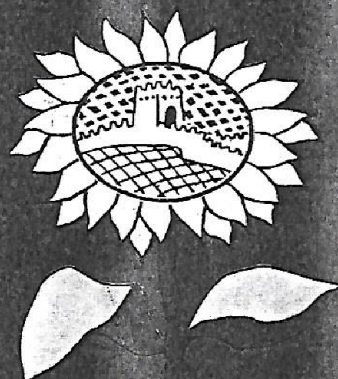


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THE COMPONENTS OF GENETIC VARIABILITY FOR BRACT LENGTH, WIDTH AND NUMBER IN SUNFLOWER (*Helianthus annuus* L.)

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Abstract

Half diallel crosses of four inbred sunflower lines were studied for genetic components of variance (D, H₁, H₂, F) for bract length, width and number in F₁ and F₂ generations.

The analysis of variance indicated the presence significant differences between the treatments.

In the heredity of bract length, width and number, the dominant components (H₁ and H₂) played a more important role than the additive ones (D). The dominant and recessive genes controlling the three traits were not symmetrically distributed in the parental lines. The parents had a greater number of dominant genes for bract number and of recessive genes for bract length and width. The average degree of dominance ($(H_1/D)^{1/2}$) and the point of intersection between the projected line of regression and the Wr axis both indicate the presence of superdominance in the heredity of the three investigated traits in F₁ and F₂ generations. The regression coefficient did not significantly deviate from the value of 1 for all three traits and in both generations, meaning there was no epistasis. Both broad and narrow sense heritability (h^2_b and h^2_n) were high for all traits.

Key-Words: Sunflower, diallel, bract length, bract width, bract number,

Introduction

Bracts, modified leaves situated at the periphery of the head of the sunflower plant, are photosynthetically active. This activity, according to RAWSON (1980), is particularly intensive at the seed formation stage. The same author argues that green bracts' photosynthetic activity is equivalent to that of

50 cm² of leaf area and that they provide as much as 40% of carbon necessary for the filling of seeds. The results of WEISHENGA (1991) indicate that the contributions of bracts to the total seed yield averages 5%, which is equivalent to the contribution of ten early stem leaves.

The objective of this study was to determine the components of genetic variability and heritability for bract length, width and number by means of half diallel cross method.

Materials and methods

In order to investigate the components of genetic variance for bract length and number, 4 inbred sunflower lines were used, namely RHA-RFYR-576, RHA-PH-BC-113, CMS-81 and KIZ. Half diallel crosses were done in the course of 1992. Plants serving as females were emasculated manually and in the early morning hours. In 1994, parental lines, F₁ and F₂ generations were planted in randomised block designs with three replications at the Experimental Field of the *Rimski Šančevi* breeding station within the Institute of Field and Vegetable Crops.

Sowing was conducted manually, on a well-prepared soil and optimal dates. The length of the rows was 3.6 m, the spacing between them 70 cm and that between the plants in a row 30 cm. There were 4 rows per replication for the parental lines and F₁ generations and 6 of them for F₂ generation.

The plant samples for analysis were taken from the central rows, 30 plants (10 per replication) from the parental lines and F₁ generation and 90 of them (30 per replication) from F₂ generation. Bract length and width were measured at the stage of full flowering and the number of bracts after a harvest by hand.

The analysis of variance suggested the existence of significant differences between the treatments.

The analysis of the components of genetic variance was conducted on the basis of the method by JINKS AND HAYMAN (1954) and regression analysis on the basis of the MATHER AND JINKS (1971) method. The latter method was also used to determine the broad and narrow sense heritability.

Results and discussion

a). *Bract length and width*

Bract length in the parental lines varied from 4,00 cm (RHA-PH-BC-113) to 8,00 cm (KIZ), in F₁ generation from 5.64 cm (RHA-RFYR-576 x RHA-

PH-BC-113) to 10.10cm (CMS-81 x KIZ) and in F_2 generation from 5.00 cm (RHA-RFYR-576 x RHA-PH-BC-113) to 8.44 cm (CMS-81 x KIZ) (Table 1).

Bract width in the parental lines, on the other hand, ranged from 1.90 cm (RHA-PH-BC-113) to 2.60 cm (KIZ), in F_1 hybrids from 2.23cm (RHA-RFYR-576 x RHA-PH-BC-113) to 3.32 cm (RHA-RFYR-576 x CMS-81) and in F_2 generation from 2.22 cm (RHA-RFYR-576 x RHA-PH-BC-113) to 3.00 cm (RHA-RFYR-576 x KIZ) (Table 1)

In the inheritance of bract length and width with F_1 and F_2 generations, the dominant effect of genes H_1 and H_2 was stronger than the additive one of gene D. The value of the F coefficient is negative in both generations and for both of the investigated traits, meaning that recessive genes prevailed over the dominant ones. The average degree of dominance ($(H_1/D)^{1/2}$) was higher than 1, which indicates superdominance with regard to all combinations. In the inheritance of bract length and width with F_1 and F_2 generations, the ratio $H_2/4H_1$ suggests that the distribution of dominant and recessive genes in the parental lines was not symmetrical. With bract length and width, the ratio of the total number of dominant genes to the total number of recessive genes (K_d/K_r) is lower than 1, indicating that recessive genes prevail in the inheritance of these two traits. Both broad and narrow-sense heritability (h^2 and h^2_b) were high for both of the investigate traits (Table 2).

Regression V_rW_r for bract length and width in F_1 and F_2 generations does not deviate significantly from 1, which is an indication of the absence of epistasis. The projected line of regression intersects the W_r axis below the value of 0 (Figures.1 i 2), which is in congruence with the average dominance degree ($(H_1/D)^{1/2}$) in the analysis of the components of genetic variance. Since, in the graph, neither of the parents is at the point where the limiting parabola and the regression line intersect, it can be concluded that neither possesses all the dominant or all the recessive genes for bract length and width, but, rather, that one of them has more dominant and less recessive genes and the other vice versa. In the distribution part of the graph, disposition of the points along the projected line of regression implies the existence of genetic divergence in the parental lines and leads to the conclusion that genotypes CMS-81 and KIZ, on the one hand, and RHA-PH-BC-113 and KIZ, on the other, have a greater number of dominant and lesser number of recessive genes for bract width and length, respectively. In contrast, genotypes RHA-RFYR-576 and RHA-PH-BC-113 contain more recessive and less dominant genes for bract width. The same is true of genotypes RHA-RFYR-576 and CMS-81, only for bract length.

b) number of bracts

In the parental lines, bract number ranged from 54.33 (RHA-RFRY-576) to 66.58 (CMS-81), with F_1 hybrids from 63.42 (RHA-RFYR-576 x KIZ) to

76.25 (RHA-PH-BC-113 x KIZ) and in F_2 generation from 57.98 (RHA-RFYR-576 x KIZ) to 73.36 (RHA-PH-BC-113 x KIZ) (Table 1.).

In the inheritance of bract number in F_1 and F_2 generations, the dominant effect of H_1 and H_2 genes was more influential than the additive one of gene D. The value of the F coefficient is positive with both generations, which means that the dominant genes prevail over the recessive ones. The average degree of dominance ($(H_1/D)^{1/2}$) is higher than 1, indicating the presence of superdominance with regard to all combinations. The ratio $H_2/4H_1$ in the inheritance of bract number in generations F_1 and F_2 shows that the distribution of dominant and recessive genes in the parental lines was not symmetrical. The ratio of the total number of dominant and the total number of recessive alleles (Kd/Kr) is higher than 1, suggesting that the dominant alleles prevail, which is in agreement with the F coefficient. The values of the broad-sense (h^2_b) and narrow-sense heritability (h^2_n) were high (Table 2.).

In generations F_1 and F_2 , regression $VrWr$ for bract number does not significantly deviate from 1, leading to the conclusion that there was no epistasis. The projected line of regression intersects the Wr axis below the value of zero. This points towards the presence of superdominance in the inheritance of bract number in generations F_1 and F_2 , which is consistent with the average degree of dominance ($(H_1/D)^{1/2}$). Based on the disposition of points in the distribution part of the graph, it can be concluded that genotypes RHA-RFYR-576 and CMS-81 contain a greater number of dominant and a lesser number of recessive genes for bract number, whereas with genotypes RHA-PH-BC-113 and KIZ it is vice versa (Figure 3.).

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Table 1. Mean bract width (BW), bract length (BL) and number of bract (BN) of parents (diagonal), F₁ generation (upper right) and F₂ generation (down left) for 4x4 diallel in sunflower (values are totalled over three replications)

Parent	Character	PARENT			
		RHA- RFYR- 576	CMS-81	RHA-PH- BC-113	KIZ
RHA-	BW	2.20	3.32	2.23	3.11
RFYR-576	BL	6.20	7.94	5.64	8.30
	BN	54.33	66.75	65.17	63.42
CMS-81	BW	2.91	2.30	3.02	2.84
	BL	6.14	6.10	7.81	10.1
	BN	62.74	66.58	71.58	68.67
RHA-PH-	BW	2.22	2.51	1.90	2.71
BC-113	BL	5.00	7.23	4.00	7.00
	BN	61.48	63.96	63.08	76.25
KIZ	BW	3.00	2.91	2.62	2.60
	BL	8.44	8.43	6.11	8.00
	BN	57.98	66.98	73.37	55.92

Table 2: Components of genetic variability

Components	Character					
	Bract length		Bract width		Bracts number	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
Vr	1.97	1.23	0.20	0.11	36.53	27.75
Wr	1.01	0.94	0.05	0.06	15.06	13.49
W	0.85	0.62	0.03	0.04	8.94	8.22
Vp	1.65	1.65	0.09	0.09	33.88	33.88
Vm	0.85	0.62	0.03	0.04	8.94	8.22
D	1.58	1.60	0.07	0.09	30.88	30.57
H ₁	5.31	2.69	0.63	0.28	112.28	82.64
H ₂	4.35	2.36	0.62	0.26	104.38	71.51
F	-0.82	-0.52	-0.03	-0.06	4.53	10.48
E	0.06	0.04	0.02	0.004	2.99	3.30
(H ₁ /D) ^{1/2}	1.83	1.30	3.08	1.80	1.91	1.64
H ₂ /4H ₁	0.21	0.22	0.24	0.24	0.23	0.22
Kd/Kr	0.75	0.78	0.85	0.66	1.08	1.23
h ² _a (%)		66.07		83.80		42.43
h ² _b (%)		97.74		99.08		91.02

Figure 1.: Regression analysis VrWr for the bract width in the F₁ and F₂ generation

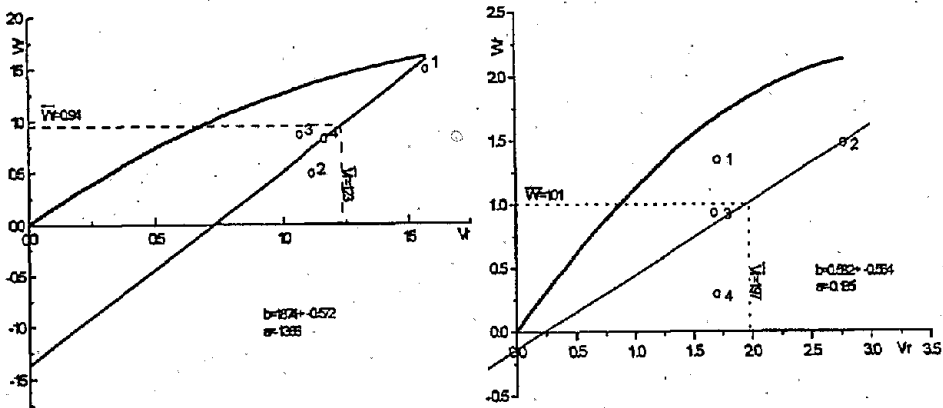


Figure 2.: Regression analysis VrWr for the bract length in the F₁ and F₂ generation

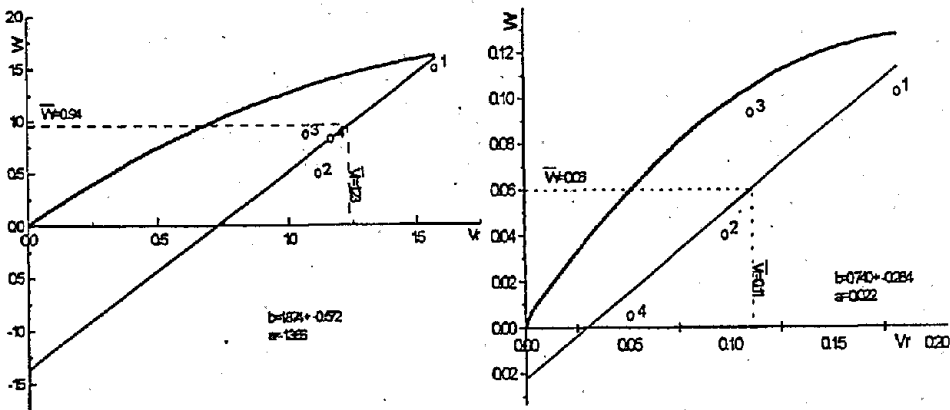


Figure 3.: Regression analysis VrWr for the number of bract in the F₁ and F₂ generations

