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Estimation of genetic parameters for yield components and seed yield in sunflower using line x tester analysis

Seyed Abbasali Andarkhor*, Valiollah Rameeh and Ramzan Ali Alitabar

Agricultural and Natural Resources Research Center of Mazandran, Sari, Iran.

Combining ability and heritability of yield and yield components of sunflower (*Helianthus annuus* L.) breeding lines were studied using line x tester analysis. Eight lines and six testers along with their 48 F1 single cross combinations and two checks were planted in simple lattice design with two replications. The results of analysis of variance revealed significant differences among the genotypes for all the traits including seed length, seed width, seed thickness, seed yield and oil yield. Line x tester analysis displayed significant effects of genotypes for all the studied traits but parents, hybrids and lines had significant differences for all the traits except seed thickness. RF81-30 and AF80-427/2/1/1 with significant positive General Combining Ability (GCA) effects for seed length and seed width were considered as good combiners for improving these traits. Non of the lines and testers had significant GCA effects for seed thickness. Most of the lines and testers with significant positive GCA effects for seed yield had significant positive GCA effect of oil yield. AF-6937*RF81-30 had significant positive specific combining ability (SCA) effects for seed width, seed yield and oil yield. The crosses including AF80-460/2/1/1 × RF81-25 and AF8-6937 × RF81-30 had significant positive specific combining ability (SCA) effects for seed yield and oil yield. Estimating low narrow sense heritability for all the traits except seed thickness indicate the importance of non additive genetics effects for them; so for improving these traits, hybrid method will be more effective.

Key words: Cross combinations, general combining ability, lattice design, oil yield, sunflower.

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is a rich source of good quality edible oil with suitable fatty acid pattern. It can be successfully grown in different parts of the world due to its wide adaptability, photo-insensitive and thermoinsensitive nature. In sunflower, being the cross-pollinated crop, heterosis can be exploited for better seed yield and other yield components. Hybrids of sunflower are more stable, highly self-fertile, with high yield performance and more uniform at maturity (Kaya and Atakisi, 2004; Seetharam, 1979; Sujatha et al., 2002). Resistance to diseases and Orobanche has also in combining ability (GCA) and specific combining ability (SCA) values. General combining ability refers to the average perfor-

mance of parental lines as reflected in its hybrid combinations and specific combining ability refers to the average performance of a particular cross. Based on the combining ability analysis of different characters, higher SCA values refer to dominance gene effects and higher GCA effects indicate a greater role of additive gene effects controlling these traits in the plants. If both creased the importance of hybrid varieties. The heterotic performance of a hybrid combination depends upon the combining abilities of its parents (Kadkol et al., 1984). Kaya and Atakisi (2004) reported that superior hybrids have been obtained by crossing cytoplasmic male sterile inbred (CMS) female and restorer lines with high general

*Corresponding author. E-mail: bessedikamina@hotmail.fr. Tel: 213 (0)559907275. Fax: 213 (0)27 773260.

the GCA and SCA effects are not significant, epistatic gene effects play an important role in determining these characters (Fehr, 1993). Due to high heterosis occurring generally in hybrids between genetically unrelated inbred lines, all crop breeders that use heterosis have the challenge to find good combiners.

Breeding programs can take advantage from such information on combining ability to find best selection strategy for developing high yielding lines and hybrids (Skoric, 1992). Also, evaluating genotypes for combining ability is important in determining appropriate procedures or genotypes to utilize efficiently in breeding programs for main yield characters in sunflower (Inamullah et al., 2006). The environmental conditions influence the evaluation of combining ability of sunflower genotypes (Petakov, 1996). Regarding combining ability analysis, SCA variance higher than GCA variance means that dominant genes have higher effects than recessive ones in determining the studied characters. Conversely, higher GCA variance indicates that additive gene effects play a more important role in determining these traits. If neither variance is significant, it implies the existence of epistatic gene effects (Marinković et al., 2000; Skoric et al., 2000). Combining ability of important sunflower yield characteristics was evaluated by many researchers. The line x tester analysis is one of the efficient methods for evaluating a large number of inbreds as well as providing information on the relative importance of general and specific combining ability effects for interpreting the genetic basis of important plant traits. Line x tester analysis has also been widely used for combining ability tests, suggested by Singh and Chaudhary (2001). Mather and Jinks (1982) reported that line x tester analysis is an extension of top cross method in which several testers are used. Virupakshappa et al. (1997) affirmed that two testers were enough to efficiently test GCA of inbred lines. Estimation of combining ability of new lines for recognition of superior parents for hybridization is necessary in sunflower breeding programs.

General and specific combining abilities as well as gene action for different agronomic traits have been estimated by many researchers (Bajaj et al., 1997; El-Hity, 1992; Hladni et al., 2006; Mihaljcevic, 1988; Orthegon- Morales et al., 1992). Over dominance gene action is reported for seed length, oil content, 100 seed weight and seed and oil yield (Gangappa et al., 1997). However, additive gene action for these traits has also been reported (Singh et al., 1989). Estimates of GCA and SCA indicating additive effects were more important for oil content (Bedove, 1985). The same importance of additive and dominance effects was reported for oil content (El-Hity, 1992; Fick, 1987). Significant negative GCA and SCA effects were found for plant height and life-cycle duration (Ghaffari et al., 2011; Khan et al., 2008) and also some researcher (Khan et al., 2009; Karasu et al., 2010) reported significant positive GCA and SCA effects for oil content, seed yield and yield associated traits.

The objectives of this study were to estimate the GCA effects of parents and also SCA effects of crosses to identify superior combiners for desired traits including yield components and also to estimate heritability of the traits in sunflower.

MATERIALS AND METHODS

The genetic materials for the study contained eight cytoplasmic male sterile (CMS) of sunflower (*H. annuus* L.) as female parents including AF80-488/1/2/1, AF80-427/2/1/1, AF80-463/1/1/1, AF80-460/2/1/1, AF80-6920, AF80-438/1/2/2, AF80-6937, AF80-533/1/1/1 and 6 testers restorers (male parents) viz., RF81-25, RF81-150/1, RF81-65, RF81-053/2, RF81-131/1 and RF81-30; and also their 48 F1 crosses. The eight CMS lines were crossed with the 6 restorers/testers in a line x tester fashion during spring 2009 to obtain sufficient seed for evaluation in the following season. The 48 F1 crosses along with their 14 parents and two checks were evaluated based on lattice design with two replications at Dashtenaz Agronomy Research Station located in Sari, Iran (53°, 11' E longitude and 36° 37' N latitude, 10.5 m above sea level) during spring 2010. Each plot consisted of four rows 5.5 m long and 60 cm apart. The distance between plants on each row was 20 cm. Sowing was done by dibbling two seeds per hill to ensure uniform stand which was later thinned to one plant per hill at V2 stage as explained by Schneiter and Miller (1981). Fertilizers were applied at the rates of 100: 70: 90 kg/ha of N: P: K, respectively. Harvesting and threshing were done manually. Data were taken on 10 randomly selected plants of each entry from each replication on the following traits. The traits including length, seed width, seed thickness, seed yield and oil yield were determined with the method as explained by Schneiter and Miller (1981). Oil content was estimated with the help of nuclear magnetic resonance spectrometry (NMR) (Madson, 1976).

Data for hybrids was subjected to "line x tester" analysis (Singh and Chaudhury, 2001) to estimate general combining ability (GCA), specific combining ability (SCA) and their respective variance components. The estimates of general combining ability and specific combining effects of parents and hybrids were detected by the equations as follows:

1) Estimation of GCA effects of parents:

a) Lines: GCA = (Xi../fr) - (X…/fmr)
b) Testers: GCA = (X.j./mr) - (X…/fmr)

Where, f = number of CMS lines (female parent), t = number of testers (male parent), r = number of replications, Xi = total of the F_1 resulting from crossing ith lines with all the testers, X.j = total of all crosses of jth tester with all the lines; X... = total of all crosses.

2) Estimation of SCA effects of the crosses:

SCA = Sij - (Xij/r) - (Xi../fr) - (X.j./mr) + (X…/fmr)

Where Xij = total of F_1 resulting from crossing ith lines with jth testers.

RESULTS AND DISCUSSION

Analysis of variance

Significant mean squares of genotypes was observed for

Table 1. Mean squares from analysis of variance for agronomic traits of 8 sunflowers lines and 6 testers.

SOV	DF	MS				
		Seed length	Seed width	Seed thickness	Seed yield	Oil yield
Rep	1	1.48**	0.570[ns]	0.288[ns]	167001.58 [ns]	1052.26 [ns]
Var	63	1.31**	0.606**	0.239*	5154996.66**	1106235.80**
C vs P vs H	2	4.37**	6.604**	2.726**	76553985.63**	16005085.54**
C vs (P, H)	1	0.77[ns]	0.462[ns]	1.009*	10629017.18**	2432666.22**
P vs H	1	7.97**	12.747**	4.442**	142478954.08**	29577504.86**
Checks (C)	1	0.30[ns]	0.256[ns]	0.123[ns]	715584.74 [ns]	93207.17 [ns]
Parent (P)	13	1.38**	0.661**	0.204[ns]	4162427.35**	613187.02**
Hybrid (H)	47	1.18**	0.342*	0.146[ns]	2485737.83**	630171.19**
Line	7	3.48**	1.229**	0.166[ns]	5848254.75**	1310557.01**
Tester	5	3.28**	0.358[ns]	0.260[ns]	4957498.69**	1687992.45**
LXT	35	0.42[ns]	0.163[ns]	0.125[ns]	1460125.749**	342976.71**
Error	63	0.32	0.192	0.150	218047.940	45818.87

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

Table 2. Genetic variance components for agronomic traits in 48 sunflower F1 hybrids.

Genetic component	Seed length	Seed width	Seed thickness	Seed yield	Oil yield
Vg	0.496	0.207	0.045	2468474.36	530208.46
Vp	0.657	0.303	0.120	2577498.33	553117.91
Cov.Hs(Vgca)	0.211	0.045	0.006	281625.07	82592.71
Va	0.423	0.090	0.013	563250.14	165185.43
Vd(Vsca)	0.052	0.015	0.012	621038.91	148578.91
Hb^2	0.755	0.682	0.372	0.95	0.95
Hn^2	0.643	0.298	0.105	0.21	0.29
Vgca/Vsca	4.048	3.068	0.503	0.45	0.55
% of lines	43.710	53.455	16.992	35.04	30.97
% of testers	29.492	11.123	19.002	21.21	28.49
% of LXT	26.799	35.423	64.006	43.74	40.53

all the traits including seed length, seed width, seed thickness, seed yield and oil yield, indicating significant genetic variation for these traits (Table 1). Variances among CMS lines used as lines were greater than the restorers (testers) for the traits including seed length, seed width and seed yield implies some degrees of maternal effects on these traits. Significant mean squares of the line x tester and non significant ratio of GCA to SCA mean squares and low narrow sense heritability estimates for all the traits indicate the importance of non additive genetic effects for controlling these traits except seed length (Table 2). General and specific combining abilities as well as gene action for different agronomic traits have been estimated by many researchers (Mihaljcevic, 1988; El-Hity, 1992; Ortegon et al., 1992; Hladni et al., 2006). Over dominance gene action is reported for plant height, head diameter, oil content, 100 seed weight and seed and oil yield (Gangappa et al., 1997). However, additive gene action for these traits has

also been reported by Singh et al. (1989).

Estimates of GCA and SCA indicating additive effects were more important for oil content (Bedove, 1985). The same importance of additive and dominance effects was reported for oil content (El-Hity, 1992; Fick, 1975).

General combining ability of parents

Combining ability effects are presented in Table 3. The restorer lines including RF81-25 and RF81-30 and also the CMS line such as AF80-438/1/2/2 with significant positive GCA effects for seed length were considered as good combiners for improving this trait (Table 3). This implies that these lines possess favorable alleles with additive genetic effects for seed length. For seed width, only one restorer lines including RF81-30 and two CMS lines such as AF80-427/2/1/1 and AF80-488/1/2/1 had significant positive GCA effect, so these lines can be

Ta**ble 3.** General combining ability for agronomic traits in sunflower restorer (lines) and CMS lines (testers).

Female (testers) and male (lines) parents		Seed length	Seed width	Seed thickness	Seed yield	Oil yield
RF81-25	T1	0.368*	0.054	-0.204*	887.33**	524.04**
RF81-150/1	T2	-0.503**	-0.175	-0.054	200.76	141.26*
RF81-65	T3	-0.370*	0.013	0.046	76.13	16.77
RF81-053/2	T4	0.146	-0.090	0.122	-664.63**	-407.13**
RF81-131/1	T5	-0.277	-0.060	-0.042	-522.95**	-258.08**
RF81-30	T6	0.636**	0.258*	0.133	23.35	-16.86
AF80-488/1/2/1	L1	-0.014	0.518**	0.116	932.88**	367.09**
AF80-427/2/1/1	L2	0.446**	0.341**	0.025	592.75**	287.97**
AF80-463/1/1/1	L3	0.095	-0.443**	-0.084	50.35	46.76
AF80-460/2/1/1	L4	0.310	0.048	0.136	-1175.69**	-530.65**
AF6920	L5	-0.064	-0.136	0.000	-87.15	10.13
AF80-438/1/2/2	L6	-0.080	-0.153	-0.167	-818.41**	-405.31**
AF-6937	L7	0.513**	0.109	0.108	246.95	303.80**
AF80-533/1/1/1	L8	-1.206**	-0.284*	-0.134	258.32	-79.78
S.E (for lines)		0.142	0.110	0.097	116.74	53.51
S.E (for testers)		0.164	0.127	0.112	134.80	61.79

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

used for increasing this trait. Non of CMS and restorer lines had significant positive GCA effect for seed thickness. RF81-25, AF80-488/1/2/1 and AF80-427/2/1/1 with significant GCA effects for seed yield were considered as superior combiners for increasing seed yield. The testers including RF81-25 and RF81-150/1 and also the lines namely, AF6920 and AF6937 had a desirable and significant positive GCA effects for oil content and also all of these genotypes except AF6920 had significant positive GCA effects for oil yield.

Significant GCA effect of 1000 seed weight was exhibited by RF81-30 and AF80-460/2/1/1, therefore, they can be recommended as valuable R-line and A-line in hybrid development programs, respectively. Significant negative GCA effects were detected for plant height and life-cycle duration (Ghaffari et al., 2011; Khan et al., 2008).

Specific combining ability of the crosses

The results of SCA effects of cross combinations are presented in Table 4. Among the crosses, AF80-427/2/1/1*RF81-65 with significant positive SCA effects for seed length was detected as superior combination for improving this trait. Although, GCA and SCA mean squares were significant for seed length but most of the crosses had non significant SCA effect for this trait, therefore, epistasis genetic effects had more important role for controlling this trait. For seed width, only AF6937*RF81-30 had significant positive SCA effect and therefore it was considered as a suitable cross for

improving this trait. Non of the crosses had significant SCA effects for seed thickness. The cross combinations including AF80-460/2/1/1*RF81-25, AF80-463/1/1/1*RF81-150/1, AF80-427/2/1/1*RF81-053/2, AF80-6920*RF81-131/1 and AF-6937*RF81-30 with significant positive SCA effects for seed yield were suitable combinations for this trait and some of these crosses had also significant positive SCA effects for 1000 seed weight. The crosses including AF80-460/2/1/1*RF81-25, AF80-460/2/1/1*RF81-150/1, AF80-427/2/1/1*RF81-053/2, AF80-438/1/2/2*RF81-30 and AF-6937*RF81-30 had significant positive SCA effects for oil content and oil yield and also these combinations can be a superior candidate for improving high oil content genotypes.

Earlier studies (Khan et al., 2009; Karasu et al., 2010) reported significant positive SCA effects for oil content, seed yield and yield associated traits.

Conclusion

Among the traits, seed length had high narrow-sense heritability and therefore this trait can be improved by selection breeding method. Variances among CMS lines used as lines were greater than restorers (testers) for the traits including seed length, seed width and seed yield, indicating some degrees of maternal effects on these traits. Non significant ratio of GCA to SCA mean squares and low narrow sense heritability estimates for all the traits except seed length indicate the importance of non additive genetic effects for controlling these traits. Among

Table 4. The crosses with superior specific combining ability effects for agronomic traits in 48 sunflower F1 hybrids.

Cross			Seed length	Seed width	Seed thickness	Seed yield	Oil yield
AF80-488/1/2/1*RF81-25	T1	L1		0.277			
AF80-427/2/1/1*RF81-25	T1	L2					
AF80-463/1/1/1*RF81-25	T1	L3					
AF80-460/2/1/1*RF81-25	T1	L4		0.327	0.152	1557.93**	861.78**
AF6920*RF81-25	T1	L5					
AF80-438/1/2/2*RF81-25	T1	L6			0.254		
AF-6937*RF81-25	T1	L7	0.267			353.74	262.29
AF80-533/1/1/1*RF81-25	T1	L8	0.187				
AF80-488/1/2/1*RF81-150/1	T2	L1				305.39	239.94
AF80-427/2/1/1*RF81-150/1	T2	L2		0.174	0.163		
AF80-463/1/1/1*RF81-150/1	T2	L3	0.265	0.383	0.221	1210.12**	490.78**
AF80-460/2/1/1*RF81-150/1	T2	L4	0.248			744.19*	393.33*
AF6920*RF81-150/1	T2	L5					
AF80-438/1/2/2*RF81-150/1	T2	L6					
AF-6937*RF81-150/1	T2	L7					
AF80-533/1/1/1*RF81-150/1	T2	L8	0.471	0.239		721.21*	290.34
AF80-488/1/2/1*RF81-65	T3	L1	0.627	0.085	0.371	567.17	281.61
AF80-427/2/1/1*RF81-65	T3	L2	0.911*		0.163	536.14	
AF80-463/1/1/1*RF81-65	T3	L3		0.180			188.15
AF80-460/2/1/1*RF81-65	T3	L4				385.22	140.33
AF6920*RF81-65	T3	L5					
AF80-438/1/2/2*RF81-65	T3	L6	0.250	0.205			
AF-6937*RF81-65	T3	L7					
AF80-533/1/1/1*RF81-65	T3	L8			0.371		
AF80-488/1/2/1*RF81-053/2	T4	L1					
AF80-427/2/1/1*RF81-053/2	T4	L2				1315.84**	747.66**
AF80-463/1/1/1*RF81-053/2	T4	L3					85.01
AF80-460/2/1/1*RF81-053/2	T4	L4	0.106	0.210			
AF6920*RF81-053/2	T4	L5			0.311		
AF80-438/1/2/2*RF81-053/2	T4	L6	0.536			438.87	
AF-6937*RF81-053/2	T4	L7					
AF80-533/1/1/1*RF81-053/2	T4	L8	0.310				
AF80-488/1/2/1*RF81-131/1	T5	L1					
AF80-427/2/1/1*RF81-131/1	T5	L2					
AF80-463/1/1/1*RF81-131/1	T5	L3					
AF80-460/2/1/1*RF81-131/1	T5	L4	0.518	0.442	0.489		
AF80-6920*RF81-131/1	T5	L5				1265.44**	516.08**
AF80-438/1/2/2*RF81-131/1	T5	L6				632.33	
AF-6937*RF81-131/1	T5	L7					
AF80-533/1/1/1*RF81-131/1	T5	L8					
AF80-488/1/2/1*RF81-30	T6	L1					
AF80-427/2/1/1*RF81-30	T6	L2					173.24
AF80-463/1/1/1*RF81-30	T6	L3			0.434		
AF80-460/2/1/1*RF81-30	T6	L4					
AF6920*RF81-30	T6	L5				710.72*	292.31
AF80-438/1/2/2*RF81-30	T6	L6				540.34	322.88*
AF-6937*RF81-30	T6	L7	0.802	0.905**	0.492	1296.97**	756.04**
AF80-533/1/1/1*RF81-30	T6	L8	0.401			460.30	
S.E			0.402	0.310	0.274	330.19	151.36

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

the combinations with significant positive SCA effects for yield and yield associated traits, at least one parent had significant positive GCA effect for these traits, therefore, for improving these traits, GCA effects of parents can be

considered as suitable criteria for SCA prediction of the crosses.

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