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COMBINING ABILITY ANALYSIS FOR SEED PROTEINS, OIL CONTENT AND FATTY ACIDS COMPOSITION IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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ABSTRACT:-Genetically diverse sunflower (*Helianthus annuus* L.) inbred lines comprising six cytoplasmic male sterile (CMS) and six fertility restorer (R_f) lines were crossed in a line x tester mating design to obtain 36 F_1 hybrids. Parental lines and F_1 hybrids exhibited mean values for seed total proteins, oil content and fatty acids composition. Among parental lines, CMS-64, CMS-53, CMS-H55-2-2-1 and CMS-53 were the best general combiners for seed total proteins, oil content, oleic and linoleic acid, respectively. Among males, C-206-R, SF-187R, RHA-295 and RHA-854 were the potential parents exhibiting desirable GCA for seed total proteins, oil content, oleic and linoleic acids, respectively. Among the F_1 hybrids, highest specific combining ability (SCA) estimates were exhibited by CMS-NDMTC x RHA-295 (3.837) for seed total proteins whereas for oil content, the hybrid CMS-53 x SF-187R exhibited the highest SCA (11.317). F_1 hybrid, CMS-NDMTC x RHA-295 (13.936) for oleic acid while CMS-53 x RHA-295 (17.986) hybrid for linoleic acid were the potential genotypes by exhibiting the maximum positive SCA values of 13.936 and 17.986, respectively. The variances due to SCA for all the quality characters were higher than GCA variances, showing non-additive type of gene action controlling the characters. Non-additive type of gene action can be utilized for varietal improvement through heterosis breeding. The lines x testers were the major contributors in inheritance of all characters studied.

Key Words: Helianthus annuus; Lines; Combining Ability; Gene Action; Cytoplasmic Male Sterile; Fertility Restorer; Heterosis Breeding; Agronomic Characters; Pakistan.

INTRODUCTION

Sunflower is the third major supplier of edible oil in the world after soybean and groundnut (Meric et al., 2003). Sunflower has emerged as a competitive oilseed crop due to its excellent nutritive properties. The sunflower cake contains 25% protein and is frequently used as a protein supplement for livestock. Its seed contains 40-50% oil. The saturated fatty acids viz., palmitic (4.7-8.2%) and stearic acid (1.7-9.1%) constitute about 10% whereas unsaturated fatty acids viz., oleic and linoleic acid constitute about 90% of total fatty acids (Przybylsky et al., 2005). High oleic acid, sunflower oil is nutritionally similar to olive oil which is

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considered superior to other types of seed oil (Doty, 1978). Grundy (1986) suggested that a diet rich in mono-unsaturated fatty acid (oleic acid) reduces cholesterol in blood plasma and therefore reduces risk of coronary heart diseases. Oil with high oleic acid content has a high degree of oxidative stability than oil low in oleic acid (Fuller et al., 1967) which is desirable for frying purposes, refining and storage. Therefore, oil with high oleic acid content has greater shelf life than that with high linoleic acid in both processed oil and seed. Therefore, it is suitable for preparations of pharmaceuticals, detergents, lubricants, metal working fluids, surfactants, or chemical synthesis (Fick and Miller, 1997; Dorrell and Vick, 1997). Oil high in linoleic acid (poly-unsaturated fatty acids) is essential for good nutrition and must be obtained from food as it cannot be produced by human body (Coons, 1960). The daily requirement of linoleic acid is about 100 mg kg^{-1} of body weight per day (Mullor, 1968). Linoleic acid is necessary for growth and reproduc-tion and protects against excessive loss of water and damage from radiation (Coons, 1960). Linoleic acid is involved in metabolism of cholesterol and may aid in excretion of cholesterol and products resulting from its breakdown (Leverton, 1974). Therefore, production of sunflower oil with high unsaturated fatty acids has become an important breeding objective. It is important to know the genetic control of saturated and unsaturated fatty acids in sunflower before going for quality improvement of edible oil through a breeding programme.

Importance of combining ability in selection of parents for hybridization has been emphasized by many workers in sunflower (Putt, 1996; Giriraj et al., 1987). The potentiality of any line to be used as a parent in hybridization depends on its per se performance and the performance of F_1 hybrid derived from it and its own GCA effects. Singh et al. (1999) in a line x tester analysis of 30 hybrids noticed the preponderance of non-additive gene action for seed yield, oil content, palmitic, stearic and linoleic acids. Skoric et al. (1978) revealed dominance and epistatic gene action for oleic acid content. While making hybrids, it is desirable if cross showing high SCA effect also has parents showing high GCA effects for the same character (Kadkol et al., 1984) in which case both additive and non-additive gene action can be utilized. Lines x testers were observed to be major contributors in inheritance of seed total proteins, oil content and all fatty acids under study. The present study is an attempt to evaluate gene action and combining ability of sunflower inbred lines and their crosses for seed proteins, oil contents and fatty acids composition in oil. In a systematic breeding programme, it is essential to identify superior parents for hybridization. In hybrid development, it is necessary to test the inbred lines and their F_1 hybrids through GCA and SCA, respectively and therefore line × tester analysis is one of the efficient methods of evaluating large number of inbred lines. The said analysis also provides information on the relative importance of GCA and SCA effects in genetic evaluation of important plant traits (Singh and Singh, 2000). The present research was an effort to develop improved and more productive F_1 hybrids through a breeding programme.

MATERIALS AND METHOD

The research was conducted in the field and laboratory conditions during 2003-04 and 2004-2005 at National Agricultural Research Centre (NARC), Islamabad, Pakistan. Among inbred lines, six cytoplasmic male sterile (CMS) lines (CMS-H55-2-2-1, CMS-NDMTC, CMS-64, CMS-303, CMS-HAR-1 and CMS-53) and six fertility restorer (R_f) (C-206R, PAC-8712, RHA-295, SF-187R, RHA-271 and RHA-854) were obtained from Oilseed Programme, NARC, Islamabad. Before crossing, the inbred lines were evaluated for seed proteins, oil content and fatty acids composition. The 36 F_1 hybrids were made by crossing inbred lines in a line × tester design during spring 2004. In autumn 2004-2005, all the parental lines and their F_1 hybrids were grown in a randomized complete block design (RCBD) with three replications. Each parental line and F_1 hybrid was planted in 5m long rows with plant to plant and row spacing of 0.3 m and 0.5 m, respectively. A basal fertilizer dose of 120 kg ha^{-1} (urea) and 60 kg ha^{-1} phosphorus (diammonium phosphate, DAP) was applied. Full dose of DAP and half dose of nitrogen were applied at the time of sowing; the remaining half dose of nitrogen was applied just before head initiation. The field was well irrigated 30 days after germination and three more irrigations were applied to the experimental block at appropriate times. At the stage of physiological maturity, when the backs of heads turned yellow, the heads were cut with sickle and sun dried. Seeds of individual heads were threshed. Field data were recorded on various parameters including seed yield and its related traits; head diameter (cm), 1000-seed weight (g), yield (kg ha^{-1}), harvest index (%), moisture factor and leaf area (cm^2). After threshing, the seeds of inbred lines and F_1 hybrids were evaluated for seed proteins, oil content (%) and fatty acids composition in oil. Seed proteins were estimated by Kjeldahl method using Kjeltech Auto Analyzer(AOAC, 1990). Oil content (%) analysis was done on Oxford NMR Analyzer. Fatty acids composition in seed oil was determined by Gas Liquid Chromatography (AOAC, 1990).

The average data was subjected to analysis of variance (Steel and Torrie, 1996) to test the significance of variance among the genotypes for seed proteins, oil content and fatty acids profile in seed oil. Combining ability studies were made by using line × tester analysis as outlined by Kempthorne (1957).

RESULTS AND DISCUSSION

Seed Proteins

The average seed proteins was 24.21% for parents vs. 21.18% for F_1 hybrids representing a net difference of 3.03%. The coefficient of variation for protein content was 2.47% suggesting a low level of variability among genotypes (Table 1). All parents including females and males were statistically significant for protein content as revealed by analysis of variance for lines x testers (Table 2). Among the restorer lines, the maximum positive GCA estimates were observed for CMS-64 (1.315) followed by CMS-53 (1.214) and CMS-H55-2-2-1 (1.188) (Table 3). The maximum negative GCA estimates

were recorded for CMS-303 (-2.369) followed by CMS-HAR-1 (-0.912) and CMS-NDMTC (-0.474). In testers, the maximum positive GCA effects were observed for C-206-R (2.403) followed by RHA-295 (1.603) whereas the maximum negative GCA estimates were observed for SF-187R (-1.680) followed by RHA-854(-1.554), RHA-271(-0.633) and PAC-8712(-0.141). Among the lines, CMS-64 was found the best general combiner for protein content as it recorded significant positive GCA effects, while among the tester, the general combiner C-206R recorded maximum positive GCA effects for protein content. These results are in agreement with those of Tan (2010) and Bedov (1985) who reported similar results while conducting trials for combining ability on sunflower lines.

Significant SCA estimates for protein content were indicated by all the F_1 hybrids except CMS-303 x SF-187R, CMS-HAR-1x C-206R, CMS-HAR-1x PAC-8712 and CMS-53x PAC-8712 which revealed non-significant SCA estimates. Sixteen crosses exhibited negative SCA values while 20 crosses showed positive SCA estimates. Highest SCA estimates for crosses were exhibited by CMS-NDMTC x RHA-295(3.837) whereas lowest SCA effects were observed for CMS-64 x RHA-295 (-5.890) (Table 4).

The values for variances of dominance and additive for protein content were 8.725 and 0.212, respectively (Table 5). The variance of dominance was higher than GCA variance showing non-additive type of gene action controlling the character. Non-additive type of gene action can be utilized for varietal improvement through heterosis breeding. The proportional contribution was 18.303 for lines, 22.539 for testers and 59.157 for lines x testers, revealing highest contribution of line x tester followed by testers for protein content (Table 6).

Seed Oil Content

Among lines, the maximum seed oil content was observed for CMS-53 (40.65%) whereas minimum in CMS-303 (25.55%) with a net difference of 15.10%. Among testers, the maximum mean value for oil content was exhibited by PAC-8712 (41.04%). Among F_1 hybrids, maximum and minimum oil contents were indicated

Table 1. Mean squares and coefficient of variation (C.V) for seed total proteins, oil content and fatty acids composition in sunflower genotypes

Source	df	Proteins	Oil Content	Palmitic Acid	Stearic Acid	Oleic Acid	Linoleic Acid
Replication	2.0	0.562	2.385	0.039	0.013	1.146	3.490
Genotypes	47.0	29.828**	51.509**	0.668**	6.072**	105.043**	125.077**
Error	94.0	0.295	0.478	0.035	0.021	0.865	0.708
C.V%		2.470	1.730	3.250	3.560	5.330	1.150

***Significant at 1% probability level*

by CMS-53 x SF-187 (57.76%) and CMS-NDMTC x RHA-295 (36.0%), respectively. The average oil percentage was 37.41% for parents vs. 40.86% for F_1 hybrids representing a net difference of 3.45%. Among genotypes, a low level of variability existed for oil content as indicated by coefficient of variation (1.73%) (Table 1). Among lines, the maximum positive GCA estimates for oil content were observed for CMS-53 (3.068) while maximum negative estimates were recorded for CMS-NDMTC (-2.418). Among testers, the SF-187R exhibited maximum positive GCA estimates (2.513) (Table 3). Among the 17 hybrids wherein positive SCA estimates were recorded, 10 hybrids revealed significant SCA effects. The cross CMS-53 x SF-187-R exhibited highest SCA effect (11.317) (Table 4), while lowest SCA effects were observed for CMS-53 x RHA-295 (-5.243).

For oil content, the estimates of SCA variance (11.084) were higher than GCA variance (0.286) indicating pre-dominance of non-additive gene action in determination of oil content (Table 5). Non-additive type of gene action for oil content has been reported by many workers (Giriraj et al., 1986; Radhika et al.,2001). This type of gene action as a predominant factor in determining the oil content has been reported by Shankara (1981), Shaktivel (2003), Ortis et al. (2005) and Reddy and Madhavilatha (2005) which can be utilized in heterosis breeding.

Table 2. Analysis of variance for lines x testers including parents for seed total proteins, oil content and fatty acisd composition in sunflower genotypes

Source	df	Proteins	Oil Content	Palmitic Acid	Stearic Acid	Oleic Acid	Linoleic Acid
Replication	2	0.562^{ns}	2.385^{ns}	0.0390^{ns}	0.013^{ns}	1.146^{ns}	3.490^{ns}
Genotypes	47	29.828**	51.509**	0.668^{ns}	6.072**	105.043**	125.077**
Parents	11	3.122*	60.214**	0.535^{ns}	6.289**	30.815**	24.76**
Crosses	35	31.961**	41.086**	0.730^{ns}	5.431**	123.559**	150.412**
Parents vs crosses	1	292.540**	320.000**	0.314^{ns}	5.661*	273.448*	267.388*
Lines	5	40.951**	57.589**	1.098^{ns}	6.060*	103.747**	79.755**
Testers	5	50.427**	61.365**	0.578^{ns}	8.193**	224.681**	245.351**
Lines x Testers	25	26.471**	33.730**	0.687^{ns}	5.954**	107.297**	143.708**
Error	94	0.295	0.478	0.035	0.020	0.865	0.708
Total	143	-	-	-	-	-	-

** and ** = Significant at 5% and 1% probability levels, respectively; ns = non-significant*

Palmitic Acid

Among the genotypes, the low level of genetic variability existed for palmitic acid as revealed by analysis of variance; the co-efficient of variation was 3.25% (Table 1). The average palmitic acid was 5.72% for parents vs. 5.37% for F_1 hybrids representing a net difference of 0.35%. The lines and testers revealed significant differences for palmitic acid as indicated by GCA estimates (Table 3). The maximum positive GCA estimates in females were observed for CMS-64 (0.381), while maximum negative GCA estimates were observed for CMS-HAR-1 (-0.298). In males, the maximum positive GCA estimates were observed for SF-187R (0.213), whereas maximum negative GCA estimates were observed for C-206-R (-0.239) followed by RHA-295 (-0.131). Saturated fatty acids are a major risk factor for heart attacks and strokes due to atherosclerosis (Anonymous, 2013). Therefore, the level of palmitic acid in edible oil should be minimized by selection of

Table 3. Estimates of GCA effects for seed total proteins, oil content and fatty acids composition in sunflower genotypes (parents)

Genotypes	Proteins	Oil Content	Palmitic Acid	Stearic Acid	Oleic Acid	Linoleic Acid
Females						
CMS H55-2-2-1	1.188*	0.215*	-0.201*	-0.362*	3.002*	-2.716*
CMS-NDMTC	-0.474*	-2.418*	0.042*	0.972*	0.348*	-1.837*
CMS-64	1.315*	-0.365*	0.381*	-0.224*	2.386*	-1.892*
CMS-303	-2.369*	0.205*	0.146*	0.259*	-1.433*	1.354*
CMS-HAR-1	-0.912*	-0.706*	-0.298*	0.052*	-0.995*	1.641*
CMS-53	1.214*	3.068*	-0.086*	-0.698*	-3.307*	3.461*
Males						
C-206-R	2.403*	-1.728*	-0.239*	-0.182*	-1.511*	1.570*
PAC-8712	-0.141*	0.543*	0.074*	-0.384*	-1.411*	-1.698*
RHA-295	1.603*	-1.924*	-0.131*	0.942*	6.862*	-7.087*
SF-187R	-1.680*	2.513*	0.213*	-0.854*	0.531*	-0.473*
RHA-271	-0.633*	-1.036*	-0.096*	0.665*	-1.612*	1.781*
RHA-854	-1.554*	1.631*	0.163*	-0.189*	-2.857*	2.570*
Standard Error	0.016388	0.026555	0.001944	0.001166	0.048055	0.039333

** Significant at 5% probability level*

parental lines with negative estimates of GCA. In present study, CMS-HAR-1 among females and SF-187R in testers were the best general combiners for palmitic acid.

Significant SCA estimates for palmitic acid was observed for 22 crosses while 14 crosses remained non-significant in SCA estimates (Table 4). Sixteen crosses exhibited negative SCA estimates whereas 20 crosses were positive for SCA effects. Maximum negative SCA estimates were indicated by CMS-64x RHA-854 (-0.907) (Table 4).

For palmitic acid, the values for variance of dominance (0.217) were higher than variance of additive (0.002) showing predominance of non-additive type of the gene action controlling the character (Table 5). Non-additive gene action for palmitic acid has been reported by Ortis et al. (2005) and Shaktivel (2003). The proportional contribution was 21.47 for lines, 11.30 for testers and 67.21 for lines x tester which showed that lines x testers were the major contributors during inheritance (Table 6).

Stearic Acid

Among genotypes, the average stearic acid was 4.45% for parents vs. 3.98% for F_1 hybrids with a net difference of 0.47%. A low level of genetic variability existed for the character as revealed by coefficient of variation (3.56%) (Table 1). Line x tester analysis of GCA for stearic acid revealed sufficient genetic variability in both lines and testers. All the parents were significantly different for GCA estimates (Table 3). Among lines, maximum GCA estimates were recorded for CMS-NDMTC (0.972), while maximum negative GCA estimates were observed for CMS-53 (-0.698) followed by CMS-H55-2-2-1 (-0.362) and CMS- 64 (-0.224). In testers, the maximum GCA estimates were recorded for RHA-295 (0.942) whereas maximum negative GCA effects were observed for SF-187R (-0.854) followed by PAC-8712 (-0.384), RHA-854 (-0.189) and C-206R (-0.182) (Table 3). The negative GCA estimates are desirable for stearic acid, therefore among female parents, CMS-53 while in male parents, the SF-187R with negative GCA estimates were the best combiners for crosses, needed for quality improvement of edible oil (Whetsell et al., 2003; Rustan and Drevon, 2005).

Significant SCA effects for stearic acid were indicated by 34 out of 36 crosses. Eighteen crosses exhibited negative SCA values while others exhibited positive SCA effects. Stearic acid being a saturated fatty acid is undesirable in sunflower seed oil, therefore negative GCA and SCA estimates are preferred. Among crosses, the lowest SCA magnitude was observed for CMS-HAR-1x RHA-271 (-2.677), followed by CMS-NDMTC x RHA-854 (-2.240) (Table 4).

Among genotypes, variance of dominance (1.977) was higher than variance of additive (0.013) showing predominance of non-additive variance controlling the character (Table 5). Present results agree those of Ortis et al. (2005) and Reddy and Madhavilatha (2005). For stearic acid, the proportional contribution of lines, testers and lines x testers was 13.76, 18.60 and 67.62, respectively revealing the major contribution of lines x testers in inheritance of character (Table 6).

Table 4. Estimates of SCA effects for seed total proteins, oil content and fatty acids composition in sunflower genotypes (crosses)

Crosses	Proteins	Oil content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid
CMS H55-2-2-1 x C-206-R	1.507*	-0.017	0.073	-0.033	-3.170*	3.666*
CMS H55-2-2-1 x PAC-8712	1.160*	1.183	0.153	-1.160*	0.080	1.410
CMS H55-2-2-1 x RHA-295	2.753*	0.870	-0.870	-0.090	-2.263*	13.020*
CMS H55-2-2-1 x SF-187R	2.253*	-1.567*	0.370*	-1.110*	-0.490	2.663*
CMS H55-2-2-1 x RHA-271	-4.913*	2.060*	-0.767*	1.337*	-4.630*	6.400*
CMS H55-2-2-1 x RHA-854	-2.740*	-2.520*	0.360*	1.237*	-4.760*	3.310*
CMS NDMTC x C-206-R	1.450*	3.280*	-0.020	1.537*	-5.503*	5.323*
CMS NDMTC x PAC-8712	0.840*	0.157	-0.453*	0.423*	-3.336*	2.960*
CMS NDMTC x RHA-295	3.837*	-0.513	0.513*	2.530*	13.936*	-15.193*
CMS NDMTC x SF-187-R	1.233*	-4.687*	-0.077	-1.813*	-4.023*	2.740*
CMS NDMTC x RHA-271	-5.277*	1.823*	-0.337*	-0.407*	2.390*	-2.050*
CMS NDMTC x RHA-854	-2.077*	-0.070	0.430*	-2.240*	-3.380*	5.896*
CMS 64 x C-206-R	2.160*	1.897*	0.350*	-0.493*	-1.586*	1.876*
CMS 64 x PAC-8712	0.683*	-0.193	-0.123*	-1.037*	-0.796*	0.376
CMS 64 x RHA-295	-5.890*	1.817*	0.327*	-0.320*	-9.193*	10.286*
CMS 64 x SF-187-R	-1.880*	-0.623	0.107	1.450*	8.923*	-8.703*
CMS 64 x RHA-271	2.500*	-1.727*	0.293*	0.830*	-1.460*	1.023*
CMS 64 x RHA-854	2.426*	-1.160*	-0.907*	-0.437*	4.183*	-4.373*
CMS 303 x C-206-R	-2.010*	-2.673*	0.563*	-0.980*	4.120*	-7.853*
CMS 303 x PAC-8712	-2.277*	-0.050	0.227*	-0.893*	0.783	-4.070*
CMS 303 x RHA-295	-2.013*	1.687*	-0.213	-1.367*	-7.000*	3.263*
CMS 303 x SF-187-R	-0.423	-1.420*	-0.567*	1.590*	-0.806	-2.886*
CMS 303 x RHA-271	3.213*	1.510*	0.060	0.730*	1.853*	-4.500*
CMS 303 x RHA-854	3.487*	0.957*	0.007	0.937*	1.116*	-5.466*

(Contd.)

Crosses	Proteins	Oil content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid
CMS HAR-1 x C-206-R	-0.577	0.963	-0.610*	0.427*	-2.406*	-3.053*
CMS HAR-1 x PAC-8712	-0.120	1.420*	-0.367*	2.427*	-0.763	-0.779
CMS HAR-1 x RHA-295	0.670*	1.380*	0.040	-0.653*	-7.046	9.370*
CMS HAR-1 x SF-187-R	-1.800*	-3.043*	-0.073	0.230*	1.273*	-2.040*
CMS HAR-1 x RHA-271	3.753*	-0.947	0.817*	-2.677*	0.540	0.756
CMS HAR-1 x RHA-854	-1.910*	0.227	0.243*	0.217*	3.666*	-4.533*
CMS 53 x C-206-R	-2.500*	-3.480*	-0.320*	-0.457*	3.816*	8.270*
CMS 53 x PAC-8712	-0.280*	-2.420*	0.617*	0.223*	4.116*	8.073*
CMS 53 x RHA-295	0.677*	-5.243*	-0.490*	0.097*	-3.673*	17.986*
CMS 53 x SF-187-R	0.627*	11.317*	0.287*	-0.360*	-4.840*	16.493*
CMS 53 x RHA-271	0.717*	-2.737*	0.053	0.167*	1.396*	8.590*
CMS 53 x RHA-854	0.796*	2.590*	-0.083	0.300*	-0.773	13.396*
Standard Error	0.313581	0.661326	0.108012	0.08366	0.536966	0.485798

** Significant at 5% probability level*

Oleic Acid

Moderate level of genetic variability existed among genotypes, the coefficient of variation was being 5.33% for oleic acid (Table 1). The average for oleic acid was 13.88% for parents vs. 18.24% for F_1 hybrids showing a net difference of 4.36%. For oleic acid, the female and male parents were significantly different for GCA estimates (Table 3). Maximum positive GCA estimates in lines were observed for CMS-H55-2-2-1 (3.002), whereas it was maximum negative for CMS-53 (-3.307). In male parents, the maximum positive GCA estimates were observed for RHA-295 (6.862) followed by SF-187R (0.531) whereas maximum negative GCA estimates were recorded for RHA-854 (-2.857). Oleic acid facilitates the improved health and oxidative stability for increased oil shelf life, flavor, durability and cold flow performance (Shannon, 2012; Anonymous, 2013) and increased values are desirable for both nutritional and storage point of view. Increasing oleic acid (more than 60%) will improve edible and industrial applications (Shannon, 2012). For quality improvement of edible oil through breeding, parental lines with positive GCA estimates for oleic acid are preferred. Therefore, CMS-H55-2-2-1 among females and RHA-295 among males are the best general combiners for high oleic acid in oil (Table 3).

Line x tester analysis of SCA for oleic acid revealed sufficient genetic

variability among crosses (Table 4). Significant SCA effects were observed for 28 crosses whereas eight cross combinations exhibited non-significant SCA estimates for oleic acid. The 19 crosses exhibited negative SCA estimates whereas all other crosses showed positive SCA effects. Highest SCA estimates among crosses were observed for CMS- NDMTC x RHA-295 (13.936) whereas the lowest were indicated by CMS-64 x RHA-295 (-9.193).

Variance of dominance (35.477) was higher than variance of additive (0.632) for oleic acid showing predominance of non-additive type of gene action controlling the character (Table 5). Non-additive type of gene action in oleic acid has also been reported by Shankara (1981) and Shaktivel (2003). Oleic acid manifested the proportional contribution of lines as 11.99, testers as 25.97 and lines x testers as 62.02 showing the major contribution of line x tester in inheritance of character (Table 6).

Linoleic Acid

The average value for linoleic acid among genotypes was 75.31% for parents vs. 72.16% for F_1 hybrids representing a net difference of 3.15%. A low level of genetic vari-ability was observed for linoleic acid as revealed by analysis of variance and the coefficient of variation was 1.15% (Table 1). Sufficient genetic variability existed among female and male parents for GCA estimates. All parents were significantly different for the chara-cter as revealed by GCA estimates. Maximum positive GCA effects in female parents were observed for CMS-53 (3.461) while negative were indicated by CMS-H55-2-2-1 (-2.716). In male parent, the maximum positive GCA effects were recorded for RHA-854 (2.570) followed by RHA-271 (1.781) and C-206R (1.570) while maximum negative GCA effects were observed for RHA-295 (-7.087) (Table 3).

A high level of genetic variability existed for linoleic acid among crosses as indicated by SCA estimates. A significant SCA was observed for crosses except CMS-H55-2-2-1 x PAC-8712, CMS-64 x PAC-8712, CMS-HAR-1 x PAC-8712 and HAR-1 x RHA-271, exhibiting non-significant SCA (Table 4). Fourteen crosses exhibited negative SCA effects while remaining were positive for SCA estimates. Highest SCA estimates for linoleic acid percentage were observed for CMS-53 x RHA-295 (17.986) expressing positive SCA magnitude while the lowest SCA effects were observed for CMS- NDMTC x RHA-295 (-15.193).

The linoleic acid exhibited the variance of dominance and variance of additive as 48.283 and 0.188, respectively showing that non-additive type of gene action was controlling the character (Table 5). Non-additive type of gene action can be utilized for varietal improvement through heterosis breeding. Linoleic acid exhibited the proportional contribution of lines, tester and lines x tester as 7.574, 23.302 and 69.122, respectively, showing the main contribution of line x tester in inheritance of this character (Table 6).

In general, the mean values of parents and F_1 hybrids, indicated low to high genetic variation for all the traits under study as revealed by analysis of variance. An increased mean value among F_1hybrids over parents was observed for oil content and oleic acid. A decrease in average mean value among F_1 hybrids over

Table 5. Estimates of genetic components for total proteins, oil content and fatty acids composition in sunflower genotypes

Gene action	Proteins	Oil content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid
Variance of dominance	8.725	11.084	0.217	1.977	35.477	48.283
Variance of additive	0.212	0.286	0.002	0.013	0.632	0.188

parents was observed for seed total proteins, palmitic, stearic and linoleic acids. The line x tester analysis of general combining ability was conducted for seed oil content, total proteins and fatty acid composition. Among female parents, the CMS-53 and CMS-H55-2-2-1, whereas in male parents, PAC-8712 and RHA-854 proved to be the potential parents exhibiting positive GCA. The F_1 hybrids, CMS-53 x SF-187-R and CMS-303 x RHA-295 are potential crosses for oil content. For seed proteins, the potential female parents were CMS-64 and CMS-53 with maximum positive GCA estimates, while in testers the C-206R and RHA-295 were the potential parents with desirable positive GCA magnitude. Saturated fatty acids are undesirable in edible oil, therefore negative GCA estimates for palmitic and stearic acids should be preferred. For palmitic acid, CMS-HAR-1 among females and C-206R among males were the potential parents possessing maximum negative GCA estimates. Among females, CMS-53 whereas in males the SF-187R were the potential parents for stearic acid with maximum negative GCA, desirable for good quality edible oil. High saturated fatty acids in edible oil are among the risk factors for human health being a major cause of cardiovascular disease. Among fatty acids, oleic and linoleic acids are the desirable unsaturated fatty acids promoting human nutrition and health (McIntyre and Hazen, 2010). For oleic and linoleic acids, maximum positive GCA estimates in female parents were observed for CMS-H55-

Table 6. Estimates of proportional contribution of lines, testers and their interactions to total variances for total proteins, oil content and fatty acids composition in sunflower genotypes

Proportional contribution	Proteins	Oil content	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid
Lines	18.303	20.023	21.475	13.764	11.995	7.574
Testers	22.539	21.336	11.304	18.609	25.977	23.302
Lines x Testers	59.157	58.639	67.219	67.626	62.027	69.122

2-2-1 and CMS-53, respectively whereas among males, the RHA-295 and RHA-854 exhibited maximum positive GCA for oleic and linoleic acids, respectively. The parental lines with large GCA for oleic and linoleic acids are preferred in sunflower breeding programme. The estimates of SCA variances were higher as compared to GCA variances for all quality characters under study indicating the predominance of non-additive gene action in determination of seed total proteins, oil content and fatty acid composition in sunflower. Our results were in accordance with the reports of Kumarswamy (1997), Rather and Sandha (1998), Rather et al. (1999) and Singh et al. (1999) who achieved similar results while conducting trials on sunflower. Our findings are in accordance with the results of Ortis et al. (2005) who reported the major contribution of line x tester in inheritance of quality characters of sunflower suggesting the presence of non-additive genes. This non-additive type of gene action can be utilized for varietal improvement through heterosis breeding.

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