

**LINE X TESTER ANALYSIS OF MORPHOPHYSIOLOGICAL TRAITS  
AND THEIR CORRELATIONS WITH SEED YIELD AND OIL CONTENT  
IN SUNFLOWER (*Helianthus annuus* L.)**

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Hladni N., D. Škorić and M. Kraljević- Balalić (2008): *Line x tester analysis of morphophysiological traits and their correlations with seed yield and oil content in sunflower (Helianthus annuus L.)*.– Genetika, Vol. 40, No. 2, 135 - 144.

One of the primary tasks of sunflower breeding is the development of inbred lines by *interspecific* hybridization for the purpose of obtaining high-yielding, stable hybrids that are characterized by altered plant appearance and the ability to produce a higher number of plants per unit area under intensive agriculture conditions. Studied in this paper by the line x tester method were seven new divergent cms inbred lines (A) lines, three Rf restorers utilized as testers, and 21 F<sub>1</sub> hybrids developed.

Significant differences in the mean values of all the traits studied were observed. Highly significant GCA and SCA values were obtained for petiole length (PL) and total leaf area per plant (TLA). The nonadditive component of genetic variance played the main role in the inheritance of

both these traits. This was confirmed by the GCA/SCA ratios for PL and LA in the F<sub>1</sub> generation, which were below the value of one (0.43 and 0.07, respectively). The greatest average contribution to the expression of PL (49.9%) and TLA (57.1%) was found in the female A lines.

A positive correlation was found between seed yield (SY) and PL (0.374\*) and TLA (0.630\*\*), while seed oil content (SOC) and TLA were found to be negatively correlated (-0.520\*\*). The findings of this study can be used in the development of new high-yielding sunflower hybrids with high yields based on interspecific hybridization.

*Key words:* combining abilities, correlations, sunflower, interspecific hybridization, gene effects

## INTRODUCTION

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 as parents lines that produce superior F<sub>1</sub> progeny over the existing hybrids for the largest number of agronomic traits.

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 yield components and the creation of a new sunflower ideotype require an increased use of wild *Helianthus* species in breeding programs.

Petiole length has caught the attention of breeders because of the possibility to change the existing sunflower plant architecture. Total leaf area depends on the position of the leaf, leaf area profile, plant development, and genotype (PANKOVIĆ *et al.*, 1991).

The objective of this study was to investigate GCA effects in new divergent inbred lines obtained by interspecific hybridization. Also studied were the SCA effects of the F<sub>1</sub> hybrids, gene effects, components of genetic variance, and average percentage contributions of the lines, testers and their interactions to the expression of PL and TLA per plant.

## MATERIALS AND METHODS

Used in this study were seven new divergent cms inbred lines (A) lines, three Rf restorers utilized as testers, and 21 F<sub>1</sub> hybrids developed at the Institute of Field and Vegetable Crops in Novi Sad. The female inbreds (Tab.1) had been developed by interspecific hybridization. The male restorer lines with good combining abilities were used as testers in the form of fertility restorers (Tab.1). The two-year trial was carried out at the 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 25 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. TLA per plant (cm<sup>2</sup>) was measured in the laboratory at flowering using the leaf area measuring device LI-300-Licor.

SY was determined by measuring total seed quantity in each individual open pollinated plant using a scale with an accuracy of 0.01 g. SOC was determined on an NMR at the chemical laboratory of the Institute's Oil Crops Department.

The calculation of mean values and correlation coefficients (*r*) as indicators of interdependence between two variables was done according to HADŽIVUKOVIĆ (1991). The mean values of the inbred lines and F<sub>1</sub> hybrids were used to calculate the values of the combining abilities and assess the gene effects for PI and LA 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<sub>1</sub> hybrids for all the traits studied, indicating the presence of genetic differences among the genotypes concerned (Tab.1).

Analysis of the combining abilities showed that the A lines and Rf testers differed significantly 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 (Tab.2).

The most pronounced highly significant positive GCA effects for TLA were observed in the female lines NS-GS-4, NS-GS-5, NS-GS-7, while NS-GS-1 and NS-GS-2 had the lowest negative GCA effect for this trait. With the Rf testers, the most pronounced positive effect was found in RHA-R-PL-2/1, while the most pronounced negative one was observed in RUS-RF-OL-168 (Tab.2).

In the case of SCA, the hybrid combinations NS-GS-4xRHA-R-PL-2/1, NS-GS-7xRHA-R-PL-2/1, NS-GS-5xRHA-N-49, and NS-GS-4xRUS-RF-OL-168 had highly significant positive PL values in the F<sub>1</sub> generation, while NS-GS-2xRHA-R-PL-2/1, NS-GS-3xRHA-N-49 and NS-GS-6xRHA-N-49 had highly significant negative ones (Tab.3).

Table. 1. Mean values of sunflower traits studied

No	Parents and hybrids	PL cm ±s	TLA m <sup>2</sup> /per plant	SY g	SOC %
1	NS-GS-1	15.8±0.41	0.464±0.012	35.6±1.46	46.3±0.49
2	NS-GS-2	17.9±0.33	0.623±0.022	52.8±1.79	49.9±0.49
3	NS-GS-3	16.8±0.35	0.606±0.016	50.5±1.25	43.1±0.33
4	NS-GS-4	20.1±0.16	0.507±0.030	55.4±2.31	29.5±0.48
5	NS-GS-5	19.9±0.29	0.394±0.012	57.0±1.50	38.1±0.47
6	NS-GS-6	12.1±0.22	0.406±0.013	32.4±1.65	37.0±0.37
7	NS-GS-7	13.8±0.22	0.531±0.021	43.8±1.75	43.1±0.55
8	RHA-R-PL-2/1	11.7±0.26	0.607±0.018	30.1±1.19	49.5±0.33
9	RHA-N-49	14.0±0.21	0.605±0.023	23.7±1.08	51.3±0.27
10	RUS-RF-OL-168	12.9±0.28	0.747±0.022	25.5±0.86	49.3±0.29
11	1x8	12.8±0.40	0.837±0.028	79.6±2.42	49.5±0.47
12	1x9	16.7±0.46	0.700±0.026	91.8±3.48	52.2±0.45
13	1x10	15.2±0.43	0.669±0.015	96.6±2.71	51.0±0.39
14	2x8	11.9±0.38	0.772±0.023	82.2±2.65	49.2±0.49
15	2x9	16.9±0.39	0.702±0.023	96.9±2.54	50.2±0.37
16	2x10	15.5±0.39	0.762±0.021	81.7±2.49	49.8±0.54
17	3x8	16.4±0.27	0.757±0.013	89.9±1.39	47.7±0.41
18	3x9	18.7±0.36	0.827±0.027	106.2±2.65	48.3±0.33
19	3x10	18.6±0.31	0.737±0.021	102.0±2.74	46.5±0.49
20	4x8	17.2±0.24	0.746±0.031	111.1±2.67	43.4±0.47
21	4x9	18.3±0.24	0.691±0.021	94.4±2.68	46.7±0.24
22	4x10	16.4±0.30	0.665±0.024	103.3±1.81	45.8±0.36
23	5x8	15.2±0.31	1.158±0.022	162.9±3.28	41.5±0.65
24	5x9	19.5±0.31	0.828±0.028	117.0±3.71	45.9±0.59
25	5x10	16.7±0.26	0.879±0.025	112.4±2.40	45.4±0.32
26	6x8	13.2±0.31	0.690±0.022	79.0±3.18	47.6±0.61
27	6x9	15.3±0.34	0.790±0.023	104.7±2.49	45.7±0.71
28	6x10	14.6±0.28	0.809±0.034	87.4±2.45	46.8±0.69
29	7x8	13.0±0.39	0.778±0.024	93.0±2.09	46.7±0.46
30	7x9	16.0±0.36	0.994±0.027	100.4±2.23	45.9±0.68
31	7x10	14.4±0.32	0.958±0.034	94.9±1.65	48.5±0.34
	LSD 5%	0.52	0.028	3.16	1.49
	LSD 1%	0.78	0.042	4.74	2.24

PL – petiole length

LA – total leaf area per plant

SY – seed yield per plant

SOC –seed oil content

Table. 2. GCA values for PL and TLA in sunflower inbreds

No.	Parents	PL	TLA
1	NS-GS-1	-0.921	-0.062
2	NS-GS-2	-1.076	-0.052
3	NS-GS-3	2.096**	-0.024
4	NS-GS-4	1.435**	0.700**
5	NS-GS-5	1.302**	0.157**
6	NS-GS-6	-1.493	-0.035
7	NS-GS-7	-1.343	0.113**
8	RHA-R-PL-2/1	-1.589	0.022**
9	RHA-N-49	1.511**	-0.007
10	RUS-RF-OL-168	0.078	-0.015
SE GCA/line		0.153	0.008
SE (GCA <sub>i</sub> - GCA <sub>j</sub> )/line		0.216	0.011
SE GCA/tester		0.100	0.005
SE (GCA <sub>i</sub> - GCA <sub>j</sub> )/tester		0.141	0.007
LSD (1-7)			
	5%	0.31	0.016
	1%	0.46	0.024
LSD (8-10)			
	5%	0.20	0.010
	1%	0.30	0.015

The hybrids NS-GS-1xRHA-R-PL-2/1, NS-GS-5xRHA-R-PL-2/1, NS-GS-3xRHA-N-49, NS-GS-7xRHA-N-49, NS-GS-6xRUS-RF-OL-168, and NS-GS-7xRUS-RF-OL-168 had highly significant positive values of SCA for TLA, whereas NS-GS-7xRHA-R-PL-2/1, NS-GS-5xRHA-N-49 and NS-GS-5xRUS-RF-OL-168 had highly significant negative ones (Tab.3).

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 selection for that trait is going in.

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 nonadditive component of genetic variance played the main role in the inheritance of PL and TLA, as shown by analysis of combining abilities and analysis of genetic variance components. This was further confirmed by the GCA/SCA ratios for PL and TLA in the F<sub>1</sub> generation, which were below the value of one (0.43 and 0.07, respectively), tab.4.

Table.3. SCA values for PL and LA in sunflower hybrids

No.	F <sub>1</sub> hybrids	PL	TLA
1	1x8	-0.506	0,080**
2	2x8	-1.300	0,004
3	3x8	0.094	-0,039
4	4x8	1.506**	0,023
5	5x8	-0.378	0,181**
6	6x8	0.467*	-0,095
7	7x8	0.117**	-0,154
8	1x9	0.278	-0,029
9	2 x9	0.667*	-0,036
10	3 x9	-0.706	0,061**
11	4 x9	-0.511	-0,002
12	5 x9	0.856**	-0,120
13	6 x9	-0.600	0,034*
14	7 x9	0.017	0,092**
15	1x10	0.228	-0,051
16	2 x10	0.633*	0,031*
17	3 x10	0.611*	-0,022
18	4 x10	0.994**	-0,021
19	5 x10	-0.478	-0,061
20	6 x10	0.133	0,061**
21	7 x10	-0.133	0,062**
SE SCA		0,264	0.014
SE(S <sub>ij</sub> - S <sub>ki</sub> )		0,374	0.019
LSD	5%	0.52	0.028
	1%	0.78	0.042

Table.4. Components of genetic variance for PL and LA

Component	PL	TLA
GCA	0.297	66739.94
F=0 V <sub>A</sub>	1.190	266959.76
F=1 V <sub>A</sub>	0.595	133479.88
F=0 V <sub>D</sub> /V <sub>A</sub>	2.299	14.65
F=1 V <sub>D</sub> /V <sub>A</sub>	1.149	7.32
SCA	0.684	977433.14
F=0 V <sub>D</sub>	2.736	3909732.54
F=1 V <sub>D</sub>	0.684	977433.14
<b>GCA/SCA</b>	<b>0.434</b>	<b>0.07</b>

These findings are not in agreement with those of MARINKOVIĆ (1993) and HLADNI *et al.* (2002), who reported greater contribution of additive genes to the expression of PL.

Additive gene action in PL inheritance was reported by NAIK *et al.* (1999), while KOVAČIK and ŠKALOUK (1990), JOKSIMOVIĆ *et al.* (1997), BATH *et al.* (2000) and HLADNI *et al.* (2003) found greater importance of the nonadditive component of genetic variance in the inheritance of this trait, which is agreement with the present findings. 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.

The greatest average contribution to the expression of PL (49.9%) and TLA (57.1%) was found in the female A lines. The contributions of the Rf testers and line x tester interaction were less significant (Tab.5).

Table. 5. Average percentage contribution of female lines, tester lines and their interactions to the expression of PL and LA

Average contribution	PL	LA
	%	%
Female lines	49.89	57.06
Testers	39.51	1.83
Line x tester	10.61	41.12

A positive correlation was found between SY and PL (0.374\*) and TLA (0.630\*\*). These findings are in agreement with those of HLADNI *et al.* (2004), MERRIEN *et al.* (1982), LAKSHMANRAO *et al.* (1985), JOKSIMOVIĆ *et al.* (1997), and DUŠANIĆ *et al.* (2004), who reported positive correlations between TLA and SY in sunflower. SOC and TLA were found to be negatively correlated (-0.520\*\*). This is in disagreement with the findings of JOKSIMOVIĆ *et al.* (1997, 1999).

The results presented in this paper show that determination of the mode of inheritance, combining abilities, and correlations between morphophysiological traits and SY and SOC makes possible the development of productive sunflower hybrids with altered plant architecture based on interspecific hybridization.

## CONCLUSION

Significant differences in the mean values of all the traits studied were observed among the genotypes (inbred lines and hybrids). The nonadditive component of genetic variance played the main role in the inheritance of PL and TLA, as shown by analysis of combining abilities and analysis of genetic variance components. This was further confirmed by the GCA/SCA ratios for PL and TLA in the F<sub>1</sub> generation, which were below the value of one. The greatest average contribution to the expression of PL (49.9%) and TLA (57.1%) was found in the female A lines. A positive correlation was found between SY and PL (0.374\*) and TLA (0.630\*\*), while SOC and TLA were found to be negatively correlated

(-0.520\*\*). 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 findings of this study can be used in the development of new sunflower hybrids with high oil yields based on interspecific hybridization.

Received June 7<sup>th</sup>, 2008

Accepted August 18<sup>th</sup>, 2008

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**LINIJ X TESTER ANALIZA MORFOLOŠKIH SVOJSTVA I NJIHOVA  
MEĐUZAVISNOST SA PRINOSOM I SADRŽAJEM ULJA  
SUNCOKRETA (*Helianthus annuus* L.)**

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I z v o d

Jedan od primarnih zadataka oplemenjivanja suncokreta je stvaranje inbred linija putem *interspecijes* hibridizacije radi dobijanja visokoprosnih i stabilnih hibrida promenjenog izgleda koji u uslovima intenzivne agrotehnike omogućavaju povećanje broja biljaka po jedinici površine.

Za linija x tester analizu korišćeno je sedam novih divergentnih (A) citoplazmatski muško sterilnih inbred linija nastalih *interspecijes* hibridizacijom, tri Rf-restorer linije kao testeri i 21 hibrid F<sub>1</sub> generacije. Dobijene su značajne razlike u srednjim vrednostima za sva ispitivana svojstva. Izračunate su visoko značajne vrednosti OKS i PKS za dužinu lisne drške (DLD) i ukupne lisne površine po biljci (ULP). Glavnu ulogu u nasleđivanju oba svojstva ima neaditivna komponenta genetske varijanse. To potvrđuje i odnos OKS/PKS u F<sub>1</sub> generaciji koji je manji od jedinice i iznosi 0.43 za DLD i 0.07 za ULP. Najveći prosečan doprinos u ekspresiji ovih svojstava imale su A-linije majke i to (49.9%) za DLD i (57.1%) za ULP. Ustanovljena je pozitivna međuzavisnost prinosa semena (PS) sa DLD (0.374\*) i ULP (0.630\*\*). Između sadržaja ulja u semenu (SU) i ULP ustanovljena je značajna negativna međuzavisnost (-0.520\*\*). Ova istraživanja mogu biti od značaja za stvaranje novih visoko prosnih genotipova suncokreta na bazi *interspecijes* hibridizacije.

Primljeno 08. VII. 2008.

Odobreno 18. VIII. 2008.