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GGE biplot analysis of Line by tester for seed yield and its attributes in sunflower

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Abstract. Nine genetically diverse sunflower promising lines in their economic trait were crossed using line by tester mating design in 2018 spring season, to estimate *per se* performance, combining ability, heterosis, gene action and heritability for earliness, yield and its attributes traits. The parents involved four sunflower CMS lines namely L1 (A3), L2 (A5), L3 (A9) and L4 (A13) (called hereafter "Lines" (as female parents) and five sunflower genotypes T1 (RF9), T2 (RF10), T3 (RF11), T4 (RF14) and T5 (RF1) as male parents (called hereafter "Tester"). In 2018 and 2019 summer season, the nine parents along with their 20 F_1s seeds were evaluated at *Shandaweel* Agricultural Research Station, ARC, Sohag Governorate, Egypt using a randomized complete blocks design with three replications. Mean squares due to parents (P), crosses (C), CMS lines (L), RF testers (T), P vs C and L x T were significant for all studied traits. A larger magnitude of non-additive gene action than additive was revealed by greater ratios (GCA/ SCA) than unity for all studied traits (except for days to 50% flowering). A5 and A13 of CMS lines and RF11 and RF14 of RF lines proved to be the best general combiners for seed weight plant^{-1} and one or more of its attributes traits. Moreover, the best cross combinations A13 x RF11, A13 x RF1 and A5 x RF9 performed better than other developed hybrids in view of seed weight plant^{-1} and one or more of its attributes, hence these F1 hybrids could further be used on commercial exploitation.

Key words: sunflower, *Helianthus annuus* L., line by tester, combining ability, heterosis, gene action

Introduction

Egypt is suffering from drastically deficit of edible oil. Therefore, Egyptian sunflower breeders seek to produce commercial sunflower for contributing in filling the gap between oil demand and supply, due to the fact that it is an excellent source of edible vegetable oil. Cytoplasmic male sterility plays an important role in developing high yielding sunflower hybrids, hence it can be widely used instead of open pollinated varieties. The assessment potential of CMS and RF lines is one of the greatest importance of sunflower breeders, a good approach for this purpose is the line by tester mating design. To provide information with regard to general combining ability (GCA) of parental genotypes, specific combining ability (SCA) of their cross combination and heterotic studies, either traditional line x tester analysis or GGE biplot analysis for Line x Tester data [1] can be used. Hladny *et al.* reported that non-additive gene action played a major role in inheritance of 100 seed weight than additive effects [2]. Also, in other reports, for seed weight, seed weight plant^{-1}, plant height and head diameter of sunflower, are more important non-additive gene action than additive ones have been reported by Škorić et al. [3]. 13 new cytoplasmic male sterile lines and 3 testers were used by Hladni et al. to develop 39 F1 hybrids, they reported that the parents and their crosses were significantly different in their mean values for plant height and head diameter [4]. The parent with more plant height was dominant over parent with head diameter while parent with more head diameter was dominant over parent with average plant height. The results exhibited significantly high positive general combining ability for plant height and head diameter in CMS line (NS-G-7) and in tester (RHA-N-49). In the newly developed hybrids, significantly high positive specific combining ability was present in NS-G-8× RUS-RF-OL-168 for head diameter and NS-G-1× RHA-N-49 for plant height. By GCA/SCA ratio in the F1 hybrids which was smaller than unit, it was confirmed that non-additive gene action played dominant role in the inheritance of both traits (plant height and head diameter). Memon et al. used cytoplasmic male sterility to develop 18 F1 hybrids inline by tester fashion, they reported that the degree of dominant genes was greater than unity of genes, hence, the main role of dominant genes was very important [5]. Therefore, estimated heritability was normally low to moderate due to dominant variance.

Therefore, the aims of this study were to estimate *per se* performance, heterosis, combining ability, gene action and heritability for earliness, yield and its attributes traits.

Materials and methods

Nine genetically diverse sunflower parental genotypes in their economic traits were mated using line by tester mating design. The parents involved four sunflower CMS lines which were designed as L1 (A3), L2 (A5), L3 (A9) and L4 (A13) as female parents (called hereafter "Lines") and five sunflower RF lines T1 (RF9), T2 (RF10), T3 (RF11),

T4 (RF14) and T5 (RF1) as male parents (called hereafter "Tester"). These parental genotypes were received from Department of Oilseed Crops Department, Field Crops Research Institute, Agricultural Research Center, Egypt.

In 2018 spring season, each of the four male parents was crossed with the five female parents to produce sufficient of seeds for 20 F1 crosses at Giza Agricultural Research Station, ARC, Giza Governorate, Egypt. In 2018 and 2019 summer seasons, the nine parental genotypes along with their 20 F1s seeds were evaluated at *Shandaweel* Agricultural Research Station, ARC, *Sohag* Governorate, Egypt. The soil texture of the experimental site was clay, including 8.02% sand, 35.46% silt and 56.52% clay, with pH of 7.6 and EC of 0.25 mmh/cm.

The experimental design was randomized complete blocks design with three replications. Each entry was contiguous sown without leaving separators in two ridges of 5 m length and 60 cm width, with a distance of 30 cm between each two hills. Four seeds were sown per hill and later thinned out to one plants per hill before the first irrigation. The other recommended packages of agronomic practices were followed as recommended by Oil Crops Research Department.

Data for the following traits were recorded on five individual guarded plants chosen at random from each plot, except for days to 50% flowering where the whole plot was used. Data included days to 50% flowering, plant height, stem diameter, head diameter, 100-seed weight and seed weight plant^{-1}. Seed oil content was determined after extraction with Soxhelt's apparatus using hexane as an organic solvent according to A.O.A.C (1990).

Statistical analysis. Analysis of variance was performed for combined data after confirmed of homogenous of error as cited by Singh and Chaudhary [6]. Combining ability analysis of line × tester was conducted based on the procedure developed by Kempthorne [7]. Mid parent heterosis was determined for individual hybrids as the percentage deviation of F1 means performance from mid parent value. Average degree of dominance (ā) was calculated according to the following equation given below [8]. For analysis of variance, the data were further subjected to biplot analysis according to the method of [9] and [10]. GGE biplot methodology for combining abilities (GCA and SCA) in a line × tester data set was used, with the following model as:

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

where Y_{ij}: genotypic value of the cross between ith line and jth tester; β_j: average value for crosses involving jth tester; λ_1: singular value for PC$_1$; λ_2: singular values for and PC$_2$; ξ_{i1} and η_{j1}: eigenvectors for PC$_1$ associated with ith line; ξ_{i2} and η_{j2}: eigenvectors for PC$_2$ associated with jth tester; ε_{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 [9, 10]. The analyses reported in this study were performed with MS-EXCEL (2007) with spreadsheet formula commands.

Results and Discussion

Genetic variability. It is apparent from the results of Table 1 that mean squares of genotypes and their components like parents, crosses and parents × crosses were highly significant (P < 0.01) for all evaluated traits, indicating the presence of wide

genetic variability in the investigated genetic materials. Again, considerable average degree of heterosis among created crosses for all studied traits as indicated by highly significance of parent's interaction with crosses, indicating that mean performance of crosses was different with difference of parents. Similarly, mean square of crosses and their populations i.e. lines, tester and line × tester was highly significant for all studied traits. Since, significance of mean square due to lines and testers (GCA) was observed for all studied traits, indicating wide genetic variability existed among CMC lines and restorer lines. Accordingly, highly significant interaction of lines with tester (SCA) was depicted for all studied traits, hence selection is possible to determinate the most preferred crosses. In consequence of substantial genetic variability among lines, tester and their crosses (lines × tester) for all studied traits as shown in Table 1, further biometrical analysis as combining ability and heterosis was valid. These results are in agreement with the results of [2, 11—15] who also reported such type of findings.

Table 1

**Mean squares of the nine sunflower parents (five RF lines and four CMS lines)
and their 20 F1 crosses for all studied traits (combined data of 2018 and 2019 summer season)**

S.O.V	df	Days to 50% flowering	Plant height	Stem diameter	Head diameter	100-seed weight	Seed weight plant^{-1}	Seed oil content
Reps	2	2.63	3.95	0.02	2.47	0.04	0.74	0.10
Entries	28	89.28**	537.81**	0.64**	22.32**	1.72**	130.81**	26.48**
Parents	8	151.29**	510.59**	0.10**	5.18**	1.37**	61.64**	7.28**
Crosses	19	60.79**	528.29**	0.28**	11.39**	0.48**	37.53**	20.73**
P vs C	1	134.44**	936.58**	11.71**	367.295**	27.97**	2456.32**	289.29**
Lines	4	142.93**	1587.56**	0.87**	34.37**	0.65**	121.66**	56.09**
Testers	3	171.22**	458.38**	0.27**	7.05**	1.22**	43.67**	37.43**
Line x tester	12	5.80*	192.67**	0.09**	4.81**	0.24**	7.96**	4.77**
Error	56	2.82	7.29	0.01	1.36	0.03	0.83	1.17
δ^2 gca		1.60	9.80	0.01	0.19	0.01	0.86	0.47
δ^2 sca		0.99	61.80	0.03	1.15	0.07	2.37	1.20
GCA/SCA		1.62	0.16	0.20	0.17	0.11	0.36	0.39

**Significant at 0.01 probability level GCA: general combining ability and SCA: specific combining ability

The highest variance due to specific combining ability was detected in plant height (61.80), stem diameter (0.03), head diameter (1.14), 100-seed weight (0.07), seed weight plant^{-1} (2.37) and seed oil content (1.20) as compared to general one. The reverse was also true in remaining traits, indicating that the non-additive gene action (non-fixable) prevailed in the inheritance of the above traits. As further confirmed by ratio of SCA to GCA variances, which was lesser than unit for the previous traits, heterosis/hybrid vigor can be commercially exploited.

Mean performance. Mean performance of nine parental sunflower genotypes along with their respective 20 F_1 crosses for all studied traits is presented in Table 2. Generally, all cross combinations were earlier by (5.93%) and shorter by (5.09%) than their respective parents. Conversely, a progressive increase was observed in stem diameter by 32.89%, head diameter by 23.58%, 100-seed weight by 19.91%, seed weight plant^{-1} by 21.80% and seed oil content by 10.01%.

**Mean performance of the nine sunflower parents (five RF lines and four CMS lines)
and their 20 F1 crosses for all studied traits (combined data of 2018 and 2019 summer season)**

	Days to 50% flowering	Plant height	Stem diameter	Head diameter	100-seed weight	Seed weight plant^{-1}	Seed oil content
A3 × Rf9	39.00	128.63	2.23	17.60	5.54	51.04	38.18
A3 × Rf10	36.67	111.77	1.80	16.50	5.41	45.67	42.83
A3 × Rf11	42.00	143.00	2.37	18.17	5.72	52.10	36.86
A3 × Rf14	45.00	153.50	2.77	21.43	6.40	54.70	37.63
A3 × Rf1	40.33	119.17	2.30	17.23	5.62	48.85	38.44
A5 × Rf9	47.33	134.67	2.30	18.63	6.22	53.61	37.34
A5 × Rf10	41.33	125.90	2.27	17.00	6.21	51.77	42.91
A5 × Rf11	49.67	151.10	2.70	21.00	6.40	55.43	40.27
A5 × Rf14	56.00	153.23	3.30	23.00	5.88	58.09	34.34
A5 × Rf1	46.33	145.71	2.43	18.60	6.50	53.11	36.90
A9 × Rf9	47.00	150.00	2.27	17.20	6.50	51.32	41.37
A9 × Rf10	43.33	126.70	2.47	16.03	5.85	47.48	43.49
A9 × Rf11	48.67	135.93	2.40	20.07	6.55	53.60	41.95
A9 × Rf14	50.33	156.07	2.63	21.47	6.57	57.20	40.81
A9 × Rf1	47.33	139.00	2.30	17.03	6.43	52.11	41.07
A13 × Rf9	44.00	154.54	2.23	19.77	6.35	52.32	37.76
A13 × Rf10	42.00	125.47	2.00	17.63	5.57	46.97	42.68
A13 × Rf11	46.33	135.33	2.50	21.03	6.40	58.52	38.81
A13 × Rf14	49.67	155.00	2.63	18.20	6.56	55.08	36.19
A13 × Rf1	44.67	144.47	2.33	19.17	6.44	54.95	37.87
A3	53.33	131.60	1.60	14.14	4.70	46.33	36.49
A5	58.00	139.69	1.83	17.07	5.66	44.22	34.26
A9	56.00	138.07	1.80	15.33	6.04	45.27	32.20
A13	53.67	130.77	1.63	13.90	5.32	42.57	35.16
Rf9	42.67	148.57	1.50	12.73	4.64	35.19	35.42
Rf10	39.33	147.87	1.33	12.83	4.72	34.29	36.19
Rf11	43.33	169.80	1.53	14.53	4.21	41.57	37.66
Rf14	44.33	160.40	1.87	14.87	5.16	44.33	35.24
Rf1	41.67	152.20	1.47	14.17	3.94	37.11	36.37
Crosses	45.35	139.46	2.41	18.84	6.16	52.70	39.38
Parents	48.83	145.85	1.64	14.43	5.06	41.72	35.33
Average	46.18	141.66	2.17	17.46	5.78	49.13	38.16
LSD 0.05	2.75	4.42	0.16	1.91	0.30	1.49	1.77
LSD 0.01	3.66	5.88	0.22	2.54	0.40	1.99	2.36

The earliest sunflower genotypes were A3 (53.33 day), Rf10 (39.33 day) and their F1 cross A3 × Rf10 (36.67 day), A3 × Rf9 (39 day) and A3 × Rf1(40.33 day), indicating that genes controlling the early flowering have been transferred from the parents to their F$_1$ progeny. Moreover, A13 (130.77 cm) and A3 (131.60 cm) of CMS lines along with Rf10 (147.87 cm) and Rf9 (148.57 cm) of Restorer lines were the shortest (dwarfeness) parents and their performance was reflected on their respective crosses A3 × Rf10 (111.77 cm), A3 × Rf1 (119.17 cm) and A13 × Rf10 (125.47 cm). Again, it was revealed that alleles controlling dwarfiness have been transmitted from parents to their offspring.

It is worthy to note that in contrast to days of 50% flowering and plant height, the highest values of the remaining traits are of the greatest important challenge for sunflower breeder. Accordingly, the largest stem diameter was detected in A5 (1.83 cm)

and A9 (1.80 cm) of CMS lines and Rf14 (1.87 cm) and Rf11 (1.53 cm) of Restorer lines and their performance were reflected on their respective crosses A5 × Rf14 (3.30 cm) followed by A3 × Rf14 (2.77 cm) and A5 × Rf11 (2.70 cm). This may be attributed to genes with positive effect on stem diameter transferred from parents to their respective F1 crosses. Similarly, the largest head diameter, again, was achieved by A5 (17.07 cm) and A9 (15.33 cm) of CMS lines and Rf14 (14.87 cm) and Rf11 (14.53 cm) of restorer lines, which inherited the largest head diameter to their respective crosses A5 × Rf14 (23.00 cm), A9 × Rf14 (21.47 cm) and A3 × Rf14 (21.43 cm). Moreover, the genes controlling the heaviest weight of 100-seed inherited form A9 (6.04 g) and A5 (5.66 g) of CMS lines and Rf14 (5.16 g) and Rf10 (4.72 g) of restorer lines to their respective crosses A9 × Rf14 (6.57 g), A13 × Rf14 (6.56 g) and A9 × Rf11 (6.55 g). Consequently, the heaviest weight of seed plant^{-1} was detected in A3 (46.33 g) and A9 (45.27 g) of CMS lines and Rf14 (44.33 g) and Rf11 (41.57 g) of restorer lines, which characterized by their ability to contribute genes with positive effect on seed weight plant^{-1} to their respective F1 crosses A13 × Rf11 (58.52 g), A5 × Rf14 (58.09) and A9 × Rf14 (57.20 g). In addition, the highest proportion of seed oil was observed in A3 (36.49%) and A13 (35.16%) of CMS lines and Rf11 (37.66%), Rf1 (36.37%) and Rf10 (36.19%) of restorer lines, as they had genes with positive effect on seed oil content and their genotypic performance was relatively reflected on some of their respective crosses A9 × Rf10 (43.49%), A5 × Rf10 (42.91%), A3 × Rf10 (42.83%) and A13 × Rf10 (42.68%). These finding is in accordance with the findings of [4, 14—16] that reported to some extent the same kind of results.

GGE biplot analysis for Line × Tester data. The 1st and 2nd principal component analysis explained most of variation in evaluated traits where 99.42, 99.26, 97.68, 93.87, 98.70, 96.59 and 99.91% of the total variation for days of 50% flowering, plant height, stem diameter, head diameter, 100-seed weight, seed weight plant^{-1} and seed oil content of the total variation. Hence, proficiency of GGE biplot for all studied traits was more precisely expressed in graphical analysis as it had the largest explanation of variation. The dispersed placement of the lines and testers on the ATC abscissa for all studied traits as in Fig. (1A1-7G3) showed significant GCA effects [10]. Similarly, the SCA effects for all studied traits were also found significant, since lines and testers showed different projections on the ATC ordinate [10].

The best combiners of parental lines for all studied traits are correctly identified by the parallel lines perpendicular onto the ATC abscissa in graphical analysis. Whereas, the best combiners of testers for all studied traits are approximated by the smallest projection of tester marker onto the ATC ordinate (most representative) coupled with the longest vector of distance between the marker of tester and plot origin (most discriminating). The best mating partners of seed yield and its components can be determined by polygon when the line and tester falling into the same sector, whereas for early flowering and maturity and dwarfness the contrast condition will be fit to identify the best cross combinations [1].

Days to 50% flowering. A graphical analysis as seen in Fig. 1 (A1) showed that negative and highly significant GCA as the best combiners of lines was observed in A3 and A13 of CMS lines for earliness in flowering, as they were placed at long distance

from the biplot origin in the negative direction of ATC abscissa. These findings were consistent with their respective GCA effects in traditional analysis (with GCA effects of –4.52** and –0.02 for CMS lines). On the other hand, the best testers combiners for earliness in flowering (Fig. 1 A2) was observed in RF10 (1.29 Discr. and 1.14 Repr.) and RF9 (1.97 Discr. and 0.15 Repr.) of RF lines, as they had the longest vector of all testers and smallest projection on ATC ordinate. This was in parallel with their respective effects of tester GCA (Table 3) in traditional analysis (with GCA effects of –4.52** and –1.02* for CMS lines). Accordingly, they are the ones who would be the best candidate from the breeder's point of view to develop genotypes with early flowering.

The A5 (1.47 Repr.) followed by A9 (1.13 Repr.) and A13 (0.48 Repr.) of CMS lines as well as RF14 (1.79 Repr.) and RF10 (1.14 Repr.) of RF lines had the highest SCA, as they had the largest projections onto the ATC ordinate (Fig. 1. A1 and A2 as well as Table 4).

The polygon view of a biplot is considered as a powerful visual tool which offers the best approach for identifying the interaction patterns between lines and testers (Fig. 1, A3). As shown in Fig. 1 A3, the hybrids taking relatively fewer days to 50% flowering are desired. Therefore, the lines A3 produced desirable cross combinations especially with testers RF10, RF9 and RF1, as well as A5 which gave the best cross combinations with Testers RF10 since this was in well agreement with their respective heterosis of mid parents (Table 5).

Plant height. Negative and highly significant GCA as the best combiners of parental lines for dwarfness was observed in A3 (4.51 Discr.) of CMS lines (Fig. 2, B1) as well as RF10 (2.45 Discr. &0.01 Repr.) and RF1 (4.02 Discr. and 0.92 Repr.) of RF lines (Fig. 2 B2), as they occupied farthest position on the ATC x-axis. This result was in well agreement with their respective GCA effects (Table 3) in traditional analysis (with GCA effects of –8.25** for CMS lines as well as –17.00** and –2.37** for RF lines).

The CMS lines A5 (3.40 Repr.) followed by A13 (2.23 Repr.) as well as the RF lines RF9 (3.84 Repr.) and RF11 (3.40 Repr.) had the highest SCA, as they had the largest projections onto the ATC ordinate (Fig. 2, B1 and B2 and Table 4).

As shown in Fig. 2, B3, the hybrids had the desired dwarfness. Therefore, the CMS lines A3 produced desirable cross combinations especially with testers RF10 and RF1, A5 with RF10, A9 with RF11, and A13 with RF11. This result was in well agreement with their respective heterosis of mid parents (Table 5).

Stem diameter. The largest projection onto the ATC abscissa (Fig. 3 C1), in reference to the highest GCA effects, were observed in A5 of CMS lines and RF14 (0.71 Discr. and 0.44 Repr.) of RF lines (Fig. 3 C2), hence these ones were identified as the best donors for improving stem diameter, which was consistent with their respective GCA effects (Table 3) in traditional analysis (with GCA effects of 0.19** of CMS lines and 0.42** of RF lines).

The largest projections onto the ATC ordinate, in reference to SCA, were detected in A9 (0.54 Repr.), A3 (0.30 Repr.) and A5 (0.24 Repr.) of CMS lines and RF10 (0.62 Repr.) and RF14 (0.44 Repr.) and thus these ones were considered as the best SCA effects (Fig. 3 C1 and C2 as well as Table 4).
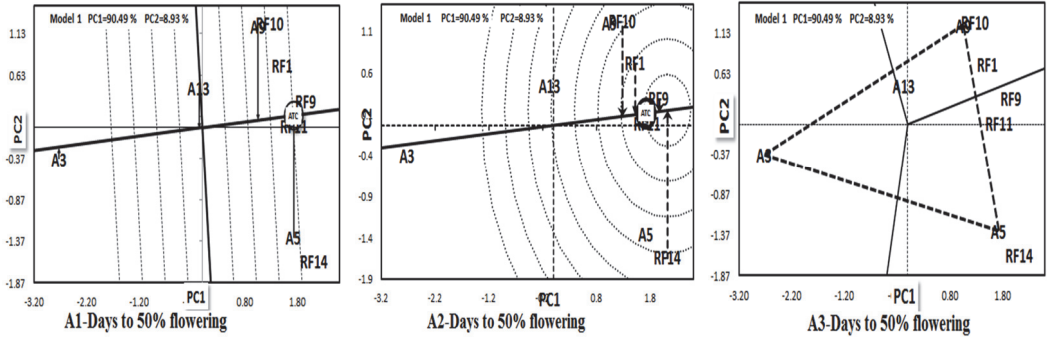
Fig. 1. Biplot of A1 (average tester coordinate), A2 (ideal tester) and A3 (polygon view)
for days to 50% flowering (combined data of 2018 and 2019 summer season)

Table 3

**General combining ability effects of the nine sunflower parents (five RF lines
and four CMS lines) for all studied traits (combined data of 2018 and 2019 summer season)**

	Days to 50% flowering	Plant height	Stem diameter	Head diameter	100-seed weight	Seed weight plant^{-1}	Seed oil content
Lines							
A3	−4.75**	−8.25**	−0.12**	−0.65*	−0.42**	−2.22**	−4.75**
A5	2.78**	2.66**	0.19**	0.81**	0.09	1.71**	2.78**
A9	1.98**	2.08**	0.00	−0.48	0.22**	−0.36	1.98**
A13	−0.02	3.50**	−0.07**	0.32	0.11*	0.87**	−0.02
LSD 5%	0.87	1.40	0.05	0.60	0.10	0.47	0.87
LSD 1%	1.16	1.86	0.07	0.80	0.13	0.63	1.16
Tester							
RF9	−1.02*	2.50**	−0.15**	−0.54	−0.01	−0.62*	−1.02*
RF10	−4.52**	−17.00**	−0.28**	−2.05**	−0.40**	−4.72**	−4.52**
RF11	1.32**	1.88*	0.08**	1.23**	0.11*	2.22**	1.32**
RF14	4.90**	14.99**	0.42**	2.19**	0.20**	3.57**	4.90**
RF1	−0.68	−2.37**	−0.07*	−0.83*	0.09	−0.44	−0.68
LSD 5%	0.97	1.56	0.06	0.67	0.11	0.53	0.97
LSD 1%	1.29	2.08	0.08	0.90	0.14	0.70	1.29

*, **Significant at 0.05 and 0.01 probability level, respectively.

Table 4

**Specific combining ability effects of the nine sunflower parents (five RF lines
and four CMS lines) for all studied traits (combined data of 2018 and 2019 summer season)**

	Days to 50% flowering	Plant height	Stem diameter	Head diameter	100-seed weight	Seed weight plant^{-1}	Seed oil content
A3 × Rf9	−0.58	−5.08**	0.09	−0.05	−0.20	1.19*	0.12
A3 × Rf10	0.58	−2.45	−0.22**	0.36	0.07	−0.08	0.45
A3 × Rf11	0.08	9.90**	−0.01	−1.25	−0.13	−0.59	−2.01**
A3 × Rf14	−0.50	7.30**	0.05	1.06	0.47**	0.66	0.98
A3 × Rf1	0.42	−9.67**	0.08	−0.12	−0.21	−1.18*	0.46
A5 × Rf9	0.22	−9.96**	−0.15*	−0.47	−0.02	−0.17	−0.29
A5 × Rf10	−2.28*	0.78	−0.05	−0.60	0.36**	2.09**	0.97
A5 × Rf11	0.22	7.10**	0.02	0.13	0.05	−1.19*	1.83**

|	Days to 50% flowering	Plant height	Stem diameter	Head diameter	100-seed weight	Seed weight plant^{-1}	Seed oil content
A5 × Rf14	2.97**	−3.88*	0.28**	1.17	−0.56**	0.11	−1.87**
A5 × Rf1	−1.12	5.96**	−0.10	−0.22	0.17	−0.85	−0.64
A9 × Rf9	0.68	5.96**	0.01	−0.62	0.12	−0.40	0.35
A9 × Rf10	0.52	2.16	0.33**	−0.28	−0.14	−0.14	−1.84**
A9 × Rf11	0.02	−7.49**	−0.09	0.48	0.06	−0.96	0.13
A9 × Rf14	−1.90	−0.46	−0.20**	0.92	0.00	1.29*	1.21
A9 × Rf1	0.68	−0.17	−0.04	−0.50	−0.04	0.21	0.15
A13 × Rf9	−0.32	9.08**	0.05	1.15	0.09	−0.62	−0.18
A13 × Rf10	1.18	−0.49	−0.06	0.52	−0.30**	−1.87**	0.43
A13 × Rf11	−0.32	−9.51**	0.08	0.65	0.03	2.73**	0.06
A13 × Rf14	−0.57	−2.95	−0.13*	−3.15**	0.10	−2.06**	−0.33
A13 × Rf1	0.02	3.88*	0.06	0.84	0.08	1.82**	0.02
LSD 5%	1.94	3.12	0.11	1.35	0.21	1.06	1.25
LSD 1%	2.59	4.16	0.15	1.80	0.28	1.40	1.67
LSD$_{5\%}$ gi-gj line	1.23	1.97	0.07	0.85	0.14	0.67	0.79
LSD$_{5\%}$ gi-gj tester	1.37	2.21	0.08	0.95	0.15	0.75	0.88
LSD$_{5\%}$ sij-skl	2.75	4.42	0.16	1.91	0.30	1.49	1.77

*, **Significant at 0.05 and 0.01 probability level, respectively.

Table 5

**Mid parent heterosis of 20 sunflower F1 crosses for all studied traits
(combined data of 2018 and 2019 summer season)**

	Days to 50% flowering	Plant height	Stem diameter	Head diameter	100-seed weight	Seed weight plant^{-1}	Seed oil content
A3 × Rf9	−18.75**	−8.17**	44.09**	30.98**	18.60**	25.21**	6.20**
A3 × Rf10	−20.86**	−20.01**	22.73**	22.34**	14.97**	13.31**	17.86**
A3 × Rf11	−13.10**	−5.11**	51.06**	26.71**	28.37**	18.55**	−0.56
A3 × Rf14	−7.85**	5.14**	59.62**	47.78**	29.86**	20.68**	4.92**
A3 × Rf1	−15.09**	−16.02**	50.00**	21.76**	30.27**	17.09**	5.51**
A5 × Rf9	−5.96**	−6.56**	38.00**	25.06**	20.71**	35.00**	7.19**
A5 × Rf10	−15.07**	−12.43**	43.16**	13.71**	19.59**	31.87**	21.83**
A5 × Rf11	−1.97	−2.35	60.40**	32.91**	29.75**	29.21**	11.98**
A5 × Rf14	9.45**	2.13	78.38**	44.05**	8.69**	31.19**	−1.18
A5 × Rf1	−7.02**	−0.16	47.47**	19.10**	35.53**	30.60**	4.49**
A9 × Rf9	−4.73**	4.66*	37.37**	22.57**	21.76**	27.56**	22.35**
A9 × Rf10	−9.09**	−11.38**	57.45**	13.85**	8.77**	19.36**	27.17**
A9 × Rf11	−2.01	−11.69**	44.00**	34.38**	27.85**	23.45**	20.11**
A9 × Rf14	0.33	4.58*	43.64**	42.16**	17.42**	27.67**	21.02**
A9 × Rf1	−3.07*	−4.23*	40.82**	15.48**	29.01**	26.50**	19.79**
A13 × Rf9	−8.65**	10.65**	42.55**	48.44**	27.55**	34.56**	6.98**
A13 × Rf10	−9.68**	−9.94**	34.83**	31.92**	10.99**	22.23**	19.63**
A13 × Rf11	−4.47**	−9.95**	57.89**	47.95**	34.43**	39.09**	6.59**
A13 × Rf14	1.36	6.47**	50.48**	26.54**	25.23**	26.76**	2.81**
A13 × Rf1	−6.29**	2.11	50.54**	36.58**	39.12**	37.91**	5.87**
LSD 5%	2.38	3.82	0.14	1.65	0.26	1.29	1.53
LSD 1%	3.17	5.09	0.19	2.20	0.35	1.72	2.04

*, **Significant at 0.05 and 0.01 probability level, respectively.
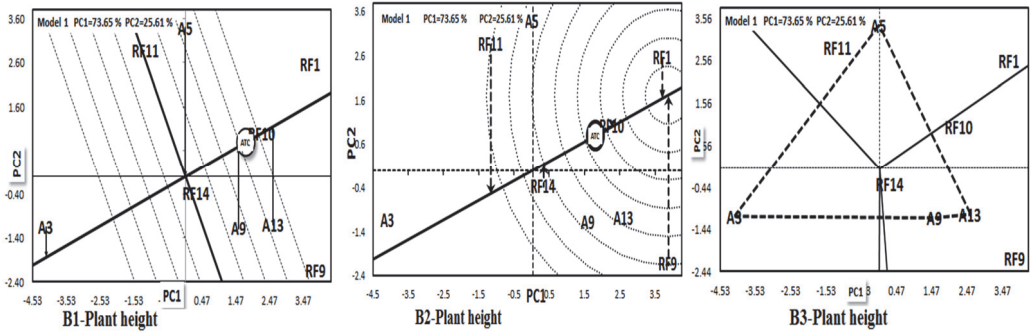
Fig. 2. Biplot of B1(average tester coordinate), B2 (ideal tester) and B3 (polygon view) for plant height (combined data of 2018 and 2019 summer season)
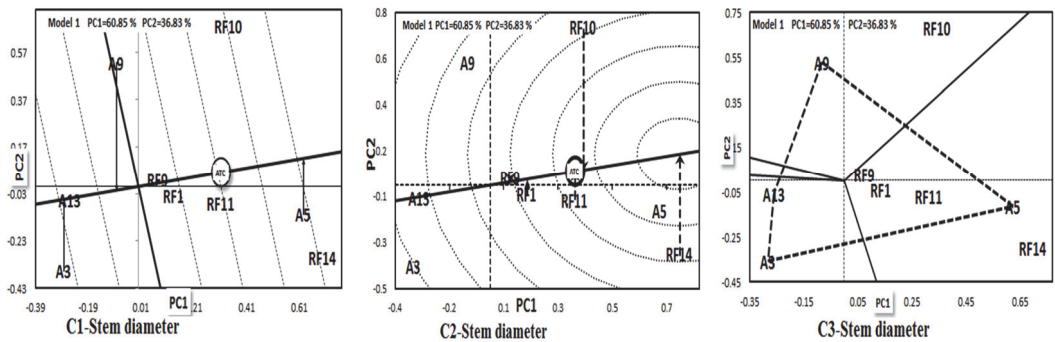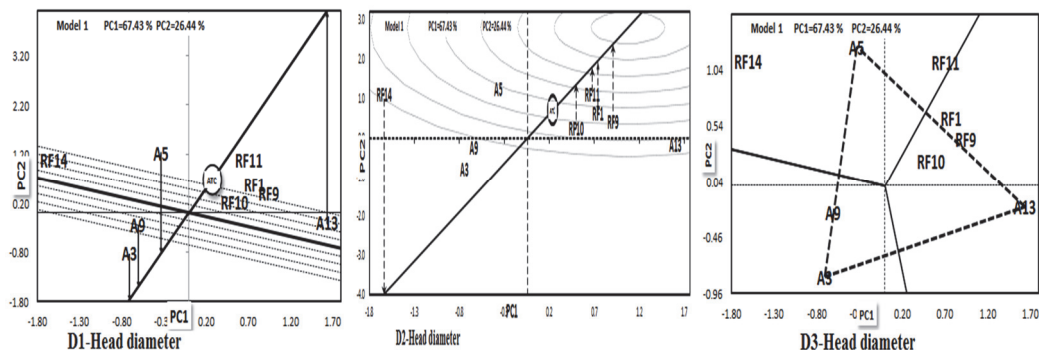

Fig. 3. Biplot of C1 (average tester coordinate), C2 (ideal tester) and C3 (polygon view) for stem diameter (combined data of 2018 and 2019 summer season)

The best cross combinations can be produced as the polygon view of a biplot (Fig. 3, C3) pointed out by crossing A5 as good specific combiner with testers RF9, RF1, RF11 and RF14 as well as A9 with RF10. This is consistent with their respective heterosis relative to mid and better parents (Table 5) in traditional analysis.

Head diameter. Among the parents (Fig. 4, D1), A5 of CMS lines and RF11 (1.93 Discr. and 0.69 Repr.) of RF lines (Fig. 4, D2) proved to be good general combiners for producing the largest head diameter, as they occupied position far away from the origin. Moreover, the remaining lines either RF or CMS depicted the lowest or negative GCA effects by occupying position in the opposite direction. These findings are consistent with their respective GCA effects (Table 3) in traditional analysis (0.81** for CMS lines and 1.23** for RF lines).

Projections of RF and CMS lines onto the ATC ordinate are approximated with their SCA effects. Accordingly, A13 (4.29 Repr.) and A5 (2.07 Repr.) as well as RF14 (5.12 Repr.) and RF9 (1.95 Repr.) were found to be the best SCA effects (Fig. 4, D1 and D2 as well as Table 4).

Genotypes having the largest diameter of head are desirable ones. Therefore, A13 produced desirable cross combination with tester Rf9, RF1 and RF10. On the other hand, A5 resulted in good cross combination especially with RF11 and RF14 (Fig. 4, D3), as proven in numerical heterosis of mid parents (Table 5).

Fig. 4. Biplot of D1 (average tester coordinate), D2 (ideal tester) and D3 (polygon view)
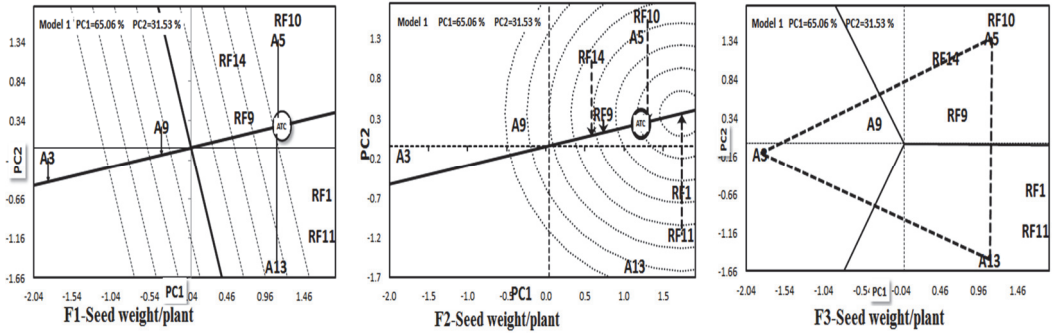for head diameter (combined data of 2018 and 2019 summer season)
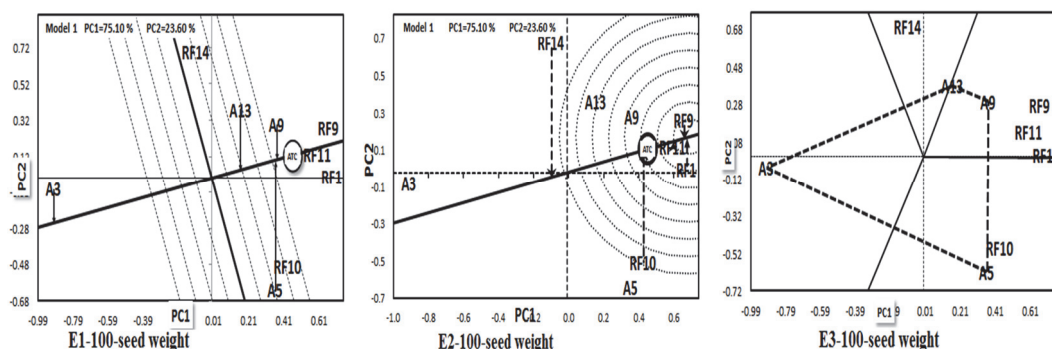
Fig. 5. Biplot of E1 (average tester coordinate), E2 (ideal tester) and E3 (polygon view)
for 100-seed weight (combined data of 2018 and 2019 summer season)

100-seed weight. Based on projection onto the ATC abscissa (Fig. 5, E1), A9 (0.38 Discr.) and A13 (0.17 Discr.) of CMS lines, as they occupied position far away from the origin, this agreed well with their respective GCA effects in traditional analysis in Table 3 (with GCA effects of 0.22** and 0.11*). Similarly, among the tester RF11, (Table 3) were identified as the best general combiners being highly discriminating (0.63) and representative (0.03). And also, this was confirmed by their respective GCA effects in traditional analysis (with GCA effects of 0.11**).

The largest projection of RF and CMS lines, in reference to the largest SCA effects, was detected in A5 (0.72 Repr.) and A13 (0.33 Repr.) of CMS lines as well as RF14 (0.72 Repr.) and RF10 (0.61 Repr.) (Fig. 5, E1 and E2 as well as Table 4).

Genotypes having the heaviest weight of 100-seed are desirable ones, therefore, two well defined groups of best cross combinations (Fig. 5, E3) were identified by the polygon view. In the first group, A5 as vertex CMS line was the best mating partners with tester RF1, whereas in the second group A9 and A13 as vertex CMS lines generated superior cross combinations with testers RF1, RF9 and RF11, as proven by numerical heterosis of mid parents (Table 5).

Seed weight pant⁻¹. The accumulative effect of stem and head diameters as well as 100-seed weight was considerable reflected on seed weight plant^{-1}. This revealed by projection of parental lines onto the ATC abscissa (Fig. 6, F1), in reference to GCA

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Fig. 6. Biplot of F1 (average tester coordinate), F2 (ideal tester) and F3 (polygon view) for seed weight plant^{-1} (combined data of 2018 and 2019 summer season)
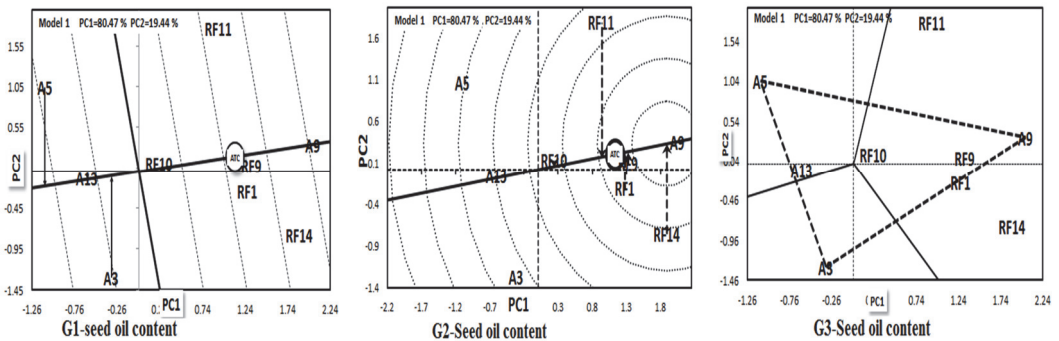
Fig. 7. Biplot of G1 (average tester coordinate), G2 (ideal tester) and G3 (polygon view) for seed oil content (combined data of 2018 and 2019 summer season)

effects, particularly in A5 (1.16 Discr.) and A13 (1.14 Discr.) of CMS lines as well as RF11 (1.74 Discr. and 1.53 Repr.) of RF lines as ideal testers of CMS (Fig. 6, F2), as they occupied a position at a longer distance from the place of origin in the positive direction of ATC abscissa, and this was consistent with their respective GCA effects in traditional analysis (Table 3) (with GCA effects of 1.71** and 0.87** of CMS lines and 2.22** of RF lines), thereby, they are behaved as the best combiner for improvement of seed weight plant^{-1}.

The largest SCA effects as the largest projection (Fig. 6, F2 and Table 4) of RF and CMS lines pointed out, was detected in A13 (1.77 Repr.) and A5 (1.09 Repr.) of CMS lines as well as Rfl11 (1.53 Repr.) and Rf10 (1.32 Repr.) of RF lines.

Genotypes having the heaviest weight of plant seed are desirable. The polygon divided the biplot into four well defined sectors (Fig. 6, F3). A13 being vertex genotype interacted positively with the testers RF1 and RF11 whereas A5 was the best mating partners with testers Rf9, Rfl14 and RF10, and this was consistent with their respective heterosis of mid (Table 5).

Seed oil content. Projection of parental lines onto the ATC abscissa (Fig. 7 G1) approximates their GCA effects. Therefore, A9 (2.06 Discr.) of CMS lines and RF10 (0.23 Discr. and 0.07 Repr.) as ideal tester of CMS (Fig 7 G2), as they occupied the position far away from the origin in the positive direction on ATC x-axis hence considered as good general combiner for improving seed oil content, and this was consistent with their respective GCA effects (Table 3) in traditional analysis (with GCA effects of 2.35** of CMS lines and 3.59** of RF lines).

The projection of parental lines on ATC y-axis refers to SCA effects. Accordingly, A3 (1.24 Repr.) and A5 (1.22 Repr.) of CMS lines as well as RF11 (1.62 Repr.) and Rf14 (1.10 Repr.) had the highest SCA effects, as they had the largest projections onto ATC ordinate (Fig. 7, G and Table 4).

The polygon (Fig. 7, G3) identified the best mating partners i.e.A9 was identified as the best specific combiners, hence it showed potential to produce superior and heterotic cross combination with all testers. And this is consistent with their respective heterosis relative to mid parents (Table 5).

It could be noticed from Table 6, that the dominance genetic variance (δ_D^2) as a portion of the total genetic variance and relative importance of SCA was larger than the additive genetic variance (δ_A^2) and relative importance of GCA for all evaluated traits except days to 50% flowering, also confirmed by greater ratio of **(ā)** than unity for all studied traits except days to 50% flowering, revealed the greater importance of dominance gene action. This was further supported by low narrow sense heritability, as seen in Table 6, for 100-seed weight (8.53%), head diameter (11.42%), plant height (13.34%), stem diameter (15.77%), seed oil content (23.80%) and seed weight plant^{-1} (25.05%) and the reverse was true in days to 50% flowering (48.59%). Heritability in broad sense along with expected genetic advance as *per cent* mean, as shown in Table 6, is considered as an effective selection tool for improving yield of sunflower than heritability estimates alone as confirmed by Johnson *et al.* [17]. This may be due to additive variance as can be predicted in the offspring of a selection cross in a systematic fashion. As presented in Table 6, high values of broad heritability coupled with high (more than 20%) values of genetic advance (as % of mean) were detected for stem diameter (33.45%), plant height (24.34%) and head diameter (24.44%), indicating the importance of additive gene effects in the inheritance of these traits, thus, selection for these traits would be effective. High heritability coupled with moderate (10…20%) expected genetic advance as *per cent* mean were recorded for 100-seed weight (18.48%), seed weight plant^{-1} (14.65%), seed oil content (12.87%) and days to 50% flowering (12.77%), indicated that these Therefore, it could be concluded that, greater importance of non-additive gene action in their expression and indicated very good prospect for the exploitation of non-additive genetic variation for most traits through hybrid sunflower breeding.

Table 6

The relative magnitudes of different genetic parameters in F1 crosses for all studied traits (combined data of 2018 and 2019 summer season)

	Days to 50% flowering	Plant height	Stem diameter	Head diameter	100-seed weight	Seed weight plant^{-1}	Seed oil content
δ_A^2	6.42	39.18	0.02	0.77	0.03	3.45	1.86
δ_D^2	3.97	247.18	0.11	4.60	0.27	9.50	4.80
δ_G^2	10.39	286.36	0.13	5.36	0.30	12.95	6.66
δ_P^2	13.21	293.65	0.14	6.72	0.33	13.78	7.83
H_n%	78.64	97.52	93.08	79.78	89.70	93.96	85.06
H_n%	48.59	13.34	15.77	11.42	8.53	25.05	23.80
(ā)	1.11	3.55	3.13	3.46	4.36	2.35	2.27
*GCA %	0.62	0.14	0.17	0.14	0.10	0.27	0.28
**SCA %	0.38	0.86	0.83	0.86	0.90	0.73	0.72
GAM	12.77	24.34	33.45	24.44	18.48	14.65	12.87

*, **Significant at 0.05 and 0.01 probability level, respectively.

Conclusion

In conclusion, A5 and A13 of CMS lines and RF11 and Rf14 of RF lines proved to be the best general combiners for seed weight plant^{-1} and one or more of its attributes traits. These lines would be used to develop hybrid seed on commercial scale. Moreover, the best cross combinations A13 × RF11, A13 × RF1 and A5 × RF9 performed better than other developed hybrids in view of seed weight plant^{-1} and one or more of its attributes, hence these F1 hybrids could further be used on commercial exploitation.

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Научная статья

GGE biplot анализ линии с помощью тестера на урожайность семян и ее признаков в подсолнечнике

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Аннотация. Девять генетически разнообразных перспективных линий подсолнечника по основным признакам урожайности были скрещены с тестером в весеннем сезоне 2018 г. для оценки их продуктивности по нескольким признакам. Родительские формы подсолнечника имели четыре типа ЦМС, а именно L1 (A3), L2 (A5), L3 (A9) и L4 (A13) (далее именуемые «Линии» (женские линии)) и пять генотипов подсолнечника T1 (RF9), T2 (RF10), T3 (RF11), T4 (RF14) и T5 (RF1) в качестве мужских линий (далее именуемые «Тестер»). В летнем сезоне 2018 и 2019 гг. девять родительских форм вместе с их семенами 20 F1 были проанализированы и получили оценку на Станции сельскохозяйственных исследований Shandaweel (ARC, Мухафаза Сохаг, Египет) с использованием рандомизированных полных блоков с тремя повторностями. Средние значения показателей для родительских форм (P), кроссов (C), линий (L), тестеров (T), P по сравнению с C и (L × T) были значимыми для всех изученных признаков. Большая величина неаддитивного действия гена, чем аддитивного, была выявлена при больших соотношениях (GCA/SCA), чем всех изученных признаков (за исключением периода до 50% цветения). A5 и A13 ЦМС линии и RF11 и RF14 линий — тестеры оказались лучшими родительскими формами по показателю массы семян с одного растения. Кроме того, были

выявлены лучшие кросс-комбинации A13 × RF11, A13 × RF1 и A5 × RF9, по сравнению с другими получившимися гибридами по признаку массы семян с одного растения и одного или нескольких сопутствующих признаков. Таким образом, полученные гибриды F1 могут в дальнейшем использоваться в коммерческих целях.

Ключевые слова: подсолнечник, *Helianthus annuus* L., линия по тестеру, комбинирующая способность, гетерозис, действие гена

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