

ANALYSIS OF THE GENETIC CONTROL OF BRANCHING TYPES IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

Ion Sandu¹⁾, Alexandru Viorel Vrânceanu²⁾ and Maria Păcureanu-Joița¹⁾

ABSTRACT

The branching character in sunflower has a high morphological variability and its genetic basis is not fully understood. The analysis of the genetic control of recessive branching was performed using 7 inbred lines with different branching types. The results obtained in F_1 suggested that nonbranching character is dominant over all the other studied types. This statement was based on the segregation ratio obtained in F_2 , 3:1 non-branched:branched, for all the studied combinations. Our data suggest that all the genes controlling this trait are located in the same locus, and induce 7 types of branching. We consider that for this character, there is a series of multiple alleles in sunflower, which are mutants considering the wild type-nonbranched. The present study emphasized a series of 7 alleles specific for the seven branching types: they were symbolized with b_1 - b_7 . The incomplete dominance between some alleles and overdominance for most of allelic combinations in heterozygous state was also reported.

Key words: braching, genetic control, locus, recessive, sunflower.

INTRODUCTION

Branching stem is frequent in wild sunflower species, expressing a high morphological variability.

Studies concerning the genetic control of this character in wild species suggested several dominant genes involved (Shull, 1908; Putt, 1940; Liashchenko, 1940; Heiser, 1954; Clement and Deihl, 1968). Hower, Blaringhem (1942) reported a recessive control in some varieties, while for other varieties a dominant type was established.

A highly branched inbred line 953-88-3 produced by crossing Sunrise x wild *H. annuus* from Texas was analysed by Putt (1964), who established that this character is controlled by a recessive gene *b* (all the F_1 plants were non-branched).

After backcrossing to the branched recessive parent, a segregation ratio of 1:1 was obtained, suggesting a heterozygous state for the dominant parent. By selfing F_1 plants, a segre-

gation ratio 3:1 was recorded (non-branched:branched).

Hockett and Knowles (1970) reported two new recessive genes, named b_2 and b_3 , which induce branching all along stalk when they are present as recessive homozygous genes. The top branching was induced when only one of the two mentioned genes was present.

Recently, Kováčik and Škaloud (1990) have reported the existence of two genes: b_1 , b_2 , inducing a segregation ratio of 9:7 (non-branched:branched); they suggested an oligogenic recessive control, with complementar interaction. Similar results were reported by Nenov and Tsvetkova (1994) from a study using a genotype with two lateral branches, crossed with two other genotypes.

MATERIALS AND METHODS

The analysis of branching genetic control in sunflower was performed using a diallel system; the crosses included 8 inbred lines expressing the dominant fertility restoration genes (*Rf*) and several branching genes. The F_1 generation and the segregation in F_2 were analysed. The main characteristics of these lines are summarized in table 1.

Table 1. Branching types of sunflower inbred lines

Genotypes	Types of branching		
	Number of branches	Length of branches (cm)	Position on the stalk
LC-1064Rf	-	-	nonbranching
LC-1066Rf	-	10-25	branches in the top of the stalk
Carg.-102Rf	-	20-50	branches all along the stalk
VF-1721Rf	-	10-15	2/3 of the stalk
S-75007Rf	-	12-40	branches in the top of the stalk
Sint/83-4200Rf	8-9	11-39	branches in the upper half

¹⁾ Research Institute for Cereals and Industrial Crops, 8264 Fundulea, Călărași County, Romania

²⁾ Academy for Agricultural and Forestry Sciences, Bucharest

SVM-8791Rf	6-7	10-30	branches in the upper half top branching
A-1566Rf	5-7	10-38	

RESULTS AND DISCUSSIONS

In order to evaluate the types of recessive genetic control of branching types, hybrids between LC-1064, which expresses the dominant genes for nonbranched stem, and 7 other genotypes expressing several types of branching were produced.

All the F_1 plants were nonbranched. After selfing a segregation of 3:1 (nonbranched: branched) in F_2 was obtained. These results support the fact that stem branching is controlled by recessive genes. Segregation data suggest that the recessive genes controlling this trait are located in the same locus, representing a series of multiple alleles; these alleles could be considered as mutants of the wild types under study. Diallel reciprocal crosses for all the studied lines didn't evinced significant differences if the genotypes were used as maternal/parental forms so there is no cytoplasmic effect. For this

reason, only the results of direct crosses are presented.

After crossing several branching types, we obtained either an intermediate type (LC-1066 x Carg. 102, Carg. 102 x VF-1721, Carg. 102 x Sint/83-4200, Carg. 102 x S-757007, Carg. 102 x SVM-8791, Carg. 102 x A-1566), or a new type, expressing a higher number of branches (Table 2).

In the first type, we suggest a case of incomplete dominance, and in the second one, an overdominance case.

The inbred lines expressing different branching types were symbolized with: LC-1066- b_1 , Carg. 102- b_2 , VF-1721- b_3 , S-757007- b_4 , Sint/83-4200- b_5 , SVM-8791- b_6 , A-1566- b_7 .

Analysing the F_2 generation (Tables 3 and 4), we obtained a segregation ratio of 1:2:1, distributed as follows: 25% of the plants expressing the maternal branching type, 25% the parental type, and 50% with a type of branching similar to F_1 .

The last situation corresponds to a het-

Table 2. Average number of branches in F_1 generation

	LC-1064	LC-1066	Carg. 102	VF-1721	S-75 7007	Sint/83-4200	SVM-8791	A-1566
LC-1064	0	0	0	0	0	0	0	0
LC-1066		7	11	12	10	10	8	12
Carg. 102			13.5	13	14	12.5	12	11
VF-1721				10	21	17	13	17
S-75 7007					7.5	11	11	11.5
Sint/83-4200						8	11.5	13
SVM-8791							6.5	8
A-1566								6

Table 3. The segregation number of branches in F_2 generation

	LC-1066 b_1	Carg. 102 b_2	VF-1721 b_3	S-75 7007 b_4	Sint/83-4200 b_5	SVM-8791 b_6	A-1566 b_7	Segregation ratio
LC-1066	7	7-11-13.5	7-12-10	7-10-7.5	7-10-8	7-8-6.5	7-12-6	1:2:1
Carg. 102		13.5	13.5-13-10	12.5-14-7.5	12.5-12.5-8	13.5-12-6.5	13.5-11-6	1:2:1
VF-1721			10	10-21-7.5	10-17-8	10-13-6.5	10-17-6	1:2:1
S-75 7007				7.5	7.5-11-8	7.5-11-6.5	7.5-11.5-6	1:2:1
Sint/83-4200					8	8-11.5-6.5	8-13-6	1:2:1
SVM-8791						6.5	6.5-8-6	1:2:1
A-1566							6	1:2:1

Table 4. Genetic structure of F_2 generation

	LC-1066 b_1	Carg. 102 b_2	VF-1721 b_3	S-75 7007 b_4	Sint/83-4200 b_5	SVM-8791 b_6	A-1566 b_7	Segregation ratio
LC-1066	b_1	$b_1-b_1 b_2-b_2$	$b_1-b_1 b_3-b_3$	$b_1-b_1 b_4-b_4$	$b_1-b_1 b_5-b_5$	$b_1-b_1 b_6-b_6$	$b_1-b_1 b_7-b_7$	1:2:1
Carg. 102		b_2	$b_2-b_2 b_3-b_3$	$b_2-b_2 b_4-b_4$	$b_2-b_2 b_5-b_5$	$b_2-b_2 b_6-b_6$	$b_2-b_2 b_7-b_7$	1:2:1
VF-1721			b_3	$b_3-b_3 b_4-b_4$	$b_3-b_3 b_5-b_5$	$b_3-b_3 b_6-b_6$	$b_3-b_3 b_7-b_7$	1:2:1
S-75 7007				b_4	$b_4-b_4 b_5-b_5$	$b_4-b_4 b_6-b_6$	$b_4-b_4 b_7-b_7$	1:2:1
Sint/83-4200					b_5	$b_5-b_5 b_6-b_6$	$b_5-b_5 b_7-b_7$	1:2:1
SVM-8791						b_6	$b_6-b_6 b_7-b_7$	1:2:1
A-1566							b_7	1:2:1

erozygous state.

For five combinations namely $b_1 \times b_2$, $b_2 \times b_3$, $b_2 \times b_5$, $b_2 \times b_6$ and $b_2 \times b_7$, the results obtained in F_2 suggest an incomplete dominance, and for all the others an overdominance relationship.

CONCLUSIONS

The studies concerning the genetic control of recessive branching in sunflower revealed a high morphological variability in the germplasm available at Research Institute for Cereals and Industrial Crops - Fundulea.

The analysis of several inbred lines expressing different branching types showed a recessive control for all the studied genotypes, with the "nonbranched" trait being dominant.

Based on F_1 dominance of "nonbranched stem" and a segregation ratio of 3:1 in F_2 for all the seven studied genotypes, we considered that the recessive genes controlling the branching type are located in the same locus, as members of a multiple alleles series.

Our data suggest the existence of seven alleles specific for the seven studied genotypes. They were symbolized with b_1 , b_2 , --- b_7 . In-

complete dominance in five combinations, b_1b_2 , b_2b_3 , b_2b_5 , b_2b_6 , b_2b_7 , and overdominance for all the other allelic combinations in heterozygous state were also evident.

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