

ESTIMATION OF THE HERITABILITY AND GENETIC VARIATION IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

J. A. KESTELOOT¹, J. HEURSEL²
and F. M. PAUWELS³

INTRODUCTION

The most important oil crop in Argentina is sunflower (*Helianthus annuus* L.). In the last years, North America and Europe have greatly increased their cropping area.

Information about genetic variance and heritability in sunflower had been reported by few authors (Kováčik and Skaloud, 1978, Luczkiewicz, 1973, Marinković, 1982, Omran et al., 1976, Pathak, 1974, Putt, 1966, Roath et al., 1982, and Shabana, 1974). Information is limited to eight characters which can be measured during or after flowering.

The objectives of this work were: 1) to find the relative importance of the GCA, SCA and RE (reciprocal effects), and 2) to find narrow sense heritability estimates for thirty characters, thirteen of them measurable in the vegetative stage.

With this information it would be possible to choose a more appropriate breeding method and to know which cultivars will produce more extreme values for the selected character. If indirect selection for high yield will be made, and if there is an hesitation about two characters, the knowledge of heritability will be one of the judgement elements to bear in mind.

MATERIALS AND METHODS

Seed of five lines (CCM 611, 7CM99, CP 331, C 104 and C10V), each of them in the sterile (Srr) and fertile (Frr) forms, were obtained from INRA (Institut National de la Recherche Agronomique) Clermont Ferrand, France. They were crossed in all combinations in the green-

house. Seed of all the hybrids and pure lines were collected. The seeds from the cross 7CM99 (Srr) × CP 331 (Frr) which did not have enough dormancy, had an irregular germination on the field and had to be eliminated from the analysis of the diallel cross.

The F₁ and pure lines were sowed at the Rijkstation voor Plantenveredeling in Merelbeke, Belgium, on May 9, 1979. The experimental layout was a randomized complete block, with 4 replications of 19 hybrids and 5 pure lines. At the end of each line in each plot, or 4 seeds of fertile plants were sown together. The experimental field was also surrounded by hermaphrodite plants. Each plot was formed by 3 rows, but only 7 plants in the central row were measured.

The data of the incomplete diallel cross were analysed according to the fixed model of Keuls and Garretsen, 1977, and Garretsen and Keuls, 1978:

$$Y_{ijk} = \mu + \lambda^*i + \lambda^*j + S^*_{ij} + r^*_{ij} + \epsilon_{ijk}$$

* = denotes the reduction of the parameters,

μ = general mean level,

$\lambda_i(j)$ = the GCA of the i^{th} (j^{th}) parent,

S_{ij} = the SCA for the cross between the i^{th} and j^{th} parents,

r_{ij} = the reciprocal effects,

ϵ_{ijk} = error term.

The heritability values were calculated by using variance estimates of the GCA, SCA, RE and error, with the assumptions that $F=1$ (F =coefficient of inbreeding) and that epistatic components of genetic variance were negligible (Garretsen and Keuls, 1973).

$$h = \frac{2 \sigma^2 \text{GCA}}{2 \sigma^2 \text{GCA} + \sigma^2 \text{SCA} + \sigma^2 \text{RE} + \sigma^2 \text{error}}$$

$\sigma^2 \text{GCA}$ = variance estimation of GCA,

$\sigma^2 \text{SCA}$ = variance estimation of SCA,

$\sigma^2 \text{RE}$ = variance estimation of RE.

¹ Faculty of Agricultural Sciences, Mar del Plata University, c.c. 276-7 620 Balcarce, Argentina.

² Institute of Ornamental Plant Growing, Caritassstraat 21, B-9 230 Melle, Belgium.

³ Faculty of Agricultural Sciences, Rijksuniversiteit Gent, Coupure 653, B-9 000 Ghent, Belgium.

RESULTS

Each pure line and hybrid were very uniform in phenotype when observed in the field.

Significant differences for all the characters measured, and low coefficient of variation for most of them were found (Table 1).

Highly significant GCA-mean squares were found for the thirty characters under study (Table 1), except for „dry leaves weight“ that had only significant GCA-mean squares. The

SCA-mean squares were highly significant for 18 characters and significant for 4. The characters „length of cotyledon“, „width of cotyledon“, „distance from ground level to cotyledon“, „distance between leaftips of first leaves“, „length of first leaf“, „width of first leaf“, „length of petiole of first leaf“, „height of plant (one month)“, „length of largest leaf“, „length by width of largest leaf“, „number of leaves“, „number of green leaves at harvest“ and „green leaves at harvest/number of leaves“ had at least significant RE-mean squares.

Table 1

Mean square and F value of GCA, SCA and RE, and mean square of error, as an estimation of heritability

Characteristics	CV	GCA		SCA		RE		Error Mean square	h
		Mean square	F value	Mean square	F value	Mean square	F value		
1. Length of cotyledon	4	0.228	70.1**	0.029	9.0**	0.069	21.2**	0.0033	0.51
2. Width of cotyledon	8	0.16	49.3**	0.01	2.9*	0.08	25.2**	0.003	0.40
3. Distance from ground level to cotyledon	9	2.24	37.4**	0.40	6.6**	0.31	5.2**	0.06	0.65
4. Distance between leaftips of first leaves	5	7.32	25.2**	0.73	2.5*	5.0	17.3**	0.29	0.34
5. Length of first leaf	4	0.76	23.8**	0.08	2.5*	0.62	19.7**	0.03	0.28
6. Width of first leaf	6	0.90	53.3**	0.04	2.3	0.35	21.1**	0.01	0.59
7. Length of petiole of first leaf	9	0.31	19.2**	0.08	4.9**	0.13	8.52**	0.01	0.40
8. Height of plant (one month)	6	182.0	67.7**	32.6	12.1**	20.3	7.5**	2.7	0.66
9. Length of largest leaf	5	7.66	23.4**	0.45	1.37	0.84	2.57*	0.32	0.75
10. Width of largest leaf	7	9.85	22.0**	0.29	0.66	0.85	1.90	0.44	0.80
11. Length by width of largest leaf	12	343.0	17.8**	611.0	0.88	1492.0	2.14*	695.0	0.73
12. Length of petiole of largest leaf	7	3.83	25.7**	0.29	1.95	0.27	1.85	0.14	0.81
13. Number of leaves	2	0.215	195.0**	0.014	12.3**	0.007	6.5**	0.0011	0.87
14. Date of flowering	2	0.107	35.7**	0.015	5.0**	0.006	2.0	0.003	0.75
15. Height of plants	4	436.0	43.6**	285.0	28.5**	11.3	1.13	10.0	0.24
16. Angle of petiole of largest leaf	8	75.7	12.5**	24.4	4.0**	5.4	0.9	6.0	0.52
17. Diameter of head	5	4.34	20.4**	1.39	6.5**	0.22	1.1	0.21	0.55
18. Diameter of sterile centre	17	4.41	18.9**	0.35	1.5	0.25	1.1	0.23	0.83
19. Dry leaves weight	12	7.45	2.87*	2.69	1.0	4.73	1.8	2.59	0.26
20. Dry stem weight	10	224.0	28.2**	55.5	6.9**	15.5	1.9	7.9	0.61
21. Dry head weight	8	19.6	5.24**	5.8	1.56	4.1	1.1	3.73	0.55
22. Dry head and stem weight	9	218.0	13.1**	89.9	5.4**	29.3	1.8	16.7	0.41
23. Total dry weight	9	208.0	7.1**	114.0	3.9**	49.0	1.7	29.0	0.28
24. Number of green leaves at harvest	10	0.5	30.9**	0.14	8.7**	0.036	2.2*	0.016	0.58
25. Percentage of grain humidity	7	70.2	60.9**	7.2	6.3**	1.5	1.3	1.2	0.83
26. Number of seeds	5	16.15	28.8**	2.17	3.9**	1.03	1.8	0.56	0.75
27. Weight of 100 seeds	6	1.37	52.1**	0.40	15.3**	0.03	1.2	0.02	0.60
28. Green leaves at harvest/number of leaves	13	94.1	24.0**	20.3	5.2**	10.1	2.6*	3.9	0.62
29. Ratio : seed yield/total dry weight	8	0.0017	5.65**	0.0008	2.64**	0.0005	1.51	0.0003	0.33
30. Seed yield	11	109.7	11.3**	62.6	6.6**	11.4	1.2	9.5	0.28

The dimension of the GCA was 4, of the SCA was 5, of the RE was 9 and of the Error was 54
 ** significant at the $P \leq 0.01$
 * significant at the $P \leq 0.05$

In the ANOVA of "seed yield" (Table 1), the F value of GCA was 1.7 times higher than the F value of SCA. If the ANOVA is done including the parents (Table 2) the F value of SCA was 5 times higher than that of GCA. In both calculations the SCA gave very significant differences ($P \leq 0.01$).

Table 2
Analysis of variance for seed yield of an incomplete diallel cross, selves included

Source of variation	Degrees of freedom	Mean square	F value
GCA	4	78.4	9.91**
SCA	10	395.2	49.9**
RE	9	11.4	1.43
Error	69	7.9	

** significant at the $P \leq 0.01$.

Comparing both analyses it is possible to conclude, for the 5 pure lines, that inbreeding was not solely responsible for the significance of the SCA. Using the Bonferroni t-test (Miller, 1966), two comparisons were made (Table 3): one to detect significant differences from zero for the GCA of each line, and the other to test the effects of the SCA in each cross. In the first comparison, it was found that the pure line CCM 611, with negative value, and the 7 CM 99, with positive value, departed significantly ($P \leq 0.05$) and very significantly ($P \leq 0.01$) respectively from zero. In the second comparison, it was found that only the hybrid 7 CM 99 \times C 10 V had positive highly significant interactions.

Table 3
Values of GCA for each pure line and SCA for each cross, selves excluded, for seed yield

Values of pure lines	GCA	SCA				
		CCM 611	7 CM 99	CP 331	C 104	C 10 V
CCM 611	-3.31*		-4.99**	-0.57	3.49	2.10
7 CM 99	7.74**			-3.81	0.69	6.23**
CP 331	-0.41				3.33	-0.82
C 104	-1.17					-7.49**
C 10 V	-2.81					

* significantly different at the 0.05 level.

** significantly different at the 0.01 level.

DISCUSSION AND CONCLUSIONS

Open pollinated varieties of sunflower will be more useful than hybrid varieties for the characters that had no significant mean squares of RE and SCA (e.g.: "diameter of sterile centre"). If one or both of these sources of variation had significant mean squares, hybrid

varieties would produce more extreme values than population varieties, the former happened for most of the characters studied.

The RE may be attributed to: 1) overall differences between male and female parents (GRE, general reciprocal effects), and/or 2) a remainder, which measures the differences between the reciprocal crosses from pairs of parents (SRE, specific reciprocal effects). One or both sources of variation had a big influence in all the characters measured in the young sunflower plant, but they were almost absent in the characters measured after the star stage.

The relative magnitude of the GCA and SCA for the characters "height of plant", "diameter of head", "weight of seeds", "seed yield" and "date of flowering" were studied by Putt (1966). The results obtained in his work coincide, except for "date of flowering". Putt (1966) found variance estimations of the same magnitude for GCA and SCA. We found a more important GCA variance estimation than that of SCA which is in accordance with the results found by Roath et al. (1982). Marinković (1982) studied the character "height of plant". His results agree with the results obtained in this work. However, for the character "number of leaves", he found that the estimation of the nonadditive sources of variation were more important than the additive ones, which is in opposition to the results presented here.

For the characters with low heritability it will be more interesting to use a selection method that gives as much information as possible about each selected material (e.g.: S_t selection). With high values of heritability, mass selection will give good advances, at a lower cost. The heritability estimates, obtained by other workers for the characters "length by width of largest leaf" (Shabana, 1974), "number of leaves" (Luczkiewicz, 1973, and Shabana, 1974) and "number of seeds" (Shabana, 1974, and Omran et al., 1976) are within the range of values found in this work. For the characters "date of flowering" (Omran et al., 1976, Shabana, 1974, and Roath et al., 1982), "diameter of head" (Pathak, 1974, Omran et al., 1976, and Shabana, 1974), "weight of seeds" (Shabana, 1974, and Omran et al., 1976) and "seed yield" (Shabana, 1974, and Omran et al., 1976) the results are not in accordance. This is probably due to the use of different estimation methods, plant material and experimental lay-out.

The conclusions of this work are: (1) RE tend to disappear after the star stage, (2) for 25 characters, hybrid varieties will produce more extreme values than population varieties, and (3) selecting for yield components, "number of seeds" is probably the most interesting character, due to the high value of GCA in relation to the other genetic sources of variation.

REFERENCES

- Garretsen, F., Keuls M., 1973, *Analysis of genetic variation in an incomplete diallel cross*, Proc. 1st Meeting of the Section Biometrics in Plant Breeding of Eucarpia, Hanover, 24—35.
- Garretsen F., Keuls M., 1978, *A general method for the analysis of genetic variation in complete and incomplete diallels and North Carolina II (NCII) designs*, part. II: Procedures and general formulae for the fixed model, *Euphytica*, 27: 49—68.
- Keuls M., Garretsen F., 1977, *A general method for the analysis of genetic variation in complete and incomplete diallels and North Carolina II (NCII) designs*, Part I: Procedures and general formulae for the random model, *Euphytica*, 26: 537—551.
- Kováčik A., Skaloud V., 1978, *Contribution to defining the inheritance of earliness in sunflower and the method of its exploitation in breeding*, Proc. 8th Int. Sunflower Conf., Minnesota, U.S.A., 437—440.
- Luczkiewicz T., 1973, *The variability and heritability of a range of features, both natural and induced by x irradiation, in the sunflower, H.a.* In: Informator o wynikach badań naukowych zakorczonych w 1983 roku. Rolonitwó, czesc I. Warsaw, Poland; Wydział Nauk Rolniczych i Lesnych PAN. 339—340 (PI) Instytut genetyki i hodowli Roslin AR, Poznan, Poland.
- Miller R. G., 1966, *Simultaneous statistical inferences*, New York, Mc Graw-Hill Book Co., 272.
- Marinković R., 1982, *Inheritance of plant height and leaf number in diallel crossings of sunflower inbreds*, Proc. 10th Int. Sunflower Conf., Surfers Paradise, Australia, 232—233.
- Omrán A. C., Abbel-Zahab A. A., Haikl M. A., 1976, *Evaluation of sunflower cultivars, heritability and variability of metric traits*, Proc. 7th Int. Sunflower Conf., Krasnodar, U.S.S.R., 361—375.
- Pathak S. R., 1974, *Yield components in sunflower*, Proc. 6th Int. Sunflower Conf., Bucharest, Romania, 271.
- Putt E., 1966, *Heterosis, combining ability, and predicted synthetics from diallel cross in sunflower (Helianthus annuus L.)*, Can. J. Pl. Sci., 46, 1.
- Roath W. W., Hamond J. J., Miller J. F., 1982, *Genetic effects of days to flowering in sunflower (Helianthus annuus L.) under short day regime*, Proc. 10th Int. Sunflower Conf., Surfers Paradise, Australia, 247—249.
- Shabana R., 1974, *Genetic variability of sunflower varieties and inbred lines*, Proc. 6th Int. Sunflower Conf., Bucharest, Romania, 263 p.

ESTIMACIÓN DE L'HERITABILITÉ ET DE LA VARIATION GÉNÉTIQUE CHEZ LE TOURNESOL

Résumé

Cinq lignées autofécondées de tournesol ont été croisées dans un système diallele incomplet et des autofécondations ont été effectuées. Des estimations de l'héritabilité en sens restreint et de l'analyse de la variance des croisements dialleles ont été obtenues, pour 30 caractères. On a déterminé des effets reciproques pour tous les caractères analysés au stade de plantule, ceux-ci étant toutefois presque absents pour les caractères analysés après la formation du bouton floral.

Des valeurs de l'héritabilité de 0,65 ou plus importantes ont été obtenues pour les caractères: la distance du niveau du sol jusqu'au cotylédon, la hauteur de la plante (âgée de 1 mois), la longueur de la plus grande feuille, la largeur de la plus grande feuille, le rapport longueur/largeur de la plus grande feuille, la longueur de petiole de la plus grande feuille, le nombre des feuilles la date de la floraison, le diamètre de la zone centrale stérile du capitule, le taux de l'humidité des graines et le nombre de celles-ci.

ESTIMACIÓN DE LA HERITABILIDAD Y DE LA VARIACIÓN GÉNÉTICA DEL GIRASOL

Resúmen

Se han cruzado cinco líneas consanguíneas de girasol en un sistema diallela incompleto y se han efectuado autofecundaciones. Se han obtenido estimaciones de la heritabilidad en sentido restringido y del análisis de la variación de la cruces diallelas, para 30 caracteres morfológicos.

Se detectaron efectos reciprocos para todos los caracteres analizados en estadio de plántula, pero éstas fueron casi ausentes para los caracteres analizados después de la formación del botón floral.

Valores de la heritabilidad de 0,65 o mayores se obtuvieron para los caracteres: distancia desde el nivel del suelo al cotiledón, altura de la planta (a un mes), longitud de la mayor hoja, amplitud de la mayor hoja, la relación longitud/amplitud de la mayor hoja, longitud del peciolo de la mayor hoja, el número de las hojas, la fecha del florecimiento, el diámetro de la zona central estéril del capítulo, el porcentaje de la humedad de las semillas y el número de semillas.