Genetic variability and selection criteria of some sunflower genotypes under different pollination methods

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Genetic variability and selection criteria of some sunflower genotypes under different pollination methods

Abstract: To determinate self-compatible genotypes for increasing autogamy yielded, the ten sunflower genotypes were sown under four pollination methods i.e., open-, self-, hand- and sib-pollinations in a randomized complete block design replicated thrice at Kafr-El-Hamam Agricultural research Station, Sharkia Governorate, Agricultural Research Center, Egypt during 2018 and 2019 summer seasons. Significant variation existed for different pollination treatments, genotypes and their interactions for all studied traits. Among the treatments, open pollination followed by sibbing one was regarded as the best pollination treatment for head diameter, number of filled seeds per head, percentage of seed setting , kernel to hull ratio, seed mass per plant, seed yield per fed and seed oil content. Autogamy studies revealed that 'L120' followed by 'L92' and 'L880' recorded higher proportion of autogamy and self-compatibility. Preferred improvement of seed mass 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.

Key words: autogamy; heritability; path analysis; sunflower

Genetska variabilnost in selekcijski kriteriji nekaterih genotipov sončnice pri različnih metodah opraševanja

Izvleček: Za določitev samokompatibilnih genotipov in povečanje samooplodive je bilo posejanih deset genotipov sončnice z različnimi načini opraševanja in sicer: navskrižno opraševanje, samoopraševanje, ročno opraševanje in opraševanje znotraj starševskih linij. Poskus je bil zasnovan kot naključni popolni bločni poskus s tremi ponovitvami na Kafr-El-Hamam Agricultural research Station, Sharkia Governorate, Agricultural Research Center, Egypt, v poletnih rastnih sezonah 2018 in 2019. Za vse preučevane lastnosti so se pokazale značilne razlike glede na način opraševanja, izbrane genotype in njihove interakcije. Med obravnavanji sta se navskrižno opraševanje in opraševanje znotraj starševskih linij izkazali kot najboljši način opraševanja glede na premer koška (glave) sončnic, število polnih zrn na košek, odstotek nastavka semen, razmerja med jedrci in luščinami, maso semen na rastlino, pridelek semena na fedan in vsebnost olja v semenu. Preučevanje avtogamije je odkrilo, da so imeli genotipi po vrstnem redu 'L120', 'L92' in 'L880' največji delež samooplodnje in samokompatibilnosti. Zaželeno izboljšanje mase semena na rastlino bi lahko dosegli z izborom genotipov, ki imajo največji premer koška, večje število polnih semen na košek, največji nastavek semen, največjo maso semen, jedrc in luščin kot je bilo dokazano z velikim fenotipskim in genotipskim koeficientom variabilnosti in velike dednosti povezano z velikim napredkom v dedovanju (kot poprečni odstotek) kot tudi z analizami korelacije med preučevanimi lastnostmi na fenotipski in genotipski ravni.

Ključne besede: avtogamija; dednost; analiza povezanih znakov; sončnica

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1   INTRODUCTION

Sunflower is a major oilseed crop in the world after soybean and groundnut. Sunflower as cross-pollinated crops, which almost dependent on pollinating insects and wind for increasing seed yield. However, only pollinating insects and winds are not sufficient to cause maximum seed yield and quality. Thus, the major challenge of plant breeder is to determinate self-compatible genotypes for increasing autogamy or selfing yielded in the absence of pollinating insects. Self-compatible genotypes have higher yields than self-incompatible ones, when bees are not abundant. Consequently, cultivating self-compatible genotypes with high yielding ability offer a great opportunity to improve seed yield and oil quality of sunflower.

Pollination methods are important factor for identifying self-compatible genotypes with high yielding ability. In this concern, seed set under self-pollination conditions is strongly correlated with self-compatibility degree (Beg et al., 1987). Earlier findings of Sameena (2003) indicated that pollen blend treatment was the best one followed by open pollination, geitonogamy and autogamy, due to its enhanced seed setting rate, higher number of filled seeds per head, kernel to hull ratio and hence seed mass per plant as well as higher seed oil content. In the same context, maximum head diameter with less empty diameter, seed setting percentage, number of filled seed per head, 100 seed mass, seed yield per plant, per plot and per ha was obtained by combination of bee pollination and hand pollination methods than that of other pollination ones as recorded by Talele (2011) and Osman and Siham (2015).

Successful sunflower breeding program depends on magnitude of genetic variability in the breeding material and knowledge of selection criteria would be effective in improving seed yield. In this respect, considerable amount of genetic variability might be affect days to first flowering, days to full flowering, plant height, stem diameter, autogamy percentage, self-compatibility percentage, head diameter, number of filled seeds per head, number of unfilled seeds per head, total number of seeds per head, seed setting percentage, 100-seed mass, kernel mass (mg), hull mass (mg), hull content (%), kernel to hull ratio, seed mass per plant, seed yield per fed and seed oil content as reported by Sameena (2003), Supriya et al. (2016), Neelima et al. (2016) and Supriya et al. (2017). High heritability coupled with high percentage of genetic advance were observed for head diameter, seed mass per plant, 100-seed mass, pollen production per plant, plant height and percentage of hull mass as reported by by Khan and Muhammad (2007), Kalukhe et al. (2010), Sudrik et al. (2014) and Seyed et al. (2014), Sheshaiah

and Shankargoud (2015), Supriya et al. (2016), Dudhe et al. (2017) and Baraiya et al. (2018).

Moreover, the selection criteria of correlation and path analyses at phenotypic and genotypic levels play a vital role in selected the best traits to improve seed mass per plant. Seed mass per plant highly significant and positively correlated with 100-seed mass, head diameter and number of filled seeds were reported by Sowmya et al. (2010), Neelima et al. (2012), Prabhakaran et al. (2013), Deengra et al. (2013) and Venkanna et al. (2014). Seed filling percentage, head diameter and hull content percentage exhibited good amount of direct effect on seed mass per plant and its correlation with these traits were also positively significant at both genotypic and phenotypic levels and it is indicated that these traits should be considered as selection criteria for higher seed yield as reported by Sowmya et al. (2010), Neelima et al. (2012), Tyagi and Khan (2013), Deengra et al. (2013) and Sanju et al. (2018).

Therefore, the present study aimed to find out the impact of pollination methods on seed yield and its attributes of some sunflower genotypes, to determinate self-compatible genotypes for increasing autogamy or selfing yielded in the absence of pollinating insects and to identify genetic variability among sunflower genotypes and selection criteria for improving yield.

2.   MATERIALS AND METHODS

2.1   SITE DESCRIPTION

Four field experiments was conducted at the experimental Farm of Kafr-El-Hamam Research Station, Zagazig, Sharkia Governorate, Agricultural Research Center, Egypt (30\ 58⁰ N, 31\ 50⁰E) during the two successive summer seasons of 2018 and 2019.

2.2   EXPERIMENTAL DESIGN

The experiment was laid out in randomized complete block design for each pollination method with three replications. Pollination methods details were practiced as follow; open pollination (OP) was done by left head of plant for open pollination without bagging to allow self and cross-pollination, self-pollination (SP) was done by bagging sunflower heads before commencement of flowering to harvesting time, hand pollination (HP) was done by gently rubbing the heads with the help of muslin cloth at flowering duration and sib-pollination (SIP) was done by collecting pollen from males plants of the same geno-

type and mixed to dust on sunflower heads of receiver female plants of the same one.

Each genotype was sown, after harvesting wheat in both seasons, in five ridges with a ridge length of 4 m spaced at 60 cm between ridges and 30 cm apart. Tested sunflower genotypes as open pollinated genotypes i.e. L125, Sakha$_{53,}$ L235, L880, L770, L92, L120, L167, L460 and L355 were received from Oil Crops Research Department, Field Crop Research Institute, Agricultural Research Center, Egypt.

2.3 AGRICULTURAL PRACTICES

Sunflower genotypes seeds were hand-planted on ridges, 60 cm as well as 30 cm apart between hills, during the first week of June in both seasons. Plants were thinned at 15 days after sowing to secure one plant per hill. Fertilizer was added in two equal portions prior to the first and the second irrigations in the form of urea (46.6 % N). All other cultural practices were applied as recommended.

2.4 DATA COLLECTED

At harvest, five guarded plants were randomly selected from the 2nd and 4th ridges, harvested, tied and left to dry to determine yield and yield attributes viz., head diameter, number of filled seeds per head, number of unfilled seeds per head, total number of seeds per head, 100-seed mass and seed mass per plant. The seed set percent was calculated by the formula given by Roath and Miller (1982) as, seed setting percentage = (number of filled seeds/ total seeds) × 100. Autogamy and self-compatibility percent was calculated by formulae given by George et al. (1980) as, autogamy % = percent seed set under self-pollination/ percent seed set under open pol-lination. Self-compatibility % = percent seed set under hand pollination/ percent seed set under open pollination. The mass of hulls and kernels recorded by drawing 100-seeds at random, and then their kernels and hulls were separated to record the mass of the separated hundred hulls and kernels. Hull percent was calculated by the following formula, Hull % = (Mass of hull / Total mass of seeds) × 100. Kernel to hull (K/H) ratio was calculated by dividing the kernel mass of hundred seed by their hull mass. Plants of central ridge from each plot were harvested for determining seed yield per m^2 and converted to seed yield in kg per fed. Seed oil content was determined according to AOAC, (1990).

2.5 STATISTICAL ANALYSIS

Analysis of variance according to Gomez and Gomez (1984) for each variable was done using randomized complete block design for all studied traits. Combined analysis of variance across the two seasons was done after confirmation of homogenous (Table 1) for all studied traits using F. max test method of Hartley (1950).

Genotypic and phenotypic coefficients of variation (Burton and DeVane 1953), estimation of broad sense heritability (H^2_b) (Hansen et al., 1956), genetic advance as percent of the mean (Johnson et al., 1955) were estimated. Phenotypic (r$_p$) and genotypic (r$_g$) correlation coefficients between two traits such as X and Y were calculated using formula of Weber and Moorthy (1952): r$_p$ = Cov$_p$ (X, Y) / (V$_p$ (X) × V$_p$ (Y))$^{0.5}$, where Cov P (X, Y) = Phenotypic covariance of traits X and Y. Vp (X) and VP (Y) = Phenotypic variance of trait X and Y, respectively. And r$_g$ = Cov$_g$ (X, Y) / (V$_g$ (X) × V$_g$ (Y))$^{0.5}$, where Cov$_g$ (X, Y) = Genotypic covariance of traits X and Y. V$_g$ (X) and V$_p$ (Y) = Genotypic variance of trait X and Y, respectively. Moreover, phenotypic and genotypic path analysis (Dewey and Lu 1959) was also done.

Table 1: Seasonal Hartley tests (F. max) of error variances for all studied traits

Item	head diameter	Number of filled seeds per head	Number of unfilled seeds per head	Total number of seeds per head	Seed setting percentage	100.seed mass	kernel mass
F. max	1.46	1.13	1.07	1.08	1.07	1.24	1.03
F. tabulated	1.48	1.48	1.48	1.48	1.48	1.48	1.48
Significance	NS	NS	NS	NS	NS	NS	NS
Item	Hull mass	Hull content	Kernel to hull ratio	Seed mass per plant	Seed yield per fed	Seed oil content	
F. max	1.18	1.24	1.12	1.24	1.11	1.43	
F. tabulated	1.48	1.48	1.48	1.48	1.48	1.48	
Significance	NS	NS	NS	NS	NS	NS	

3 RESULTS AND DISCUSSION

3.1 ANALYSIS OF VARIANCE

The combined analyses of variance for all studied traits of 10 sunflower genotypes over years and pollination methods are presented in Table 2. In this respect, the main effects of years, pollination methods and genotypes were highly significant for all studied traits, indicating that significant effect of these main effects on the performance of all studied traits. The interactions of year with pollination methods and with genotypes had insignificant effect on the performance of all studied traits. This indicated that the pollination methods and tested sunflower genotypes had the same ranks from year to another. Moreover, the insignificant triple interaction among year, pollination methods and genotypes was observed for all studied traits. This indicated that climatic conditions of two years had the same effect on pollination methods and tested sunflower genotypes, hence it was ignored in discussion. However, the interaction of pollination methods with tested sunflower genotypes was highly significant for all studied traits. This indicated that tested sunflower genotypes significantly differed from pollination method to another for all studied traits, hence it was considered as important interaction to discussion. Similar significant interactive effect of pollination methods with sunflower genotypes were reported by Supriya et al. (2016), Neelima et al. (2016) and Supriya et al. (2017).

3.2 POLLINATION METHODS EFFECTS

The results of pollination methods in Table (3) revealed that there were significant differences between various pollination treatments for all studied traits. Similar significant effects of pollination methods were reported by Talele (2011) and Osman and Siham (2015).

As shown in the combined analysis, obviously, open pollination gave the highest values for head diameter, number of filled seeds per head, percentage of seed setting, kernel to hull ratio, seed mass per plant, seed yield per fed and seed oil content. It exceeds self-pollination by 25.10 %, 41.45 %, 44.03 %, 3.55 %, 56.68 %, 57.25 %, 15.16 %, respectively. This may be due to the effective transfer of foreign pollens by pollinating insects to the

Table 2: Combined analysis of variance for all studied traits of 10 sunflower genotypes over two years and four pollination methods

SOV	df	Head diameter	Number of filled seeds per head	Number of unfilled seeds per head	Total number of seeds per head	Seed setting percentage	100.seed mass	Kernel mass
Year (Y)	1	**	**	**	**	*	**	**
Pollination methods (P)	3	**	**	**	**	**	**	**
Y x P	3	NS	NS	NS	NS	NS	NS	NS
Reps in Y x P	2	NS	NS	NS	NS	NS	NS	NS
Genotypes (G)	9	**	**	**	**	**	**	**
P x G	27	**	**	**	**	**	**	**
Y x G	9	NS	NS	NS	NS	NS	NS	NS
Y x P x G	27	NS	NS	NS	NS	NS	NS	NS
Error	237							

SOV	df	Hull mass	Hull content	Kernel to hull ratio	Seed mass per plant	Seed yield per fed	Seed oil content
Year (Y)	1	**	**	**	**	**	**
Pollination methods (P)	3	**	**	**	**	**	**
Y x P	3	NS	NS	NS	NS	NS	NS
Reps in Y x P	2	NS	NS	NS	NS	NS	NS
Genotypes (G)	9	**	**	**	**	**	**
P x G	27	**	**	**	**	**	**
Y x G	9	NS	NS	NS	NS	NS	NS
Y x P x G	27	NS	NS	NS	NS	NS	NS
Error	237						

Table 3: Comparison of means of pollination methods for all studied traits across 2018 and 2019 seasons

Pollination methods	Head diameter (cm)	Number of filled seeds per head	Number of unfilled seeds per head	Total number of seeds per head	Seed setting percentage	100-Seed mass (g)	Kernel mass (mg)
Open	19.54	471.92	101.99	573.91	81.52	6.07	483.92
Selfing	14.63	276.32	316.72	593.03	45.63	6.66	552.33
Hand	17.48	340.78	201.15	541.93	62.00	6.52	535.63
Sibbing	18.95	444.22	132.72	576.93	76.41	6.26	505.03
LSD$_{5\%}$	0.24	1.55	1.55	2.28	0.21	0.05	1.46

Pollination methods	Hull mass (mg)	Hull content (%)	Kernel to hull ratio	Seed mass per plant (g)	Seed yield per fed (kg)	Seed oil content (%)	
Open	172.99	0.39	2.80	42.62	1112.22	42.08	
Selfing	204.40	0.89	2.70	18.46	475.44	35.70	
Hand	189.05	0.60	2.84	25.27	773.90	37.49	
Sibbing	183.71	0.44	2.75	35.42	953.64	39.96	
LSD$_{5\%}$	1.20	0.01	0.02	0.51	10.38	0.36	

receptive stigma, thereby increasing percentage of seed setting and gave higher number of filled seeds per head. The reverse was true, with selfing, which pollination had the highest values of number of unfilled seeds per head, total number of seeds per head, 100-seed mass (g), kernel mass (mg), hull mass (mg) and percentage of hull content. It exceeds open pollination by 210.53 %, 3.33 %, 9.78 %, 14.14 %, 18.16 %and 129.63 % in the respective order. Other methods, hand and sib-pollination had the moderate effect on most of studied traits.

3.3 GENOTYPIC EFFECTS

It is apparent from the pooled data in Table (4) that significant differences were detected among the ten tested sunflower genotypes for all studied traits, indicated that there is valuable genetic variation in these genotypes to warrant selection for improvement sunflower crop. Similar significant genotypic effects for all studied traits were reported by Supriya et al. (2016), Neelima et al. (2016) and Supriya et al. (2017). Irrespective of pollination methods imposed, 'Sakha 53' (21.55 cm) followed by 'L120' (19.83 cm) behaved as the largest head diameter; 'L120' (534.95) followed by 'L880' (503.37) gave more filled seeds per head; 'L120' (80.07 %) followed by 'L92' (76.59 %) had the highest proportion of seed setting; 'L355' (6.76 g) followed by 'L167' (6.73 g) possessed the biggest mass of 100-seed; 'L355' (538.58 mg) followed by ''L880 (535.33 mg) had the biggest mass of kernel; 'L880' (199.71 mg) followed by 'L355' (198.61 mg) expressed the highest mass of hull; the highest proportion of hull was detected in 'L355' (1.07 %) followed by 'L167' (0.82 %);

'L120' (2.98 %, 37.28 g, 1022.95 kg and 42.86 %) followed by 'L92' (2.83 %, 33.83 g, 890.05 kg and 40.21 %) behaved as the largest ratio of Kernel to hull, seed mass per plant, seed yield per fed and seed oil content, respectively. Hence, these genotypes are the best stock for improving sunflower crop in terms of most studied traits.

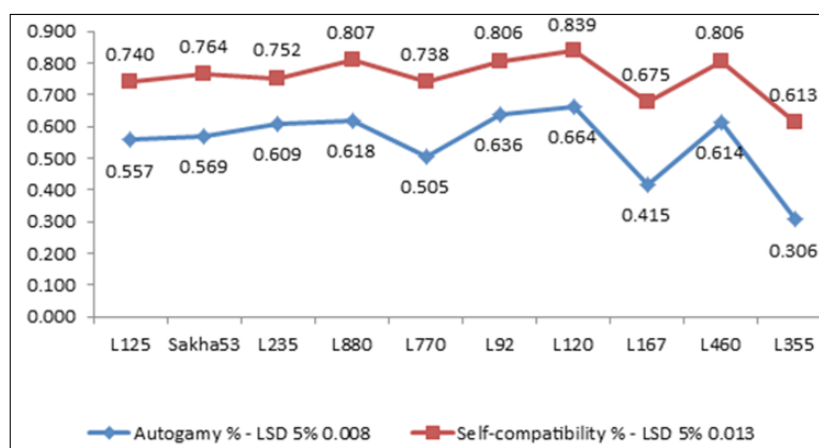### 3.4 PERCENTAGE OF AUTOGAMY AND SELF-COMPATIBILITY

A genotype is considered self-fertile if the maximum percentage of seed setting takes place under self-pollination. Among the ten sunflower genotypes as shown in Fig. (1), L120 recorded the highest proportion of autogamy on one hand (0.664 %) followed by L92 (0.636 %) and L880 (0.618 %). On the other hand, L120 (0.839 %), L880 (0.807 %) and L92 (0.806 %) behaved as self-compatible sunflower genotypes. This may be due to these genotypes possessed a high number of florets per unit area, a random orientation of stigmas, and the stigma receptive surface vertically presented. Thus, these genotypes can be used in sunflower breeding program to increasing proportion of self-compatibility.

3.5 INTERACTION EFFECTS

The interactive effect of pollination methods with ten sunflower genotypes was significant for all studied traits, as combined analysis shown in Table (5), indicated that traits of sunflower genotypes especially yield and yield-components varied according to pollination meth-

Table 4: Comparison of means of ten sunflower genotypes for all studied traits across 2018 and 2019 seasons

Sunflower genotypes	Head diameter (cm)	Number of filled seeds per head	Number of unfilled seeds per head	Total number of seeds per head	Seed setting percentage	100-Seed mass (g)	Kernel mass (mg)
L125	16.45	349.12	173.17	522.28	66.82	6.55	522.50
Sakha 53	21.55	379.45	206.02	585.47	64.66	6.04	506.42
L235	17.21	376.61	171.39	548.00	69.05	6.51	518.21
L880	18.60	503.37	198.52	701.89	71.99	6.16	535.33
L770	16.08	321.95	180.00	501.95	64.32	6.59	528.33
L92	18.26	452.70	139.17	591.87	76.59	6.28	506.75
L120	19.83	534.95	131.83	666.78	80.07	5.70	492.83
L167	15.79	264.95	245.50	510.45	51.97	6.73	532.50
L460	17.68	420.20	154.50	574.70	73.23	6.42	510.83
L355	15.06	229.78	281.33	511.12	45.19	6.76	538.58
LSD 5%	0.37	2.45	2.46	3.60	0.33	0.07	2.31

Sunflower genotypes	Hull mass (mg)	Hull content (%)	Kernel to hull ratio	Seed mass per plant (g)	Seed yield per fed (kg)	Seed oil content (%)	
L125	188.58	0.58	2.77	30.96	795.79	38.32	
Sakha$_{53}$	190.30	0.54	2.66	28.48	849.66	40.06	
L235	186.70	0.52	2.78	31.54	822.01	39.14	
L880	199.71	0.41	2.68	28.45	824.84	38.48	
L770	190.43	0.64	2.78	29.61	770.06	37.77	
L92	178.80	0.41	2.83	33.83	890.05	40.21	
L120	166.05	0.32	2.98	37.28	1022.95	42.86	
L167	191.89	0.82	2.78	26.75	746.59	36.51	
L460	184.30	0.46	2.78	32.36	842.15	39.69	
L355	198.61	1.07	2.71	25.14	723.89	35.04	
LSD 5%	1.90	0.02	0.03	0.81	16.42	0.57	

Figure 1: Autogamy percentage and self-compatibility percentage of ten sunflower genotypes across 2018 and 2019 summer seasons

Table 5: Comparison of means of pollination methods interaction with ten sunflower genotypes across 2018 and 2019 summer seasons

Interaction	Head diameter (cm)	Number of filled seeds per head	Number of un-filled seeds per head	Total number of seeds per head	Seed setting percentage	100-seed mass (g)	Kernel mass (mg)
OP x L125	17.67	428.12	93.25	521.37	82.12	6.20	489.83
OP x Sakha 53	25.67	459.78	125.33	585.12	78.58	5.72	467.50
OP x L235	18.63	449.10	88.81	537.91	83.49	6.18	478.33
OP x L880	20.10	608.12	95.68	703.79	86.41	5.97	507.50
OP x L770	17.42	422.45	97.92	520.37	81.18	6.21	494.17
OP x L92	19.87	534.45	58.93	593.38	90.07	6.02	473.83
OP x L120	22.35	626.45	50.92	677.37	92.49	5.55	458.83
OP x L167	17.38	356.45	155.58	512.03	69.61	6.35	496.17
OP x L460	19.10	517.45	77.92	595.37	86.91	6.08	475.50
OP x L355	17.17	316.78	175.58	492.37	64.34	6.38	497.50
SP x L125	13.67	247.12	293.25	540.37	45.73	6.81	551.17
SP x Sakha 53	17.88	266.12	328.92	595.03	44.72	6.41	540.83
SP x L235	14.47	302.12	292.25	594.37	50.83	6.76	548.50
SP x L880	15.53	394.12	344.25	738.37	53.38	6.37	567.50
SP x L770	13.23	214.12	308.58	522.70	40.96	6.90	565.17
SP x L92	15.38	356.12	265.58	621.70	57.28	6.54	538.50
SP x L120	17.10	409.12	257.25	666.37	61.41	6.01	523.83
SP x L167	12.87	152.12	374.25	526.37	28.90	7.04	567.50
SP x L460	14.73	318.12	277.58	595.70	53.40	6.71	545.50
SP x L355	11.45	104.12	425.25	529.37	19.66	7.07	574.83
HP x L125	16.68	295.12	190.58	485.70	60.76	6.65	536.17
HP x Sakha 53	20.07	325.78	216.58	542.37	60.07	6.19	531.83
HP x L235	17.40	319.12	189.25	508.37	62.77	6.63	535.17
HP x L880	18.55	478.12	207.92	686.03	69.69	6.64	549.17
HP x L770	16.03	291.12	194.58	485.70	59.94	6.68	539.17
HP x L92	18.17	397.12	149.92	547.03	72.60	6.43	529.17
HP x L120	19.33	491.12	141.92	633.03	77.59	5.79	515.83
HP x L167	15.77	228.12	257.25	485.37	47.00	6.81	541.50
HP x L460	17.90	388.12	165.58	553.70	70.09	6.53	533.17
HP x L1250	14.93	194.12	297.92	492.03	39.45	6.84	545.17
SIP x L355	17.80	426.12	115.58	541.70	78.66	6.55	512.83
SIP x Sakha 53	22.57	466.12	153.25	619.37	75.26	5.86	485.50
SIP x L235	18.33	436.12	115.25	551.37	79.10	6.49	510.83
SIP x L880	20.20	533.12	146.25	679.37	78.47	5.64	517.17
SIP x L770	17.63	360.12	118.92	479.03	75.18	6.59	514.83
SIP x L92	19.63	523.12	82.25	605.37	86.41	6.13	485.50
SIP x L120	20.53	613.12	77.25	690.37	88.81	5.46	472.83
SIP x L167	17.13	323.12	194.92	518.03	62.37	6.72	524.83
SIP x L460	19.00	457.12	96.92	554.03	82.51	6.37	489.17
SIP x L355	16.70	304.12	226.58	530.70	57.30	6.75	536.83
LSD 5%	0.74	4.90	4.91	7.20	0.66	0.15	4.61

OP: open pollination, SP: self-pollination, HP: hand-pollination and SIP: sib-pollination

Table 5: Continued

Interaction	Hull mass (mg)	Hull content (%)	Kernel to hull ratio	Seed mass per plant (g)	Seed yield per fed (kg)	Seed oil content (%)
OP x L125	174.97	0.41	2.80	42.77	1058.32	41.60
OP x Sakha 53	171.23	0.37	2.73	41.51	1183.29	42.79
OP x L235	170.52	0.38	2.81	43.54	1103.32	43.12
OP x L880	180.80	0.30	2.81	39.64	1147.50	41.72
OP x L770	178.63	0.42	2.77	42.17	1025.86	40.25
OP x L92	164.73	0.31	2.88	46.50	1176.32	44.11
OP x L120	149.53	0.24	3.07	48.98	1352.95	45.15
OP x L167	180.80	0.51	2.75	39.50	995.90	39.36
OP x L460	167.60	0.32	2.84	43.72	1119.19	43.56
OP x L355	191.07	0.60	2.60	37.86	959.51	39.13
SP x L125	208.00	0.84	2.65	19.20	466.24	34.72
SP x Sakha 53	209.67	0.79	2.58	17.11	466.93	38.24
SP x L235	206.80	0.68	2.65	19.80	479.53	35.64
SP x L880	209.20	0.53	2.71	14.65	404.00	35.57
SP x L770	208.93	0.98	2.71	17.18	446.16	34.67
SP x L92	191.11	0.54	2.82	21.17	493.70	36.61
SP x L120	185.13	0.45	2.83	24.20	642.11	42.00
SP x L167	209.67	1.38	2.71	16.06	441.73	33.05
SP x L460	203.53	0.64	2.68	20.09	484.64	35.86
SP x L355	212.00	2.04	2.71	15.17	429.33	30.61
HP x L125	186.67	0.63	2.87	25.48	724.45	37.18
HP x Sakha 53	197.47	0.61	2.69	24.64	794.77	39.55
HP x L235	185.93	0.58	2.88	26.11	761.40	37.69
HP x L880	210.33	0.44	2.61	25.82	799.93	37.92
HP x L770	187.17	0.64	2.88	24.06	695.90	36.77
HP x L92	183.90	0.46	2.88	29.20	840.51	39.24
HP x L120	171.03	0.35	3.02	34.16	974.37	41.20
HP x L167	188.68	0.83	2.87	18.68	685.58	34.52
HP x L460	185.33	0.48	2.88	27.62	785.18	38.87
HP x L1250	193.95	1.00	2.81	16.93	676.94	31.98
SIP x L355	184.70	0.43	2.78	36.41	934.14	39.78
SIP x Sakha 53	182.83	0.39	2.66	30.67	953.63	39.66
SIP x L235	183.57	0.42	2.78	36.72	943.80	40.12
SIP x L880	198.50	0.37	2.61	33.70	947.93	38.72
SIP x L770	187.00	0.52	2.75	35.02	912.33	39.38
SIP x L92	175.47	0.34	2.77	38.46	1049.67	40.88
SIP x L120	158.50	0.26	2.98	41.79	1122.37	43.09
SIP x L167	188.40	0.58	2.79	32.77	863.13	39.09
SIP x L460	180.73	0.40	2.71	38.02	979.57	40.47
SIP x L355	197.43	0.65	2.72	30.59	829.78	38.43
LSD 5%	3.79	0.03	0.07	1.61	32.83	1.13

OP: open pollination, SP: self-pollination, HP: hand-pollination and SIP: sib-pollination

ods. Similar significant interactive effect of pollination methods with sunflower genotypes were reported by Supriya et al. (2016), Neelima et al. (2016) and Supriya et al. (2017). As shown in pooled data of pollination methods interaction with ten sunflower genotypes, the largest head diameter (25.67) was recorded by 'Sakha 53' under open pollination, the highest number of filled seeds per head (626.45), percentage of seed setting (92.49 %), kernel to hull ratio (3.07), seed mass per plant (48.98 g), seed yield per fed (1352.95 kg) and seed oil content (45.15 %) was recorded by 'L120' under open pollination. Conversely, the biggest mass of 100-seed (7.07), kernel (574.83), hull (212.00) and hull content (2.04) was detected in 'L355' with self-pollination. This indicated that possibility selection of genotypes on pollination methods, where performance of genotypes varied according to pollination method used.

3.6 GENETIC VARIABILITY

To have better understanding of the extent of genetic variability for the ten sunflower genotypes, phenotypic (PCV)and genotypic (GCV) coefficient of variation, heritability in broad sense (H^2b) and expected genetic advance as percent mean were computed for all studied traits as presented in Table (6). Phenotypic coefficient of variation (PCV) was slightly higher than genotypic coefficient of variation (GCV) for all studied traits, indicating negligible influence of environmental conditions on the expression of all traits. Consequently, the selection would be effective to genetic improvement of the studied traits for these materials. High PCV and GCV as shown

in combined analysis, were observed for head diameter, number of filled seeds per head, number of unfilled seeds per head, total number of seeds per head, percentage of seed setting, percentage of hull content , seed mass per plant and seed yield per fed, and dropped to moderate for 100-seed mass, hull mass and seed oil content, while drastically reduced for kernel mass and kernel to hull ratio. High heritability in broad sense was recorded for all studied traits, indicates a genotype can be identified by its phenotypic performance, thus making the selection more effective for improving these traits. That has been observed in earlier studies by Neelima et al. (2012), Tyagi and Khan (2013), Deengra et al. (2013) and Sanju et al. (2018).

Heritability in broad sense along with expected genetic advance as percent mean, as shown in Table (6), is normally more useful in predicting the genetic gain under selection than heritability estimates alone as confirmed by Johnson et al. (1955). High values of heritability coupled with high values of genetic advance percentage (more than 20 %) were detected for head diameter, number of filled seeds per head, number of unfilled seeds per head, total number of seeds per head, percentage of seed setting , hull content percentage, seed mass per plant and seed yield per fed, indicating the importance of additive gene effects in the inheritance of these traits, thus, selection for these traits would be effective for improving seed mass per plant. High heritability coupled with moderate expected percentage of genetic advance (10-20 %) were recorded for 100-seed mass, hull mass and seed oil content, indicated that these traits appear to be controlled by both additive and non-additive gene action. However high heritability coupled with low expected percentage of

Table 6: Pooled analysis of genetic parameters for all studied traits across 2018 and 2019 seasons

Genetic parameter	Head diameter	Number of filled seeds per head	Number of unfilled seeds per head	Total number of seeds per head	Seed setting percentage	100-Seed mass	Kernel mass
GCV	11.10	25.43	24.75	11.84	16.12	5.10	2.80
PCV	11.24	25.53	24.85	11.94	16.20	5.20	2.87
H^2 bs	97.40	99.25	99.22	98.43	98.91	96.17	95.55
GV %	22.56	52.19	50.79	24.21	33.02	10.31	5.64

Genetic parameter	Hull mass	Hull content	Kernel to hull ratio	Seed mass per plant	Seed yield per fed	Seed oil content
GCV	5.07	35.30	2.92	11.43	10.00	5.38
PCV	5.20	38.67	3.14	11.68	10.21	5.55
H^2 bs	94.87	83.33	86.58	95.86	95.93	93.83
GV %	10.16	66.39	5.59	23.06	20.17	10.73

GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, H2bs: Broad-sense heritability and GV %: Expected genetic advance as percent of mean

genetic advance (less than 10 %) were recorded for kernel mass and kernel to hull ratio, indicated that an increased influence of environmental conditions on this character. Thus selection procedure involving progeny testing are recommended for this trait.

3.7 ASSOCIATION OF TRAITS AND PATH ANALYSIS (AS SELECTION CRITERIA)

Phenotypic and genotypic correlation were estimated between seed mass per plant and its attributes for the 10 sunflower genotypes based on average of 2018 and 2019 summer seasons as presented in Table (7). Seed mass per plant was positively and significant or highly significant correlated with head diameter, number of filled seeds per head, total number of seeds per head, percentage of seed setting and kernel to hull ratio at phenotypic and genotypic levels, indicating that selection will be more effective for the largest head diameter, more of filled seeds, the highest proportion of seed setting and kernel to hull ratio. These findings are confirmed by those of Tyagi and Khan (2013), Deengra et al. (2013) and Sanju et al. (2018). Furthermore, positive and significant or highly significant phenotypic and genotypic correlation was detected among the previous traits i.e. head diameter, number of filled seeds per head, total number of seeds per head, percentage of seed setting and kernel to hull ratio at phenotypic and genotypic levels, indicated that selection practiced for any one of the previous traits would improve the other ones, especially seed mass per plant. Therefore, these traits could be considered as indicators to achieve desirable genetic improvement for seed mass per plant of sunflower.

For further clarification about interrelationships between seed mass per plant and its attributes, the phenotypic and genotypic path analysis divided phenotypic and genotypic correlation into direct and joint effects, where seed mass per plant was considered a dependent variable and yield attributes were independent variables as shown in Table (8) and Fig.(2).

A critical perusal of phenotypic and genotypic path analysis revealed that seed setting percentage had the highest positive direct effects ($p = 0.598$, G = 1.759) on seed mass per plant, followed by kernel mass only at genotypic level (1.122). The highest positive direct effects of the two previous mentioned traits in addition to their highly significant correlation coefficient with seed mass per plant indicated that the direct selection through these two traits would be effective for sunflower improvement.

Conversely, the direct effects of head diameter, number of filled seeds per head, 100-seed mass and hull mass on seed mass per plant were negative and negligible, although their phenotypic and genotypic correlation with seed mass per plant were positive and highly significant. Consequently, the indirect effects of the previous mentioned traits would be more effective to improve seed mass per plant of these materials than direct ones. The highest positive phenotypic and genotypic indirect effects on seed mass per plant were detected for head diameter ($p = 0.367$, G = 1.102) through seed setting percentage followed by 100-seed mass ($p = 0.303$, G = 1.232), kernel mass only at phenotypic level (0.322) and hull mass ($p = 0.081$, G = 0.458); number of filled seeds per head *via* seed setting percentage ($p = 0.554$, G =

Table 7: The pooled phenotypic (above diagonal) and genotypic (below diagonal) correlations of seed mass per plant and its attributes across 2018 and 2019 summer seasons

Traits	HD	FS	UFS	TS	SS	HSM	KM	HM	HC	KHR	SMP
HD	1	0.70**	-0.46**	0.69**	0.61**	-0.89**	-0.73**	-0.41**	-0.70**	0.07	0.45**
FS	0.72**	1	-0.78**	0.90**	0.93**	-0.87**	-0.64**	-0.58**	-0.93**	0.44**	0.76**
UFS	-0.47**	-0.78**	1	-0.43**	-0.95**	0.59**	0.76**	0.78**	0.90**	-0.63**	-0.93**
TS	0.71**	0.90**	-0.44**	1	0.68**	-0.84**	-0.40*	-0.30	-0.72**	0.20	0.46**
SS	0.63**	0.93**	-0.96**	0.68**	1	-0.74**	-0.73**	-0.69**	-0.98**	0.52**	0.88**
HSW	-0.92**	-0.89**	0.61**	-0.87**	-0.76**	1	0.76**	0.62**	0.77**	-0.41**	-0.66**
KW	-0.74**	-0.66**	0.78**	-0.41**	-0.76**	0.78**	1	0.89**	0.70**	-0.63**	-0.85**
HW	-0.42**	-0.59**	0.81**	-0.30	-0.72**	0.64**	0.92**	1	0.61**	-0.91**	-0.93**
HC	-0.76**	-1.01**	0.98**	-0.78**	-1.04**	0.86**	0.78**	0.70**	1	-0.41**	-0.81**
KHR	0.08	0.47**	-0.70**	0.20	0.58**	-0.45**	-0.71**	-0.92**	-0.53**	1	0.83**
SMP	0.46**	0.79**	-0.96**	0.48**	0.91**	-0.70**	-0.91**	-1.01**	-0.93**	0.94**	1

HD-head diameter, FS-number of filled seeds per head, UNS-number of filled seeds per head, TS-Total number of seeds per head, SS-seed setting percentage, HSM-100-seed mass, KM-kernel mass, HM-hull mass, HC-hull content, KHR-kernel to hull ratio and SMP-seed mass per plant

Table 8: Pooled phenotypic (P) and genotypic (G) path analysis of seed mass per plant and its attributes traits across 2018 and 2019 summer seasons

Traits		P1	P2	P3	P4	P5	P6	Correlation
Head diameter (P1)	P	-0.571	-0.056	0.367	0.303	0.322	0.081	0.446
	G	-0.216	-1.279	1.102	1.232	-0.834	0.458	0.462
Filled seeds per head (P2)	P	-0.402	-0.080	0.554	0.294	0.285	0.113	0.763
	G	-0.155	-1.786	1.637	1.188	-0.738	0.640	0.787
Seed setting percentage (P3)	P	-0.351	-0.074	0.598	0.251	0.326	0.134	0.884
	G	-0.135	-1.662	1.759	1.018	-0.848	0.774	0.906
100.seed mass (P4)	P	0.510	0.069	-0.443	-0.339	-0.339	-0.121	-0.662
	G	0.200	1.589	-1.342	-1.334	0.874	-0.689	-0.703
Kernel mass (P5)	P	0.414	0.051	-0.438	-0.258	-0.445	-0.174	-0.850
	G	0.161	1.175	-1.329	-1.040	1.122	-0.997	-0.909
Hull mass (P6)	P	0.237	0.046	-0.410	-0.210	-0.397	-0.195	-0.930
	G	0.092	1.059	-1.262	-0.853	1.037	-1.079	-1.006
Residual effect	P	0.057						
	G	0.305						
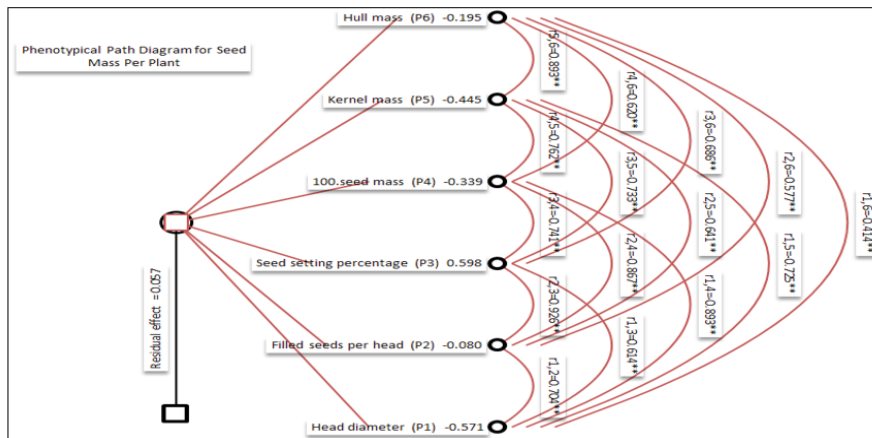
Figure 2a: Phenotypic path diagram for seed mass per plant

1.637), followed by 100-seed mass (*p* = 0.294, G = 1.188), kernel mass only at phenotypic level (0.285) and hull mass (*p* = 0.113, G = 0.640); seed setting percentage via 100-seed mass (*p* = 0.251, G = 1.018), followed by kernel mass at only phenotypic level (0.326) and hull mass (*p* = 0.134, G = 0.774); 100-seed mass (*p* = 0.510, G = 0.200) followed by number of filled seeds per head (*p* = 0.069, G = 1.589) followed kernel mass at only genotypic level (0.874); kernel mass via head diameter (*p* = 0.414, G = 0.161) followed number of filled seeds per head (*p* = 0.051, G = 1.175) and hull mass via head diameter (*p* = 0.237, G = 0.092) followed by number of filled seeds per head(*p* = 0.046, G = 1.059).

It is apparent from the above-mentioned results, it can be concluded that preferred improvement of seed mass per plant may be achieved through selecting genotypes having

the biggest head diameter, more number of filled seeds per head, the highest proportion of seed setting and the heaviest seed, kernel and hull mass. These results agreed with those of Tyagi and Khan (2013), Deengra et al. (2013) and Sanju et al. (2018).

The residual effect being 0.057 and 0.305 at phenotypic and genotypic levels, respectively indicated that independent traits which are included at the phenotypic and genotypic path analysis, explained 94.3 and 69.5 % of the total variation, respectively in seed mass per plant. The highest 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 highest effect on seed mass per plant.
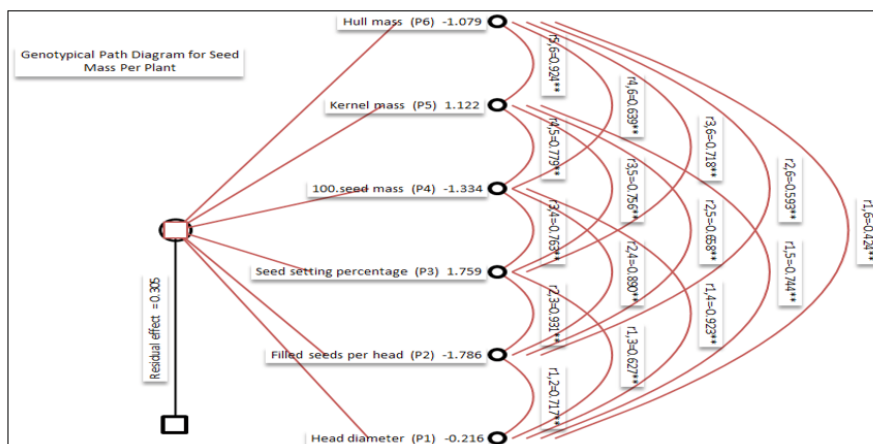
Figure 2b: Genotypic path diagram for seed mass per plant

4 CONCLUSION

From above-mentioned results, it can be concluded that open pollination followed by sibbing one was superior to other pollination methods and leading to high seed mass per plant and higher accumulation of oil content. Higher seed yield was achieved due to high seed set percent, number of filled seeds per head, high kernel to hull ratio and higher kernel proportion in seed. Genotypes L120 followed by L92 and L880 behaved as self-compatible sunflower genotypes. Selection would be more effective to improve seed mass per plant through selecting genotypes having the largest head diameter, more 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.

5 ACKNOWLEDGEMENTS

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