

GENETIC STUDY OF SHORT PETIOL TRAIT AND ITS USE IN SUNFLOWER BREEDING

A.V.Vrânceanu, Monica Luoraş and F.M.Stoehescu
 Research Institute for Cereals and Industrial Crops
 8264 - Fundulea, Romania

SUMMARY

The mutant "short petiol" discovered at Fundulea in an inbred originated from the Romanian variety Orizont represents an important agronomical trait permitting the reconstruction of plant architecture with the view of increasing plant population per unit area and maximizing yield capacity. The hybridological study revealed the cumulative action of at least two dominant genes (denominated with the symbol Ps). The inheritance of this trait permits its transfer into different genotypes, through backcrosses and selection, without selfing after each backcross generation, as in the case of the recessive traits. A certain number of sunflower inbreds have been already converted and used in short petiol hybrid breeding programme.

INTRODUCTION

Photosynthesis intensity of the leaves situated on the lower part of the stem decreases along with the plant population increase, so, an important aim of sunflower breeding has to be the creation of a certain plant architecture, which would permit a more efficient utilization of light (V r â n c e a n u, et al., 1974; A r n o u x, 1978; V r â n c e a n u, 1978; S k o r i ć, 1980). "Short petiol" may be considered an important trait because brings the blade near the stem and so gives the possibility to increase considerably plant population per area unit without decreasing photosynthetic activity of each plant.

"Short petiol" mutants have a low frequency in the frame of different sunflower genotypes. L u c z i e w i c z (1975) isolated plants with short and thick petiol from the variety Karlik '68. These plants gave normal F_1 plants when crossed with normal inbreds. Segregation ratio in F_2 was closed to the theoretical ratio 9 normal: 7 mutant, this indicating the action of two complementary recessive genes for this trait. Two "short petiol" mutant plants were detected in the Romanian inbred O-7657, in 1981. They were used in genetic studies and as sources for getting inbreds and hybrids with this trait.

MATERIALS AND METHODS

The mutant plants were selfed. Mutant plants of next generation were crossed to three normal inbreds with long petiol. F_2 generations were obtained by selfing F_1 mutant plants, having the petiol length of 0-8 cm. F_3 generations resulted from selfing of F_2 mutant plants and BC_1 generation from the cross of F_1 mutant plants to the parental inbreds. The mutant plants were grouped in four classes with the following intervals: 0-2 cm, 2-4 cm, 4-6 cm and 6-8 cm, measuring the petiol length of the leaves situated at the stem middle. The plants with petiol longer than 8 cm were considered normal.

Segregation ratios were assessed using the χ^2 test.

Generation mean analyses were used to quantify possible polygenic effects using the methods described by M a t h e r and J i n k s (1971).

Each of the generation mean can be expressed in terms of the following effects: a = pooled additive effect; d = pooled dominance effect ; aa = pooled additive x additive epistatic effect; ad = pooled additive x dominance epistatic effect; and dd = pooled dominance x dominance epistatic effect. The equations are as follows: $P_1 = m + a + aa$; $P_2 = m - a + aa$; $F_2 = m + 0.5 d + 0.25 dd$; $F_3 = m + 0.25 d + 0.0625 dd$; $BC_1 I = m + 0.5 a + 0.25 d + 0.25 aa + 0.125 ad + 0.625 dd$; $BC_1 II = m - 0.5 a + 0.25 d + 0.25 aa - 0.125 ad + 0.625 dd$. The parameters in the above equations were estimated using an unweighted least square analysis. The significance of genetic effects were evaluated from an analysis of variance of generation means. Twenty seven valuable normal inbreds have been already converted into "short petiol" ones, in order to produce hybrids with the respective trait.

RESULTS

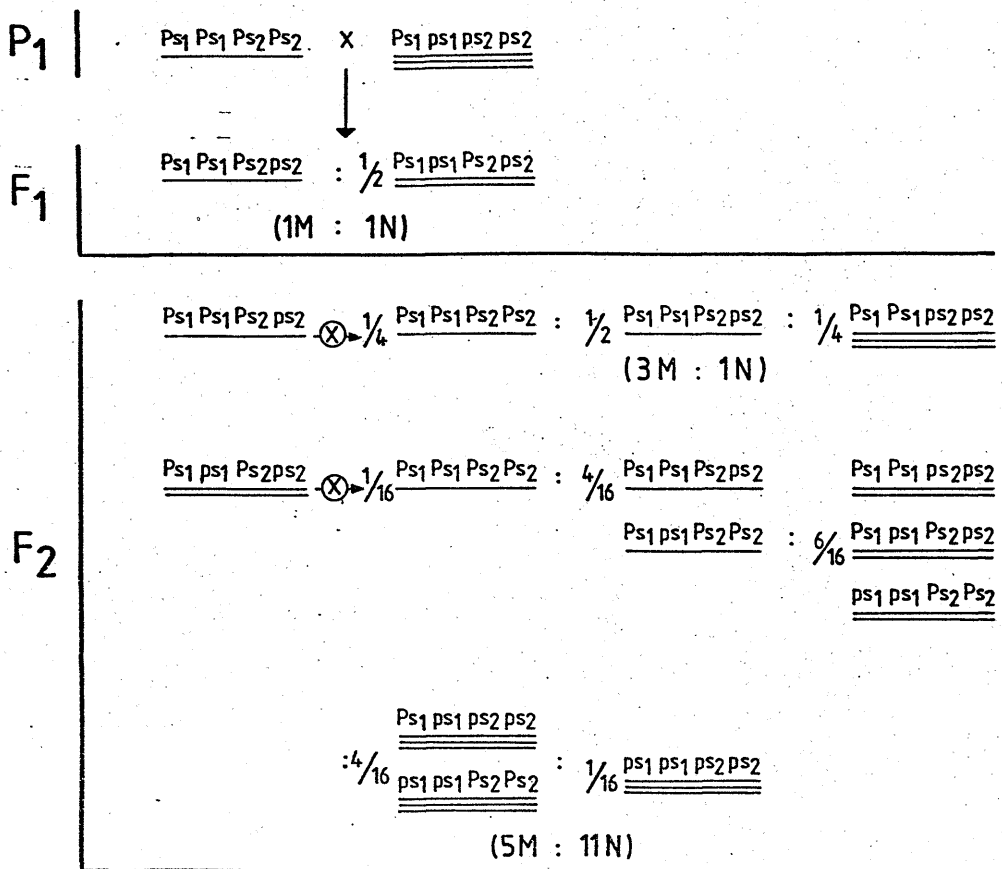
Segregating generations contained mutant individuals with different petiol length, suggesting thus a rather complex genetic inheritance. Table 1 contains the individual distribution in 6 classes, means and variances of the parents and F_1 , F_2 , F_3 and BC_1 generations.

Table 1

Distribution, means and variances of petiol length (cm) for parental and segregating generations F_1 , F_2 , F_3 , and BC_1 , from the cross O=7657 M x three normal inbreds.

Generation		Class interval (cm)						n	\bar{x}	Variance
		0-2	2-4	4-6	6-8	8-10	10			
P_1	O=7657 M	47	13					60	2.0	1.0
P_2	I O=7704						20	20	12.0	0.9
	II O=7754						20	20	12.4	1.0
	III O=7823						20	20	11.2	0.8
F_1	I $P_1 \times P_2$ I	23	7	8		7	40	85	8.0	6.1
	II $P_1 \times P_2$ II	76	27	8	3	2	89	203	6.0	6.25
	III $P_1 \times P_2$ III	30	19	14	4	3	48	118	7.0	6.6
F_2	I	18	90	3	2	4	24	141	5.0	5.0
	II	5	20	3		1	7	36	5.0	6.25
	III	5	49	4		6	92	156	9.0	6.4
$BC_1 I$	I	13	18	7	4		21	63	6.0	
	II	7	12	1			11	31	7.0	
	III	4	8	4			22	38	10.0	
$BC_1 II$	I	7	30	60	27	3	23	150	6.0	
	II	1	13	20	7	4	30	75	8.0	
	III		6	15	4	2	18	45	8.0	
F_3	I	6	20	2	2		0	30	3.0	
	II	2	40	18	2		58	110	9.2	
	III		20	12			28	60	8.0	

Scheme 1. Segregating ratio short petiol: long petiol for two dominant genes with cumulative effect (hypothesis)



----- short petiol
 ===== intermediate
 ===== long petiol

M - mutant
 N - normal

For the genetic analysis of F_1 and F_2 generations presented in Scheme 1, all plants with petiol shorter than 8 cm were considered mutants and with petiol longer than 8 cm normal individuals. In order to interpret the segregation ratios in F_1 and F_2 generations the hypothesis of existing at least two dominant genes with cumulative action was emitted. The mutant plants were considered homozygous for the dominant alleles Ps_1 and Ps_2 , and the inbreds with normal phenotype as heterozygous for one gene and recessive homozygous for the other gene.

Segregation in F_2 was evaluated supposing that the "short petiol" individuals possess at least three dominant alleles, and the normal or almost normal genotypes less than two dominant alleles of the two genes. Data presented in Table 2 validate this hypothesis in six out of seven cases, in which χ^2 had values lower than those for $P = 5\%$.

Table 2

Segregating ratio short petiol : long petiol in F_1 and F_2 generations when the mutant inbred O-7657 was crossed to three normal inbreds

Generation	Plants total number	Observed ratio		Test for "two dominant genes with cumulative effect" hypothesis			
		long petiol	short petiol	theoretical ratio:	2	P	
				short petiol			
				long petiol			
F_1	I	85	38	47	1 : 1	0.96	0.50-0.30
	II	203	114	89	1 : 1	3.80	0.05-0.01
	III	118	67	51	1 : 1	2.17	0.20-0.10
TOTAL	406	219	187	1 : 1	2.53	0.20-0.10	
F_2	I	141	113	28	3 : 1	1.99	0.20-0.10
	II	33	25	8	3 : 1	0.01	0.90-0.95
	III	156	58	98	5 : 11	0.61	0.30-0.20

All three F_1 generations segregated in a ratio closed to the theoretical one, 1 mutant : 1 normal. Two F_2 generations segregated in a ratio closed to 3 mutant : 1 normal but the third F_2 generation suggested significantly the ratio 5 mutant : 11 normal. Results of analyses among generation means using an additive - dominance model showed dominance effect were higher than additive ones, but associated with a greater standard error. Additive x dominance and dominance x dominance effects had negative large magnitudes which suggest certain interallelic gene relationships (Table 3).

DISCUSSIONS

The "short petiol" trait discovered at the Research Institute of Fundulea, is a heritable character and so, selection of inbreds similar to the mutant phenotype, is possible. When "short petiol" was considered simply inherited, the segregation ratio in F_1 and F_2 generations evidenced two dominant genes with cumulative effects.

Table 3

Genic effect estimation and standard errors for
 "short petiol" trait in O-7657 M x O-7704 sunflower
 inbred crosses

Genic effect	Genic effect estimation	Standard error
Mean (m)	6.78	1.75
Additive (a)	5.23	0.19
Dominance (d)	8.79	4.15
Additive x additive (aa)	-1.80	1.14
Additive x dominance (ad)	-6.62	2.12
Dominance x dominance (dd)	-3.94	1.18

If more than two dominant genes act cumulatively for the expression of this character, the number of normal petiol phenotypes would decrease and intermediate phenotypes would increase proportionally (Scheme 1). When a polygenic inheritance was supposed, a prevalent dominant gene effect was found.

Results of this study demonstrate the high heritability of "short petiol" trait and the magnitude of the dominant gene effects indicates that the respective trait can be transferred to different genotypes, through backcross and selection, without selfing after each backcross generation as in the case of recessive characters.

The important additive gene effect indicates that repeated selection for very short petiol in a population should be effective, providing even less-petiol individuals or inbreds.

CONCLUSIONS

"Short petiol" represents an important agronomical trait permitting the reconstruction of the plant architecture for increasing plant population per unit area and maximizing yield capacity. This mutant has a low frequency in cultivated sunflower genotypes.

The "short petiol" mutant discovered at Fundulea is determined by at least two dominant genes with cumulative effect, so only backcrosses and selection, without selfing after each backcross generation are needed for its transfer to other genotypes.

Repeated selection for very short petiol in a population is effective, and could result even in less-petiol individuals or inbreds.

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