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PHENOTYPIC STABILITY OF YIELD COMPONENTS IN PROTEIN SUNFLOWER

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Phenotypic stability of the yield components of three sunflower (*Helianthus annuus* L.) inbred lines in their third, fourth and fifth year of self-pollination was analysed. Stability parameters were calculated following an Eberhart and Russell (1966) model. According to regression coefficients, the investigated lines showed satisfactory stability of the protein content in seeds and weight per 1000 seeds. The line D4441 in the third year of self-pollination was identified as the most stabile one regarding protein content. As for weight per 1000 seeds, the best genotype stability was detected in the line Rs 4 I 10 in its fourth year of self-pollination.

Key words: sunflower, phenotypic stability, regression coefficient, protein content, weight per 1000 seeds

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INTRODUCTION

Protein sunflower originates from North America. The population of western parts of North America and Mexico had been first to recognize the potential for multiple uses of sunflower (ROSENGARTEN, 1985). Indians had used it as nourishment, consuming it raw or grinding it and mixing with maize flour before baking (HENDERSON, 1987). The Spaniards had transferred it to Europe in the 16th century. Today, protein sunflower attracts considerable attention of the food processing industry worldwide, as well as in this country. Its uses are expanding – whether wholemeal or hulled, it can be consumed fried, raw, salted, unsalted, or mixed with various spices. Hulled kernel may be added to ice-creams, salads or sweets topped with chocolate.

Besides being bred for the main seed yield components and high genetic yielding potential, hybrids of the protein type of sunflower should also be characterized by good adaptability and stability, appropriate seed size, shape and colour, high content of kernel, uniformity of seed size, easy hulling and long and safe seed storage. In this type of hybrid, the content and quality of proteins is very important (FICK and MILLER, 1997). To ensure further yield increase, it is therefore essential to focus more attention on analysing the variability of individual characters that have direct or indirect effect on yield (KRALJEVIĆ-BALALIĆ and BOROJEVIĆ, 1982; DENČIĆ, 1994, NURMINIEMI, 1996).

High yield is an expression of different yield components and complexes of other plant properties under given environmental conditions. Stable and high yield does not depend only on the genotype but on interaction of genotype and the environment as well. There is a whole series of models that enable analysis of the adaptiveness of a genotype to particular environmental conditions. The most widely employed model of stability has been proposed by EBERHART and RUSSELL (1966). A stable genotype under such model is one that has high average yield, a regression coefficient of around 1.0 (bi $\approx$ 1) and a regression deviation as low as possible ($S^2_{di} \approx 0$).

This research aimed to determine the variability of the investigated phenotypic characters of several inbred sunflower lines, their genotype/environment interaction, and the degree of stability depending on the homozygosity level (year of self-pollination) and environmental effects.

MATERIALS AND METHODS

Three promising inbred sunflower lines in their third, fourth and fifth year of self-pollination were used in this investigation. The chosen lines originated from the protein cultivar Kolos, which had been selected in the Agricultural and Technological Research Centre in Zaječar. The cultivar Kolos itself was the standard. The chosen lines S_3, S_4 and S_5 were sown according to a random block design with three replications in the experimental fields of the Agricultural and Technological Research Centre in Zaječar, the Agricultural School in Leskovac and the Stig Agricultrual Institute in Požarevac over the 1997-1998 period. Sowing was done upon thoroughly tilled soil at optimal timing for the given locality.

The experimental data was processed by the analysis of variance in a three-factorial experiment and the stability parameters were calculated from the regression analysis using the EBERHART and RUSSELL (1966) method:

$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$

where:

Y_{ij}- yield average of *i* genotype in *j* locality

μ_i- yield average of *i* genotype in all localities

β_i- regression coefficient indicating genotype reaction to different localities

I_j- ecological index, average of all genotypes in all localities from which the average of all genotypes in *j* locality is deducted

δ_{ij}- regression deviation of *i* genotype in *j* locality

Two stability parameteres were calculated: regression coefficient b_i:$b_i = \sum yij\ Ij \sum I^2_j$ and mean regression variance S^2_{di}:

$S^2_{di} = [\sum \delta^2_{ij} / (n-2)] - S^2e/r$.

S^2e/r - mid-square error in analysis of variance

r - number of blocks

n- number of localities

The student t-test was used to test the regression coefficient significance, and the average coefficient standard error was employed.

RESULTS AND DISCUSSION

Table 1. Protein contents (%) for sunflower lines in S3, S4 and S5 generations of self-pollination per locality (average per annum)

INBRED LINE		LOCALITIES		
		ZAJEČAR Average ± δ	LESKOVAC Average ± δ	POŽAREVAC Average ± δ ξ
1.	Rs 4 I 10-S_3	21.75 ± 1.9	22.24 ± 3.2	22.15 ± 1.7
2.	Rs 4 I 10- S_4	21.21 ± 2.1	22.04 ± 3.3	22.12 ± 1.1
3.	Rs 4 I 10-S_5	20.07 ± 1.8	21.92 ± 3.4	21.80 ± 0.27
4.	D 4441- S_3	20.55 ± 1.7	21.71 ± 3.9	21.92 ± 2.0
5.	D 4441- S_4	20.12 ± 1.4	19.94 ± 2.3	19.91 ± 2.8
6.	D 4441- S_5	18.85 ± 2.1	19.44 ± 2.6	19.18 ± 3.1
7.	Ko 7 - S_3	21.25 ± 1.7	21.92 ± 4.0	21.83 ± 2.3
8.	Ko 7 - S_4	20.59 ± 2.1	21.17 ± 4.4	21.44 ± 2.4
9.	Ko 7 - S_5	19.56 ± 2.9	21.05 ± 4.0	21.23 ± 2.6
10.	Kolos-standard	19.99 ± 3.2	22.64 ± 3.5	21.66 ± 1.7

Locality: LSD 0.05 = 0.389; 0.01 = 0.51; Genotype x Locality: LSD 0.05 = 1.232; 0.01 = 1.628

Means and variance components. - Proteins are the second most important reserve compound in sunflower seeds. Protein content in the seed, as well as yield components, are determined by a number of genes (minor genes or polygenes), and they are the result of interactions between those genes and environmental factors. BEDOV and ŠKORIĆ (1981) had reported finding protein content in the seed to vary between 16% and 29% in the examined material of different genetic origin. STANOJEVIĆ *et al*. (1998) reported protein content in the seed to depend on ecological factors and locality.

We found significant differences in the seed protein contents of the investigated lines in their S_3, S_4 and S_5 generations of self-pollination. The higest mean for the localities in Zaječar (21.75%), Leskovac (22.24%) and Požarevac (21.75%) was found for the line Rs 4 I 10-S_3. The lowest mean value for protein content was found in the line D 4441 in all localities (Zaječar 18.85%, Leskovac 19.44%, Požarevac 19.18%), Table 1.

Table 2. ANOVA for protein contents in seeds of different sunflower lines in S3, S4 and S5 generations of self-fertilization.

Source of variation	Degree of freedom (DF)	Mean squares (MS)	F-relation	Variance components σ2	%
Years –G	1	755.22	670.12***		
Localities – L	2	19.03	16.45***		
G x L	2	43.17	37.32***		
Genotype – S	9	14.25	12.32***	0.65	26.42
S x G	9	3.99	3.45***	0.15	6.10
S x L	18	1.23	1.06 ns	0.00	0.00
S x G x L	18	2.65	2.29**	0.50	20.32
	118	1.16		1.16	47.15
Total				2.46	100.00

The percentages of accountability of the genotype (26.42%) and genotype/year/locality interaction (20.32%) are comparatively equal. The high proportion of this property is attributable to experimental error (47.15%), Table 2.

Table 3. Weight per 1000 seeds (g) for sunflower lines in S3, S4 and S5 generations of self-pollination per locality (average per annum)

INBRED LINE		LOCALITIES		
		ZAJEČAR Average ± δ	LESKOVAC Average ± δ	POŽAREVAC Average ± δ
1.	Rs 4 I 10-S_3	109.9 ± 13.5	127.8 ± 17.1	115.0 ± 18.3
2.	Rs 4 I 10- S_4	108.4 ± 16.9	120.8 ± 12.8	113.1 ± 13.1
3.	Rs 4 I 10-S_5	83.6 ± 15.4	116.2 ± 11.5	102.5 ± 18.3
4.	D 4441- S_3	94.9 ± 28.2	81.0 ± 6.4	75.2 ± 2.1
5.	D 4441- S_4	70.9 ± 8.7	71.9 ± 7.3	69.0 ± 5.0
6.	D 4441- S_5	63.9 ± 4.6	62.18 ± 9.4	53.3 ± 11.2
7.	Ko 7 - S_3	106.7 ± 14.1	122.7 ± 5.1	104.2 ± 7.1
8.	Ko 7 - S_4	96.9 ± 9.5	118.6 ± 6.5	99.3 ± 10.0
9.	Ko 7 - S_5	91.1 ± 13.0	107.6 ± 8.8	97.1 ± 9.0
10.	Kolos-standard	118.0 ± 14.0	125.8 ± 14.0	110.1 ± 7.3

Locality: LSD 0.05 = 2.966; 0.01 = 3.920; Genotype x Locality: LSD 0.05 = 9.449; 0.01 = 12.448

Weight per 1000 seeds represents a relationship between weight and seed number. JOVANOVIĆ *et al*. (1998) reported 80.2-122.1 g weight per 1000 seeds in their investigation of inbred lines, while MIHALJČEVIĆ (1989) found an interval of 40.6-63.4 g. Weight per 1000 seeds measures seed size, and the highest mean value for that character was found in the line Rs 4 I 10 in its third generation of self-pollination in all localities. Mean weight per 1000 seeds was 109.9 g in the Zaječar locality, 127.8 g in the locality Leskovac, and 115.0 g in the locality Požarevac. The smallest seeds, i.e. the lowest average weight per 1000 seeds in the investigated lines, was found in the line D 4111 in its fifth generation of self-pollination in all localities (63.9 in Zaječaru, 63.9 in Leskovcu and 69.0 g in Požarevac), Table 3.

Table 4. ANOVA for weight per 1000 seeds of different sunflower lines in S3, S4 and S5 generations of self-fertilization

Source of variation	Degree of freedom (DF)	Mean squares (MS)	F-relation	Variance components σ2	%
Years –G	1	3215.65	47.78***		
Localities – L	2	2556.32	37.98***		
G x L	2	727.10	10.80***		
Genotype – S	9	7374.27	109.57***	360.03	64.75
S x G	9	772.20	11.45***	64.08	11.52
S x L	18	317.02	4.71***	20.26	3.64
S x G x L	18	195.43	2.90***	43.37	7.80
	118	68.32		68.32	12.29
Total				556.06	100.00

All factors were found to have highly significant effect on the weight per 1000 seeds, the lowest effect of 3.64% being the genotype/year/locality interaction, which agrees with the findings reported by Mikliča, 2001, Table 4.

Stability parameters. - Looking at both stability parameters, the line Rs 4 I 10 approached closest the average stability genotype regarding protein content in its fourth generation of self-pollination, while the line D 4441 achieved the same in the third, and the line Ko7 in the fourth generation of self-pollination. All three lines in all three years of self-pollination were found to have better stability regarding protein content in different localities and in both years of investigation that the standard cultivar Kolos (b_i =2,28), tab.5.

The high variation in the values of the stability parameters b_i and S^2_{di}, acquired by the regression analysis, stresses the differences in reaction of the investigated material to the existing environmental conditions of the experiments. All three lines approached the average stability genotype regarding weight per 1000 seeds in their fourth year of self-pollination, tab.6.

Table 5. Stability parameters for sunflower lines in S3, S4 and S5 generations for protein content

Inbred line	b_i	S^2_{di}
Rs 4 I 10-S_3	0.46	-0.17
Rs 4 I 10- S_4	0.90	-0.16
Rs 4 I 10-S_5	1.84	-0.17
D 4441- S_3	1.27	-0.11
D 4441- S_4	-0.20	-0.17
D 4441- S_5	0.48	-0.15
Ko 7 - S_3	0.65	-0.17
Ko 7 - S_4	0.71	-0.12
Ko 7 - S_5	1.61	-0.12
Kolos-standard	2.28	0.05

Standard error of average coefficient of regression *Sbi*: 0.285

Table 6. Stability parameters for sunflower lines in S3, S4 and S5 generations for weight per 1000 seeds

Inbred line	b_i	S^2_{di}
Rs 4 I 10-S_3	1.17	-10.55
Rs 4 I 10- S_4	0.88	3.32
Rs 4 I 10-S_5	1.97	206.48
D 4441- S_3	-0.25	186.68
D 4441- S_4	0.18	-10.66
D 4441- S_5	0.39	40.05
Ko 7 - S_3	1.56	-11.67
Ko 7 - S_4	1.83	-3.45
Ko 7 - S_5	1.17	13.70
Kolos-standard	1.10	11.00

Standard error of average coefficient of regression *Sbi*: 0.815

CONCLUSION

Based on data of the ecological stability of 10 sunflower genotypes, obtained using the EBERHART and RUSSELL (1966) method in three localities and in two years of investigation, it is possible to make the following conclusions:

The ANOVA results for overall samples show satisfactory stability of the investigated characters, but differences were observed by examining the reactions of individual genotypes to the changeable limiting factors of the environment.

The analysis of sunflower genotypes in their different years of self-pollination and cultivated in three different agroecological localities over two years showed that it would be possible to develop sunflower genotypes that would satisfy both criteria, i.e. good characters and high stability under different conditions. It could facilitate the choice of parents for ensuing sunflower breeding programmes.

The results of this investigation showed that it is possible to select the best lines as early as in the S_3 generation, and then to continue the self-pollination process, which increases the efficacy of breeding.

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FENOTIPSKA STABILNOST KOMPONENATA PRINOSA PROTEINSKOG SUNCOKRETA

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Izvod

Proteinski suncokret vodi poreklo sa područja Severne Amerike. Danas proteinski tip suncokreta privlači pažnju prehrambene industrije u celom svetu, a takođe i u našoj zemlji. Pored oplemenjivanja na glavne komponente prinosa semena i stvaranja visokog genetskog potencijala za prinos, hibridi proteinskog tipa treba da su dobre adaptabilnosti i stabilnosti, zatim veoma je važna krupnoća semena, oblik i boja, visok udeo jezgre, uniformnost u krupnoći semena, lako ljuštenje i dugotrajno i bezbedno čuvanje semena. Kod ovog tipa hibrida veoma je bitan visok sadržaj proteina i njihov kvalitet. U radu je analizirana fenotipska stabilnost komponenata prinosa tri inbred linije suncokreta (*Helianthus annuus* L.) u trećoj, četvrtoj i petoj godini samooplodnje. Parametri stabilnosti su izračunati primenom modela EBERHART and RUSSELL (1966). Ispitivane linije su, prema koeficijentu regresije pokazale zadovoljavajuću stabilnost za sadržaj proteina u semenu i masu 1000 semena. Kao najstabilnija za sadržaj proteina pokazala se linija D4441 u trećoj godini samooplodnje. Za masu 1000 semena najbolju stabilnost genotipa ostvarila je linija Rs 4 I 10 u četvrtoj godini samooplodnje.

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