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Research article

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Evaluation of some sunflower genotypes for agronomic traits and oil quality

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Abstract: The present investigation was carried out to evaluate agronomic performance and oil quality of seven sunflower genotypes at Shandaweel Research Station, Agricultural Research Center, Sohag, Egypt during 2018 and 2019 summer seasons. These genetic materials were sown in a randomized complete block design having three replications. Significant genetic variations among evaluated sunflower genotypes for agronomic traits and oil quality were observed. The superior sunflower genotypes were Line 120 for seed yield per hectare (3102.38 kg), Sakha 53 for seed oil content (44.63 %) and Line 125 for oil quality where it contained the highest proportion of unsaturated fatty acids (89.20 %). The phenotypic coefficients of variation were slightly higher than genotypic coefficients of variation for all studied traits. High heritability (exceeded 60%) and genetic advance as percent of mean (ranged from medium to high, exceeded 10%) was observed for most studied traits. Seed yield per plant positively correlated with plant height, stem diameter, head diameter, and 100-seed weight and most chemical traits at phenotypic and genotypic levels. Maximum phenotypic direct effects on seed yield per plant were observed for 100-seed weight, head diameter and total unsaturated fatty acids. While, the highest genotypic direct effect on seed yield per plant was observed for head diameter. Hence, most studied traits could be employed as selection criteria for improving evaluated sunflower genotypes.

Keywords: genetic parameters; mean performance; selection criteria.

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Introduction

Sunflower is one of the important oil crops in Egypt, and the agricultural policy in Egypt is concerned with expanding its cultivation, as it has a great potential to increase the local oil production to cover the increased domestic consumption of edible oil. Identify the nature of genetic variability in a sunflower population is an important objective for a breeding program to improve the yield and oil quality potential of genotypes.

To infer the genetic variability, some genetic criteria i.e. phenotypic and genotypic coefficients of variation, heritability and genetic advance were estimated for agronomic traits and oil quality in the previous studied literature for achieving the effective improvement in the yield and oil quality potential of sunflower genotypes. Of them, study of Singh et al. (2019) showed that genetic variability was significant for all studied traits. Moreover, the highest phenotypic and genotypic coefficients of variations as well as high heritability coupled with high genetic advance over mean were detected in seed yield and hull content followed by seed oil content, 100-seed weight and plant height. Dudhe et al. (2020) revealed that days to maturity was less affected by environment due to it having high heritability coupled with high genetic advance as percent of mean (GAM), this refers to role of additive gene action in its inheritance. However, the non-additive gene action played a major role in inheritance of seed yield per plant, head diameter and oil content as evidenced by moderated heritability along with moderated-to-lowed GAM for these traits. Moreover, the correlation of head diameter, 100-seed weight and plant height was positive with seed yield per plant, whereas seed yield per plant had a negative correlation with oil content. Similarly, Ahmed et al. (2020) showed that tested sunflower genotypes had valuable genetic variability, and they added that effective improvement for seed yield can be achieved through two traits of head diameter and 100-seed weight. In addition, Abdelsatar et al. (2020) illustrated that desirable improvement of seed yield per plant may be achieved through selecting genotypes having the largest head diameter, bigger number of filled seeds per head, the highest proportion of seed setting and the heaviest seed, kernel and hull mass as proven by high phenotypic and genotypic coefficient of variation and high heritability coupled with high genetic advance (as % of mean) as well as correlation and path analyses at both phenotypic and genotypic levels.

The above-mentioned studies have focused on the importance of identifying the genetic variation among genotypes and importance of determining the selected traits in improving the yield and oil quality potential of sunflower genotypes. Therefore, our efforts in this research were limited to evaluate seven sunflower genotypes through agronomic traits and oil quality, and their improving through estimating some genetic parameters and determining the selection traits to improve seed yield and oil quality potential of sunflower genotypes.

Materials and methods

Seven sunflower genotypes were evaluated in a field trial using randomized complete block design with three replications during summer seasons of 2018 and 2019 at Shandaweel Agricultural Research Station, ARC, Sohag, Egypt. Names and pedigree of the seven genotypes are shown in Table 1.

The experimental plots consisted of three ridges with a ridge length of 4 m length, 60 cm ridge to ridge distance and 25 cm plant to plant distance. Sowing was done in hill on ridges by placing three seeds in hill to ensure uniform stand and was later thinned to one plant per hill at 15 days after sowing stage as recommended.

All other agricultural practiced were done as recommended by Oil crops Research Department, Field Crops Research Institute, Agricultural Research Center, Giza, Egypt.

Collected data

Agronomic traits: At maturity, 10 sunflower plants were randomly taken from each genotype in each replication for recording the agronomic traits. Agronomic traits represented in number of days to 50% flowering plants as flowering date (N^0), plant height (cm), stem diameter (cm), head diameter (cm), 100-seed weight (g), seed yield per plant (g) and seed yield per hectare (kg)

Oil quality: Oil quality represented in oil percentage (%), total protein content (%), total saturated fatty acids content, total unsaturated fatty acids content, oleic acid (C18:1), linolic acid (C18:2) and linolenic acid (C18:3). Samples of seeds were oven dried, ground finely and stored in small bags for chemical analysis. Extraction of oils, the method used to extract from the seed was the Association of Official Analytical Chemists (AOAC 2005). Oil Percentage was determined according to AOAC (1990). Total protein content, the method used to determine it in the seed was AOAC (2000). Gas liquid chromatography (Aglent 6890 GC, USA) used for determination and identification of the

Table 1: Names and pedigree of seven sunflower genotypes studied.

Name	Pedigree
Sakha 53	Mayak × Bulgarian1
Giza 102	Indian line × Mayak
Line 120	Mayak × Bulgarian2
Line 990	Bulgarian 59 × Bulgarian 52
Line 770	Bulgarian 53 × Bulgarian 49
Line 465	Bulgarian 53 × Bulgarian 52
Line 125	Mayak × Bulgarian3

fatty acids composition, in Central Laboratory of Food Technology Research Institute, ARC, Egypt, according to Zygadloet al. (1994).

Statistical analysis

Standard statistical analysis of variance was performed using randomized complete block design with three replications according to Gomez and Gomez (1984). The combined analysis of variance (across the two seasons) was done according to Snedecor and Cochran (1989), which was performed after confirmation of the homogeneity test.

The phenotypic and genotypic coefficient of variability was computed according to Singh and Chaudhury (1999).

$$\mathrm{PCV}\ (\ \%\ ) = \frac{\sqrt{\delta^2 ph}}{\overline{x}} \times 100$$

$$\mathrm{GCV}\ (\%) = \frac{\sqrt{\delta^2 g}}{\overline{x}} \times 100$$

where:

$\delta^2 ph$ = phenotypic variance.

$\delta^2 g$ = genotypic variance.

$\overline{x}$ = grand mean of trait

Heritability in broad sense was computed by the formula suggested by Falconer (1989).

$$h_b^2 = \frac{\delta^2 g}{\delta^2 ph} \times 100$$

where:

$\delta^2 ph$ = phenotypic variance.

$\delta^2 g$ = genotypic variance.

Genetic advance was worked out as per the formula given by Singh and Chaudhury (1999).

$$\text{GA as } \%\text{ of mean (GAM)} = \left(\left(k \times \delta_{ph} \times h_b^2\right)/\overline{x}\right) \times 100.$$

where, k = The standardized selection differential at 5% selection intensity and (k = 2.063). δ_{ph} = Phenotypic standard deviation, h_b^2 = broad sense-heritability and $\overline{x}$ grand mean of trait.

Correlation coefficients at phenotypic and genotypic levels for seed yield per plant and yield related traits were evaluated utilizing the formula suggested by Miller et al. (1958) and Kashiani and Saleh (2010).

$$rp_{xy} = \frac{\delta^2 p_{xy}}{\sqrt{\delta^{2p_x}} \times \sqrt{\delta^{2p_y}}} \times 100$$

where,

rp_{xy} = phenotypic correlation coefficient between traits x and y,

$\delta^2 p_{xy}$ = is the phenotypic covariance of xy,

δ^{2p_x} = is the phenotypic variance of x,

δ^{2p_y} = is the phenotypic variance of y.

$$rg_{xy} = \frac{\delta^2 g_{xy}}{\sqrt{\delta^{2g_x}} \times \sqrt{\delta^{2g_y}}} \times 100$$

where,

rg_{xy} = genotypic correlation coefficient between traits x and y,

$\delta^2 g_{xy}$ = is the genotypic covariance of xy,

δ^{2g_x} = is the genotypic variance of x,

δ^{2g_y} = is the genotypic variance of y.

Phenotypic and genotypic path coefficient analyses were carried out as suggested by Dewey and Lu (1959) using phenotypic and genotypic correlation coefficients, respectively to determine the direct and indirect effects of yield related traits (independent variables, causes) on seed yield per plant (dependent variable, effect) at phenotypic and genotypic levels based on the following equation:

$$r_{ij} = p_{ij} + \sum r_{ik} p_{kj}$$

where, r_{ij} = Mutual association between the independent trait (i) and dependent trait, seed yield per plant (j) as measured by correlation coefficients at phenotypic and genotypic levels. p_{ij} = Components of direct effects of the independent trait (i) as measured by path coefficients at phenotypic and genotypic levels and $\sum r_{ik} p_{kj}$ = summation of components of indirect of a given independent trait (i) on a given dependent trait (j) via all other independent traits (k).

The contribution of the remaining unknown factor was measured as the residual factor (p_r) at phenotypic and genotypic levels, which is calculated as:

$$p_r = \sqrt{\left(1 - \sum r_{ij} p_{ij}\right)}$$

The r_{ij} = denote correlations between all possible combinations of independent traits, p_{ij} = denote direct effects of various traits on trait j.

The magnitude of p_r indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary 1999) (Table 1).

Results and discussion

Agronomic performance and oil quality

The presented data in Table 2 showed the significant differences among sunflower genotypes for all studied traits. Hence, possibility of further improvement for these traits within these breeding materials was effective. The earlier genotype in days to 50% flowering (47.75 days) was shown for Line 125. In contrast, Line 990 and Sakha 53 were the latest (50.78 days) in days to 50% flowering. This varied range of difference is available in the present materials that can help the Egyptian breeder in any breeding program for selection for earliness. Concerning Line 990 recorded tallest plant height (163.25 cm), while the shortest genotype was shown by Giza 102 (136.67 cm). Line 770 had the highest value for stem diameter but the lowest value

Table 2: Agronomic performance and oil quality of seven sunflower genotypes across two summer seasons.

Genotype	Agronomic traits							Oil quality						
	Days to 50 flowering (N^0)	Plant height (cm)	Stem diameter (Cm)	Head diameter (cm.)	100-seed weight (g.)	Seed yield per plant (g.)	Seed yield per hectare (kg.)	Seed oil content (%)	Total protein content (%)	Saturated fatty acids	Unsaturated fatty acids (%)	Oleic acid (C18:1) (%)	Linolic acid (C18:2) (%)	Linolenic acid (C18:3) (%)
Sakha 53	50.78	147.93	2.07	17.94	6.58	40.29	3089.68	44.63	17.56	15.26	87.27	22.77	64.37	0.13
Giza 102	48.33	136.67	1.64	17.35	6.16	43.65	3037.14	38.69	19.30	13.28	86.78	18.02	68.65	0.11
L120	48.73	142.42	1.45	18.01	6.42	43.66	3102.38	40.93	19.11	12.35	87.05	17.02	69.90	0.12
L990	50.78	163.25	1.56	20.22	6.70	44.21	2731.87	40.48	19.00	14.31	84.51	17.37	67.01	0.14
L770	48.00	160.40	2.29	19.03	6.38	43.85	2422.42	41.23	19.49	14.01	83.31	16.73	66.47	0.12
L465	48.89	146.48	2.02	20.07	6.59	45.04	2580.91	43.51	18.14	13.92	88.09	16.54	71.44	0.12
L125	47.75	158.97	2.18	20.37	6.83	46.13	2578.61	42.97	18.20	15.62	89.20	21.10	67.97	0.13
LSD 5%	1.03	2.69	0.14	0.78	0.19	1.93	182.96	1.91	0.89	0.69	2.48	1.18	1.77	0.01
LSD 1%	1.45	3.77	0.20	1.09	0.27	2.70	256.50	2.68	1.25	0.97	3.48	1.65	2.47	0.02

was detected by Line 120. The largest head diameter (20.37 cm) was for Line 125 and the lowest value (17.35 cm) was for Giza 102. These results are in agreement with the findings of Ahmed et al. (2020) and Abdelsatar et al. (2020).

Line 125 had the heaviest of 100-seed weight (6.83 g) while the lowest mean of 100-seed weight was shown for Giza 102. Highest seed yield per plant was obtained by Line 125, while the lowest yield was obtained from Sakha 53. On the other hand, the highest seed yield per hectare was obtained by Line 120, while the lowest was for Line 770.

These differences among sunflower genotypes for all studied traits may be due to the variances in their genetically constituents. Similar results were reported by Ibrahim (2012), Ali et al. (2014), Abd EL-Satar et al. (2017), Ahmed et al. (2020) and Abdelsatar et al. (2020).

As shown in Table 2, sunflower genotypes significantly differed in all chemical composition of sunflower seeds traits across two summer seasons. The highest oil content was shown by the locally bred Sakha 53 compared to Giza 102 which had the lowest oil percentage. While the highest total protein content was obtained by Line 770, the lowest value was shown by Sakha 53. Maximum saturated fatty acids were detected by Line 125 as the highest value (15.62%), but the lowest value (12.35%) was recorded by Line 120. On the other hand, the highest content of unsaturated fatty acids (89.20%) was recorded by Line 125, but the lowest value (83.31%) was shown by Line 770. Sakha 53 recorded the highest value of oleic acid (C18:1), while Line 465 recorded the lowest value. On the other hand, Line 465 had the highest linoleic acid content, but Sakha 53 recorded the lowest proportion. The highest proportion of linolenic acid was achieved by Line 990, while Giza 102 possessed the lowest proportion. Sakha 53 was superior in seed oil content, while Line 125 had the good oil quality via its contained the highest proportion of unsaturated fatty acids. These findings are in accordance with these obtained by Ibahim (2012), Abd EL-Satar et al. (2017) and Abdelsatar et al., (2020).

Genetic parameters for all studied traits

To check the amount of genetic variability for tested sunflower genotypes, the mean, the range, genotypic and phenotypic variances, genotypic (GCV) and phenotypic (PCV) coefficient of variation, broad sense-heritability (h^2_b), and genetic advance as % of mean (GAM) were computed for agronomic traits and oil quality (Table 3). High magnitude of variation in the tested breeding material was reflected by broad range for all studied traits. These results are in confirmation with Abd EL-Satar et al. (2017) and Abdelsatar et al. (2020).

Table 3: Estimates of genetic variability for all studied traits.

Characters	Mean	Range	GV	PV	GCV	PCV	h^2_b	GA% Mean
Days to 50% flowering	49.04	47.75–50.78	1.46	1.80	0.99	1.22	0.81	4.58
Plant height	150.87	136.67–163.25	101.02	103.31	22.32	22.82	0.98	13.59
Stem diameter	1.89	1.45–2.18	0.11	0.11	1.89	2.00	0.95	34.80
Head diameter	19.00	17.35–20.37	1.49	1.68	2.62	2.95	0.89	12.49
100-Seed weight	6.52	6.16–6.83	0.05	0.06	0.24	0.29	0.80	6.07
Seed yield per plant	43.83	40.29–46.13	2.86	4.04	2.18	3.07	0.71	6.70
Seed yield per hectare	2791.86	2422.42–3102.38	75698.21	86275.53	903.80	1030.08	0.88	19.04
Oil content	41.78	38.69–44.63	3.75	4.90	2.99	3.91	0.77	8.36
Total protein content	18.69	17.65–19.49	0.44	0.69	0.78	1.23	0.64	5.82
Saturated fatty acids	14.11	12.35–15.62	1.19	1.34	2.82	3.17	0.89	15.05
Unsaturated fatty acids	85.89	84.38–87.65	1.19	1.34	0.46	0.52	0.89	2.47
Oleic acid	18.51	16.54–22.77	5.80	6.24	10.45	11.24	0.93	25.90
Linoleic acid	67.97	64.37–71.44	5.07	6.05	2.49	2.97	0.84	6.25
Linolenic acid	0.12	0.11–0.14	0.0001	0.0002	0.03	0.04	0.72	15.01

PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; h_2b, broad sense heritability; GA% mean, genetic advance as percent of mean.

Data in Table 3 showed that the agronomic traits such as plant height and seed yield per hectare and oil quality such as oil content, oleic acid and linoleic acid recorded the highest phenotypic and genotypic variation than the other studied traits. Phenotypic coefficient of variation (PCV) was slightly higher than genotypic one (GCV) for all studied traits (Table 3), indicating negligible influence of environment on the expression of all traits. Where, seed yield per hectare showed high PCV and GCV estimates. Plant height was moderate PCV and GCV, and the remaining traits recorded low PCV and GCV.

Oleic acid had the highest phenotypic and genotypic variation than the other chemical traits, while linoleic acid and oil content recorded moderate PCV and GCV and unsaturated fatty acids showed low coefficient of variation at two levels. There is enough focused for selection based on these traits, and the diverse genotypes can provide materials for an effective breeding program. The finding of Abd EL-Satar et al. (2017), Ahmed et al. (2020), and Abdelsatar et al. (2020) corresponds with the present study.

The heritability estimates (Table 3) were high for all studied traits for evaluated genotypes, which supported selection for improving these traits, and have been detected in earlier studies by Abd EL-Satar et al. (2017), Ahmed et al. (2020) and Abdelsatar et al. (2020).

Estimates of heritability along with genetic advance (as percent of mean) are more important for selection than heritability alone. This was confirmed by Johnson et al. (1955) who discovered efficient use of broad sense-heritability along with genetic advance (as percent of mean), which would give a more reliable index of selection value. High broad sense-heritability and high genetic advance as percent of mean (Table 3) were observed for stem diameter and oleic acid indicating that these traits were controlled by additive gene effects would likely to be effective. Plant height, head diameter, seed yield per hectare, total saturated fatty acids and linolenic acid had high broad-sense heritability, and moderate genetic advanced. In the same context, Ahmed et al. (2020) and Abdelsatar et al. (2020) observed high heritability estimates and high genetic advance as percent of mean for head diameter, plant height, stem diameter and seed yield per plant in sunflower genotypes.

Selection criteria for all studied traits

Phenotypic and genotypic correlations

Correlation coefficient analysis at phenotypic and genotypic levels was estimated between various traits and seed yield per plant to determine the selected traits for improvement in yield and oil quality potential. Phenotypic (r_p) and genotypic (r_g)

correlation were estimated between seed yield per plant and its related traits for seven sunflower genotypes across two seasons (Table 4). Seed yield per plant was positively correlated with plant height, stem diameter, head diameter and 100-seed weight and most chemical traits at phenotypic and genotypic levels, indicating that selection using these traits will be more effective for improving evaluated sunflower genotypes. These findings are confirmed by those of Abd EL-Satar et al. (2017), Ahmed et al. (2020) and Abdelsatar et al. (2020).

The correlation at phenotypic and genotypic levels were positive between seed yield per plant and plant height ($P = 0.294$ and $G = 0.304$), stem diameter ($P = 0.006$ and $G = 0.085$), head diameter ($P = 0.631$ and $G = 0.707$), 100-seed weight ($P = 0.301$ and $G = 0.304$), total protein content ($P = 0.296$ and 0.251), unsaturated fatty acids ($P = 0.338$ and $G = 0.019$), linoleic acid ($P = 0.783$ and $G = 0.422$) and linolenic acid ($P = 0.052$). Similarly, positive correlation was detected between head diameter and plant height ($P = 0.723$ and $G = 0.765$), stem diameter ($P = 0.310$ and $G = 0.337$), 100-seed weight ($P = 0.749$ and $G = 0.842$), oil content ($P = 0.302$ and $G = 0.325$), saturated fatty acids ($P = 0.469$ and $G = 0.697$), unsaturated fatty acids ($P = 0.010$ and $G = 0.035$), linoleic acid ($P = 0.129$ and $G = 0.223$) and linolenic acid ($P = 0.527$ and $G = 0.642$). Likewise, positive correlation was observed between 100-seed weight and days to 50% flowering ($P = 0.224$ and $G = 0.277$), plant height ($P = 0.609$ and 0.690), stem diameter ($P = 0.250$ and 0.334), head diameter ($P = 0.749$ and $G = 0.842$), oil content ($P = 0.543$ and $G = 0.698$), saturated fatty acids ($P = 0.634$ and $G = 0.755$), unsaturated fatty acids ($P = 0.275$ and $G = 0.393$), oleic acid ($P = 0.379$ and $G = 0.415$) and linolenic acid ($P = 0.832$ and $G = 0.930$). Thus, selection practiced for any one of the previous traits would automatically improve the other ones, especially seed yield per plant. Therefore, these traits could be considered as indicators to achieve desirable genetic improvement for seed yield per plant and oil quality of sunflower.

Phenotypic and genotypic path analysis

For further clarification about interrelationships between seed yield per plant and its related traits, the phenotypic and genotypic path analysis divided phenotypic and genotypic correlation into direct (in bold) and indirect effects, where seed yield per plant was considered a dependent variable and yield related traits were independent variables as shown in Table 5 and Figure 1.

Maximum phenotypic direct effects were observed for 100-seed weight (0.688) followed by total unsaturated fatty acid (0.842) and head diameter (0.706). While genotypic direct effects were observed for head diameter (0.886).Hence, preferred improvement may be achieved through selecting genotypes with 100-seed weight, head diameter. Furthermore, the highest phenotypic and genotypic indirect effects on seed yield per plant were detected for plant height ($P = 0.510$ and $G = 0.677$),

Table 4: The pooled phenotypic (above diagonal) and genotypic (below diagonal) correlations for all studied traits across two seasons.

	days to 50 flowering, X1	plant height, X2	Stem diameter, X3	Head diameter, X4	100-weight weight, X5	Oil percentage, X6	Total protein, X7	Total Saturated Fatty acids, X8	Total Unsaturated Fatty acids, X9	Oleic acid (C18:1), X10	Linoleic acid (C18:2), X11	Linolenic acid (C18:3), X12	Seed yield per plant, X13
X1	1.000	0.093	−0.251	−0.047	0.224	0.199	−0.302	0.155	−0.136	0.253	−0.388	0.467	−0.554
X2	0.143	1.000	0.392	0.723	0.609	0.175	0.001	0.529	−0.388	0.028	−0.399	0.596	0.294
X3	−0.332	0.423	1.000	0.310	0.250	0.552	−0.351	0.627	0.064	0.336	−0.281	0.012	0.006
X4	−0.005	0.765[a]	0.337	1.000	0.749	0.302	−0.204	0.469	0.010	−0.120	0.129	0.527	0.631
X5	0.277	0.690	0.334	0.842[a]	1.000	0.543	−0.456	0.634	0.275	0.379	−0.128	0.832[a]	0.301
X6	0.295	0.199	0.633	0.325	0.698	1.000	−0.828[a]	0.512	0.330	0.470	−0.166	0.424	−0.198
X7	−0.448	0.038	−0.395	−0.202	−0.712	−0.943[b]	1.000	−0.517	−0.438	−0.580	0.175	−0.405	0.296
X8	0.226	0.577	0.697	0.483	0.755[a]	0.707	−0.768[a]	1.000	0.211	0.714	−0.528	0.546	−0.052
X9	−0.227	−0.434	0.035	0.112	0.393	0.535	−0.841[a]	0.276	1.000	1.000	0.456	0.112	0.338
X10	0.287	0.042	0.349	−0.125	0.415	0.635	−0.835[a]	0.761	0.472	1.000	−0.558	0.394	−0.469
X11	−0.498	−0.408	−0.345	0.223	−0.122	−0.238	0.198	−0.589	0.325	−0.680	1.000	−0.299	0.783[a]
X12	0.619	0.718	0.048	0.642	0.930[b]	0.471	−0.536	0.683	0.103	0.497	−0.451	1.000	0.052
X13	−0.673	0.304	0.085	0.707	0.304	−0.279	0.251	0.016	0.019	−0.397	0.422	−0.023	1.000

[a,b] Significant at 0.05 and 0.01 probability levels, respectively.

Table 5: Pooled phenotypic and genotypic path analysis of seed yield per plant and its related traits across two seasons (on diagonal are direct effects).

	Path analysis	Days to 50% flowering, X1	plant height, X2	Stem diameter, X3	Head diameter, X4	100-seed weight, X5	Oil percentage, X6	Total Protein, X7	Total Saturated Fatty acids, X8	Total Unsaturated Fatty acids, X9	Oleic acid (C18:1), X10	Linoleic acid (C18:2), X11	Linolenic acid (C18:3), X12	Correlation with seed yield per plant
X1	*P*	**−0.439**	−0.030	0.022	−0.033	0.154	−0.093	−0.003	−0.006	−0.114	−0.263	0.416	−0.166	−0.554
	G	**−0.805**	−0.012	0.139	−0.005	−0.007	−0.002	−0.011	−0.002	0.018	0.051	−0.085	0.049	−0.673
X2	*P*	−0.041	**−0.320**	−0.035	0.510	0.420	−0.081	0.000	−0.020	−0.327	−0.029	0.428	−0.212	0.294
	G	−0.115	**−0.085**	−0.177	0.677	−0.019	−0.001	0.001	−0.006	0.034	0.007	−0.069	0.057	0.304
X3	*P*	0.110	−0.125	**−0.088**	0.219	0.172	−0.256	−0.003	−0.024	0.054	−0.350	0.301	−0.004	0.006
	G	0.268	−0.036	**−0.419**	0.299	−0.009	−0.005	−0.010	−0.008	−0.003	0.062	−0.059	0.004	0.085
X4	*P*	0.021	−0.231	−0.027	**0.706**	0.515	−0.140	−0.002	−0.018	0.009	0.125	−0.139	−0.188	0.631
	G	0.004	−0.065	−0.141	**0.886**	−0.023	−0.002	−0.005	−0.005	−0.009	−0.022	0.038	0.051	0.707
X5	*P*	−0.098	−0.195	−0.022	0.529	**0.688**	−0.252	−0.004	−0.024	0.231	−0.394	0.138	−0.297	0.301
	G	−0.223	−0.059	−0.140	0.746	**−0.027**	0.001	−0.004	0.004	−0.020	0.056	−0.021	−0.009	0.304
X6	*P*	−0.087	−0.056	−0.049	0.213	0.373	**−0.464**	−0.007	−0.019	0.278	−0.488	0.178	−0.151	−0.279
	G	−0.237	−0.017	−0.265	0.288	0.004	**−0.007**	−0.023	−0.008	−0.042	0.112	−0.040	0.038	−0.198
X7	*P*	0.133	0.000	0.031	−0.144	−0.314	0.384	**0.009**	−0.038	−0.369	0.603	−0.188	0.144	0.251
	G	0.360	−0.003	0.165	−0.179	0.004	0.007	**0.024**	0.008	0.066	−0.147	0.034	−0.043	0.296
X8	*P*	−0.068	−0.169	−0.055	0.331	0.436	−0.237	0.009	**−0.038**	0.177	−0.743	0.567	−0.194	0.016
	G	−0.182	−0.049	−0.292	0.428	0.010	−0.005	−0.019	**−0.011**	−0.021	0.134	−0.100	0.054	−0.052
X9	*P*	0.060	0.124	−0.006	0.007	0.189	−0.153	−0.004	−0.008	**0.842**	−0.504	−0.489	−0.040	0.019
	G	0.183	0.037	−0.015	0.099	−0.007	−0.004	−0.020	−0.003	**−0.078**	0.083	0.055	0.008	0.338
X10	*P*	−0.111	−0.009	−0.030	−0.085	0.261	−0.218	−0.005	−0.027	0.408	**−1.040**	0.598	−0.140	−0.397
	G	−0.231	−0.004	−0.146	−0.111	−0.008	−0.005	−0.020	−0.008	−0.037	**0.176**	−0.115	0.040	−0.469
X11	*P*	0.170	0.127	0.025	0.091	−0.088	0.077	0.002	0.020	0.384	0.580	**−1.073**	0.107	0.422
	G	0.401	0.035	0.145	0.198	0.003	0.002	0.005	0.006	−0.025	−0.120	**0.170**	−0.036	0.783
X12	*P*	−0.205	−0.190	−0.001	0.372	0.573	−0.197	−0.004	−0.021	0.094	−0.410	0.321	**−0.356**	−0.023
	G	−0.498	−0.061	−0.020	0.569	0.003	−0.003	−0.013	−0.008	−0.008	0.088	−0.077	**0.080**	0.052
Residual	*P*	0.286												
	G	0.368												

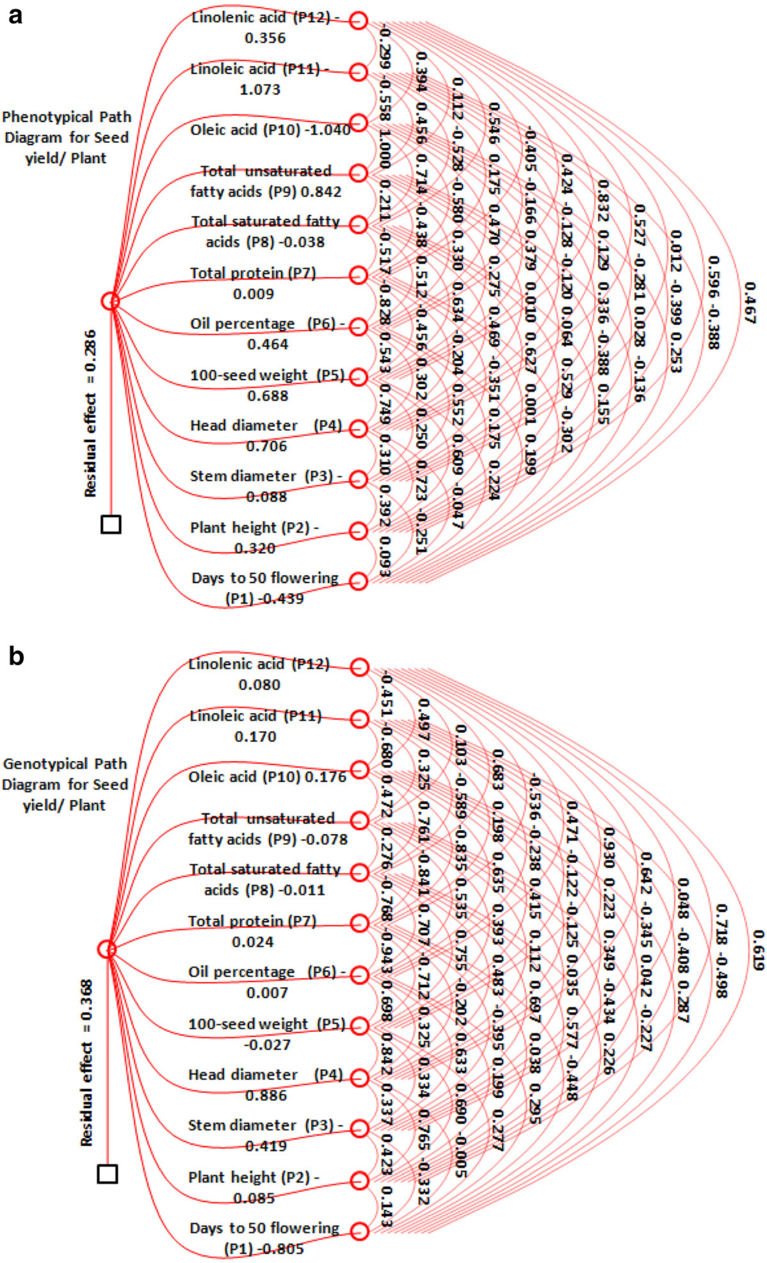

Figure 1: (a) Phenotypic path diagram for seed yield per plant. (b) Genotypic path diagram for seed yield per plant.

steam diameter (P = 0.219 and G = 0.299), 100- seed weight (P = 0.529 and G = 0.746), oil percentage (P = 0.213 and G = 0.288), total saturated fatty acids (P = 0.331 and G = 0.428) and linolenic acid (P = 0.372 and G = 0.569) via head diameter and stem diameter (P = 0.110 and G = 0.268), total protein (P = 0.133 and G = 0.360) and linoleic acid (P = 0.170 and G = 0.401) via days to 50% flowering, considered as identical reflection for the previous results of correlation at both phenotypic and genotypic levels (Table 5).These results agreed with those of Abd EL-Satar et al. (2017), Ahmed et al. (2020) and Abdelsatar et al. (2020).

The residual effect being (0.286) and (0.368) at phenotypic and genotypic levels, respectively indicated that independent traits which are included at the phenotypic and genotypic path analysis, explained (71.4) and (63.2 %) of the total variation, respectively in seed yield per plant. The high residual effects of phenotypic and genotypic path analyses, indicated that the presence of other traits that are not included in the present study were associated with the high effect on seed yield per plant. These results agreed with Abd EL-Satar et al. (2017), Ahmed et al. (2020) and Abdelsatar et al. (2020).

Conclusion

In conclusion, evaluated sunflower genotypes have valuable genetic variation, which gives the good opportunity for effective selection on genetic basis within these genotypes for seed yield and oil quality. Moreover, efficiency of some studied traits *i.e.* head diameter and 100-seed weight in improving seed yield per plant were observed, as they had the highest broad-sense heritability with genetic advance as percent of mean, in addition to their significant association with seed yield per plant and their direct and indirect positive effect on seed yield per plant.

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