

## LINE × TESTER ANALYSIS OF YIELD AND YIELD RELATED ATTRIBUTES IN DIFFERENT SUNFLOWER GENOTYPES

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### Abstract

This paper encompasses the study of line x tester analysis to chalk out genetic implications regarding yield and yield relating components in different genotypes of sunflower. Eight parents (four CMS lines and four restorers) along with their sixteen F<sub>1</sub> hybrids were considered and planted in Randomized Complete Block Design (RCBD) replicated thrice at experimental area of Oilseed Research Program, National Agriculture Research Centre (NARC), Islamabad, Pakistan in 2011. Combining ability for some important morphological traits included days to flower initiation, days to flower completion, days to maturity, plant height, head diameter and seed yield plant<sup>-1</sup>. In this concern general combining ability (GCA), reciprocals combining ability (RCA) and specific combining ability (SCA) for all traits were studied. The GCA and SCA variances due to lines and testers interaction were significant for all the characters. However, the magnitude of GCAs from CMS lines (females) and restorers (pollinators) were higher than the SCA indicating preponderance of additive genes in the expression of all the traits. Among the lines, CMS-HA-54 whereas in testers, RHP-71, by manifesting maximum GCA effects were considered as the best general combiners for almost all the traits indicating the presence of more additive gene effects in these parents, therefore may serve as potential parents for hybridization and to improve the characters studied. Among the F<sub>1</sub> hybrids, CMS HA-99 x RHP-76 (1.54, 212.65) and CMS HA-101 x RHP-73 (0.91, 432.73) were found as the best specific combiners for head or capitulum and seed yield. Hence, if farming community and researchers include these hybrids in their selection and hybridization program for the trait under study optimum result may be obtained.

### Introduction

Knowledge of the nature of inheritance and the way in which parents can transmit favorable alleles for desirable traits to their progeny enhances breeder's ability to select genetically superior parents and practice selection within segregating population. Good combining ability implies to the ability of a parent to produce superior progeny when combined with another parent (Khan *et al.*, 2008). General combining ability (GCA) provides an evaluation of the degree of mainly additive gene action, while specific combining ability (SCA) refers to the performance of two particular lines in a specific cross and it thus reflects non-additive types of gene interaction. Common technique has been extensively used in sunflower to classify parental lines in terms of their ability to combine and express hybrid vigor in cross combination. The resulting total genetic variation is partitioned into general and specific combining ability effects. In the present study, these techniques were applied to set of 16 crosses derived from 4 lines and 4 testers.

A breeder always tries to find out new combinations with high yielding, hybrid stability with outstanding performance in various features for a crop like sunflower (*Helianthus annuus* L.) which is an important cultivated oil crop in the world after soybean, oil palm and rapeseed (Fernandez *et al.*, 2004; Siddiqi *et al.*, 2012; Semerci, 2012). Among different oilseed crops grown in the country, sunflower has become the most important one due to its higher yield potential, shorter maturity duration and wider adaptability under different climatic conditions (Arshad *et al.*, 2010; Rehman *et al.*, 2012;

Onemli, 2012). General and specific combining abilities effects are meaningful biometrical techniques which aid in framing the breeding scheme for any crop particularly when one intends to produce a hybrid of his own choice. Earlier studies led to the selection of inbred with high GCA, predominance of non-additive gene action for major yield components and oil contents. It has been proved experimentally that parental lines with high GCA produce higher yielding hybrids than lines with low GCA (Marinkovic, 1993). The main objectives of sunflower breeding are improvements in seed yield and oil content per unit area, sink capacity, harvest index, resistance to major diseases and pests, and plant architecture (Škorić *et al.*, 2002; Bedove, 1985). Oil contents in the seed are greatly affected by genotype, soil and climatic conditions and the intensity of cultivation practices (Marinkovic *et al.*, 2003). Over-dominant gene action is reported for plant height, head diameter, oil contents, 100-seed weight, seed and oil yield, to estimate GCA and SCA as well as genetic variance components for different agronomic traits in sunflower (*Helianthus annuus* L.) inbred lines (Gangappa *et al.*, 1997). However, additive gene action for these traits has also been reported (Singh *et al.*, 1989). Estimates of GCA and SCA indicating additive effects were more important for oil contents (Bedov, 1985). Additive gene action has the greatest effect on flowering (Alvarez *et al.*, 1992). Thus keeping in view the pivotal importance of combining ability as well line x tester analysis 8 parents (4 CMS lines and 4 restorers) along with their 16 F<sub>1</sub> hybrids were used to study the mechanism as well as mode of inheritance so as to help sunflower breeders to decide for efficient breeding strategies to improve the valuable characters.

## Materials and Methods

The present research was conducted in the experimental area of Oilseed Research Program, NARC, Islamabad during spring seasons of 2010 and 2011. The experimental material comprised of four cytoplasmic male sterile (female) lines and four restorer (male) lines, developed by Oilseed Research Program. The CMS (A) lines were CMS HA-25, CMS HA-54, CMS HA-99 and CMS HA-101 and restorer lines RHP-69, RHP-71, RHP-73 and RHP-76. During first growing season (spring, 2010), hybrid combinations were developed by making crosses of the above mentioned CMS and restorer lines. Plants in both CMS and restorer lines were bagged before flower initiation and were pollinated twice. Pollen from restorer lines were collected to pollinate CMS flowers of the respective pairs when 50 and 75 percent disc florets opened. Flowers were bagged again after pollination to avoid contamination. The seeds were harvested and threshed carefully to avoid any physical contamination at maturity and kept separately.

Hybrid combinations developed by crossing the CMS and restorer lines during spring, 2010 were planted for evaluation during spring, 2011. Planting was done on raised beds (ridges) by dibbling 2-3 seeds hill<sup>-1</sup> during both seasons and one plant hill<sup>-1</sup> was maintained by manual thinning to maintain optimum plant population after emergence of seedlings. Randomized Complete Block Design (RCBD) was used with three replications.

Parental material and hybrids were planted in 4 rows of 5 meter length. Row to row distance of 75 cm was kept, while plant to plant distance was maintained at 25 cm. During growing season, weeds were eradicated manually. Earthing up was done to eradicate the weeds and protect the crop from lodging by winds/storm. Fertilizers (Urea and DAP) were applied @ 120 Kg N and 60 Kg P ha<sup>-1</sup>. All phosphorus and half nitrogen fertilizer was applied at the time of seed bed preparation while remaining half N was applied after 45 days of planting. Ten randomly selected plants from each line and hybrid were used for recording data on seed yield, plant height and head diameter. The analysis of variance to determine the differences among the genotypes (Parents and F<sub>1</sub>'s) was carried out according to Steel & Torrie (1980) procedure. The mean squares from line x tester analysis and combining ability (GCA and SCA) effects were calculated by following the statistical procedures adopted by (Kempthorn, 1957).

## Results and Discussion

Data presented in Table 1 revealed highly significant differences amongst the genotypes for most of the traits under study. The total variations for various traits were partitioned into general combining ability and specific combining ability and have been discussed separately for each trait as under.

**Table 1. Analysis of variance for mean square of yield and yield related components in sunflower genotypes, during spring 2011.**

Source of variance	df	Days to flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	Head diameter (cm)	Seed yield kg ha <sup>-1</sup>
Replications	2	1.29	1.01	5.38	1220.67	0.59	48957.56
Treatments	23	38.27**	53.21**	102.37**	991.11**	36.15**	1512941.84**
Error	46	14.93	18.38	24.62	416.80	2.54	27071.87
CV (%)		4.41	4.41	4.44	11.50	9.08	7.13

\*\* Highly significant (p<0.0)

**Days to flower initiation:** Data pertaining to flower initiation revealed that significant variation amongst the mean exists (Table 1). Comparing parents mean along with their hybrid variations were noted in results. Amongst parent RHP-71 and CMS-54 has initiated flowering in 82 to 83 days respectively, where as flower initiation was very late (96 days) in the parent RHP-73. Furthermore, CMS HA-54 showed minimum days (83) for flower initiation. This parameter is closely related to earliness of plant maturity so less days required for heading show early flowering and in turn early maturity, which save time and is also helpful in escaping from various biotic and abiotic stresses. In cross combinations, lowest mean value of 83 days was recorded in CMS HA-54 × RHP-76, CMS HA-99 × RHP-71, whereas, maximum (91 days) in CMS HA-54 × RHP-69 (Table 2). Data analyzed for GCA revealed that sufficient variation was found among the female and male parents for days to flower initiation (Table 4). Among the female parent

lines, maximum positive GCA effects (1.395) were indicated by CMS HA-99, Which indicates that this parent is the best general combiner for the trait under study while maximum negative GCA estimates (-1.104) were indicated by CMS HA-25 indicating that this parent does not affect the earliness regarding flower initiation. For a particular trait higher value of GCA is of prime importance. Therefore attention should be given to parent with high GCA value irrespective of the sign positive or negative. Among the male parents, maximum positive GCA estimates (0.81) were expressed by RHP-69, while maximum negative GCA (-0.94) effects by RHP-76. As per Table 5 pertaining to SCA effects it has been noted that maximum SCA effects for the parameter focused have been noted in cross CMS-HA-54 x RHP-69 with value 3.52 although both of them have small value of GCA. They show highest SCA value when crossed with their hybrid, which indicates that it is not necessary for the parents to be a good general combiner for hybrid

production. Table 5 further elucidated that CMS-HA-99 × RHP-76 showed higher SCA value i.e., 2.94. Highest negative SCA effects (-4.06) for this character were observed in the cross combination of CMS HA-99 × RHP-71, followed by CMS HA-101 × RHP-69 (-3.40). Morpho-physiological characteristic of sunflower genotypes indicated that the trait is controlled by non-additive gene action. Variance of dominance was observed as 3.91 and additive variance was -0.42 for days to flower initiation (Table 6). Khurana *et al.*, (1996), Lande *et al.*, (1997), Singh & Singh (2002) and Gill *et al.*, (2003) also reported similar findings in their studies.

**Days to flower completion:** As per parents days for the complete blooming of flowers ranged from 91-105, wherein tester RHP-71 took minimum days while CMS (HA-99) and tester (RHP-73) took maximum days (105) (Table 2). Amongst crosses three crosses viz., CMS HA-25 × RHP-69, CMS HA-99 × RHP-71 and CMS HA-101 × RHP-76 took minimum days (92) for flower completion. Probing into (Table 4) showing the GCA effects, the female parents (CMS HA-25) expressed maximum negative GCA effect (-1.44) and maximum positive effects (1.65) was observed in CMS-HA-99.

Among the male parents, maximum positive GCA effects (1.98) were recorded for RHP-69, whereas maximum negative GCA estimates (-1.19) were observed for RHP-71. The SCA for days to flower completion revealed maximum positive SCA effects for days to flower completion (3.52) in cross combination of CMS HA-54 × RHP-69 followed by CMS HA-99 × RHP-69 (2.60). The highest negative SCA value for this character was observed in the cross combination of CMS HA 25 × RHP-69 (-3.65) followed by CMS-HA-99 × RHP-71 with SCA magnitude of -3.56 (Table 5). The Genotypes exhibited the additive and dominance variances of -0.08 and 2.76, respectively, suggesting the expression of non-additive type of gene action for days to flower completion (Table 6). Variation in days to flower completion is important because it allows the development of cultivars/hybrids adapted to specific growing regions. Secondly it also has deep concern with grain filling. Sunflower hybrids with later flowering tend to have smaller grain filling period (Putt, 1940). The results have great analogy with the previous findings of Sakthivel *et al.*, (2003 a), Burli *et al.*, (2001), Ashok *et al.*, (2000), Gangappa *et al.*, (1997), Khurana *et al.*, (1996) and Kandhola *et al.*, (1995 b).

**Table 2. Mean performance for yield and yield related components in sunflower genotypes, during spring, 2011.**

Parents/F <sub>1</sub> hybrids	Days to flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	Head diameter (cm)	Seed yield kg ha <sup>-1</sup>
CMS HA-25	91	103	122	183	22.68	1953
CMS HA-54	83	98	106	144	19.32	1988
CMS HA-99	92	105	125	172	20.77	1794
CMS HA-101	84	101	116	164	21.07	2042
RHP-69	89	101	114	139	9.67	1071
RHP-71	82	91	110	177	11.33	1113
RHP-73	96	105	125	161	13.00	1309
RHP-76	91	100	108	131	8.67	711.3
CMS HA-25 × RHP-69	84	92	107	183	18.57	2545
CMS HA-25 × RHP-71	86	94	110	179	19.07	3264
CMS-HA-25 × RHP-73	87	95	109	188	18.23	2907
CMS HA-25 × RHP-76	85	95	107	183	17.57	2900
CMS HA-54 × RHP-69	91	101	116	198	19.60	2984
CMS HA-54 × RHP-71	87	95	111	200	18.20	3082
CMS HA-54 × RHP-73	85	95	108	188	17.97	2690
CMS HA-54 × RHP-76	83	93	104	178	16.57	2300
CMS HA-99 × RHP-69	91	102	117	194	19.87	2310
CMS HA-99 × RHP-71	83	92	107	197	17.23	2608
CMS HA-99 × RHP-73	88	96	111	182	18.17	1964
CMS HA-99 × RHP-76	90	98	114	177	19.87	2485
CMS HA-101 × RHP-69	84	94	111	188	18.13	2521
CMS HA-101 × RHP-71	88	96	111	178	18.23	2672
CMS HA-101 × RHP-73	89	97	113	197	19.27	3260
CMS HA-101 × RHP-76	84	92	106	182	17.37	2879
<b>Range</b>	<b>82-96</b>	<b>91-105</b>	<b>106-125</b>	<b>131-200</b>	<b>8.67-22.68</b>	<b>711.3-3264</b>

**Days to maturity:** Maturity duration in Sunflower is an important selection criterion. It is planted in two major cropping systems i.e., Rice and Cotton. Farmers demand early maturing hybrids with higher yield potential, so that the planting, harvesting and threshing of major crops in the cropping system may not be delay. Days to maturity were recorded when back of the heads turned yellow and bracts started turning brown in color. Data presented in Table 1 revealed that there was significant variation in maturity duration of parental material and hybrid combinations. Average days to maturity ranged from 106 to 125. Female parent line, CMS HA-54 was earliest in maturity and took minimum (106) days, whereas CMS-HA-99 and RHP-73 were latest in maturity with maximum (125) days to maturity. Among hybrid combinations, maximum (117) days were taken by CMS HA-99  $\times$  RHP-69 and minimum (104) in CMS HA-54  $\times$  RHP-76 (Table 2). Data presented in Table 4 revealed that among female parent lines, CMS HA-99 had the maximum positive GCA value (2.54), while maximum negative GCA value was observed in CMS HA-25 (-1.88). Among male parents maximum positive GCA effects (2.625) for days to maturity were recorded for RHP-69 whereas maximum negative GCA value (-2.208) in RHP-76. CMS HA-54  $\times$  RHP-69 exhibited maximum positive SCA effects (3.88), followed by CMS HA-99  $\times$  RHP-76 (3.71). Highest SCA negative effects for days to maturity were recorded in combination of CMS-HA-99  $\times$  RHP-71 (-4.71) followed by CMS HA-25  $\times$  RHP-69 (-4.04) (Table 5). Early maturity is desirable. It not only saves the crop from any type of weather upsets but also beneficent in evolving new varieties. Hence negative combining ability effects for this trait is preferred. Variance of dominance was 4.02 and variance of additive gene action was 0.24 (Table 6). The Genotypes exhibited the additive and dominance variances of 0.24 and 4.02, respectively, suggesting the expression of non-additive type of gene action is controlling the trait under study. Which also shows that epistasis is involved in the manifestation of this trait. Present outcome of the research coincides with the findings of (Kinman, 1975). Who emphasized to focus early maturing in sunflower breeding if one wanted to develop hybrids/cultivar. Our results are also supported by the previous work of Ashok *et al.*, (2000), Khurana *et al.*, (1996) and Kandhola *et al.*, (1995 b).

**Plant height (cm):** Hybrids with shorter height and higher yield potential respond better to higher inputs due to better tolerance against lodging. Data presented in Table 2 revealed that height of parental lines and hybrid combinations ranged from 131 to 200 cm. Among parent lines, RHP-76 attained the minimum height of (131 cm) and maximum height of (183 cm) was recorded in CMS HA-25. However, height of the hybrid combinations ranged from 177 to 200 cm. Cross, CMS HA-54  $\times$  RHP-71 had the maximum height of (200 cm) whereas minimum plant height was recorded in CMS-HA-99  $\times$  RHP-76 of (177 cm). Data presented in Table 4 revealed that among the female parent lines, maximum positive

GCA effects (3.81) were observed for CMS HA-54, however, highest negative GCA effects (-3.69) were recorded for CMS HA-25. Among male parents, RHP-6 expressed maximum positive GCA estimates (3.65) for plant height and maximum negative GCA effects (-6.85) by RHP-76. Eight out of sixteen crosses manifested negative SCA estimates for plant height. The highest positive SCA effects for plant height were recorded by the cross combination, CMS HA-101  $\times$  RHP-73 (8.69) followed by cross CMS HA-99  $\times$  RHP-71 (8.02). The lowest SCA effects (-9.56) for this character were observed in CMS HA 101  $\times$  RHP-71 (Table 5).

Plant height exhibited -77.34 as variance of dominance and 0.10 as variance of additive indicating the presence of additive type of gene action (Table 6). Additive type of gene insolvent is good for a breeder. This may enhance the heritability value. And higher value of heritability means early selection will bring fruitful result regarding the parameter focused for that particular crop. Radhika *et al.*, (2001) and Burli *et al.*, (2001) were also of the same opinion regarding selection strategy for any breeding programme.

**Head diameter (cm):** Head Diameter in sunflower is also an important agronomic trait; normally ranges from 15 to 30 cm. Bigger heads have more number of seeds and also contribute towards better yield potential. However, in addition to head size, other factors, like number of filled seeds, seed size are also important. Average head diameter recorded in parental lines and hybrid combinations varied between 8.7 and 22.7 cm (Table 2). Among parents, minimum head diameter of (8.7 cm) was recorded in RHP-76 and maximum (22.7 cm) in CMS HA-25. In hybrid combinations, maximum head diameter of (19.9 cm) was recorded in CMS HA-99  $\times$  RHP-69 and CMS HA-99  $\times$  RHP-76 each. CMS HA-54  $\times$  RHP-76 produced heads of minimum size (16.6 cm). Parents and parents vs crosses showed highly significant differences for mean square in line  $\times$  tester analysis for head diameter (Table 3). Among female parent lines, CMS HA-99 expressed maximum positive GCA (0.39) effects, whereas maximum negative GCA (-0.31) in CMS HA-54. Among male parents, maximum positive GCA estimates (0.65) were recorded in RHP-69 and maximum negative GCA effects (-0.46) in RHP-76 (Table 4). Table 5 shows maximum SCA estimates (1.54) for head diameter were found in CMS HA-99  $\times$  RHP-76, followed by CMS HA-25  $\times$  RHP-71 (0.92). Seven out of sixteen crosses showed negative SCA estimates for head diameter. The highest negative SCA estimates for head diameter (-1.34) were exhibited by the cross combination of CMS HA-99  $\times$  RHP-71 followed by CMS HA-54  $\times$  RHP-76 (-1.06). Evaluation for genetic components revealed that head diameter manifested 0.212 as variance of dominance and -0.04 as variance of additive showing prevalence of non-additive gene action (Table 6). Our findings are supported by Kumar *et al.*, (1998), Sassikumar (1999), and Shekar *et al.*, (1998). Goksoy *et al.*, (2000) also found similar results.

**Table 3. Analysis of variance for line × Tester analysis for various yield components in sunflower genotypes, during spring 2011.**

Source of variance	df	Days to flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	Head diameter (cm)	Seed yield kg ha <sup>-1</sup>
Replication	2	1.29	1.01	5.37	1220.7	0.58	48958
Treatments	23	38.26**	53.20**	102.37**	991.1**	36.14**	1512942**
Parents	7	73.04**	62.47**	174.89**	1057.5*	97.88**	777671**
Parents vs crosses	1	60.06*	403.34**	529.00**	12600.1**	106.46**	23541095**
Crosses	15	20.58	25.54	40.68	186.2	2.64	387525**
Lines	3	13.18	21.18	42.47	114.9	1.00	765219**
Tester	3	9.74	26.57	47.91	261.7	2.70	231682**
Line × tester	9	26.66	26.65	36.67	184.8	3.17	313574**
Error	46	14.92	18.37	24.62	416.8	2.53	27072

\*\* Significant at 1% level of probability

\*Significant at 5% level of probability

**Table 4. Estimates of GCA effects for seed yield and yield related traits in sunflower genotypes, during spring 2011.**

Lines/Tester	Days to flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	Head diameter (cm)	Seed yield kg ha <sup>-1</sup>
CMS-HA-25	-1.10	-1.44	-1.88	-3.69	-0.03	193.19
CMS-HA-54	0.06	0.40	-0.79	3.81	-0.31	53.35
CMS-HA-99	1.40	1.65	2.54	0.48	0.39	-368.98
CMS-HA-101	-0.35	-0.60	0.13	-0.60	-0.05	122.44
RHP-69	0.81	1.98	2.63	3.65	0.65	-120.90
RHP-71	-0.60	-1.19	-0.46	1.56	-0.21	196.02
RHP-73	0.73	0.31	0.04	1.65	0.02	-5.48
RHP-76	-0.94	-1.10	-2.21	-6.85	-0.46	-69.65

**Table 5. Estimation of SCA effects for seed yield and yield related traits in sunflower genotypes, during 2011.**

F <sub>1</sub> Hybrids	Days to flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	Head diameter (cm)	Seed yield kg ha <sup>-1</sup>
CMS-HA-25 × RHP-69	-1.98	-3.65	-4.04	-3.90	-0.44	-238.27
CMS-HA-25 × RHP-71	1.10	1.19	2.38	-6.15	0.92	163.81
CMS-HA-25 × RHP-73	0.44	0.69	0.88	3.10	-0.14	8.31
CMS-HA-25 × RHP-76	0.44	1.77	0.79	6.94	-0.33	66.15
CMS-HA-54 × RHP-69	3.52	3.52	3.88	3.27	0.87	340.56
CMS-HA-54 × RHP-71	0.94	0.02	1.29	7.69	0.33	122.31
CMS-HA-54 × RHP-73	-2.06	-1.48	-2.21	-4.73	-0.13	-68.52
CMS-HA-54 × RHP-76	-2.40	-2.06	-2.96	-6.23	-1.06	-394.35
CMS-HA-99 × RHP-69	1.85	2.60	2.21	2.60	0.43	89.23
CMS-HA-99 × RHP-71	-4.06	-3.56	-4.71	8.02	-1.34	70.65
CMS-HA-99 × RHP-73	-0.73	-1.06	-1.21	-7.06	-0.63	-372.52
CMS-HA-99 × RHP-76	2.94	2.02	3.71	-3.56	1.54	212.65
CMS-HA-101 × RHP-69	-3.40	-2.48	-2.04	-1.98	-0.86	-191.52
CMS-HA-101 × RHP-71	2.02	2.35	1.04	-9.56	0.10	-356.77
CMS-HA-101 × RHP-73	2.35	1.85	2.54	8.69	0.91	432.73
CMS-HA-101 × RHP-76	-0.98	-1.73	-1.54	2.85	-0.15	115.56
S.E (s.i.)	-4.06	-3.56	-4.71	8.02	-1.34	70.65

**Table 6. Estimates of genetic components for seed yield and yield related traits in sunflower genotypes, during spring 2011.**

Gene action	Days to flower initiation	Days to flower completion	Days to maturity	Plant height (cm)	Head diameter (cm)	Seed yield kg ha <sup>-1</sup>
Variation due to additive type of gene action	-0.4	-0.1	0.2	0.1	0.0	5135.0
Variation due to non-additive type of gene action	3.9	2.8	4.0	-77.3	0.2	95501.0

**Seed yield (kg ha<sup>-1</sup>):** Seed yield has been recorded which is the major factor that determines the commercial success of crops' cultivars. Better yield means better profit and higher income for the customers of the seed industry and the growers. Seed yield recorded for different parental lines and crosses ranged from 711 to 3246 kg ha<sup>-1</sup>. Among parent lines, lowest seed yield (711.3 kg) was recorded in RHP-76 while highest mean value of (2042 kg) was obtained in CMS HA-101. In cross combinations, the highest seed yield of 3264 kg was recorded in CMS HA-25 × RHP-69, followed by CMS HA-101 × RHP-73 and CMS HA-54 × RHP-71 with 3260 and 3082 kg ha<sup>-1</sup>, respectively. Minimum seed yield of 1964 kg ha<sup>-1</sup> was recorded in CMS HA-99 × RHP-73 (Table 2). The data analyzed for the GCA effects statistically showed that maximum positive value for seed yield was exhibited by the female parent CMS HA-25 (193.19), whereas maximum negative GCA (-386.98) values were estimated for CMS HA-99. Among male parent lines, RHP-71 had a maximum (196.02) positive effects, whereas male parent RHP-69 exhibited maximum negative (-120.90) effects (Table 4). As per their GCA values regarding female parent CMS HA-25 with value 193.19 and lower value of pollinator i.e. RHP 71 with value 196.02 these can further be explored as female line or restorer parent in any line x tester analysis. Data presented in Table 5 revealed that SCA effects for seed yield in the crosses were significantly different (Table 5) does not show significance) The highest positive SCA effects for seed yield (432.73 kg ha<sup>-1</sup>) were exhibited by the cross combination of CMS HA-101 × RHP-73, followed by CMS HA-54 × RHP-69 (340.56). Six out of 16 crosses manifested negative SCA effects. The highest negative SCA effects (-394.35) were exhibited were recorded in the cross combination of CMS HA-54 × RHP-76 followed by CMS HA-99 × RHP-73 (-372.52). Variances recorded due to additive and non-additive types of gene action were 5135 and 95501 respectively for seed yield (Table 6). Our findings are in agreement with the previous research work of Radhika *et al.*, (1999).

## Conclusion

The genotypes studied in this experiment were differed significantly for all the traits. Parent showed highly significant differences for all the traits. Crosses exhibited highly non- significant variation for all traits. Line × tester showed highly non-significant variation for all the traits except seed yield. Overall results revealed that among male parents, RHP-71 proved to be the best combiner for yield and its most of the related characters

while among female parents, CMS-HA-25 exhibited its superior GCA effects for grain yield. The SCA effects revealed that cross CMS-HA-101 x RHP-73 could be the better choice for seed yield and CMS-HA-99 x RHP-71 for early maturity. Female line CMS-HA-25 and male RHP-71 and among the crosses CMS-HA-101 x RHP-73 and CMS-HA-99 x RHP-71 were the best specific combiners for head and seed yield. For majority of the traits, both these parents and crosses may be preferred for hybridization and selection programmes and for hybrid crop development.

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