Introduction

Identification of superior parents for hybridization is an important step in plant breeding. Combining ability of parental lines should be estimated to find the best hybrid combinations. Furthermore, estimation of gene effects could be done by analyzing combining ability values based on F_1 mean values. Combining ability of inbred lines could be estimated with various methods such as top cross. Line $\times$ tester analysis is an extension of this method in which several testers are used (Kempthorne 1957).This study was conducted to evaluate gene action and combining ability for yield, agronomic traits through line $\times$ tester analysis with 36 hybrids, developed from eight testers and four lines. Gene action and combining ability for seed yield and other yield attributing agronomic traits were studied in the sunflower hybrids. The cytoplasmic male sterile lines were used as female lines while

some new male inbreds were introduced as testers in the form of fertility restorers. The main objectives of sunflower breeding programs are the development of productive F1 hybrids with high seed and oil yield. Sunflower oil yield is determined as the product of seed yield per unit area and the oil percentage in grains. Therefore, consideration of both components is important when breeding for high oil yield (Fick and Miller, 1997). National sunflower hybrid (development of new hybrid) breeding programme is a continuous programme which started in our country early 1980s. Sunflower hybrid breeding was started economically in discovering **CMS** by Leclercq in 1960 and restorer genes by Kinman in 1970. Heterosis of sunflower has been exploited only over the past few decades. Hybrid sunflower became a reality with the discovery of cytoplasmic male sterility and

effective male fertility restoration system during 1970. Hybrid vigor has been the main driving force for acceptance of this oilseed crop. Utilization of heterosis has allowed sunflower to become one of the major oilseed in many countries of Eastern and Western Europe, Russia and South America and is an important crop in the USA, Australia, South Africa, China, India and Turkey. Sunflower hybrid breeding has thus played a vital role in improvement of this crop. Increasing seed and oil yields is the top priority of most sunflower breeding programs. Getting benefit from use of heterosis is the main purpose in sunflower hybrid breeding.

In India, the sunflower is grown on about 0.55 million ha (Anonymous, 2016, Padmaiah *et.al.*2015) and mostly grown in the states of Karnataka, Maharastra, AP and Tamil Nadu with potential scope of growing in the non-traditional areas like West Bengal (Dutta, 2015).   In West Bengal, Sunflower is second important oilseed crop after rapeseed-mustard during *rabi*-summer season and it was grown on about 21,000 ha in last *rabi* season (2016-17). Due to short winter spell and delayed and heavy rainfall during rainy season, the sowing of mustard was delayed which ultimate reduced the production of rapeseed-mustard. The delayed sowing also invites the insect pests in most of the years. Sunflower being a photoperiod neutral crop has wide scope to replace the rapeseed-mustard cultivation with high yield potentiality.

Materials and Methods
The crossing was affected in the line x tester fashion and the resultant hybrids were subjected to combining ability studies. The experiment was conducted in randomized complete block design with three replicates for two years 2015-16 and 2016-17 at AICRP-Sunflower, Nimpith Centre.

Gene action and combining ability for seed yield and other yield attributing agronomic traits were studied in the sunflower hybrids. The cytoplasmic male sterile lines(4) were used as female lines while some new male inbreds (9) were introduced as testers in the form of fertility restorers. The genotypes (parents and hybrids) were raised in Randomized Block Design with two replications where in each replications were represented by three rows of three meter length. The soil texture was clay loam in "On station" plots. Three irrigations were provided during the cropping period. One foliar spray was given with Boron (@ 2g/lit. of water in ray floret stage. The row per plot were five in number with a row spacing of 60 cm and plant to plant spacing was 30 cm. Uniform dose of fertilizer @80 kg N,40 Kg P_2O_5 and 40 kg K_2O per ha was applied. The germinated seed of sunflower used as the planting materials and one per hill were maintained

throughout the cropping period. The data was recorded in ten randomly selected plants from each plot of all replications on the following characters viz., days to 50% flowering, days to maturity, plant height at harvest (cm), head diameter per plant (cm), seed weight per head (g), 100-seed weight (g), husk (hull) content (%), volume weight (g/100cc). The seed yield (kg/ha), oil percentage and oil yield (kg/ha) were estimated on plot basis. The mean values were subjected to statistical analysis. In the very first year (2014-15), 36 of hybrids (developed from line X tester mating design) were evaluated and next two year, 2015-16 and 2016-17, 36 superior hybrids were evaluated for performance (seed yield, oil yield and other agronomical important traits) at research farm under AICRP Sunflower, Nimpith Centre in Randomized complete block design with three replications. The data pertaining to seed yield and other yield attributing traits for these test hybrids are presented in Table 2(polled data of 2015-16 &2016-17).Components of variance due to GCA and SCA were estimated from the expectation of mean squares of the ANOVA for combining ability. The estimates were used to compute predictability factors following Baker,1978.

Predictability factor (PF) = $2V_{GCA}/(2V_{GCA}+V_{SCA})$
The predictability factor indicates the relative importance of additive gene action in predicting the expression of characters in the progenies.
Estimates of the *gca effects* of 13 parents for 13 quantitative traits revealed that none of the parents had good general combining ability for all the traits studied. Therefore, to determine overall best combining parents for 13 quantitative traits separately, each parent was given a score for each trait as per their *gca effects*. A score of '+1' was assigned for any significant *gca effects* in desirable direction, while '–1' for any significant *gca effects* in undesirable direction. A score of '0' was assigned for any non-significant *gca effects* in any direction. The sum total of the scores over the 13 quantitative traits for each parent was used for judging the overall combining ability effects.
Genetic dissimilarity among the parents was estimated from the Euclidian distance matrix. Euclidian distance is a multivariate generalization of the Pythagorean Theorem. Euclidian distance was estimated by the following formula.

$$D_{rs}= \left(\sum(X_{rj}-X_{sj})^2\right)^{1/2}$$

Where, X_{rj} and X_{sj} is the rth and sth object measured on jth variable.

Once the distance matrix was found, dendogram was constructed based on Unweighted Pair Group

Method using Arithmatic average (UPGMA) (Sneath and Sokal, 1973). Clustering was performed using Windostat version 8.6. Clustering pattern of the 13 parents was also confirmed by plotting parental genotypes on first and second principal component (PC1 and PC2) axis.

Results and Discussion
Analysis of the combining abilities for plant height(cm), head diameter (cm), number of filled grain per head , grain filling %, 100 seed weight(g), 100 kernel weight(g), volume weight(g/100cc), hull content(%), seed yield per plant, seed yield (kg/ha) and oil yield (kg/ha) had shown that there are significant differences between the Rf-lines and A-testers with respect to the GCA. The inbred lines and their F_1hybrids differed significantly in their mean values of the traits under the present study(Table-1).Highly significant means square due to parents x environments and hybrids x environments were observed for all the agronomic traits indicated appreciable influence of environment for expression of this traits in parents and F_1s. Whereas, parents *vs* hybrids x environments was highly significant for all the agronomic traits which revealed greater effect of environment on hybrids compared to parents in expression of these traits and existence of overall heterosis for these characters.

Volume weight, 100-seed weight, and seed yield and hull content recorded significant mean squares due to lines, testers as well as line x tester on the basis of pooled analysis, with high magnitude of variance for lines and testers as compared to L x T. This indicated significant contribution of lines, testers towards GCA and line x tester interaction towards SCA. The magnitude of estimated component of GCA and SCA variances revealed greater importance of SCA for all the characters. Among interactions, line x environments, testers x environments and line x tester x environments were highly significant for aforesaid traits except for lines x environments in hull content indicated that estimates of GCA and SCA variances were influenced by the environments. The SCA: GCA ratio s indicated that the most of the total genetic variation for aforesaid characters were resulted in by the non-additive gene effects.Oil content recorded significant mean squares due to lines, testers as well as line x tester with high magnitude of variance for lines and testers as compared to L x T on the basis of analysis. This indicated significant contribution of lines, testers towards GCA and line x tester interaction towards SCA.

Highly significant interaction between line x environments, testers x environments and line x testers x environments suggested that lines, testers and hybrids were influenced by environments. The values

of SCA: GCA ratio indicated that the most of the total genetic variation for aforesaid characters were resulted in by the non-additive gene effects in all the environments and on the basis of pooled analysis. The similar type of findings also reported by Patil *et al.* (2012), Jondhale, *et al.* (2012).The most prominent positive effect of the GCA for days to 50% flowering was found in the CMS lines in CMS-107A and Pet-2-7-1A and for the same traits among the Rf-lines in R-12-96, EC-601878 and EC-601858, while the most prominent negative effect was observed among the lines in CMS-10A whereas among the Rf-lines most prominent negative effect of the GCA for days to 50% flowering was observed in R-6D-1,R-138-2 and R-1-1respectively.The GCA/SCA ratio for days to 50% flowering was less than 1, namely 0.10 (Table 3). Our analysis of genetic variance components showed that non-additive gene action played a significant role in the inheritance of days to 50% flowering trait in sunflower (Table 2).The most prominent positive effect of the GCA for plant height was found in the CMS lines in CMS-107A and for the same traits among the Rf-lines in R-12-96, R-630,R-107and R-104, while the most prominent negative effect was observed among the lines in P-2-7-1A and P-89-1A and whereas among the Rf-lines most prominent negative effect of the GCA for plant height in was observed in and EC-601858 and EC-601978respectively. The GCA/SCA ratio for plant height was less than 1, namely 0.47 (Table 3). Our analysis of genetic variance components showed that additive as well as non-additive gene action played a more or less equal role in the inheritance of plant height (Table 2).

The most prominent positive effect of the GCA for head diameter was found in the CMS lines in CMS-107A and for the same traits among the Rf-lines in R-12-96 and R-104 and while the most prominent negative effect was observed among the lines in CMS-Pet-89-1A whereas among the Rf-lines most prominent GCA negative effect for the same trait was observed in EC-601858. (Table 3). For head diameter CMS 107A and R-12-96 and R-104 showed positive and significant GCA effects. Thus these parents could be adjudged good general combiners for head diameter.The GCA/SCA ratio for head diameter (cm) was less than 1, namely 0.30 (Table 3). The study's results indicate that the non-additive component had a more significant role in the inheritance of head diameter in the F1 hybrid combinations (Table 2).

Though sunflower hybrids are high yielders, the G × E interaction influence their performance (Balu *et al.* 2007). Chandra *et al.* (2011) reported a significant line × tester × environment effects for different yield attributing traits in sunflower. Ortis *et al.* (2005) reported significant line × environment and tester ×

environment for all traits and, also, significant line× tester × environment effects for all traits except plant height. Highly significant positive effects of the GCA for number of filled grain per head were observed among the A-lines in Pet-89-1A and CMS-10A where as highly significant positive effects of the GCA for volume weight same trait were observed in the three Rf-lines, viz. R-12-96, EC-601978 and R- 630. (Table -2). Highly significant negative effects of the GCA for same trait was found among the A-lines in Pet-2-7-1A and CMS-107A and among the Rf-lines inR-138-2 and Rha-1-1 respectively. For number of filled seed per head, Pet-89-1A and CMS-10A and R-12-96, EC-601978 and R- 630 showed positive and significant GCA effects. Thus these parents could be adjudged good general combiners for increasing number of filled seeds per head.

The GCA/SCA ratio for number of filled seeds per head was less than 1, namely 0.17 (Table 3). The study's results indicate that the non-additive(non-additive gene action) component had a more significant role in the inheritance of number of filled grain per head in the F1 hybrid combinations in sunflower (Table 2).

The most prominent positive effect of the GCA for seed filling was found among the CMS lines in Pet-2-7-1A and   from the Rf line most prominent positive effect of the GCA for the grain filling was found in EC-601958,EC-601878 R-107 and R-6D-1 and most significant negative effect was observed in P-89-1A and CMS-107A respectively and for the same trait, prominent negative GCA effect grain filling was observed among the Rf-lines in   R-630,R-138-2 and R-104   respectively (Table-2). For seed filling % Pet-2-7-1A and EC-601958, EC-601878 R-107 and R-6D-1 showed positive and significant GCA effects. Thus these parents could be adjudged good general combiners for increasing the autogamy % (seed filling %) in sunflower hybrids. The GCA/SCA ratio for autogamy % (seed filling %) was less than 1, namely 0.11 indicated that non-additive gene action played a significant role in the inheritance of autogamy % (seed filling %) (Table 2).

Highly significant positive effects of the GCA for 100 seed weight (g) were observed among the A-lines Pet-2-7-1A. (Table-2).For 100 seed weight, CMS 852A and CMS-853A and EC-601858, Rha-1-1 and R-104 showed positive and significant GCA effects. Thus these parents could be adjudged good general combiners for 100-seed weight. The GCA/SCA ratio for 100 seed weight (g) was less than 1, namely 0.10 (Table 2) indicated that non-additive gene action played a significant role in the inheritance of 100 seed weight trait in sunflower. Highly significant positive effects of the GCA for 100 seed kernel weight were

observed in the Rf-lines EC-601958, R-104 and Rha-1-1 and among the A-lines in P-2-7-1A. Highly significant negative effects for same trait were found in CMS-P-89-1A and among the Rf lines in R-12-96, R-630 and RHA-6D-1 (Table 2). The GCA/SCA ratio for 100 seed kernel weight (g) was less than 1, namely 0.17 (Table 2). The study's results indicate that the non- additive component of genetic variance had a more significant role in the inheritance of 100 kernel seed weight in the F1 hybrid combinations (Table 2) in sunflower.

Highly significant positive effects of the GCA for volume weight (g/100cc) were observed in the Rf-lines R-12-96, R-104 and R-6D-1 and among the A-lines in P-89-1A. Highly significant negative effects for same trait were found in CMS-10A and among the Rf lines in R-107, RHA-1-1 and R-630.For volume weight CMS P-89-1A and R-12-96, R-104 and R-6D-1 showed positive and significant GCA effects. Thus these parents could be adjudged good general combiners for increasing volume weight. The GCA/SCA ratio for volume weight (g/100cc) was less than 1, namely 0.07. Analysis of genetic variance components showed that non-additive gene action played a significant role in the inheritance of volume weight in sunflower. For the hull content (%) lower magnitude is desirable. Highly significant negative effects for same trait were found in CMS-107A and CMS-10A and among the Rf lines in EC-601958,EC-601978,R-138-2,   RHA-107.   Highly   significant positive effects of the GCA for hull content % were observed in the Rf-lines R-12-96 and R-630 and among the A-lines in P-89-1A and CMS-P-2-7-1A. For hull content (%), CMS-107A and CMS-10A and EC-601958, EC-601978, R-138-2 and R-107 showed negative and significant GCA effects. Thus these parents could be adjudged as good general combiners to get low hull content sunflower hybrids. The GCA/SCA ratio for hull content (%) was less than 1, namely 0.06 (Table 3) indicated that non-additive gene action played a significant role in the inheritance of hull content (%) in sunflower. Highly significant positive effects of the GCA for seed yield per plant were observed in the Rf-lines R-12-96, R-104 and EC-601978 and among the A-lines in Pet-2-7-1A. Highly significant negative effects for seed yield were observed in the Rf-lines in R-6D-1, RHA-1-1, R-138-2,R-630 and R-107 among the female parents in CMS-P-89-1A and CMS-107A where as non significant positive effects of the GCA for seed yield per plant were observed in EC-601958 (:Table-2.).

The GCA/SCA ratio for seed yield per plant was lower than 1.0 namely 0.07, indicating that the non-additive component of genetic variance played a significant role in the inheritance of the seed yield trait in sunflower. The study's results indicate that the non-additive component had a more significant role in the

inheritance seed yield trait in the F1 hybrid combinations (Table 2).Highly significant positive effects of the GCA for seed yield (kg/ha) were observed in the Rf-lines R-12-96, R-104, EC-601978 and R-630 and among the A-lines in Pet-2-7-1A and CMS-107A. Highly significant negative effects for seed yield were observed in the Rf-lines in R-6D-1, RHA-1-1, R-138-2 and R-107 among the female parents in CMS-P-89-1A. The GCA/SCA ratio for seed yield (kg/ha) was lower than 1.0 namely 0.07, indicating that the non-additive component of genetic variance made a significant role in the inheritance of the seed yield trait in sunflower. The results indicate that the non-additive component had a more significant role in the inheritance seed yield trait in the F1 hybrid combinations in sunflower under present study.

Highly significant positive effects of the GCA for seed oil content were observed in the Rf-lines R-138-2, R-104 and EC-601978 and among the A-lines in Pet-89-1A. Highly significant negative effects for seed yield were observed in the Rf-lines in R-12-96 and RHA-1-1, among the female parents in CMS-P-2-7-1A (Table-2).The GCA/SCA ratio for seed oil content was less than 1, namely 0.05 (Table 2.) indicating that the non-additive component of genetic variance made a significant role in the inheritance of the trait oil content in sunflower. The other components of genetic variance showed that the contribution of the non-additive component of genetic variance is very significant contribution for the expression of this trait than that of the additive one. The highest positive value of the GCA for oil yield (kg/ha) was found in those lines that had positive GCA values for either seed yield or seed oil content or both. Significant positive GCA values for this trait were found in those lines that had either negative GCA values for both seed yield and seed oil content or a very high negative GCA value for seed yield or seed oil content (Table 2). Significant positive GCA values for this trait were found in the Rf-lines R-104, EC-601978 R-630 and EC-601958 and among the A-lines in Pet-2-7-1A. Highly significant negative effects for seed yield were observed in the Rf-lines in R-6D-1, RHA-1-1, R-630 and R-107 among the female parents in CMS-107A.

The GCA/SCA ratio for oil yield (kg/ha) was lower than 1 namely 0.06, indicating that the non-additive component of genetic variance made a significant role in the inheritance of the trait oil yield (kg/ha) in sunflower. The other components of genetic variance showed that the contribution of the non-additive component of genetic variance highly significant and key contribution for the expression of this trait than that of the additive one (Table-2). Additive gene action was reported for head diameter (Gvozdenovic *et al.* 2005), however, non-additive

gene effects have also been reported for plant height (Gvozdenovic *et al.* 2005, Gourishankar *et al.* 2007) and days to 50% flowering (Gourishankar *et al.* 2007). Karasu *et al.* (2010) showed significant general combining ability for plant height, seed number per head, 1000 seed weight and seed yield. Ortis *et al.* (2005) stressed the preponderance of additive type of gene effects for 1000 seed weight and seed yield in sunflower.

Four testers *viz.,* R-104, R-12-96, EC-601978 and EC-601958 exhibited higher gca effects for most of the traits studied (seed yield, head diameter, no. of filled seeds/head, oil %), therefore, these parents can be considered as the good combiners. For hull content, among lines Pet-2-7-1A and P-89-1A and among testers EC-601978, R-138-2 R-107 and EC-601958 exhibited significant negative GCA effects therefore, these parents can be considered as the good combiners (Table-3) for developing low hull content sunflower hybrids. The importance and predominance of non-additive or dominance effects for seed yield in sunflower was also highlighted by many earlier workers like Permeshwarappa *et al.* (2008), Karasu *et al.* (2010), Chandra *et. al.*(2013). Therefore, production of hybrid varieties in this crop is justified due to the existence of additive as well as non-additive non-additive type of gene action for seed and oil yield trait. Hybridization helps to augment the desirable genes of various parents in one combination. Higher seed volume weight in sunflower is often associated with higher seed yield as well as oil content. R-104, R-138-2 and EC-601958 recorded significant and positive GCA effects, therefore, these parents can be considered as the good combiners (table-3) for introgression of higher seed volume weight in new sunflower hybrids.

For 100 seed weight P-2-7-1A and EC-601958, RHA-1-1 and R-104 showed positive and significant GCA effects. Thus these parents could be adjudged good general combiners for 100-seed weight. The estimation of SCA variance was higher than GCA variance, for all the characters which indicate non-additive gene action had more effect for inheritance of yield attributing traits in sunflower; the present findings also supported by Chandra *et. al.*(2011). The importance of non-additive gene action in the inheritance of many of the yield attributing traits in sunflower was reported by Shinde *et al.* (2016). Singh and Kumar (2018) in order to identify good general combiners for yield attributing traits, they noticed both GCA and SCA variance differed significantly for the traits. They also indicated suitability of material for cross combinations based on higher magnitude of non-additive gene action for seed yield and attributing traits in sunflower.

There are significant differences among the sunflower genotypes (inbred lines and F1 hybrids) tested with regard to the mean values of all the traits involved; for each of the traits, highly significant positive and negative GCA values were recorded which was reflected from the hybrid combinations; The GCA/SCA ratio for all the traits were lower than one and majority of the cases and the values of the GCA/SCA ratio were found lower than 0.5 indicated that the non-additive component of genetic variance plays the main role in the inheritance of the most of the yield attributing traits concerned under present study except plant height. For hull content, Pet-2-7-1A and P-89-1A among lines, and among testers EC-601978, R-138-2 R-107 and EC-601958 exhibited significant negative GCA effects, therefore, these parents can be considered as the good combiners (Table-3) for developing low hull content sunflower hybrids.Seed yield, the final expression of above component traits, was found to record high significant mean square for lines, testers and line x tester interaction. The significant mean squares indicated significant contribution of lines and testers towards general combining ability variance component for the trait. Whereas significant mean square for line x tester indicates the significant contribution of crosses for specific combining ability variance component. Significant L x T proved that variation among hybrid combination was considerably higher. Five parents, R-104, R-12-96, EC-601978, EC-601958 and P-2-7-1A had significant positive *gca effect* for seed yield and some other yield components like head diameter, 100 seed weight and volume weight (g/100cc). Thus these genotypes appeared to possess high concentration of additive genes for seed yield and component traits. Most of these parents also possessed high *per se* performance for seed yield as well as its important component traits.

Acknowledgement

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Table 1. Analysis of Variance (Mean squares) for Combining ability

Source of variation	d.f.	Days. to 50% flowering	Plant height (cm)	Head Diameter .(cm)	No. of filled Grain/hd.	Autogamy %	100.seed wt(g)	100 kernel Wt(g)	Hull Cont%	Vol. Wt(g/100CC)	Seed. yield/Plant (g)	Seed yield/ (Kg/ha)	Oil cont. %	Oil Yield (Kg/ha)
Location	1	6.18	2010.7**	5.17**	9448.0**	250.0**	0.54	0.648	0.302	207.20**	238.2**	326716.4**	36.61**	90212.8**
Repl./Loc	2	11.91**	274.4**	1.88	13121.5**	15.61**	0.61	0.0005	3.40	9.51**	26.2**	273720.5**	2.47	42789.3**
Line	3	56.31**	1836.1**	2.01	40390.2**	31.70**	5.28**	2.18**	27.36**	20.68**	395.6**	111693.5**	6.40**	8475.7**
Tester	8	87.75**	666.4**	1.87	44918.1**	65.39**	1.99*	1.34**	31.50**	6.02**	127.7**	200252.5**	8.60**	24668.5**
Line X Tester	24	15.45**	188.0**	2.75	36651.2**	27.15**	1.10*	0.863	46.48**	9.82**	50.7**	104727.2**	11.83**	11874.2**
L X Loc.	3	0.75	1.08	0.002	2639.1**	0.03	0.004	0.001	4.51	4.10	0.45	871.4**	0.18	338.5**
T X Loc.	8	0.091	0.50	0.0013	4726.5**	0.04	0.002	0.0004	0.521	24.33**	0.31	688.4**	0.15	220.4**
L X T X LC	24	0.066	0.125	0.0008	2239.4**	0.027	0.0009	0.0003	2.60	23.82**	0.33	484.5**	0.13	360.5**
Error	70	0.247	2.94	0.02	29.6	0.265	0.338	0.194	10.99	4.18	0.18	177.8	0.17	23.8
V_{GCA}		2.16	40.12	0.30	175.3.2	0.82	0.09	0.035	0.65	0.505	0.568	1959.6	0.167	183.7
V_{SCA}		7.70	92.53	1.37	16840.2	13.45	0.38	0.33	17.25	2.82	25.26	51774.7	5.83	5819.20
Predictability Factor		0.362	0.475	0.304	0.172	0.110	0.321	0.170	0.068	0.264	0.052	0.071	0.055	0.060
Gene action		Non-additive	Additive and non-additive	Non-additive	Non-additive	Non-additive	Non-additive	Non-additive	Non-additive	Non-additive	Non-additive	Non-additive	Non-additive	Non-additive

 Significant at 5% level; ** Significant at 1% level.

Table 2. *gca* effects and performance *per se* of the parents for yield attributing traits in sunflower.

Name of the parent	50% Flowering.		Plant Height(cm)		Head Diameter (cm)		Seed Yield (kg/ha)		No. of filled seeds/ Head		Autogamy(Seed Filling) %	
CMS Line(L)	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*
P-2-7-1A	0.35*	68.33	-6.94**	139.61	0.00	14.60	72.44**	1845.0	-41.4 **	600.44	1.39**	87.28
P-89-1A	-0.20	67.78	-3.42**	143.13	-0.31**	14.28	-21.09**	1751.5	15.74**	657.58	-0.58**	85.31
CMS-10A	-1.57**	66.41	0.73	147.28	0.05	14.66	8.22	1780.8	36.01**	677.85	-0.30**	85.59
CMS-107A	1.43**	69.40	9.63**	156.18	0.26*	14.86	-59.56**	1713.0	-10.36**	631.48	-0.52**	85.37
S. Em(±)	0.06	-	0.21	-	0.02	-	4.25	-	6.74	-	0.06	-
GM	-	67.98	-	146.55	-	14.60	-	1772.6	-	645.3	-	86.06
RHA-6D-1	-2.85**	65.13	1.20 *	147.76	-0.18*	14.42	-116.2**	1656.4	-17.27 **	624.57	0.42**	86.31
R-12-96	2.64**	70.62	8.94**	155.49	0.43**	15.04	70.2**	1842.8	87.00**	728.84	-0.44**	85.45
R-630	-1.31**	66.67	4.13**	150.68	-0.20**	14.41	-62.6**	1709.1	39.05**	680.89	-3.88**	82.01
EC-601758	1.98**	69.96	-11.10**	135.45	-0.68**	13.92	17.3	1789.9	-3.43	638.41	2.27**	88.16
EC-601978	3.47**	71.45	-8.79**	137.76	0.12*	14.73	214.9**	1987.6	61.95**	703.78	2.02**	87.91
R-138-2	-3.04**	64.95	0.87*	147.48	0.10*	14.70	-66.03**	1706.6	-51.86 **	589.97	-2.17**	83.72
R-1-1	-1.28*	66.70	-2.59**	143.42	0.07	14.67	-97.3**	1675.3	-75.69**	566.15	0.80*	86.68
R-107	0.47*	68.45	3.67**	150.22	-0.07	14.53	-71.4**	1701.2	-21.93**	619.91	1.53**	87.42
R-104	-0.11	67.87	3.66**	150.21	0.42**	15.02	111.1**	1883.6	-17.82**	624.02	-0.55**	85.34
S. Em(±)	0.10	-	0.35	-	0.03	-	6.93	-	11.01	-	0.10	-
GM	-	67.98	-	146.50	-	14.60	-	1772.5	-	641.83	-	85.88

*, **: Significant at P=0.05 and 0.01, respectively

Table 2. Continued….

Name of the parent	100 seed wt.(g)		100 kernel wt(g)		Hull Cont. (%)		Vol. Wt (g/100cc)		Oil%		Oil Yield (kg/ha)	
CMS Line(L)	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*	*gca*	*per se*
P-2-7-1A	0.57**	5.71	0.34**	3.68	0.61**	36.73	-0.15	36.39	-0.44**	34.95	15.32**	642.0
P-89-1A	-0.25**	4.89	-0.23**	3.10	0.82**	36.94	1.03**	37.57	0.56**	35.95	3.28**	629.9
CMS-10A	-0.18*	4.96	-0.10*	3.23	-0.39**	35.73	-0.80**	35.74	0.03	35.42	2.70**	629.3
CMS-107A	-0.14*	5.00	0.00	3.33	-1.04**	35.08	-0.09	36.45	-0.16*	35.23	-21.30**	605.4
S. Em(±)	0.07	-	0.05	-	0.41	-	0.25	-	0.05	-	1.90	-
GM	-	5.14	-	3.34	-	36.46	-	36.57	-	35.38	-	633.73
RHA-6D-1	-0.25*	4.89	-0.22*	3.12	0.34	36.46	0.47*	37.01	0.07	35.46	-39.91**	586.8
R-12-96	-0.54**	4.60	-0.54**	2.80	3.39**	39.51	0.77**	37.31	-1.45**	33.94	-0.65	626.0
R-630	-0.33*	4..81	-0.23*	3.11	0.68*	36.80	-0.47*	36.07	0.15*	35.54	-17.57**	609.1
EC-601758	0.34*	5.48	0.31**	3.64	-0.71*	35.41	0.02	36.56	0.61*	36.00	12.61**	639.3
EC-601878	0.15	5.29	0.15*	3.49	-1.12**	35.00	-0.38	36.16	-0.17*	35.22	73.54**	700.2
R-138-2	0.01	5.15	0.04	3.38	-0.75**	35.36	-0.02	36.52	1.09**	36.48	-5.02**	621.7
R-1-1	0.38**	5.51	0.26**	3.59	-0.34	35.78	-0.75**	35.78	-0.72*	34.67	-47.87**	578.8
R-107	-0.21	4.93	-0.08	3.26	-1.01**	35.11	-0.60**	35.94	0.19*	35.58	-21.03**	605.6
R-104	0.46**	5.60	0.30**	3.64	-0.48	35.64	0.95**	37.48	0.23*	35.62	45.90**	672.6
S. Em(±)	0.12	-	0.09	-	0.67	-	0.41	-	0.08	-	3.10	-
GM	-	5.12	-	3.34	-	36.12	-	36.54	-	35.40	-	626.7

*, **: Significant at P=0.05 and 0.01, respectively

Table 3. Scoring of parents in respect of rank in GCA effect for thirteen for yield and yield contributing characters

Name of the parent	Days. to 50% flowering	Plant height (cm.)	Head Dia. (cm.)	Seed yield /plant (g.)	Seed yield (kg/ha)	No .of filled Grain/ Head	Autoga my (%)	100 seed weight(g)	100 kernel wt(g)	Hull content (%)	Vol. Wt. (g/100cc)	Oil content %	Oil Yield (Kg/ha)	TOTAL
P-2-7-1A	+1	-1	0	+1	+1	-1	+1	+1	+1	+1	0	-1	+1	**5**
P-89-1A	0	-1	-1	-1	-1	+1	-1	-1	-1	+1	+1	+1	+1	-2
CMS-10A	-1	0	0	0	0	+1	0	-1*	-1	-1	-1	0	+1	-2
CMS-107A	+1	+1	+1	-1	+1	-1	-1	-1	0	-1	0	-1	-1	-3
RHA-6D-1	-1	1	0	-1	-1	0	+1	-1	1	0	+1	0	-1	-1
R-12-96	+1	+1	+1	+1	+1	+1	-1	-1	-1	+1	+1	-1	0	4
R-630	-1	+1	0	-1	+1	+1	-1	-1	-1	+1	-1	+1	-1	-2
EC-601858	+1	-1	-1	0	+1	0	+1	0	+1	-1	0	+1	+1	3
EC-601978	+1	-1	0	+1	+1	+1	+1	0	+1	-1	0	-1	+1	4
R-138-2	-1	+1*	0	-1	-1	-1	-1	0	0	-1	0	+1	-1	-6
R-1-1	-1	-1	0	-1	-1	-1	+1	+1	+1	0	-1	-1	-1	-5
R-107	+1	+1	0	-1	-1	-1	+1	0	0	-1	-1	+1	-1	-2
R-104	-0	+1	+1	+1	+1	0	-1	+1	+1	0	+1	+1	+1	**8**

A score of '+1' was assigned for any significant *gca effects* in desirable direction, while '−1' for any significant *gca effects* in undesirable direction. A score of '0' was assigned for any non-significant *gca effects* in any direction.