

## GENETIC VARIABILITY OF SUNFLOWER VARIETIES AND INBRED LINES

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Sunflower (*Helianthus annuus* L.) has assumed its international importance after the development of the Russian varieties with high oil content. The wide adaptability of sunflower to varying soil and climatic conditions has made its cultivation possible to occur beyond areas suited for maize production.

The main objective of the present investigation is to evaluate the variability which exists in main yield components of divergent sunflower varieties as compared with inbred lines which are used for the exploitation of hybrid vigour. This estimation could be of help in determining the contribution of each of these characters alone and in combination with the other characters for oil synthesis and for yield formation. This would provide new information for sunflower breeders; and, thus, breeding for yield of seed and oil could be more reliable.

### MATERIAL AND METHODS

This investigation was carried out at the Agricultural Experiment Station at Rimski Šančevima of the Institute for Agricultural Research, and of the Faculty of Agriculture, the University of Novi Sad, Yugoslavia. The investigation was performed during the growing successive seasons of 1972 and 1973.

The materials of the experiment were selected from ten genetically different sunflower populations, i.e., four Russian varieties, one Novi Sad's new selected strain, and five Novi Sad's inbred lines in the ninth and tenth generations of inbreeding.

The analysis has been done on 18 of the physiological, morphological, and chemical characters of sunflower. However, for the purpose of the paper we will discuss only the characters: days to flowering, plant height, leaf area, number of leaves per plant, number of seeds per head, seed yield per plant, 1000-seed weight and oil percentage of dry seed, for the varieties only.

A randomized block design with five replications was used in the two years of investigation. Each plot consisted of seven rows 4.8 meter long and 70 centimeters apart. The seeds were planted in hills spaced 40 cm apart in the row. The size of plot was  $4.8 \times 4.9 = 23.52$  square meters, of  $\frac{1}{425}$  h. Each plot was planted by hand on April 10 and April 11 in 1972 and 1973, respectively. All the varieties and inbred lines were planted on the same day at the same rate and in the same uniform field which had been prepared and fertilized as uniformly as possible.

Genotypic variance, error variance, interaction variance and phenotypic variance for the characters were calculated from the mean squares in the table of analysis of variance, as described by Miller et al. (11) and widely used by many investigators in various crops. Then, heritability was estimated by dividing the genotypic variance by the total phenotypic variance and multiplying by 100. Heritability was also estimated as twice the regression coefficient as described in sunflower by Schuster (16) and applied by Nikolič-Vig et al (12).

Genetic coefficient of variation was calculated by dividing the square root of the genetic variance by the population mean and multiplying by 100 (3).

To predict expected genetic advance the following formula was used.

$$\text{Expected genetic advance} = \frac{\delta_g^2}{\delta_{ph}} \times K$$

Where  $\delta_{ph}$  is the phenotypic standard deviation,  $\delta_g^2$  genotypic standard deviation and K is the selection differential. In this investigation, the K has value of 2.06 and 1.16 which is the expectation in the case of 5% and 30% selection intensities in large samples (11).

## RESULTS AND DISCUSSION

The estimates of variance components showed that the magnitudes of the interaction components were variable. For the characters: leaf area, number of leaves per plant, plant height, number of seeds per head, oil percentage and 1000-seed weight, the magnitudes of the interaction components were of negative values (table 1). In order to obtain unbiased estimates of the components of variance, the negative values had been used as such it were in the calculations. Negative estimates for several traits were reported also in cotton by Miller et al. (11). Since the true parameters cannot be negative, these values should be interpreted as being estimates of variances which were zero or small positive quantities. These negative estimates are suggestive of the size of sampling errors involved. Consequently, it may be concluded that the estimate of genotype x environmental interaction is of a great value in obtaining unbiased estimates of the genotypic components of variance. Moreover, its magnitude is of a great help to the breeders to explain the misjudgments which may result from the conclusions based on single trial in a single year.

Table 1

**Estimates of variance components, and population mean for the different characters**

Characters	Genotypic variance $V_g^2$	Phenotypic variance $V_{ph}^2$	Interaction variance $V_{gy}^2$	Error variance $V_e^2$	Population mean
Seed yield	88.50	166.55	61.51	47.29	108.77
Days to flowering	25.55	26.15	0.33	0.43	66.56
Leaf area	2454675	2769025	— 100107	364404	7519
No. of leaves	4.02	4.26	— 0.44	0.46	30.50
Plant height	233.43	364.83	— 28.37	145.56	171.80
No. of seeds	27231	29349	— 242	2239	1326
Oil %	0.31	0.48	— 0.20	0.27	48.62
1000-seed weight	10.48	15.92	— 1.26	5.44	66.56

The genetic coefficient of variation ranged from 1.2% for oil percentage to 21.4% for plant height (table 2). Although, the previous studies indicated that the genetic coefficient of variation helps to measure the range of genetic variability in the various characters, it was not possible to estimate heritable variation with the help of genetic coefficient of variation alone. Genetic coefficient of variation together with the heritability estimates would give the best values of the amount of advance to be expected from selection (3), when these genotypes crossed or mixed together.

Table 2

**Estimates of heritability ( $h^2$ ), Genetic coefficient of variation (G.C.V.), Expected genetic advance (E.G.A.) and Expected genetic advance as the percentage of mean**

Characters	$h^2$ %	G.C.V. %	E.G.A. k = 1.16	E.G.A. %	E.G.A. k = 2.06	E.G.A. %
Seed yield	68.7	13.5	7.95	7.3	14.11	13.4
Days to flowering	97.7	7.6	5.79	8.7	10.28	15.4
Leaf area	88.8	20.8	1171.00	22.8	3039.00	40.4
No. of leaves	94.4	6.6	2.26	7.4	4.02	13.2
Plant height	90.4	21.4	14.19	8.7	25.19	14.7
No. of seeds	92.8	12.4	184.5	13.9	327.70	24.7
Oil %	64.6	1.2	0.52	1.1	0.93	1.9
1000-seed weight	65.8	4.0	3.05	3.8	5.42	6.7

Heritability as twice the regression ( $b \times 2$ )

$h^2$  for yield =  $42.0 \pm 160.0\%$

$h^2$  for oil =  $44.0 \pm 45.0\%$

High heritability estimates, in the broad sense, were obtained for days to flowering followed by number of leaves and number of seeds per head (table 2). On the other hand, medium heritability was shown for oil

percentage, 1000-seed weight and seed yield per plant. This confirms the results of several investigators in other crops. For example, Majumdar et al. (10) reported a range from 49.61 per cent for yield per plant to 98.63 per cent for days to maturity and they estimated the heritability in broad sense for a collection of groundnut varieties.

In sunflower, Pustovoit (14) reported medium heritability for oil percentage. Furthermore, Nikolić-Vig et al. (12) obtained medium heritability (57%) for the variety VNIIMK 8931 but a relatively high heritability (75%) for Peredovik in which the estimates were calculated on the base of the regression coefficient. The last method was also calculated for both seed yield per plant and oil percentage over all the varieties (table 2). It should be emphasized, however, that in the heritability estimates based on regression, the estimate may be affected by the contraction or expansion of the phenotypic scale caused by the genotype x environment interaction and it is, may be, the main reason for the cases in which heritability estimate larger than 100% has been obtained. In contrast to the heritability estimates obtained for oil by (14) and (12), Schuster (16) reported low heritability estimates for oil percentage in sunflower. These differences in the estimates of heritability may be due to the differences in the material, environments and methods of estimation.

Expected genetic advance was calculated on the bases of 5% selection intensity if selection is to be practiced for one character, and 30% intensity when equal attention will be paid for the selection of two or three characters, simultaneously (table 2). Leaf area and number of seeds per head showed high heritability estimates with very high expected genetic advance which may indicate that the high heritability obtained in those characters was due to the additive genetic effects (13). On the other hand, days to flowering showed the highest heritability but low genetic advance which suggests that high heritability estimate for this character was probably due to non-additive (dominance, overdominance or epistasis) gene effects (13).

Thus, it may be concluded from the various genetic parameters studied that a considerable amount of genetic variability exists over all the genotypes used. So, a breeding programme of mass selection for the superior genotypes from a crossed population of these varieties would be effective for a number of characters such as: leaf area and number of seeds per head. Also, mass selection or recurrent selection would be satisfactorily effective if they followed by the recombination of the superior genotypes of the varieties or the inbred lines which will combine well with each other in all combinations in order to develop hybrid varieties or synthetic varieties.

In the last decade, great attention as well as intensive researchs have been made by Borojević and his team in Yugoslavia (1) to create a model for high-yielding wheat varieties. This aim could be reached also in sunflower by the accumulation of data, from divergent

Table 3

Simple ( $r_a$ ) and partial ( $r_b$ ) coefficient of correlation between seed-yield and some other characters for five varieties during two-years (10 variants)

Characters		Flow. $X_1$	Leaf area $X_2$	Number of leaves $X_3$	Plant height $X_4$	Number of seeds $X_5$	Oil % $X_6$	1000-seed weight $X_7$
Yield of seed g/pl.	$r_a$	0.926**	0.917**	0.632*	0.919**	0.938**	-0.161	0.462
	$r_b$	0.186	0.528	0.626	-0.841**	0.982**	-0.656*	0.975**
1 Flowe- ring (days)	$r_a$		0.957**	0.709*	0.960**	0.922**	-0.235	0.338
	$r_b$		0.157	-0.249	0.391	-0.167	0.351	-0.201
2 Leaf area (cm <sup>2</sup> /pl.)	$r_a$			0.742*	0.969**	0.904**	-0.307	10.340
	$r_b$			-0.032	-0.579	-0.512	0.279	-0.461
3 Number of leaves per plant	$r_a$				0.678*	0.803**	0.100	-0.273
	$r_b$				0.634*	-0.626	0.620	-0.746*
4 Plant height (cm)	$r_a$					0.897**	-0.393	0.408
	$r_b$					0.886**	-0.849**	0.871**
5 Numer of seeds per head	$r_a$						-0.027	0.142
	$r_b$						-0.740	-0.972**
6 Oil per- centage	$r_a$							-0.472
	$r_b$							0.699*

\* Significant

\*\* Highly significant

materials in wide range of environments, about the nature of genetic variability for each parameter and the association between the different parameters. The correlation between the 8 characters represented here are summarized in table 3. The dependence of seed yield per plant on each character may also be illustrated by the following regression equations ( $\hat{Y}$ ):

$$\hat{Y}_y \quad 1...7 = 873.0290 + 0.0842 x_1 + 0.0012 x_2 + 0.9555 x_2 \\ - 0.3049^* x_4 + 0.0978^{**} x_5 - 1.1904 x_6 + 1.4522^{**} x_7$$

From the data in table 3 and the regression equation it may be concluded that:

The decisive role in the formation of the seed-yield per plant in sun-flower varieties, under the conditions of this investigation, were played

first by 1000-seed weight followed by number of seeds per head and plant height (table 3). Furthermore, the decisive role in the synthesis of oil for the varieties of sunflower were played first by plant height followed by number of seeds per head, 1000-seed weight and seed yield.

Many investigations were reported in regards to correlation between some of sunflower parameters (2, 4, 5, 6, 7, 8, 9, 14 and 15). In some of these studies, positive correlation coefficient was observed between seed yield and oil content per seed which is in a quite contrast with the negative relation obtained here. The reason for that may be attributed to the differences in the methods of estimation. The previous association may be based on the simple correlation only in which the correlation between two characters should be affected by the effect of the other characters. On the other hand, the highly negative correlation coefficient obtained in this research was based on the partial correlation in which the effect of the other characters are omitted or its effect kept constant. Moreover, the calculation for the two parameters from the fluctuations in one genotype may be of different attitude than that based on number of divergent genotypes.

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