

GENETICS OF LEAF LENGTH AND WIDTH IN SUNFLOWER (*Helianthus annuus* L.)

Radovan Marinković, Jovan Joksimović, Branislav Dozet

Faculty of Agriculture, Institute of Field and Vegetable Crops, Novi Sad, Yugoslavia

SUMMARY

A set of diallel crosses which included six inbred lines from a gene pool of the Institute of Field and Vegetable Crops in Novi Sad was analyzed for components of genetic variability (D, H₁, H₂, F, h²) of leaf length and width. The dominant component (H₁) was highly significant for both traits, the additive one (D) was not. The dominant and recessive genes that controlled the two traits were not uniformly distributed in the parent lines. Superdominance was registered for both traits. Leaf width was controlled by at least four genes, leaf length by at least three. High values of the wide-sense heritability (h²_b) and low values of the narrow-sense heritability (h²_n) were found for both traits.

Key words: Sunflower, leaf length, leaf width, diallel, component of genetic variability, heritability.

INTRODUCTION

When analyzing heterosis expressed in crosses of homozygous lines, it is important, both theoretically and practically, to study genetic traits of these lines. This is usually done by means of diallel crossing which supplies ample information about the experimental material.

The leaf, which forms the major part of organic matter, is the most frequently studied organ of the sunflower plant. However, attention has been given to leaf area, per plant or unit area, and its correlation with yield (Prokofev and Diakov, 1961; Vrebalov, 1979; Marinković, 1980; Rawson, 1980). The data on the leaf parameters would usually exhaust themselves by the statement that the leaves in the F₁ generation are longer and wider than those of the parents (Marozov, 1947). The other data were scant. This is why we decided to study the genetics of leaf length and width in diallel crosses of sunflower.

MATERIAL AND METHOD

Six sunflower inbred lines from a gene pool of the Institute of Field and Vegetable Crops in Novi Sad were selected for diallel crossing, without reciprocals, aimed at the genetic study of leaf length and width: L-1, L-10, L-15, L-17, L-21, and L-24. The female plants were emasculated manually in early morning hours to prevent selfing.

The F₁ hybrids and their parents were sown at the experiment field of the Institute of Field and Vegetable Crops at Rimski Šančevi. The sowing was done in three replicates, after the system of random blocks. The length of rows was 3.6 m, the distance between rows 70 cm, and the distance within rows 30 cm. Each combination was sown manually in four rows. The experimental plot was cultivated and hoed to control weeds.

Leaf length and width were measured at the stage of full flowering. The measuring was done with a ruler, on 20 plants in the two inner rows in each small plot. The first and the last plant in each row were not measured.

The values used in the diallel analysis were the average values for 60 plants per treatment (parents and hybrids).

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

The statistical analysis was done according to a model proposed by Hayman (1954). The narrow- and wide-sense heritability were calculated after the method of Mather and Jinks (1971).

RESULTS AND DISCUSSION

Leaf width in the parent lines ranged from 19.20 to 22.80 cm, in L-21 and L-17, respectively, and leaf length from 20.23 to 22.33 cm, in L-10 and L-17, respectively. In the F₁ hybrid combinations, the smallest values of leaf length and width were found in the combinations L-10 x L-15 and L-1 x L-10, 22.00 and 23.23 cm, respectively; the largest width was found in the combinations L-1 x L-15 and L-21 x L-24, 25.70 cm, the largest length in the combination L-17 x L-21, 27.77 cm (Table 1).

Table 1. Mean leaf width (LW) and leaf length (LL) of parents (diagonal) and F₁ hybrids (upper right) for 6x6 diallel in sunflower (values are totalled over three replications)

Parent	Character	PARENT					
		L-1	L-10	L-15	L-17	L-21	L-24
L-1	LW	20.47	23.33	25.70	24.63	22.27	24.60
	LL	21.30	23.23	24.73	25.80	25.93	25.60
L-10	LW		19.57	22.00	24.03	23.27	25.60
	LL		20.23	25.30	26.13	25.43	26.70
L-15	LW			21.13	23.07	22.80	24.17
	LL			21.77	25.20	26.13	26.00
L-17	LW				22.80	25.53	25.57
	LL				22.33	27.77	25.73
L-21	LW					19.20	25.70
	LL					21.57	26.97
L-24	LW						22.53
	LL						20.30

The statistical analysis revealed highly significant differences between the treatments (parents and hybrids) which indicated the presence of genotypic variability within the gene pool.

The analysis of components of genetic variability showed that the dominant component (H₁) was highly significant for both traits, while the additive one was non-significant. Based on the additive-dominance model, additive genetic variance was about 0.03 and 0.19 that of the dominance components for leaf length and width, respectively.

The component H_2 was highly significant for both traits, indicating that the dominant genes that controlled the traits were not symmetrically distributed in the parent lines (Table 2). The overall dominance effects of heterozygous loci (h^2) were significant for both traits, indicating that the dominance effect was due to heterozygosity.

Table 2. Components of genetic variability

Components	Character	
	Leaf length	Leaf width
Vr	4.27	3.18
Wr	0.19	0.93
W	0.26	0.50
Vp	0.70	2.23
Vm	0.26	0.50
D	0.55±0.71	2.05±0.20
H ₁	16.63±1.81	10.73±0.50
H ₂	15.75±1.61	10.34±0.47
F	0.46±1.74	0.51±0.40
h^2	14.21±1.16	28.42±0.32
E	0.14±0.27	0.18±0.07
$(H_1/D)^{1/2}$	5.49	2.29
$k=h^2/H_2$	3.56	2.75
$H_2/4H_1$	0.24	0.24
$((4DH_1)^{1/2}+F)/((4DH_1)^{1/2}-F)$	1.16	1.12
u	0.62	0.60
v	0.38	0.40
$h^2a(\%)$	10.63	28.36
$h^2b(\%)$	96.93	95.32

A positive value of F showed that dominant genes prevailed over the recessive ones in the parent lines. Another proof for the uneven distribution of dominant and recessive genes in the parents was the value of the ratio $H_2/4H_1$. The ratio was 0.24 for both traits, i.e., lower than the maximum value of 0.25 which is obtained when $u=v=0.5$, i.e., $H_1=H_2$. This was also supported by the value of the ratio $((4DH_1)^{1/2}+F)/((4DH_1)^{1/2}-F)$. The values of this ratio for leaf width and length, 1.16 and 1.12, respectively, indicated that dominant genes prevailed in the parents for both traits. When parents contain an equal number of dominant and recessive genes, the ratio equals one and $F=0$. When parents contain more recessive genes, the value of the ratio is negative.

The ratio $(H_1/D)^{1/2}$, which stands for the average degree of dominance in all loci, was greater than one for both leaf length and width (5.49 and 2.29, respectively). It means that superdominance was expressed for both traits. In the case of partial dominance, the value of the ratio is lower than zero; in the case of full dominance, the value is one.

The ratio h^2/H_2 , which represents the number of genes that control a trait, was 3.56 for leaf width and 2.75 for leaf length. These values indicated that leaf width was controlled by at least four genes, leaf length by at least three genes.

Two kinds of heritability were analyzed: the narrow-sense heritability (h^2a), i.e., a ratio between additive and total phenotypic variance, and the broad-sense heritability

(h^2b), i.e., a ratio between genetic and total phenotypic variance. High values of the broad-sense heritability and low values of the narrow-sense heritability were obtained for both, leaf length (10.63 and 96.93, respectively) and leaf width (28.36 and 95.32, respectively). These values indicated that the dominant component prevailed in the genetic control of both traits.

REFERENCES

- Hayman, B. I., 1954. The theory and analysis of diallel crosses I. *Genetics* 39, 787-805.
- Marinković, R., 1980. Nasleđivanje veličine lisne površine suncokreta u F_1 generaciji i komponente genetske varijabilnosti (Inheritance of leaf area in F_1 generation of sunflower and components of genetic variability). *Arhiv za polj. nauke* 41, 385-392.
- Mather, K., and J. L. Jinks, 1971. *Biometrical Genetics*. 2nd ed., p. 382., London, New York, Chapman and Hall.
- Morozov, V. K., 1947. Selekcija podsolnečnika v SSSR. Pišćepromizdat, Moskva.
- Prokofev, A. A., A. B. Djakov, 1961. Listovij aparat i nakoplenie zapasnih veščestv v semenah podsolnečnika. *Botaničeskij žurnal* 46:10.
- Rawson, H. M., and G. A. Constable, 1980. Carbon production of sunflower cultivars in field and controlled environments. I Photosynthesis and transpiration of leaves, stems and heads. *Aust. J. Plant Physiol.* 7, 555-573.
- Vrebalov, T., 1979. Uloga listova u formiranju prinosa zrna i sadržaja ulja suncokreta (The role of leaves in the formation of grain yield and oil content of sunflower). *Zbornik radova Instituta za ratarstvo i povrtarstvo u Novom Sadu* 12, 199-206.

GENÉTICA DE LA LONGITUD Y ANCHURA DE LA HOJA EN GIRÁSOL (*Helianthus annuus* L.)

RESUMEN

Un juego de cruces dialélicos que incluían seis líneas puras de una colección del Instituto de Field Vegetable Crops de Novi Sad fue analizado para los componentes de variabilidad genética (D, H_1, H_2, F, h^2) para anchura y longitud de la hoja. El componente de dominancia (H_1) fue altamente significativo para ambos caracteres, mientras que el aditivo (D) no lo fue. Los genes dominantes y recesivos para ambos caracteres no estuvieron uniformemente distribuidos en las líneas parentales. Para ambos caracteres se encontró superdominancia. La anchura de la hoja estuvo controlada por al menos cuatro genes, y la longitud por al menos tres. Se encontraron para ambos caracteres altos valores de la heredabilidad en sentido amplio (h^2b) y bajos valores de la heredabilidad en sentido estrecho.

GÉNÉTIQUE DE LA LONGUEUR ET LA LARGEUR DES FEUILLES CHEZ LE TOURNESOL (*Helianthus annuus* L.)

RÉSUMÉ

Des croisements dialléliques comprenant six lignées issues d'un pool génétique de l'Institut de Field and Vegetable Crops de Novi Sad, ont permis d'analyser les composantes de la variabilité génétique (D, H_1, H_2, F, H^2) relative à la longueur et la largeur des feuilles. La composante dominante (H_1) est hautement significative pour les deux caractères alors que la composante additive (D) ne l'est pas. Les gènes dominants et récessifs pour les deux caractères ne sont pas distribués uniformément dans les lignées parentales. Une super dominance pour les deux caractères a été mise en évidence la largeur des feuilles est contrôlée par au moins quatre gènes et la longueur par au moins trois. Pour ces deux caractères nous avons trouvé des valeurs élevées tant pour l'héritabilité au sens large (h^2b) que pour l'héritabilité au sens stricte (h^2n).