

INHERITANCE OF BRANCHING TYPES IN SUNFLOWER

Ion SANDU, Alex V. VRÂNCEANU, Dan-Sorin CRAICIU,
Ilie BĂLANA and Maria PĂCUREANU
Research Institute for Cereals and Industrial Crops
Fundulea 8264 Călărași (România)

Abstract

The branching character in sunflower has a high morphological variability. The type of branching can be short or long, profuse or scarce, basal or top, or all stem type.

The branching character in sunflower wild species is dominantly inherited, whilst in cultivated sunflower it is mainly determined by recessive genes. The study carried out at the Research Institute for Cereals and Industrial Crops Fundulea included different types of branching and nonbranching (monoheaded) type. The purpose of the study was to determine the inheritance of the branching character as result of crosses between the different types. Different types of branching in cultivated sunflower are controlled by different recessive genes, and the influence of environment was also demonstrated. The types with recessive genes are widely used as restorer lines in sunflower hybrid production. The result of the crosses between two inbred branching types was an intermediante type. The F₂ generation segregated in 1:2:1 ratio for this character.

Key words: sunflower, inheritance, branching, dominance, recessiveness.

Introduction

The branching character is very common in wild species of sunflower, showing a wide range of morphological variability. Using test crosses within wild species (PUTT 1940, LIASKENKO 1940 and HEISER 1954) it was demonstrated that the branching character is dominantly inherited.

PUTT identified a single dominant gene named *Br*₁ which controls all stalk branching.

Later (HOCKETT and KNOWLES 1970) reported two dominant genes *Br*₂ and *Br*₃, the first one controlling the top branching. Together the two mentioned genes control the branching over the whole length of the stalk. KOVACIK and SKALOUD 1990, reported two dominant complementary genes which together control the branching all along the main stalk. The branches were shorter if one of

the two dominant genes were present. PUTT 1964, established that the intensive branching of the inbred 953-88-3 was inherited by a recessive gene named "b". It is supposed that the origin of "b" gene is a wild species from Renner - Texas. This type of branching being recessive, is fully subordinated by the dominant "non branching" character. The F₁ generation will exhibit only non branched plants.

HOCKETT and KNOWLES 1970, reported a further two recessive genes, named "b₂" and "b₃", which induced branching all along the stalk when they were present as recessive homozygous.

The top branching was induced when only one of the two mentioned genes were present. KOVACIK and SKALOUD (1990) reported two genes "b₁" and "b₂" which segregated in the ratio 9:7 (nonbranched : branched) in the F₂ generation.

If one or other of two aforementioned genes were present as homozygous recessive than the plants were branched. The study of the "branching" character of the stalk constituted the aim of many research projects in sunflower. NENOV and TSVETKOVA, 1994, studied the inheritance of branching types. VRANCEANU 1985, studied the use of recessive branching types in sunflower seed production. This topic still needs to be continued to gain a better knowledge of the phenomenon.

Materials and methods

The research was carried out during 1993-1995 at the Research Institute for Cereals and Industrial Crops Fundulea. 9 sunflower inbred lines were included in a diallel crosses, both directly and reciprocally. The inbreds had dominant genes for pollen fertility restoration (Rf) and genes which control the branching character. The F₁ generation and the segregation ratio in the F₂ were analysed.

The studied inbreds were:

1. Rf 1064 - nonbranching type.
2. Rf 1066 - 6-8 branches in the top of the stalk having the length of 10-25 cm.
3. Rf 102 - branches all along the stalk, the length of branches being 20-50 cm.
4. Rf 1721 - 2/3 of the stalk length branched and the branches having a length of 10-15 cm.
5. Rf 70007 - 7-9 branches in the top of the stalk with a length of 12-40 cm.
6. Rf 420 - 8-9 branches in the upper half, with a length of 11-39 cm.
7. Rf 8791 - top branching (6-7 branches) with the length of 10-30 cm.
8. Rf 1566 - top branching (5-7 branches together), with a length of branches 10-38 cm.
9. Rf 8740 - two symmetric basic branches with a length of 40-60 cm.

Because of the strong interaction with the environment, the study of morphological characters of parental lines and F₁ and F₂ generation was made in 1995.

Results, discussion and conclusion

Crossing the Rf 1064 nonbranched type with all other types of branching, in F₁ generation only nonbranched plantes were obtained. After the selfing of the F₁ generation, the segregation ratio in F₂ was 3:1 (nonbranched to branched).

This fact demonstrates the genetic inheritance by the recessive genes, with the "nonbranched type" character being dominant.

The reciprocal crosses do not show significant differences among the parental lines used as the male or female. The crosses between different branching types produced an intermediate type in the F₁ generation. This type was intermediate for the number and length of branches and the position and angle of branch insertion.

The data presented in Table 1 demonstrated that the heterozygous structure induced an intermediate expression of the character.

Table 1

Average number of branches in F₁ generation

Female \ Male	RF 1064	RF 1066	RF 102	RF 1721	RF 75007	RF 420	RF 8791	RF 1566	RF 8740
RF 1064	0	0	0	0	0	0	0	0	0
RF 1066		7	11	12	10	10	8	12	0
RF 102			13.5	13	14	12	12	11	0
RF 1721				10.5	21	17	13	17	0
RF 75007					7.5	11	11	11.5	0
RF 420						8.3	11	13	0
RF 8791							6.5	8	0
RF 1566								6	0
RF 8740									2

The F₂ generation presented a large variability. By crossing the nonbranched Rf 1064 with different types of branching in the F₂ generation, the segregating ratio was 3:1 (nonbranched to branched).

The branched plants were divided in several phenotypic groups:

Rf 1064 x Rf 1066 70 nonbr. : 27 br. (9:2:8:6:2)

Rf 1064 x Rf 102 78:22 (10:4:6:1:1)

Rf 1064 x Rf 1721 64:18 (12:3:3)

Rf 1064 x Rf 75007 61:35 (18:7:6)

Rf 1064 x Rf 420 66:21 (8:6:2:2:1:1:1)

Rf 1064 x Rf 8791 68:30 (12:9:4:3:1:1)

Rf 1064 x Rf 1566 68:21 (7:7:7)

Rf 1064 x Rf 8740 73:20 (8:4:4:4)

The number of phenotypic groups for the segregating plants was between 3 and 7. This demonstrated that polygenic control of inheritance is involved. The number of phenotypic groups (3,4 or 7) depends on the active number of alleles. The crosses between branching types recessively inherited produced in the F₁ generation, a new type intermediate for number, length, angle and position of branches.

The fact that in the F₂ generation all plants were branched, demonstrated that the alleles are situated on the same chromosome. The analysis of the F₂ generation demonstrated that useful type of plants are located in phenotypic groups with an intermediate type of branching. The continuous phenotypic variation between the parental lines demonstrated the presence of 3 phenotypic groups, and the action of 2 pairs of genes. The 2 pairs of genes are contributing to the development of the same character, having a cumulative effect. The alleles of those genes could present dominance or recessiveness.

A particular response in the F₂ generation had the RF-8740 combination showing two basal branches with all combinations of branching type. In this case, in the F₂ generation, the segregating ratio was 2:1. The branched plants were assigned to the abovementioned 3 phenotypic groups.

Crossing Rf-1066 by RF 8740 produced:

- plants totally branched with variable length, increasing from the base to the top.
- plants branched all along the stalk, more numerous in the upper half.
- plants with 11-12 ramifications in the upper half.
- plants with 6-9 branches at the top of the stalk.
- two headed plants.
- five headed plants.
- plants having 2-3 branches at base.

Segregating ratio was 62:3 (3:4:8:10:1:1:3).

This segregation of the F₂ generation demonstrated that the branching genes were located at different loci of the same chromosome, polygenes being involved.

The study of the branching character demonstrated that the phenomenon is very complex. There are several genes with individual effects, small and additive for branching character.

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