

INHERITANCE OF SELF-INCOMPATIBILITY  
IN SUNFLOWER

Aurelio Luciano, Ing. Agr.  
Sunflower Section  
Agricultural Experiment Station  
Pergamino, Argentina

It was mentioned before that the production and utilization of single cross hybrids in sunflower are the most desirable means of obtaining higher yields.

Hybrids between selected inbreds may yield as much as 72 to 132 percent above the yield of standard commercial varieties. The major obstacle to the utilization of sunflower hybrids is the lack of an economical and efficient means of making the crosses.

As we know, sunflower is a monoecious plant with the male and female organs in the same flower; and thus, the percentage of hybrid plants obtained from crossing blocks will depend upon the self-incompatibility of the female line and the insect population. This percentage is variable within the same hybrid combination in different years. The commercial hybrids released up to this time have this serious fault.

For this reason the utilization of heterosis in sunflower will be delayed until a better understanding of the inheritance of self-incompatibility or the discovery of cytoplasmic male sterility.

The concept of heritability is associated with the relative importance of heredity and environment in determining the expression of characters.

To know the heritability of a character in a specific population is very helpful for estimation of gain to be expected under selection.

The objective of this investigation is the study of the inheritance of self-incompatibility and determination of its heritability value in order to estimate the efficiency of selection for this character. If the estimation of heritability is high, it should be possible to develop self-incompatible lines for use as female parent in the production of commercial hybrids.

The following lines were used in the present study:

Line HA 42 (953-102-1-1-22-12-T1-B-B-9) which is closely related to line 22 from Canada. It is considered a self-fertile line by its seed production under bags.

Line HA 38 (Hopi-04-01-B1-3-1-2-1-1) developed at College Station, Texas, was derived from the open-pollinated progeny of a rust resistant plant found in the Hopi variety.

Line S-37-388T. The original line S-37-388 was developed in Canada from the Mennonite variety. The modified line used in this study resulted from a single cycle of recurrent selection for increased self-incompatibility and larger seed size at College Station, Texas. It is the most self-incompatible line available at present.

F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub> and F<sub>4</sub> generations of the following crosses were used:

S-37-388T × HA 42 (cross No. T 56002)

S-37-388T × HA 38 (cross No. T 61002)

Self-pollination of plants in F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub> and F<sub>4</sub> generations at College Station, Texas. Some of the F<sub>3</sub> and F<sub>4</sub> were grown at Pergamino, Argentina.

Counting of fertile seed of each self-pollination was practiced in all generations. One of the methods of estimating heritability is by measuring the regression of offspring on parent.

Three practices have been used here:

1. Repeat the parent's records with each offspring's record.
2. Regress the average of all the offspring on a parent on the parent's record.
3. Kempthorne and Tandon weighted regression technique.

The estimate b, the regression of offspring's phenotype on the phenotype of the parent, in a random mating population without epistasis will equal

$$1/2 \frac{\sigma_g^2}{\sigma_p^2} \quad \text{but} \quad \frac{\sigma_g^2}{\sigma_p^2} = h^2 = \text{heritability in the narrow sense.}$$

then  $h^2 = 2b$ . Heritability in the narrow sense, if epistasis and dominance are negligible, is equal to the double of the estimate of b.

The regression coefficients and heritability values for the cross T 56002 are shown in the following table.

Regression method <sup>1/</sup>	College Station		College Station		Pergamino (Argentina)	
	F <sub>2</sub> - F <sub>3</sub>		F <sub>3</sub> - F <sub>4</sub>		F <sub>3</sub> - F <sub>4</sub>	
	b	h <sup>2</sup>	b	h <sup>2</sup>	b	h <sup>2</sup>
A	.01 NS	.02	.34**	.68	.24**	.49
B	.65 NS	1.30	.28**	.57	.29**	.59

<sup>1/</sup> A - repeating the parent's records with each offspring's record.  
 B - average of all the offspring of a parent on the parent's record.

The above data indicate that: (1) F<sub>3</sub> - F<sub>4</sub> regression coefficient at both locations was highly significant and (2) the regression of F<sub>2</sub> - F<sub>3</sub> was not significant.