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

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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 F1 suggested that nonbranching character is dominant over all the other studied types. This statement was based on the segregation ratio obtained in F2, 3:1 nonbranched: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 b1 - b7. The incomplete dominance between some alleles and overdominance for most of allelic combinations in heterozygous state was also reported.

Key words: branching, 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; Put, 1940; Liashcenko, 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 F1 plants were nonbranched).

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 F2 plants, a segregation ratio 3:1 was recorded (nonbranched:branched).

Hockett and Knowles (1970) reported two new recessive genes, named b2 and b3, 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, Kováčík and Skaloud (1990) have reported the existence of two genes: b1, b2, inducing a segregation ratio of 9:7 (nonbranched: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 F1 generation and the segregation in F2 were analysed. The main characteristics of these lines are summarized in table 1.

Table 1. Branching types of sunflower inbred lines

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Number of branches</th>
<th>Length of branches (cm)</th>
<th>Position on the stalk</th>
</tr>
</thead>
<tbody>
<tr>
<td>LC-1064Rf</td>
<td>-</td>
<td>10-25</td>
<td>nonbranched branches</td>
</tr>
<tr>
<td>LC-1066Rf</td>
<td>-</td>
<td>20-50</td>
<td>branches all along the stalk</td>
</tr>
<tr>
<td>Carg.-102Rf</td>
<td>-</td>
<td>10-15</td>
<td>2/3 of the stalk branches in the top of the stalk</td>
</tr>
<tr>
<td>VF-1721Rf</td>
<td>-</td>
<td>12-40</td>
<td>branches in the upper half</td>
</tr>
<tr>
<td>S-75007Rf</td>
<td>-</td>
<td>11-39</td>
<td></td>
</tr>
<tr>
<td>Sint/83-4200Rf</td>
<td>8-9</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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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 F₁ plants were nonbranched. After selfing a segregation of 3:1 (nonbranched: branched) in F₂ 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 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-b₁, Carg. 102-b₂, VF-1721-b₃, S-757007-b₄, Sint/83-4200-b₅, SVM-8791-b₆, A-1566-b₇.

Analysing the F₂ generation (Tables 3 and 4), we obtained a segregation ratio of 1:2:1, distributed as follows: 25% of the plants expressed the maternal branching type, 50% with a type of branching similar to F₁.

The last situation corresponds to a het-
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 \(b_1, b_2, \ldots, b_7\). Incomplete 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.

REFERENCES
