

## Inheritance of Fertility Restoration in Wild Sunflowers

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### Abstract

The presence of the genes for pollen fertility restoration was studied in 75 populations of wild *H. annuus* and *H. petiolaris* that were collected in the Great Lakes Region and Central Great Plains of the USA. The inheritance of pollen fertility restoration was studied in ten crosses. The populations of wild *H. annuus* were included in all ten crosses. Research on 10 sources of pollen fertility restoration revealed that this character was controlled in eight cases by one single dominant gene and in two cases by two complementary genes.

**Key words:** Wild species, inheritance, rf genes.

### Introduction

The discovery of cytoplasmic male-sterility in sunflower by LECLERCQ (1969) and the subsequent identification of restorer genes for pollen fertility by KINMAN (1970), ENNS ET AL. (1970) and VRANCEANU AND STOENESCU (1971) has led to the widespread use of cms in the production of sunflower hybrids.

VRANCEANU and STOENESCU (1973), FERNANDEZ ET AL. (1974) and FICK and ZIMMER (1974) reported that they discovered the genes for pollen restoration fertility in cultivated sunflower. However, the highest number of genes for the restoration of pollen fertility was discovered in wild sunflower species (DOMINGUEZ GIMENEZ and FICK, 1975; FICK ET AL., 1974; FICK ET AL., 1976; ŠKORIĆ ET AL., 1988; JAN, 1990; CHRISTOV, 1992).

The objective of this investigation was to find new sources of the genes for pollen fertility restoration in some wild sunflower species (wild *H. annuus* and *H. petiolaris*), to determine the number of genes and type of gene action controlling fertility restoration of cms.

## Materials and methods

Seventy-five populations of wild sunflower *H. annuus* and *H. petiolaris* collected from the Great Lakes Region and Central Great Plains of the United States were crossed with the cytoplasmic male-sterile inbred lines V-8931-3-4 (L-1). The L-1 is a selection from the variety VNIIMK-9831, that was converted to male sterility by back-crossing to the cms source discovered by LECLERCQ (1969).

The crosses between the line L-1 and wild populations *H. annuus* and *H. petiolaris* were performed at the experiment fields of the Institute of Field and Vegetable Crops - Novi Sad at the location of Rimski Šančevi in the summer of 1993. The plants of the line L-1 were isolated with paper bags before the beginning of flowering. Pollen mixture that was put on the plants was collected from 10-15 plants per every population. The plants of the populations were also isolated with paper bags. The seed of  $F_1$  was sown the next year at the same experiment field. All the seed produced in the crosses was sown. Before flowering, all plants were isolated with bags. In the stage of flowering, restoration of fertility was determined primarily by visual observations of the pollen and by staining with aceto carmine. All  $F_1$  plants were fertile in 15 of 75 crosses. The populations of wild *H. annuus* were included in all 15 crosses. These 15 crosses were selected for the study of the inheritance of pollen fertility restoration. The mixture of pollen was collected from each cross and was put on the plants of the line L-1. In that way, the seed of  $BC_1$  was produced. Due to the fact that the plants were isolated, the seed of the  $F_2$  generation was obtained at the end of the growing period.

The seed of  $BC_1$  and  $F_2$  generation was sown at the experiment field in 1995. The presence and absence of pollen on the plants was determined in the period of flowering as it was done in the previous year. Due to the fact that a large number of plants was destroyed because of various reasons, we selected 10 crosses for the further analysis (Table 1).

Goodness of fit of observed male-fertile to male-sterile plants to the expected number in the various populations was tested by the  $X^2$  method.

## Results and discussion

The analysis of pollen in the  $F_1$  plants discovered that the genes for pollen fertility restoration are present in a large number of wild population of *H. annuus*. However, in 15 crosses all  $F_1$  plants were fertile, which indicates that the populations of wild *H. annuus* were homozygous dominant for fertility restoring genes. The presence of fertile and sterile plants in some crosses suggested that one or more of the 15 plants used in the bulk pollination of

cms L-1 were either heterozygous or homozygous recessive for fertility restoration. The absence of fertile  $F_1$  plants in some crosses indicated that there was no dominant gene for fertility restoration of these 15 plants of the populations from which pollen was collected.

The results of the analysis of the presence of pollen in the plants of the  $F_2$  and  $BC_1$  generation and the expected relation of segregation of fertile and sterile plants for ten crosses used for the study of the inheritance of pollen fertility restoration is presented in Table 1.

In the crosses 1, 2, 3, 4, 5, 7, 9 and 10 the segregation of fertile and sterile plants in  $BC_1$  generation was near 1:1. Due to the fact that in the  $F_2$  generation the relation of the segregation of fertile and sterile plants was near 3:1, it can be considered that a single dominant gene is responsible for fertility restoration of male sterile cytoplasm. ENNS ET AL. (1970), KINMAN, (1970), LECLERCQ, (1971) and VRANCEANU and STOENESCU (1971) wrote about the control of pollen fertility restoration by a single dominant gene.

Unlike the above mentioned crosses, the crosses 6 and 8 had the segregation relation of fertile and sterile plants in  $BC_1$  generation approximately 3:1 and in  $F_2$  generation it was approximately 9:7. This indicates that two complementary dominant genes control fertility restoration in these two cases. FICK and ZIMMER (1974), DOMINGUEZ GIMENEZ and FICK (1975), RADDY and THAMMI RAYU (1977) and MEGALE ET AL. (1988) also reported that they discovered the effect of two independent dominant genes on pollen fertility restoration in some crossing combinations.

In these studies, no case was found in which three or more genes are responsible for pollen fertility restoration. However, VRANCEANU and STOENESCU (1978) reported the three cases in which fertility restoration was conditioned by three complementary genes and in one case by the cumulative action of two non-allelic dominant genes. DOMINGUEZ GIMENEZ and FICK (1975) and WHELAN (1980) reported that they discovered the cases in which fertility restoration was controlled by four non-allelic genes.

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**Table 1.** Number of male-fertile (MF) and male-sterile (MS) plants in F<sub>1</sub>, F<sub>2</sub> and BC<sub>1</sub> generations and Chi-square analysis

Cross	Genera- tion	No. of plants		Expected ratio	X <sup>2</sup>	P
		MF	MS			
1. L <sub>1</sub> x ANN-2005	F <sub>1</sub>	37	0			
	F <sub>2</sub>	31	11	3:1	0.032	0.80-0.90
	BC <sub>1</sub>	27	23	1:1		
2. L <sub>1</sub> x ANN-2038	F <sub>1</sub>	25	0			
	F <sub>2</sub>	35	10	3:1	0.185	0.60-0.70
	BC <sub>1</sub>	50	45	1:1		
3. L <sub>1</sub> x ANN-2130	F <sub>1</sub>	39	0			
	F <sub>2</sub>	25	8	3:1	0.010	0.90-0.95
	BC <sub>1</sub>	32	30	1:1		
4. L <sub>1</sub> x ANN-2131	F <sub>1</sub>	28	0			
	F <sub>2</sub>	35	11	3:1	0.029	0.80-0.90
	BC <sub>1</sub>	41	44	1:1		
5. L <sub>1</sub> x ANN-2153	F <sub>1</sub>	28	0			
	F <sub>2</sub>	24	7	3:1	0.097	0.75
	BC <sub>1</sub>	52	48	1:1		
6. L <sub>1</sub> x ANN-2169	F <sub>1</sub>	30	0			
	F <sub>2</sub>	42	30	9:7	0.127	0.50-0.75
	BC <sub>1</sub>	58	20	3:1		
7. L <sub>1</sub> x ANN-2171	F <sub>1</sub>	20	0			
	F <sub>2</sub>	29	10	3:1	0.077	0.80-0.90
	BC <sub>1</sub>	50	52	1:1		
8. L <sub>1</sub> x ANN-2197	F <sub>1</sub>	26	0			
	F <sub>2</sub>	40	27	9:7	0.324	0.05-0.10
	BC <sub>1</sub>	58	24	3:1		
9. L <sub>1</sub> x ANN-2225	F <sub>1</sub>	28	0			
	F <sub>2</sub>	39	12	3:1	0.059	0.80-0.90
	BC <sub>1</sub>	35	32	1:1		
10. L <sub>1</sub> x ANN-2231	F <sub>1</sub>	31	0			
	F <sub>2</sub>	50	18	3:1	0.079	0.80-0.90
	BC <sub>1</sub>	24	28	1:1		