Gene effects and combining abilities of sunflower morphophysiological traits

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ABSTRACT

The development of sunflower hybrids with high genetic potentials for seed and oil yields requires information on the GCA and SCA for agronomically important traits in the F_1 generation. In this study were used seven new divergent cms inbred lines (A) lines, three Rf restorers utilized as testers, and 21 F_1 hybrids developed at the Institute of Field and Vegetable Crops in Novi Sad. Significant differences were found between the A lines, Rf testers and their F_1 hybrids for petiole length (PL), total leaf number per plant (TLN), total leaf area per plant (TLA), seed yield per plant (SY), seed oil content (OC), and oil yield per plant (OY). Analysis of variance of the combining abilities revealed highly significant differences for GCA and SCA. The nonadditive component of genetic variance (dominance and epistasis) contributed more to total genetic variance, as evidenced by the GCA/SCA ratio in the F_1 generation being below the value of one for all the traits studied. The greatest average contribution to the expression of all of the traits was found in the female A lines, while the contributions of the Rf testers and line x tester interaction were less significant. Evaluation of the combining abilities of the line NS-GS-5 suggests that this line could justifiably be used as a parent in breeding programs for increasing sunflower seed and oil yields. Analysis of SCA for OY per plant identified the following hybrids as promising: NS-GS-5xRHA-R-PL-2/1, NS-GS-6xRHA-N-49, NS-GS-2xRHA-N-49, NS-GS-1xRUS-RF-OL-168.

Key words: GCA – *H. annuus* – interspecific hybridization – SCA.

INTRODUCTION

Sunflower is the main crop for producing vegetable oil in Serbia. NS sunflower hybrids are developed primarily for Serbian growing conditions while taking into account the limiting factors present in the domestic sunflower production. They are the dominant brand on the Serbian sunflower market and are also grown on over two million hectares in various markets abroad (Miklič et al., 2007).

Plant height, head size, form, and position on the stem, and leaf number, size, duration, and distribution on the plant all play important roles in defining optimum plant architecture for a sunflower hybrid (Škorić et al., 1989; 2002). Breeding for morphophysiological yield components and the creation of a new sunflower ideotype require an increased use of wild *Helianthus* species in breeding programs. One of the surest ways to increase the genetic variability of sunflower is by the use of interspecific hybridization (Škorić et al., 2007). The main precondition for designing the model of a hybrid is to obtain parental lines possessing desirable genes so as to be able to pair up parent lines that produce superior F_1 progeny over the existing hybrids for the largest number of agronomic traits.

Petiole length (PL) has caught the attention of breeders because of the possibility of changing existing sunflower plant architecture. The shortening of the sunflower petiole so that it is closer to the stem results in the faster conveyance of photoassimilates from the leaf blade to the sinks as well as in an increased plant number per unit area (Marinković et al., 2003).

Along with leaf size, total leaf number per plant (TLN) determines the total leaf area for accumulation, which makes it necessary to know the genetics of this trait (Marinković et al., 2003). Total leaf area (TLA) depends on the position of the leaf, leaf area profile, plant development, and genotype (Panković et al., 1991).

One of the main directions of sunflower breeding both in Serbia and elsewhere is the development of hybrids with high genetic potential for seed yield and altered plant architecture capable of adapting to the conditions of the specific area in which they are being grown. Seed oil content (OC) depends on the genotype, soil and climate conditions, and the level of cultural practice used. OC is greatly influenced by the origin of the material and the year of study (Hladni et al., 2006). It ranges from 38.1 to 49.2% depending on the location (Škorić et al., 1996) and from 36.0 to 54.4% according to year (Škorić and Marinković, 1990).

Oil yield (OY) is the main indicator of any sunflower hybrid's productivity (Škorić et al., 2005) and is dependent on SY and OC. Nonadditive gene action in OY inheritance has been reported by Škorić et al. (2000), Laureti and Del Gatto (2001), Ortis (2005) and Gvozdenović (2006).

The objective of this study was to investigate GCA effects in new divergent inbred lines obtained by interspecific hybridization, SCA effects of the F_1 hybrids, gene effects, components of genetic variance, average percentage contributions of the lines, testers and their interactions to the expression of the six morphophysiological traits studied (PL, TLN, TLA, SY, OC, OY).

MATERIALS AND METHODS

Seven new divergent cms inbred lines (A) lines, three Rf restorers utilized as testers, and 21 F_1 hybrids developed at the Institute of Field and Vegetable Crops in Novi Sad were used in this study. The female inbreds (NS-GS-1, NS-GS-2, NS-GS-3, NS-GS-4, NS-GS-5, NS-GS-6, NS-GS-7) had been developed by interspecific hybridization. The male restorer lines (RHA-R-PL-2/1, RHA-N-49, RUS-RF-OL-168) with good combining abilities were used as testers in the form of fertility restorers. The F_1 hybrids had been developed by crossing each tester with each female inbred line. The trial was carried out at the Institute's Experiment Field at Rimski Šančevi.,There were three replications, and the experiment was designed according to the line x tester method. The lines and hybrids were planted manually at an optimum time on a well-prepared soil. The plots consisted of four rows with 12 plants in each. The row-to-row spacing was 70 cm and the plants were spaced at 30 cm intervals within the rows. Each trait was analyzed on a sample consisting of 30 plants (10 per replicate) taken from the middle rows in each block. PL (cm) was determined in the field at budding by measuring the 12th leaf. TLN and TLA (expressed as cm^2) were determined in the laboratory at flowering by counting the total number of leaves (dry and green) and using a device for measuring leaf area LI-300- Licor, respectively. SY was determined by measuring total seed quantity in each individual open pollinated plant using a scale with an accuracy of 0.01 g. OC was determined on an NMR at the chemical laboratory of the Institute's Oil Crops Department.

Mean values were calculated according to Hadživuković (1991). The mean values of the inbred lines and F_1 hybrids were used to calculate the values of the combining abilities and assess the gene effects for morphophysiological traits using the line x tester method (Singh and Choudhary, 1976).

RESULTS AND DISCUSSION

Significant differences were observed among the A lines, Rf testers and their F_1 hybrids for all the traits studied, indicating the presence of genetic differences among the genotypes concerned .

The mean values of the inbred lines and F_1 hybrids were used to calculate the combining abilities in order to estimate gene effects for all the morphophysiological traits under study. Analysis of the combining abilities showed that the A lines and Rf testers differed in their GCA.

Highly significant positive GCA values for PL were found in the female inbreds NS-GS-3, NS-GS-4, and NS-GS-5 and the male inbred RHA-N-49, so these lines can be regarded as good general combiners for this trait. Highly significant negative GCA effects and the lowest PL means were recorded in the female inbred lines NS-GS-6 and NS-GS-7. These lines, along with the male inbred RHA-R-PL-2/1, can be considered poor general combiners for PL. In the case of SCA, the hybrid combinations NS-GS-4xRHA-R-PL-2/1(4x8), NS-GS-7xRHA-R-PL-2/1(7x8), NS-GS-5xRHA-N-49(5x9), and NS-GS-4xRUS-RF-OL-168(4x10) had highly significant positive PL values in the F_1 generation, while NS-GS-2xRHA-R-PL-2/1(2x8), NS-GS-3xRHA-N-49(3x9) and NS-GS-6xRHA-N-49(6x9) had highly significant negative ones. The nonadditive component of genetic variance played the main role in the imheritance of PL, as shown by analysis of combining abilities and analysis of genetic variance components. This was further confirmed by the GCA/SCA ratio for PL in the F_1 generation, which was below the value of one (0.43) (Table 1). These findings are not in agreement with those of Marinković (1993) and Hladni et al. (2002), who reported a greater contribution of additive genes to the expression of PL.

The female inbreds NS-GS-1 and NS-GS-3 and the male tester RUS-RF-OL-168 had highly significant positive GCA values for TLN and can hence be considered good general combiners for this trait. The female inbreds NS-GS-6 and NS-GS-7 and the male inbred RHA-R-PL-2/1 had highly significant negative GCA effects and are therefore poor general combiners for TLN. The hybrids NS-GS-6xRHA-R-PL-2/1(6x8), NS-GS-1xRHA-N-49(1x9), and NS-GS-4xRUS-RF-OL-168(4x10) had highly significant SCA values for TLN. The main role in the inheritance of TLN was that of the nonadditive component of genetic variance, as confirmed by the GCA/SCA ratio being below one (0.40) in the F_1

generation (Table 1). Additive gene action in the inheritance of TLN has been reported by Hladni et al. (2000), whereas Nedeljković et al. (1992), Kumar et al. (1998), and Naik et al. (1999) found nonadditive gene action in the inheritance of this trait.

The most highly significant positive GCA effects for TLA were found in the female inbreds NS-GS-4, NS-GS-5 and NS-GS-7, while the lowest negative ones were recorded in NS-GS-1 and NS-GS-2. Among the Rf testers, RHA-R-PL-2/1 had the most pronounced positive GCA effect for TLA, while RUS-RF-OL-168 had the most pronounced negative one. The hybrids NS-GS-1xRHA-R-PL-2/1(1x8), NS-GS-5xRHA-R-PL-2/1(5x8), NS-GS-3xRHA-N-49(3x9), NS-GS-7xRHA-N-49(7x9), NS-GS-6xRUS-RF-OL-168(6x10), and NS-GS-7xRUS-RF-OL-168(7x10) had highly significant positive values of SCA for TLA, whereas NS-GS-7xRHA-R-PL-2/1(7x8), NS-GS-5xRHA-N-49(5x9) and NS-GS-5xRUS-RF-OL-168(5x10) had highly significant negative ones. In the inheritance of TLA, the dominant component of genetic variance predominated, as confirmed by a GCA/SCA ratio of less than one (0.07) (Table 1). These findings are in agreement with those of Kovačik and Škaloud (1990), Joksimović et al. (1997), Bath et al. (2000) and Hladni et al. (2003).

Highly significant positive GCA values for SY were found in the female inbreds NS-GS-4 and NS-GS-5, while the lines NS-GS-1 and NS-GS-2 had highly significant negative ones. The largest highly significant positive value of SCA for SY was found in the hybrid NS-GS-5xRHA-R-PL-2/1(5x8). The nonadditive component of genetic variance was more influential in the inheritance of SY, as confirmed by the GCA/SCA ratio being below one in the F_1 generation (0.08) (Table 1). Studies of the mode of inheritance of SY in sunflower have produced varying results. In agreement with the present findings, greater contribution of nonadditive genetic variance in the inheritance of this trait has been reported by Škorić et al. (2000), Hladni et al. (2002), and Gvozdenović (2006). Marinković et al. (2000) and Shekar et al. (2000), on the other hand, have reported greater contribution of additive genetic variance. Qingyu et al. (2002) has found equal contributions of the additive and nonadditive components of genetic variance in SY inheritance.

Highly significant positive values of GCA for OC were found in NS-GS-1 and NS-GS-2, while NS-GS-4 and NS-GS-5 had highly significant negative ones. The largest highly significant positive SCA value for OC was recorded in the hybrid NS-GS-6xRHA-R-PL-2/1(6x8), while the highest negative one was observed in NS-GS-5xRHA-R-PL-2/1(5x8). As evidenced by the GCA/SCA ratio being smaller than one (0.33), tab. 1, genes with nonadditive effects had more influence in the inheritance of OC, which is in agreement with the results of Marinković (1993) and Škorić et al. (2000).

The female inbred NS-GS-5 had the largest highly significant positive effect for OY and was deemed the best general combiner for the trait. Highly significant negative OY values were found in NS-GS-1, NS-GS-2, NS-GS-6, and NS-GS-7. The male inbred RHA-N-49 was the best general combiner for OY, as it had the largest positive GCA effect for this trait. The hybrid NS-GS-5xRHA-R-PL-2/1(5x8), which had the best SCA for OY, had been developed by crossing one parent with good GCA with one with poor GCA for the trait. Highly significant average values of SCA for OY were recorded in the hybrids NS-GS-1xRUS-RF-OL-168(1x10), NS-GS-6xRHA-N-49(6x9), and NS-GS-2xRHA-N-49(2x9). The nonadditive component of genetic variance was more significant in the inheritance OY, since the GCA/SCA ratio was below the value of one (0.07) (Table 1). These results are in agreement with Škorić et al. (2000) and Gvozdenović (2006).

The greatest average contribution to the expression of PL (49.9%), TLN (75.6%), TLA (57.1%), SY (61.5%), OC (77.3%), and OY (56.3%) was found in the female A lines. The contributions of the Rf testers and line x tester interaction were less significant (Table 2).

The differences in the findings of different authors referenced in the present paper can be attributed to the divergence of the material used in their studies. Identification of inbred lines with high positive GCA values is of great importance for the development of new productive sunflower hybrids. None of the inbred lines from the present study (either male or female) had a highly significant positive or negative effect for all six traits studied.

One of the goals of sunflower breeding is to decrease PL, so any line with a negative GCA value for this trait is considered desirable in a breeding program. In the present study, the lines NS-GS-6 and NS-GS-7 had the lowest highly significant negative values of PL and were rated the best general combiners for this trait. These findings are in agreement with those of Marinković (1982), who argues that in studying a particular trait advantage should be given to the line that is the best combiner for that particular trait regardless of whether the value is positive or negative, which depends on the direction in which selection for that trait goes.

Table 1. Values of GCA inbred lines and SCA hybrids for sunflower morphophysiological traits

No.	Parents and hybrids	PL	TLN	TLA	SY	OC	OY
	GCA values						
1	NS-GS-1	-0.921	0.659	-0.062	-10.053	3.56**	-1.221
2	NS-GS-2	-1.076	-0.486	-0.052	-12.439	2.38**	-3.468
3	NS-GS-3	2.096**	2.881**	-0.024	-0.072	0.15	0.466
4	NS-GS-4	1.435**	0.170	0.700**	3.521**	-2.067	-0.272
5	NS-GS-5	1.302**	0.014	0.157**	31.356**	-3.10	10.769**
6	NS-GS-6	-1.493	-2.297	-0.035	-9.021	-0.64	-4.700
7	NS-GS-7	-1.343	-0.941	0.113**	-3.292	-0.30	-1.574
8	RHA-R-PL-2/1	-1.589	-0.573	0.022**	0.273	-0.82	-1.070
9	RHA-N-49	1.511**	-0.259	-0.007	2.219**	0.49	1.758
10	RUS-RF-OL-168	0.078	0.832	-0.015	-2.492	0.33	-0.688
LSD (1-7) 5%		0.31	0.29	0.016	1.826	0.86	1.232
1%		0.46	0.43	0.024	2.739	1.29	1.848
LSD (8-10) 5%		0.20	0.19	0.010	1.196	0.56	0.806
1%		0.30	0.75	0.015	1.794	0.85	1.209
SCA values							
1	1x8	-0.506	-0.949	0.080**	-10.01	-0.60	-4.891
2	2x8	-1.300	-0.138	0.004	-5.01	0.31	-1.661
3	3x8	0.094	0.329	-0.039	-9.75	1.10**	-3.317
4	4x8	1.506**	-0.794	0.023	7.94**	-1.07	2.800*
5	5x8	-0.378	0.295	0.181**	31.88**	-1.95	11.188**
6	6x8	0.467*	1.173**	-0.095	-11.64	1.73**	-3.433
7	7x8	0.117**	0.084	-0.154	-3.41	0.52	-0.686
8	1x9	0.278	1.037**	-0.029	0.22	0.84	0.482
9	2x9	0.667*	0.548*	-0.036	7.75**	-0.02	3.592**
10	3x9	-0.706	-0.552	0.061**	4.60*	0.26	2.384*
11	4x9	-0.511	-0.175	-0.002	-10.80	0.91	-4.222
12	5x9	0.856**	-0.252	-0.120	-15.98	1.16**	-5.276
13	6x9	-0.600	-0.308	0.034*	12.10**	-1.53	3.816**
14	7x9	0.017	-0.297	0.092**	2.10	-1.63	-0.777
15	1x10	0.228	-0.087	-0.051	9.78**	-0.24	4.410**
16	2x10	0.633*	-0.410	0.031*	-2.74	-0.29	-1.932
17	3x10	0.611*	0.224	-0.022	5.15**	-1.32	0.933
18	4x10	0.994**	0.968**	-0.021	2.86	0.16	1.422
19	5x10	-0.478	-0.043	-0.061	-15.90	0.79*	-5.912
20	6x10	0.133	-0.865	0.061**	-0.46	-0.20	-0.384
21	7x10	-0.133	0.213	0.062**	1.31	1.12	1.463
LSD 5%		0.52	0.50	0.028	3.16	0.564	2,134
1%		0.78	0.75	0.042	4.74	0.846	3.201
	GCA	0,30	0.21	66739.94	16.03	0.41	1,93
	SCA	0,68	0,52	977433.14	201.15	1.23	26,02
	GCA/SCA	**0.43**	**0.40**	**0.07**	**0.08**	**0.33**	**0.07**

PL – petiole length
TLN – total leaf number per plant
TLA – total leaf area per plant
SY – seed yield per plant
OC – seed oil content
OY – oil yield per plant

Table 2. Average percentage contributions of the female lines, testers and their interactions to the expression of sunflower morphophysiological traits.

Average contribution	PL	TLN	TLA	SY	OC	OY
	%	%	%	%	%	%
Female line	**49.89**	**75.63**	**57.06**	**61.51**	**77.29**	**56.33**
Tester line	39.51	12.65	1.83	1.20	5.65	4.01
Line x tester	10.61	11.71	41.12	37.29	17.06	39.66

If the goal is to change sunflower plant architecture, then the NS-GS-7 genotype with its highly significant negative GCA value for PL and highly significant positive GCA value for TLA is desirable in breeding programs. The line NS-GS-5 had highly significant positive effects for four traits (PL, TLA, SY, OY), while the line NS-GS-4 had these effects for three of the characters (PL, TLA, SY).

Based on the GCA values, selection was made of the lines with the best GCA for PL and TLN (NS-GS-3), TLA (NS-GS-4), SY and OY (NS-GS-5), and OC (NS-GS-1). Combining all the positive traits in a single hybrid combination is very difficult. The hybrid NS-GS-5xRHA-R-PL-2/1(5x8) had the best SCA for SY and OY and highest average values of those traits. Highly significant positive values of SY and OY were found in the hybrids NS-GS-6xRHA-N-49(6x9), NS-GS-2xRHA-N-49(2x9), and NS-GS-1xRUS-RF-OL-168(1x10).

The assessment of the combining abilities of the female line NS-GS-5 indicates that this line could justifiably be used as a parent in breeding for increased oil yield in sunflower. The hybrids NS-GS-5xRHA-R-PL-2/1(5x8), NS-GS-1xRUS-RF-OL-168(1x10), NS-GS-6xRHA-N-49(6x9), and NS-GS-2xRHA-N-49(2x9), obtained by interspecific hybridization, have been identified in the present study as promising because of their high SCA for OY, and, as such, should be subjected to further testing. The findings of this study can be used in the development of new sunflower hybrids with high oil yields based on interspecific hybridization.

CONCLUSIONS

Significant differences in the mean values of all the traits studied were observed among the inbred lines (females and testers) and the F_1 hybrids.

Analysis of the combining abilities showed that the A lines and Rf testers differed in their GCA and SCA for all the traits studied. The nonadditive component of genetic variance played the main role in the inheritance of all the traits, as evidenced by the GCA/SCA ratio being below the value of one. The greatest average contribution to the expression of all the traits was found in the female A lines, while the contributions of the Rf testers and line x tester interaction were less significant.

Evaluation of the combining abilities of the line NS-GS-5 suggests that this line could justifiably be used as a parent in breeding programs for increasing sunflower oil yields. The hybrids NS-GS-5xRHA-R-PL-2/1(5x8), NS-GS-1xRUS-RF-OL-168(1x10), NS-GS-6xRHA-N-49(6x9), and NS-GS-2xRHA-N-49(2x9), obtained by interspecific hybridization, have been identified as promising due to their high SCA for OY, and, as such, should be subjected to further tests in the future.

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