

## GENE EFFECTS AND COMBINING ABILITIES FOR 1000-SEED MASS IN SUNFLOWER (*HELIANTHUS ANNUUS*)

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### Abstract

Significant differences in the mean values of 1000-seed mass were found among the sunflower (*Helianthus annuus* L.) genotypes studied (eight inbred lines and 15 F1 hybrids). The mean value of 1000-seed mass was 46.88 g in the female inbreds, 43.52 g in the restorers and 57.45 g in the F1 hybrids. Heterosis and dominance of the better parent manifested themselves in the inheritance of 1000-seed mass in 12 and three combinations, respectively. The nonadditive component of genetic variance played the main role in the inheritance of this trait. The major portion of nonadditive genetic variance was due to superdominance. The inbred lines were found to have different alleles for 1000-seed mass. Standard deviation and coefficient of variation were used as indicators of variability. The influence of genotype and environmental factors and their interactions on total phenotypic variance was determined by the variance analysis model for a two-factorial trial with year as one of the factors. Analysis of phenotypic variance components showed that genotype had the largest contribution in the expression of the trait in the inbreds (78.9%) as well as in F1 hybrids (73.7%). Analysis of combining abilities by the line x tester method (Singh and Choudhary, 1976) revealed that significantly different GCA effects occurred among the inbred lines studied. Inbred lines and F1 hybrids with positive and negative GCA and SCA effects were identified. The inbred lines HA-22 and RHA-C-B were identified as the best general combiners for this trait, and their hybrid combination (NS-H-59) was the only one with a significantly positive SCA value. The GCA/SCA ratio was less than 1. The GCA/SCA showed that the main portion of total genetic variance was nonadditive in character.

### Introduction

In our country, sunflower is the main cultivated oil crop and over 85% of edible oil is obtained from its seed. It is grown on 160-210,000 hectares annually (Škorić et al., 2004). The main advantages of introducing hybrids into production are utilization of the phenomenon of heterosis, uniformity of the F1 generation, and easier incorporation of resistance to diseases and other desirable traits. According to Škorić (1989), sunflower genotypes have been

developed that have a genetic potential for seed yield of over 7 t/ha. Seed yield is a complex trait. It is a result of the influence of a large number of factors, both individual and joint, and is polygenic in character (Borojević, 1992). 1000-seed mass is one of the three most important factors affecting sunflower seed yield. In high-oil genotypes of cultivated sunflower, this mass most often ranges between 40 and 100 g (Fick, 1978). Marinković (1997) studied 16 oil-type varietal populations and found mean values of 1000-seed mass that ranged between 43.79 and 74.29 g. A lot of data have been published on the mode of inheritance of 1000-seed mass in the F1 generation, but they are not mutually consistent, because different materials were used in different studies. Gorbačenko (1979) found cases of intermediacy and dominance of the better parent in the inheritance of this trait. Fick (1978) found intermediacy to be the most common mode of inheritance, while Morozov (1947) and Putt (1966) found cases of heterosis in their studies. In Marinković and Škorić (1985), superdominance, intermediacy and dominance of the better parent manifested themselves in the inheritance of this trait in the F1 generation. To sum up, the type of gene action in the inheritance of 1000-seed mass depends on the origin of the genotype. In Kovačik and Škaloud (1972), the nonadditive component of genetic variance was around nine times higher than the additive one in the inheritance of this trait. Putt (1966) and Marinković and Škorić (1985), on the other hand, reported that both variance components contributed to 1000-seed mass inheritance. Similar results have been obtained by Rao and Singh (1977). Significant influence on increase of sunflower seed yield may be exerted by selection of inbreds for increased 1000-seed mass values and high heterosis in the hybrid combination. For this reason, we carried out a study to obtain information on the expression of 1000-seed mass in sunflower in terms of its phenotypic variability, mode of inheritance, effects of genotype, environmental factors and their interactions, effects of combining abilities of inbred lines and F1 hybrids, and components of genetic variance.

## **Materials and Methods**

Our experimental material was selected at the Institute of Field and Vegetable Crops in Novi Sad. It included five female inbred lines (L-1/L-5) used in their fertile form, three inbreds (T-6/T-8) used as testers in the form of fertility restorers, and their 15 single-cross F1 hybrids. Over a period of two years, the inbreds and F1s were sown at the Institute's Experiment Field at Rimski Šančevi using a randomized block design with four replicates.

The 1000-seed mass of the inbred lines and F1 hybrids was determined by the standard method in the laboratory. The average seed sample from 10 plants per replicate was used for analysis. The mode of inheritance was determined using the significance test of generation means relative to parental average, while the influence of genotype and environmental factors and their interactions on total phenotypic variance was determined by the variance analysis model for a two-factorial trial with year as one of the factors (Borojević, 1992). Analysis of combining abilities using the line x tester method (Singh and Choudhary, 1976) provided information on the following: significance of differences between the variation sources, general combining ability (GCA) of the inbreds, specific combining ability (SCA) of the F1 hybrids, and components of genetic variance in the expression of 1000-seed mass.

## Results and Discussion

The mean values of 1000-seed mass in the inbreds ranged between 26.23 (RHA-N-K) and 54.08 g (RHA-178) (Table 1). The variability of the F1 hybrids was greater with the means ranging from 47.55 (NS-H-64) to 69.29 g (NS-H-59). The F1 mean values of this trait were 18.4% higher than in the female inbreds and 24.3% higher than in the restorers. If all plants in a progeny of the same genotype are homozygous (in the case of inbreds) or heterozygous (in the case of F1 hybrids), variability occurring among the individual plants in such progenies is not heritable, but is a result of action of environmental factors.

Table 1. Mean values and mode of inheritance of 1000-seed mass in inbred lines and F1 hybrids of sunflower.

Inbred lines		RHA-178 T-6	RHA-C-B T-7	RHA-N-K T-8
		54.08±1.54	50.24±0.86	26.23±0.68
CMS-V-8931-3-4 50.75±1.59	L-1	NS-H-47 (d) 65.51±0.73	NS-H-57 (h) 59.29±1.21	NS-H-66 (d) 49.12±1.34
CMS-V-8931-5-4 48.07±1.84	L-2	NS-H-48 (h) 58.00±.87	NS-H-58 (h) 57.58±0.78	NS-H-65 (d) 50.75±1.16
HA-22 47.41±0.89	L-3	NS-H-49 (h) 59.07±0.99	NS-H-59 (h) 69.29±1.64	NS-H-70 (h) 57.29±1.01
HA-74 48.99±1.79	L-4	NS-H-50 (h) 58.58±1.28	NS-H-60 (h) 62.24±0.86	NS-H-68 (h) 54.24±0.97
HA-BCPL 39.19±1.20	L-5	NS-H-51 (h) 60.14±0.70	NS-H-61 (h) 62.04±0.90	NS-H-64 (h) 47.55±0.59

LSD (0.05)=2.75

LSD (0.01)=3.66

In the inheritance of 1000-seed mass in the F1 hybrids, positive heterosis (h) was found in 12 and dominance (d) in three hybrid combinations (Table 1). These results supported our assumption that the inbred lines involved in the study are of genetically divergent origin.

ANOVA of the inbreds revealed highly significant F values for the variation sources genotype, year and genotype x year interaction. Analysis of phenotypic variance components showed that genotype (78.92%) had the greatest contribution to total variance (Table 2).

Table 2. ANOVA and components of phenotypic variance of 1000-seed mass in sunflower inbreds.

Source of variation	Degree of freedom	Mean square		Component of variance		
				$\sigma^2$	%	
Replicate	3	6.857		Not relevant		
Genotype	7	636.815	**	M1	72.28	78.92
Year	1	130.959	**	M2	2.76	2.93
Genotype x year	7	42.610	**	M3	8.51	9.04
Error	45	8.567		M4	8.57	9.11
Total	63				94.12	100.00

Variance analysis of 1000-seed mass of the F1 hybrids revealed highly significant F values of genotype. The largest contribution to total phenotypic variance was that of genotype (73.7%), followed by error (19.26%), genotype x year interaction (5.76%) and year (1.28%) (Table 3).

Table 3. ANOVA and components of phenotypic variance of 1000-seed mass in F1 hybrids.

Source of variation	Degrees of freedom	Mean square		Component of variance	
				$\sigma^2$	%
Replicate	3	1.502		Not relevant	
Genotype	14	241.475 **	M1	28.16	73.70
Year	1	31.982	M2	0.49	1.28
Genotype x year	14	16.162	M3	2.20	5.76
Error	87	7.357	M4	7.36	19.26
Total	119			38.21	100.00

Based on their GCA means, the inbreds were divided into two groups: those with a positive (four lines) and those with a negative (four lines) GCA effect. The best general combiners were the RHA-C-B and HA-22 inbreds, as they had a highly significant positive GCA effect (Table 4). The RHA-N-K and CMS-V-8931-3-4 inbreds had a highly significant negative GCA effect for 1000-seed mass and are presumed to be poor general combiners.

Table 4. GCA effect for 1000-seed mass in sunflower inbreds.

No.	Inbred line		Year 1	Year 2	Mean
1	CMS-V-8931-3-4	L-1	-3.487 **	-2.122	-2.471 **
2	CMS-V-8931-5-4	L-2	-2.240 *	-1.596	-2.001 *
3	HA-22	L-3	6.134 **	2.907 *	4.438 **
4	HA-74	L-4	0.146	1.833	0.907
5	HA-BCPL	L-5	-0.553	-1.023	-0.873
LSD (0.05)			1.833	2.671	1.588
LSD (0.01)			2.441	3.556	2.115
6	RHA-178	T-6	-0.209	2.402 *	1.013
7	RHA-C-B	T-7	5.228 **	3.725 **	4.643 **
8	RHA-N-K	T-8	-5.019 **	-6.127 **	-5.656 **
LSD (0.05)			1.419	2.070	1.230
LSD (0.01)			1.889	2.756	1.638

The stability of the GCA effect for this trait over the two study years was observed in all the inbreds except RHA-178 (Table 4).

Judging by the mean values of the SCA in the F1 hybrids, the SCA effect does not depend on environmental factors. A significant positive SCA value was found only in the hybrid combination HA-22 x RHA-C-B (Table 5), which was obtained by crossing inbreds with highly significant positive GCA effects, i.e., the best general combiners. This was probably a result of the action of additive x additive gene interaction, and since heterosis and

dominance manifested themselves in the inheritance of 1000-seed mass, the additive component was still present. A highly significant negative SCA value was found in the hybrid combination HA-22 x RHA-178, while a significant negative effect was observed in the HA-BCPL x RHA-N-K combination, which involved lines with poor GCA. The stability of SCA effects for 1000-seed mass was observed in all 15 hybrid combinations (Table 5).

Table 5. SCA effect for 1000-seed mass in F1 hybrids.

No.	F1 hybrid		Year 1	Year 2	Mean
1	NS-H-47	L-1 x T-6	1.36	0.35	0.52
2	NS-H-57	L-1 x T-7	-1.40	-0.58	-0.32
3	NS-H-66	L-1 x T-8	0.05	0.23	-0.20
4	NS-H-48	L-2 x T-6	0.65	2.26	1.54
5	NS-H-58	L-2 x T-7	-2.29	-2.39	-2.50
6	NS-H-65	L-2 x T-8	1.63	0.12	0.96
7	NS-H-49	L-3 x T-6	-4.15 *	-3.68	-3.83 **
8	NS-H-59	L-3 x T-7	3.26 *	2.61	2.76 *
9	NS-H-70	L-3 x T-8	0.89	1.07	1.06
10	NS-H-50	L-4 x T-6	-0.70	-1.04	-0.79
11	NS-H-60	L-4 x T-7	-0.07	-1.11	-0.76
12	NS-H-68	L-4 x T-8	0.77	2.15	1.54
13	NS-H-51	L-5 x T-6	2.84	2.10	2.55
14	NS-H-61	L-5 x T-7	0.50	1.47	0.82
15	NS-H-64	L-5 x T-8	-3.34 *	-3.56	-3.37 *
LSD (0.05)			3.174	4.627	2.752
LSD (0.01)			4.227	6.161	3.665

The GCA/SCA ratio was below the value of 1. Since GCA is thought to be indicative of additive and SCA of nonadditive genetic variance, our results can be said to support the notion that 1000-seed mass in sunflower is determined by additive and nonadditive gene action. The nonadditive component of genetic variance had more control over the inheritance of 1000-seed mass (Table 6).

Table 6. Components of genetic variance of 1000-seed mass in sunflower.

1000-seed mass		$V_A$	$V_D$	$V_D/V_A$	GCA	SCA	GCA/SCA
Year 1	F=0	11.584	25.575	2.208	2.896	6.394	0.453
	F=1	5.792	6.394	1.104			
Year 2	F=0	9.133	18.691	2.047	2.284	4.673	0.489
	F=1	4.567	4.673	1.023			
Mean	F=0	9.861	23.927	2.426	2.465	5.982	0.412
	F=1	4.93	5.982	1.213			

## Conclusions

Significant differences in the mean values of 1000-seed mass were found among the sunflower genotypes (inbred lines and F1 hybrids) studied. The mean value of 1000-seed mass was 46.88 g in the female inbreds, 43.52 g in the restorers and 57.45 g in the F1 hybrids. Heterosis and dominance of the better parent manifested themselves in the inheritance of 1000-seed mass. The nonadditive component of genetic variance played the main role in the inheritance of this trait. The major portion of nonadditive genetic variance was due to superdominance. The inbred lines were found to have different alleles for 1000-seed mass. Inbred lines and F1 hybrids with positive and negative GCA and SCA effects were identified. The inbred lines HA-22 and RHA-C-B were identified as the best general combiners for this trait, and their hybrid combination (NS-H-59) was the only one with a significantly positive SCA value. The GCA/SCA ratio was less than 1. Additive and nonadditive gene action controlled the expression of 1000-seed mass.

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