



## Combining ability estimation for yield and its components of sunflower inbred lines



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### Abstract

The objective of this investigation was to determine the combining ability for yield and its components in sunflower A-line by tester mating design among seven cytoplasmic male sterile lines and five restorer lines were selected to produce 35 crosses. Parents and crosses were evaluated during the summer of 2017 year. Results indicated that the mean squares due to parents, crosses, parent's vs crosses except for days to 50% flowering and number of seeds plant<sup>-1</sup>. Lines, testers, and line x tester were significant for all studied traits. A<sub>14</sub> and A<sub>31</sub> of A-lines and Rf<sub>1</sub> and Rf<sub>20</sub> of Rf testers proved to be the best general combiners for seed yield plant<sup>-1</sup> and the most of its attributes. Moreover, the best cross combinations were of A<sub>4</sub> × Rf<sub>14</sub>, A<sub>6</sub> × Rf<sub>14</sub>, A<sub>31</sub> × Rf<sub>8</sub>, A<sub>28</sub> × Rf<sub>20</sub>, A<sub>23</sub> × Rf<sub>20</sub>, A<sub>1</sub> × Rf<sub>1</sub> and A<sub>14</sub> × Rf<sub>11</sub> that performed better than other developed hybrids in the view of seed yield plant<sup>-1</sup> and one or more of its attributes. The ratio of  $\sigma^2$  GCA/ $\sigma^2$  SCA was less than unity for all the traits indicating that non-additive gene effects played an important role in the inheritance of these traits. The biplot graphic allowed a rapid and effective overview of general combining ability (GCA) and specific combining ability (SCA) effects of inbred lines, best lines, and testers as well as their performance in crosses.

**Keywords:** Combining ability, gene action, hybrids, GGE biplot, line × tester

### 1. Introduction

Sunflower (*Helianthus annuus* L.) is one of the three crop species along with soybean and canola that account for approximately of the world vegetable oil. Sunflower is grown on 27.02 million hectares in the world, producing 54.92 million metric tons of seed yield (USDA 2021). Egypt production of edible vegetable oils has been suffering several problems due to the lower domestic production of oil crops that resulted in failing to meet the needs of domestic consumption. Recently, the state began to pay attention to the expansion of crop cultivation to meet the growing demand to meet the needs of the population.

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 reflect 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. The importance of hybrid cultivars in sunflower has recently increased because of their higher seed yield compared to open cross-pollinated varieties in many countries in the world. Hybrids of sunflower are more stable, highly self-fertile, with high yield performance, and more uniform at maturity [1].

The two types of combining ability, general (GCA) and specific (SCA), have been recognized in quantitative genetic. General combining ability is regarded as additive gene effects, while specific combining ability reflects the non-additive gene actions [2]. Numerous investigators found that the non-additive genetic effects played an effective role in the inheritance of seed yield and other agronomic traits [3-5]. While, Ciric et al. [6], Golabadi et al. [7] showed that the additive gene effects represented the major role in the inheritance of seed yield or other agronomic traits.

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Thus, keeping in view, the pivotal importance of combining ability as well line x tester analysis of 12 parents (7 CMS lines and 5 restorers) along with their 35 F<sub>1</sub> hybrids were used to study the mechanism as well as mode of inheritance to help sunflower breeders to decide for efficient breeding strategies to improve the valuable characters. A biplot approach [8] has been developed for analyzing the data regarding combining abilities, heterosis and relationships among parents. This approach provides a graphical demonstration of the data using principal components (PC1 and PC2) which are obtained through principal component analysis. Keeping in view the importance of combining ability and heterosis in plant breeding.

The objectives of the present study were: (i) to estimate both general and specific combining ability effects of some new sunflower inbred lines and crosses respectively, and (ii) to identify the most superior and hybrids for use in hybrid sunflower

breeding programs aiming to have highly and stable seed yield.

## 2. Materials and Methods

Twelve parental sunflower genotypes were used in present investigation. A-lines were A<sub>1</sub> (L<sub>1</sub>), A<sub>4</sub> (L<sub>2</sub>), A<sub>6</sub> (L<sub>3</sub>), A<sub>14</sub> (L<sub>4</sub>), A<sub>23</sub> (L<sub>5</sub>), A<sub>28</sub> (L<sub>6</sub>), and A<sub>31</sub> (L<sub>7</sub>) they were obtaining by backcrossing and selection for 6 generation (A<sub>5</sub> with L<sub>39</sub>). The tester, Rf-lines, Rf<sub>1</sub> (T<sub>1</sub>), Rf<sub>8</sub> (T<sub>2</sub>), Rf<sub>11</sub> (T<sub>3</sub>), Rf<sub>14</sub> (T<sub>4</sub>), and Rf<sub>20</sub> (T<sub>5</sub>) are male restorer lines, Rf<sub>1</sub> and Rf<sub>20</sub> were obtained by self-pollination from A<sub>12</sub> x Rf<sub>15</sub> and A<sub>1</sub> x Rf<sub>16</sub> for 6 generation are presented in Table (1). All possible combinations crosses were executed by using line × testers mating design to produce 35 F<sub>1</sub> seed during year 2016-summer season. The 35 F<sub>1</sub> crosses and their parents were evaluated during 2017 at Giza Agricultural Research station, Field Crops Research Institute, A.R.C. Egypt (22°, 32° N latitude and 24°, 37° E longitude).

**Table 1.** A- Lines and restorers (*cms* and *Rf*) were used.

CMS/Rf	Habitus	Source	Type
A <sub>1</sub>	Non-branched, Single headed	Argentina	Oilseed
A <sub>4</sub>	Non-branched, Single headed	Romania	Oilseed
A <sub>6</sub>	Non-branched, Single headed	U.S.A	Oilseed
A <sub>14</sub>	Non-branched, Single headed	Romania	Oilseed
A <sub>23</sub>	Non-branched, Single headed	Russia	Oilseed
A <sub>28</sub>	Non-branched, Single headed	Russia	Oilseed
A <sub>31</sub>	Non-branched, Single headed	Egypt	Oilseed
Rf <sub>1</sub>	Branched, Multi headed	Egypt	Oilseed
Rf <sub>8</sub>	Branched, Multi headed	Egypt	Oilseed
Rf <sub>11</sub>	Branched, Multi headed	Egypt	Oilseed
Rf <sub>14</sub>	Branched, Multi headed	Egypt	Oilseed
Rf <sub>20</sub>	Branched, Multi headed	Egypt	Oilseed

The experiment was designed as randomized complete block design (RCBD) with three replications. The plot size was 4 rows, 4 meter long and 60 cm apart. Planting was done in hills spaced 20 cm apart. Seedling were thinned to one plant per hill before the first irrigation (two weeks after planting in both seasons). The cultural practices followed as the recommendations for oil seed sunflower production. Ten plants were selected at random from each plot to record the data on days to 50 % flowering, plant height, head diameter, 100 seed weight, seed yield/plant and seed oil content which was determined according to AOAC [9] using *soxhlet* apparatus and diethyl ether as a solvent. The data was subjected to combined analysis of variance across two seasons according to Steel and Torrie [10] after insurance of the

homogeneity of individual error terms. The estimates of combining ability effects (GCA and SCA) were made following Kempthorne [11] & Singh and Chaudhary [12]. Biplot analysis for combining ability: Following analysis of variance the data were subjected to biplot analysis according to the method of Yan and Hunt [8] and Bertoia et al. [13]. GGE biplot methodology for combining abilities (GCA and SCA) in a line × tester data set was used, with the following model as:

$$Y_{ij} - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

Where: Y<sub>ij</sub>: genotypic value of the cross between *i*th line and *j*th tester; β<sub>j</sub>: average value for crosses involving *j*th tester; λ<sub>1</sub>: singular value for PC1; λ<sub>2</sub>: singular values for and PC2; ξ<sub>i1</sub> and η<sub>j1</sub>:

eigenvectors for PC1 associated with  $i$ th line;  $\xi_{i2}$  and  $\eta_{j2}$ : eigenvectors for PC2 associated with  $j$ th tester;  $\epsilon_{ij}$ : overall residual of the model associated with the combination of line  $i$  and tester  $j$ .

Symmetrical scaling was carried out for Principal components scores for entries and testers Yan and Hunt, [8], Bertoia et al. [13]. The analyses reported in this study were performed with the GGE-biplot software. Which are a windows-based application that generates biplots for a two-way data set [14].

### 3. Results and Discussion

#### 3.1. Analysis of variance

The analysis of variance (Table 2) showed significant differences among genotypes for all studied traits, indicating a wide genetic variability in this material. Results revealed that parents, crosses, parents' vs crosses (except days to 50% flowering and number of seeds) showing the presence of heterotic effects as non-additive genetic variance in the crosses, lines, testers and lines  $\times$  testers. Similar results were obtained by Imran et al. [15], Cvejic et al. [16], Bhoite et al. [17], Telangre et al. [18], Rizwan et al. [4] and Ahmed et al. [5].

**Table 2.** Analysis of variance for combining ability effects of the studied sunflower traits.

S.O.V	df	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	100-seed weight (g)	Number of seeds plant <sup>-1</sup>	Oil seed content (%)	Seed yield plant <sup>-1</sup> (g)
Rep	2	5.63	9.71	2.77	0.22	11685.58	7.16	23.91
Genotypes	64	32.67**	1690.82**	18.96**	6.46**	214841.36**	39.24**	689.28**
Parent (P)	14	15.07**	1943.36**	23.25**	4.22**	133481.97**	29.61**	593.75**
Crosses (C)	49	39.10**	1504.55**	10.70**	6.33**	246390.79**	42.25**	499.95**
P vs. C	1	7.57	5246.16**	252.50**	35.82**	37113.89	42.57**	8177.57**
Line	9	117.44**	5198.25**	24.33**	0.82**	560910.48**	87.73**	713.55**
Tester	4	40.39**	1360.70**	11.61**	48.91**	632588.76**	47.23**	1417.14**
L x T	36	19.30**	605.10**	7.14**	0.60**	103394.54**	30.05**	293.68**
Error	128	2.03	77.07	1.23	0.13	13615.64	2.65	46.57

\* and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

#### 3.2. Mean performance

Data in Table (4) are shown the mean performance of sunflower lines, tester, and their F<sub>1</sub> hybrids for studied traits. Significant differences were found among the Rf- testers and A- lines and their F<sub>1</sub> hybrids regarding to days to 50% flowering, plant height, head diameter, 100- seed weight (g), number of seeds plant<sup>-1</sup>, oil seed content (%), and seed yield plant<sup>-1</sup> (g), indicating the existence of genetic differences among the genotypes.

Among the Rf-testers, the earliest days to flowering was observed in Rf<sub>8</sub> (49 days) and the latest was Rf<sub>14</sub> (53.3 days). Among A-lines, A<sub>14</sub> was the earliest (46.8 days) and A<sub>1</sub> was the latest (54.6 days). Among F<sub>1</sub> hybrids the combination of A<sub>14</sub>  $\times$  Rf<sub>8</sub> had the lowest number of days to flowering of 47 days. The highest number of days to flowering of 59 days was found in the combination of A<sub>1</sub>  $\times$  Rf<sub>20</sub>. the shortest plant height was observed in Rf<sub>8</sub> (94.3cm) and the highest was Rf<sub>14</sub> (161.3 cm). Among A-lines, A<sub>4</sub> was the shortest (122 cm) and A<sub>1</sub> was the highest (172.9 cm), while 106.7 cm was

recorded in with the combination of A<sub>4</sub>  $\times$  Rf<sub>8</sub> to 208.7 cm with the hybrid combination of A<sub>1</sub>  $\times$  Rf<sub>20</sub>. The narrowest head diameter among the A-lines was found in A<sub>6</sub> (15.03 cm) and the widest in A<sub>4</sub> (19.50 cm), while among Rf-testers the lowest value of head diameter was recorded in Rf<sub>11</sub> (11.67 cm) and the highest was in Rf<sub>14</sub> (13.33 cm), F<sub>1</sub> hybrids head diameter ranged from 16.0 cm at the two combinations of A<sub>6</sub>  $\times$  Rf<sub>11</sub> and A<sub>23</sub>  $\times$  Rf<sub>11</sub> to 22.3 cm with the combination of A<sub>14</sub>  $\times$  Rf<sub>11</sub>. The lightest 100-seed weight among the A-lines was found in A<sub>14</sub> (5.67g) and the heaviest in A<sub>28</sub> (6.46 g), while among the Rf-testers the lowest value was recorded in Rf<sub>8</sub> (3.64 g) and the highest in Rf<sub>20</sub> (7.57 g), and F<sub>1</sub> hybrids ranged from 5.20 g at the combination of A<sub>31</sub>  $\times$  Rf<sub>1</sub> to 10.24 g at the combination of A<sub>23</sub>  $\times$  Rf<sub>20</sub>. The lowest number of seeds plant<sup>-1</sup> among the A-lines was found in A<sub>6</sub> (708.1) and the highest in A<sub>14</sub> (1322.5), among the Rf-testers the lowest value was recorded in Rf<sub>20</sub> (637) and the highest in Rf<sub>1</sub> (1240.2), while F<sub>1</sub> hybrids ranged from 630.4 seeds at the combination of A<sub>6</sub>  $\times$  Rf<sub>1</sub> to 1600.6 seeds at the combination of A<sub>14</sub>  $\times$  Rf<sub>1</sub>. The lowest seed oil content among the A-

lines was found in A<sub>4</sub> (31.04%) and the highest in A<sub>31</sub> (39.63%), among the Rf-restorers the lowest value was recorded in Rf<sub>20</sub> (30.24%) and the highest in Rf<sub>1</sub> (40.83%), while F<sub>1</sub> hybrids ranged from 27.59 % at the combination of A<sub>28</sub> × Rf<sub>11</sub> to 43.03% at the combination of A<sub>31</sub> × Rf<sub>1</sub>. As regards seed yield, the lowest-yielding A-line was in A<sub>4</sub> with

43.13 g, while the highest-yielding in A<sub>31</sub> with 74.93 g. Among the Rf-testers, Rf<sub>8</sub> had the lowest and Rf<sub>20</sub> the highest seed yield (33.69 and 51.33 g, respectively), while F<sub>1</sub> hybrids ranged from 52.06 g at the combination of A<sub>28</sub> × Rf<sub>11</sub> to 93.24 g at the combination of A<sub>28</sub> × Rf<sub>20</sub>.

**Table 3.** Mean performance of sunflower lines, testers and their F<sub>1</sub>hybrids for studied traits.

Genotype	Days to 50% flowering	Plant height (cm)	Head diameter (cm)	100-seed weight (g)	Number of seeds	Oil seed content (%)	Seed yield plant <sup>-1</sup> (g)
A <sub>1</sub>	54.6	172.9	17.43	6.04	1079.1	35.25	64.21
A <sub>4</sub>	52.1	122.0	19.50	6.02	1069.6	31.04	74.93
A <sub>6</sub>	53.2	129.0	15.03	6.1	708.1	35.62	57.16
A <sub>14</sub>	46.8	133.2	17.03	5.67	1322.5	37.19	52.63
A <sub>23</sub>	53.4	134.2	18.73	6.11	849.0	33.37	70.67
A <sub>28</sub>	54.1	149.1	18.33	6.46	1015.4	34.19	66.14
A <sub>31</sub>	50.5	125.3	17.17	5.96	1188.9	39.63	43.14
Rf <sub>1</sub>	52.3	103.7	13.00	4.14	1240.2	40.83	37.08
Rf <sub>8</sub>	49.0	94.3	12.67	3.64	925.8	35.78	33.69
Rf <sub>11</sub>	51.3	155.0	11.67	4.01	876.7	35.16	35.17
Rf <sub>14</sub>	53.3	161.3	13.33	4.40	840.6	32.63	48.06
Rf <sub>20</sub>	51.3	94.7	12.67	7.57	637.0	30.24	51.33
A <sub>1</sub> *R <sub>1</sub>	53.0	172.0	20.67	6.10	1546.8	38.39	90.22
A <sub>1</sub> *R <sub>8</sub>	55.3	154.3	16.33	5.91	974.3	32.57	56.63
A <sub>1</sub> *R <sub>11</sub>	53.3	192.3	17.67	5.70	1027.1	36.04	58.53
A <sub>1</sub> *R <sub>14</sub>	55.7	182.7	19.00	6.71	911.0	34.71	71.00
A <sub>1</sub> *R <sub>20</sub>	59.0	208.7	18.00	9.14	787.5	31.75	72.60
A <sub>4</sub> *R <sub>1</sub>	53.7	142.7	21.33	6.11	1412.9	35.77	85.73
A <sub>4</sub> *R <sub>8</sub>	56.0	106.7	16.50	6.00	757.5	33.33	54.36
A <sub>4</sub> *R <sub>11</sub>	50.3	138.0	16.50	5.51	945.7	39.45	56.36
A <sub>4</sub> *R <sub>14</sub>	56.0	146.0	18.33	6.39	1221.7	35.72	80.54
A <sub>4</sub> *R <sub>20</sub>	48.0	108.7	16.67	9.45	821.8	39.17	79.59
A <sub>6</sub> *R <sub>1</sub>	51.9	145.0	17.33	6.50	630.4	31.80	54.89
A <sub>6</sub> *R <sub>8</sub>	51.5	131.7	16.73	6.36	662.1	31.69	54.89
A <sub>6</sub> *R <sub>11</sub>	51.0	142.0	16.00	6.33	666.3	30.53	55.00
A <sub>6</sub> *R <sub>14</sub>	51.0	135.0	18.67	6.55	930.1	31.88	69.67
A <sub>6</sub> *R <sub>20</sub>	54.3	125.3	15.33	8.18	776.9	29.29	70.69
A <sub>14</sub> *R <sub>1</sub>	48.0	147.7	19.67	6.65	1600.6	30.65	89.59
A <sub>14</sub> *R <sub>8</sub>	47.0	138.7	19.33	5.43	1399.3	36.15	79.01
A <sub>14</sub> *R <sub>11</sub>	49.3	146.0	22.33	5.35	1548.0	30.60	86.09
A <sub>14</sub> *R <sub>14</sub>	48.0	147.7	18.67	6.02	1144.9	40.75	74.57
A <sub>14</sub> *R <sub>20</sub>	53.7	121.0	18.67	8.67	819.6	32.67	72.90
A <sub>23</sub> *R <sub>1</sub>	57.0	160.3	18.67	6.06	1168.9	36.39	67.76
A <sub>23</sub> *R <sub>8</sub>	55.7	140.7	17.67	5.74	777.4	31.74	55.10
A <sub>23</sub> *R <sub>11</sub>	53.0	124.0	16.00	5.55	824.5	34.82	52.85
A <sub>23</sub> *R <sub>14</sub>	56.3	146.3	15.90	6.35	653.3	30.65	52.06
A <sub>23</sub> *R <sub>20</sub>	48.0	134.7	21.00	10.24	757.4	30.18	82.90
A <sub>28</sub> *R <sub>1</sub>	57.0	169.3	20.33	6.76	1317.6	37.42	84.48
A <sub>28</sub> *R <sub>8</sub>	55.3	141.0	19.33	6.07	735.0	28.77	58.16
A <sub>28</sub> *R <sub>11</sub>	55.7	139.7	18.33	5.29	1100.6	27.59	69.50
A <sub>28</sub> *R <sub>14</sub>	54.7	181.0	17.00	6.81	847.5	29.41	55.73
A <sub>28</sub> *R <sub>20</sub>	51.3	153.7	20.93	9.85	907.4	30.63	93.24
A <sub>31</sub> *R <sub>1</sub>	49.7	118.7	20.67	5.20	1332.0	43.03	81.31
A <sub>31</sub> *R <sub>8</sub>	50.0	137.0	20.00	5.82	1274.8	38.15	80.09
A <sub>31</sub> *R <sub>11</sub>	49.0	143.3	20.00	5.41	1177.6	36.40	72.71
A <sub>31</sub> *R <sub>14</sub>	55.7	144.0	20.67	6.35	1253.5	34.26	59.38
A <sub>31</sub> *R <sub>20</sub>	48.0	116.7	21.33	9.86	820.4	31.19	83.06
Mean	52.2	141.6	17.83	6.37	1007.1	34.14	65.86
L.S.D (5%)	2.3	14.2	1.8	0.6	189.0	2.6	11.1

### 3.3. Combining ability analysis

#### 3.3.1. General combining ability effects

The general combining ability effects ( $\hat{g}_i$ ) of the testers and parental inbred lines for all traits are presented in Table (3). From the breeder's point of view, high negative values of days to 50% flowering and plant height along with high positive values for yield and its components would be useful for sunflower breeding program.

#### 3.3.2. Estimates of combining ability effects

The combining ability analysis revealed that among the lines A<sub>14</sub> and A<sub>31</sub> were good general combiners for seed yield plant<sup>-1</sup>, head diameter, number of seeds plant<sup>-1</sup> and days to 50% flowering (Table 4). The lines identified on the basis of their GCA were good general combiner's viz., A<sub>4</sub> and A<sub>31</sub> for plant height and oil content, A<sub>28</sub> for 100-seed weight, A<sub>6</sub> for plant height. Among the testers Rf<sub>1</sub> was a good general combiner for head diameter, number of seeds plant<sup>-1</sup>, oil seed content and seed yield plant<sup>-1</sup> whereas Rf<sub>20</sub> for days to 50%

flowering, plant height, 100-seed weight and seed yield plant<sup>-1</sup>.

### 3.4. Genetic components analysis

The genetic components of the studied traits were calculated and reported in Table 4. The variance of A line ( $\delta^2_1$ ) (CMS lines) and Rf tester ( $\delta^2_2$ ) (restorer fertility lines) were significant for all the studied traits, implying the important effects of both additive and dominance gene actions on the genetic control of the investigated traits. The variance among the CMS lines (A lines), for all the traits, were greater than that among the Rf testers (restorer), indicating the possible existence of some degree of maternal effects for the genetic control of the studied traits. Variance of SCA was greater than the variance of GCA for all studied traits, which indicates that higher amount of genetic variability was caused by SCA effect (Table 4). Results suggest that the traits were under greater influence of non-additive type of gene action. These results are in contrary to those of Dudhe et al. [19], Hladni et al. [20], Andarkhor et al. [3], Golabadi et al. [7], Patil et al. [21], Rizwan et al. [4] and Ahmed et al. [5].

**Table 4.** General combining ability effects of the A-lines and Rf-testers for the seed yield and its components.

Inbred lines	Flowering	Plant height	Head diameter	100-seed	Number seeds	Oil content	Seed yield
<b>Lines</b>							
A <sub>1</sub>	2.902**	36.789**	-0.283	0.043	32.712	0.875	-0.540
A <sub>4</sub>	0.435	-16.811**	-0.750	0.023	15.286	2.874**	0.998
A <sub>6</sub>	-0.411	-9.400**	-1.803**	0.115	-283.488**	-2.779**	-9.288**
A <sub>14</sub>	-5.098**	-5.011	1.117**	-0.445**	285.859**	0.348	10.116**
A <sub>23</sub>	1.635**	-4.011	-0.770	0.121	-180.341**	-1.058	-8.184**
A <sub>28</sub>	2.435**	11.722**	0.571	0.285*	-35.041	-3.052**	1.905
A <sub>31</sub>	-1.898**	-13.278**	1.917**	-0.142	165.012**	2.791**	4.993*
L.S.D 5%	1.031	6.360	0.804	0.262	84.533	1.178	4.944
L.S.D 1%	1.365	8.418	1.065	0.347	111.887	1.560	6.544
<b>Testers</b>							
Rf <sub>1</sub>	0.574	5.603*	1.193**	-0.616**	270.373**	2.392**	8.822**
Rf <sub>8</sub>	0.615	-9.494**	-0.631	-0.766**	-69.436	-0.615	-7.710**
Rf <sub>11</sub>	-0.698	1.265	-0.497	-1.077**	24.769	-0.183	-5.897**
Rf <sub>14</sub>	1.540**	9.456**	-0.297	-0.215	-22.065	0.096	-4.181*
Rf <sub>20</sub>	-2.031**	-6.830*	0.231	2.673**	-203.641**	-1.690**	8.966**
L.S.D 5%	0.871	5.375	0.680	0.222	71.443	0.996	4.178
L.S.D 1%	1.153	7.114	0.900	0.294	94.562	1.318	5.530
GCA	0.39	17.58	0.07	0.11	2794.18	0.24	4.03
SCA	5.76	176.01	1.97	0.16	29926.30	9.14	82.37
GCA/SCA	0.07	0.10	0.04	0.69	0.09	0.03	0.05

\* and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

Positive as well as negative and significant estimates of SCA effects were observed among the crosses for seed yield (Table 5). Out of the 35 crosses, seven crosses have shown significant positive SCA effects for seed yield plant<sup>-1</sup>. The cross A<sub>4</sub>×R<sub>14</sub> (13.41) followed by A<sub>6</sub>×R<sub>f<sub>14</sub></sub> (12.83), A<sub>31</sub>×R<sub>f<sub>8</sub></sub> (12.49), A<sub>28</sub>×R<sub>f<sub>20</sub></sub> (12.05), A<sub>23</sub>×R<sub>f<sub>20</sub></sub> (11.80), A<sub>1</sub>×R<sub>f<sub>1</sub></sub> (11.63) and A<sub>14</sub>×R<sub>f<sub>11</sub></sub> (11.55) showed high positive significant effect for this trait. The cross A<sub>14</sub>×R<sub>f<sub>14</sub></sub>, A<sub>28</sub>×R<sub>f<sub>1</sub></sub>, A<sub>4</sub>×R<sub>f<sub>20</sub></sub>, A<sub>31</sub>×R<sub>f<sub>1</sub></sub> and A<sub>4</sub>×R<sub>f<sub>11</sub></sub> showed positive significant for seed oil content, A<sub>6</sub>×R<sub>f<sub>20</sub></sub>, A<sub>1</sub>×R<sub>f<sub>1</sub></sub>, A<sub>14</sub>×R<sub>f<sub>11</sub></sub>, A<sub>6</sub>×R<sub>f<sub>14</sub></sub>, A<sub>31</sub>×R<sub>f<sub>8</sub></sub> and A<sub>4</sub>×R<sub>f<sub>14</sub></sub> for number of seeds plant<sup>-1</sup>, A<sub>23</sub>×R<sub>f<sub>20</sub></sub>, A<sub>31</sub>×R<sub>f<sub>8</sub></sub> and A<sub>6</sub>×R<sub>f<sub>11</sub></sub> for 100-seed

weight, A<sub>14</sub>×R<sub>f<sub>11</sub></sub>, A<sub>23</sub>×R<sub>f<sub>20</sub></sub>, A<sub>4</sub>×R<sub>f<sub>1</sub></sub> and A<sub>6</sub>×R<sub>f<sub>14</sub></sub> for head diameter showed the highest positive significant SCA effect. Whereas, the highest significant negative SCA effect for maturity and physiological traits was shown by A<sub>23</sub>×R<sub>f<sub>20</sub></sub>, A<sub>1</sub>×R<sub>f<sub>1</sub></sub>, A<sub>4</sub>×R<sub>f<sub>20</sub></sub> and A<sub>6</sub>×R<sub>f<sub>14</sub></sub> for days to 50% flowering, A<sub>31</sub>×R<sub>f<sub>1</sub></sub>, A<sub>28</sub>×R<sub>f<sub>11</sub></sub>, A<sub>23</sub>×R<sub>f<sub>11</sub></sub>, A<sub>1</sub>×R<sub>f<sub>8</sub></sub> and A<sub>1</sub>×R<sub>f<sub>1</sub></sub> for plant height. Similar finding for identification of superior inbred lines and hybrids based on GCA and SCA effects for seed yield and its components in sunflower were also reported by Hladni et al. [20], Patil et al. [21], Rizwan et al. [4] and Ahmed et al. [5].

**Table 5.** Specific combining ability for agronomic traits in 35 sunflower F<sub>1</sub> hybrids.

Hybrid	Days to flowering	Plant height	Head diameter	100-seed w.	Seeds number	Oil content %	Seed yield plant <sup>-1</sup> g
A <sub>1</sub> *R <sub>1</sub>	-2.841*	-15.603*	1.140	0.005	227.073*	1.304	11.625*
A <sub>1</sub> *R <sub>8</sub>	-0.549	-18.173*	-1.370	-0.038	-5.617	-1.503	-5.440
A <sub>1</sub> *R <sub>11</sub>	-1.235	9.068	-0.170	0.069	-46.989	1.528	-5.450
A <sub>1</sub> *R <sub>14</sub>	-1.140	-8.789	0.964	0.211	-116.225	-0.081	-5.405
A <sub>1</sub> *R <sub>20</sub>	5.765**	33.497**	-0.565	-0.247	-58.212	-1.248	-6.140
A <sub>4</sub> *R <sub>1</sub>	0.292	8.664	2.273*	0.032	110.567	-3.308*	5.589
A <sub>4</sub> *R <sub>8</sub>	2.585*	-12.240	-0.736	0.072	-204.957*	-2.745*	-9.248*
A <sub>4</sub> *R <sub>11</sub>	-1.769	8.335	-0.870	-0.104	-110.995	2.946*	-9.055
A <sub>4</sub> *R <sub>14</sub>	1.660	8.144	0.764	-0.086	210.871*	-1.063	13.409*
A <sub>4</sub> *R <sub>20</sub>	-2.769*	-12.903	-1.431	0.086	-6.486	4.170**	-0.695
A <sub>6</sub> *R <sub>1</sub>	-0.621	3.619	-0.673	0.330	-373.160**	-1.629	-14.964**
A <sub>6</sub> *R <sub>8</sub>	-1.042	5.372	0.550	0.343	-1.617	1.268	1.572
A <sub>6</sub> *R <sub>11</sub>	-0.255	4.924	-0.316	0.627*	-91.589	-0.328	-0.132
A <sub>6</sub> *R <sub>14</sub>	-2.493*	-10.267	2.150**	-0.021	219.011*	0.747	12.826*
A <sub>6</sub> *R <sub>20</sub>	4.411**	-3.648	-1.711	-1.279**	247.354*	-0.058	0.698
A <sub>14</sub> *R <sub>1</sub>	0.492	1.864	-1.260	0.043	27.693	-5.906**	0.332
A <sub>14</sub> *R <sub>8</sub>	-0.882	7.960	0.230	-0.031	166.270	2.601	6.291
A <sub>14</sub> *R <sub>11</sub>	2.765*	4.535	3.097**	0.203	220.765*	-3.381*	11.554*
A <sub>14</sub> *R <sub>14</sub>	-0.807	-1.989	-0.770	0.008	-135.502	6.490**	-1.681
A <sub>14</sub> *R <sub>20</sub>	-1.569	-12.370	-1.298	-0.223	-279.226**	0.196	-16.496**
A <sub>23</sub> *R <sub>1</sub>	2.426*	13.530	-0.373	-0.116	62.193	1.240	-3.195
A <sub>23</sub> *R <sub>8</sub>	1.051	8.960	0.450	-0.283	10.536	-0.403	0.680
A <sub>23</sub> *R <sub>11</sub>	-0.302	-18.465*	-1.350	-0.162	-36.535	2.248	-3.390
A <sub>23</sub> *R <sub>14</sub>	0.793	-4.322	-1.650	-0.221	-160.935	-2.201	-5.892
A <sub>23</sub> *R <sub>20</sub>	-3.969**	0.297	2.922**	0.782**	124.741	-0.885	11.797*
A <sub>28</sub> *R <sub>1</sub>	1.626	6.797	-0.047	0.419	65.627	4.268**	3.436
A <sub>28</sub> *R <sub>8</sub>	-0.082	-6.440	0.777	-0.121	-177.164	-1.376	-6.348*
A <sub>28</sub> *R <sub>11</sub>	1.565	-18.532*	-0.356	-0.590	94.198	-2.991*	3.178
A <sub>28</sub> *R <sub>14</sub>	-1.673	14.611*	-1.890*	0.071	-112.069	-1.453	-12.314*
A <sub>28</sub> *R <sub>20</sub>	-1.435	3.564	1.515	0.220	129.408	1.552	12.048*
A <sub>31</sub> *R <sub>1</sub>	-1.374	-18.870**	-1.060	-0.713*	-119.993	4.031**	-2.822
A <sub>31</sub> *R <sub>8</sub>	-1.082	14.560*	0.097	0.057	212.550*	2.158	12.494*
A <sub>31</sub> *R <sub>11</sub>	-0.769	10.135	-0.036	-0.043	-28.855	-0.021	3.294
A <sub>31</sub> *R <sub>14</sub>	3.660**	2.611	0.430	0.039	93.878	-2.440	-11.752*
A <sub>31</sub> *R <sub>20</sub>	-0.435	-8.436	0.569	0.661*	-157.579	-3.728**	-1.213
L.S.D (5%)	2.306	14.221	1.799	0.587	189.021	2.635	11.055

\* and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

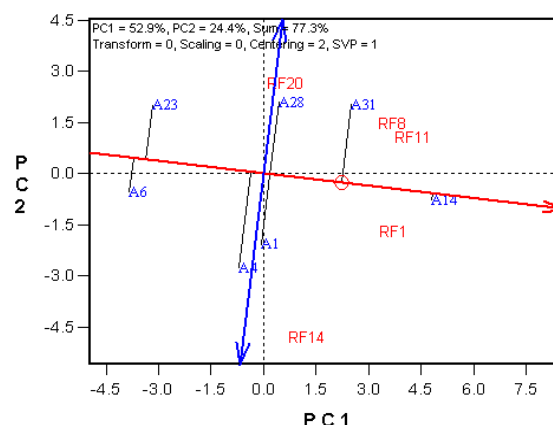
### 3.5. Biplot Analysis

#### 3.5.1. General and Specific Combining Ability

Figure 1 is the Average Tester Coordination (ATC) view of the biplot brought up by the Average Tester Coordination function of GGE biplot for seed yield plant<sup>-1</sup>. A GGE biplot is said to adequately approximate the variability in the two-way data when the first two PCs explain more than 60% of the variability in the data, and the combined interaction effect account for more than 10% of the total variability [22, 23]. The small circle on the average tester axis represents the average tester, which is defined by the average PC1 and PC2 values of all testers [24]. The line passing through the biplot origin and the average tester is referred to as average tester axis or ATC abscissa. The perpendicular line to the ATC passing through the origin of biplots shown with both side arrow heads in Fig. 1 is referred to as ATC ordinate.

Projection of the entries onto the ATC abscissa denotes GCA effects of the entries. The arrow head indicates the highest GCA effects. Thus, A<sub>14</sub> displayed highest GCA effects, and the relationship among the lines was A<sub>14</sub>>A<sub>13</sub>>A<sub>28</sub>>A<sub>1</sub>>A<sub>4</sub>> A<sub>23</sub>>A<sub>6</sub> for GCA effects. Observed relationship was comparable according to conventional GCA analysis which brought out the line A<sub>14</sub> with significant and positive GCA effects (10.12\*\*). Whereas, line A<sub>6</sub> showed significantly negative GCA effects (-9.28\*\*), followed by A<sub>23</sub> (-8.18\*\*).

The study clearly brought out A<sub>6</sub> to be a poor combiner for these traits, while A<sub>14</sub> to be best. Similarly, GCA for the testers was also visualized by switching the role of line and testers. The GCA relationship among testers was Rf<sub>20</sub>> Rf<sub>1</sub>> Rf<sub>8</sub>> Rf<sub>11</sub>> Rf<sub>14</sub> (Fig. 1). When compared these results to the conventional GCA analysis which revealed the testers Rf<sub>20</sub> and Rf<sub>1</sub> with significant and positive *gca* effects (8.97\*\* and 8.82\*\*). Whereas, Rf<sub>8</sub>, Rf<sub>11</sub> and Rf<sub>14</sub> showed negative *gca* effects for seed yield plant<sup>-1</sup> trait.

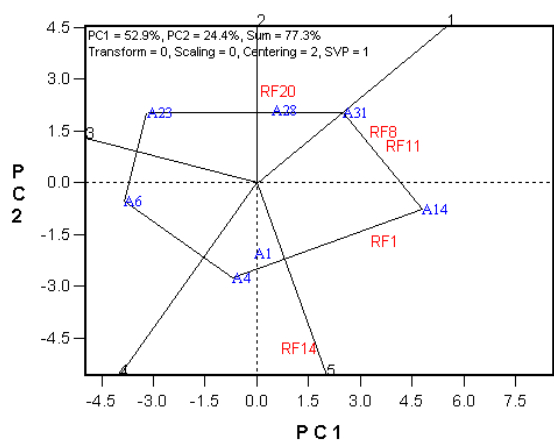


**Figure 1.** Biplot based on seed yield data explaining combining ability in sunflower genotypes.

The projections of the lines onto the ATC ordinate indicate their SCA effects [8]. Yan and Hunt [8] pointed out that in conventional analyses, SCA is associated with crosses rather the parents. However, GGE biplot of such crosses bring out this additional advantage. Observed SCA indicates the tendency of the lines to produce superior hybrids with specific testers. In the current study A<sub>14</sub> followed by A<sub>31</sub> showed the highest SCA. Among testers the highest SCA effect was noticed in Rf<sub>20</sub> followed by Rf<sub>1</sub> and Rf<sub>14</sub>, while that was in Rf<sub>8</sub> and Rf<sub>11</sub> in decreasing order. However, identified genotypes with the highest SCA not necessarily indicate always SCA towards positive direction but bring out only higher numerical values without the sign of it. Akinwale et al. [24] with GGE biplot analysis of a line x tester data set of Singh and Chaudhary [12]. Successfully identified lines with better SCA.

The polygon view of ‘Which-won-where’ analysis of GGE biplot provides us opportunity to visualize which tester combines well with which line [8]. The entries located on the vortex of the polygon are the best mating partners with the testers in the same sector and the poorest-mating partners with the testers in another sector. Similarly, lines at the vortex of opposite sector will be poorest with the testers in facing section. For SY, A<sub>14</sub> and A<sub>31</sub> combine well with Rf<sub>1</sub>, Rf<sub>8</sub> and Rf<sub>11</sub> testers, as all of them fall in the same sector at vortex of which A<sub>14</sub> was placed and A<sub>28</sub> combines well with Rf<sub>20</sub> testers (Fig. 2). All other lines were poor combiners with the testers. Yan and Hunt [8] were first to indicate possibility to identify best combiners using GGE biplot approach in diallel crosses. Subsequently,

GGE approach has been deployed in identifying best combiners in Khalil and Raziuddin [25] in Brassica; Bertoia et al. [13] in maize, Darvishzadeh et al. [26] in sunflower.

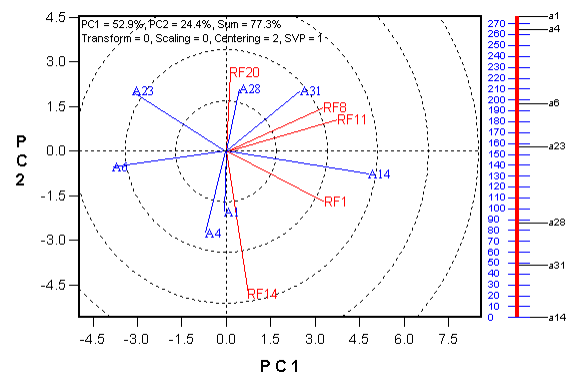


**Figure 2.** Biplot based on seed yield data explaining specific cross combination in sunflower genotypes

### 3.6. Relationship among Genotypes

The interrelationship among genotypes is visualized in Fig. 3. The lines that connect the biplot origin and the markers of the genotypes are known as vectors. The angle between vectors of two genotypes relates to the correlation coefficient between them, and the linear map to the right of the graph (in degrees) help in explaining the relationship among them [25]. For positive relationship between two genotypes the angle between their vectors must be smaller than  $90^\circ$  [14, 28, 29]. Thus, based on Fig 3, entries  $A_1$  and  $A_4$  showed a strong and positive relationship between them, and were too close to each other (almost  $0^\circ$  angle). The entry  $A_{14}$  is also lying close to both  $A_1$  and  $A_4$  (angle  $< 90^\circ$ ), and predicted a positive relationship among them. Similarly, the angles between  $A_{14}$  and  $A_{31}$ ,  $A_{31}$  and  $A_{28}$  were also smaller which also exhibited the positive relationship among them. However, the negative relationship was observed between two groups i.e ( $A_4, A_{28}$ ) and ( $A_6, A_{14}$ ), meaning that these genotypes were apparently different from one to another. Tester  $Rf_8$  and  $Rf_{11}$  showed positive and strong relationship (Fig. 3). Moreover, the testers ( $Rf_8$  and  $Rf_{11}$ ) showed an equal and positive relationship with  $Rf_1$  and  $Rf_{20}$ , since they are located in-between their vectors, but tester  $Rf_1$  and  $Rf_{20}$  were negatively correlated (angle  $> 90^\circ$ ). Similarly,  $Rf_{14}$  and  $Rf_{20}$

were located in opposite directions (angle  $> 140^\circ$ ) exhibiting negative relationship.



**Figure 3.** Biplot based on line x tester data in sunflower for seed yield explaining relationship among lines and testers.

## 4. Conclusion

Significant differences were found among the A lines, Rf testers and their  $F_1$  hybrids for all studied traits. Analysis of variance of the combining abilities revealed highly significant differences for A-lines,  $A_{14}$  and  $A_{31}$  and Rf-testers  $Rf_1$  and  $Rf_{20}$  proved to be the best general combiners for seed yield plant<sup>-1</sup> and the most of its attributes. Moreover, the best cross combinations were  $A_4 \times Rf_{14}$ ,  $A_6 \times Rf_{14}$ ,  $A_{31} \times Rf_8$ ,  $A_{28} \times Rf_{20}$ ,  $A_{23} \times Rf_{20}$ ,  $A_1 \times Rf_1$  and  $A_{14} \times Rf_{11}$ . The main role in inheritance for all studied traits is played by non-additive component of the genetic variance which is confirmed by the GCA/SCA relation in  $F_1$  generation that is less than one. The combination of the lxt mating design and GGE biplot in the same time gives the most important information for parental choice.

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