GENETIC RESEMBLANCE OF SUNFLOWER CULTIVARS TESTED IN INTERNATIONAL TRIALS

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INTRODUCTION

Genetic diversity is considered one of the most important factor securing crop stability. A large genetic diversity would reduce the yield fluctuation in a certain area because different genotypes react differently to the environmental variation. Also, it is well known that the appearance and spreading of the new, more virulent races of the pests are positively correlated with the area occupied by the corresponding genes for resistance.

A greater genetic diversity at territorial level may be achieved in sunflower by means of a higher number of different hybrids but the number *per se* does not constitute an adequate solution, taking into account that certain hybrids could be genetically related and the cultivation of more alike genotypes may be equivalent to the extension of a single one.

Presently sunflower breeders seeking yield improvement are generally faced with a relative vast array of potential parent genotypes among which only a limited number of crosses can be made in order to obtain new valuable initial breeding material. The choice is usually based on a combination of yield data, visual assessment of agronomic characteristics and pest resistance, and very seldom the pedigree knowledge. Genetic investigations based on test crosses are costly and so quite rare. It is generally assumed that maximum improvement of the initial material can be obtained from crosses which release the maximum amount of variations between parents which are genetically diverse.

From this point of view, our attempts to evaluate the genetic relationship among hybrids, which constitute the aim of this paper, could be of a certain usefulness.

MATERIALS AND METHODS

The identification of the genotype structures fitting properly the ecological conditions of different regions has been one of the main purposes of the F.A.O. Research Network on Sunflower. All sunflower cultivars tested since the Network's establishment have represented the latest achievements of the main sunflower breeding centres from all over the world (Annex 1). Trials have been conducted with 101 F_1 hybrids and 13 open pollinated varieties (OPV) in four biennial cycles, starting from 1976, under a wide range of environments from Europe, Near and Middle East, Africa, Latin America and U.S.A. and their results were published in the Information Bulletin HELIA, numbers 1, 2, 3, 5 and 7.

The estimation of the relationship degree of sunflower cultivars on genealogy basis requires the knowledge of parental genetic origin, which is not always accessible. Such an approach has also the inconvenience that divergent inbreds could be often selected from the same source material, while similar ones may arise from distinct origins.

The genetic resemblance estimation on the basis of common allele percentage is also difficult and relative for this study, because the number of the identified genes in sunflower is still small and the existence of their alleles in the tested genotypes has been only approximately investigated.

A more complete assessment of the genetic resemblance has been done for some groups of cereal cultivars, on the basis of their yield response to a large range of environments.

Johnson (1977), working with corn hybrids, elaborated a model which provides weighted estimates of hybrid means, coefficients of the regression of each hybrid on an environmental index and coefficients of the regression of each hybrid on a set of orthogonal residual vectors. Genotypic similarity was defined as the euclidian distance between genotypes in the space whose coordinate axes were the locations. A claster analysis arranged the hybrids into groups that were differentiable in terms of means and stability.

Habgood (1977) proposed a method of estimating the genetic diversity of self-fertilizing cereal cultivars based on genotype-environment interactions. The degree of similarity or diversity between each pair of genotypes in an array is estimated by the correlation over

Annex 1

Sunflower cultivars tested in the F.A.O. international trials in the period of 1976—1983

Supplying country 1	Biennial cycles 2	Cultivars (SH=single hybrids, TH=three-way hybrids, OPV=open pollinated varieties) 3
Argentina (Continental)	1980—1981	Contiflor (SH)
Bulgaria (General Toshevo)	1976—1977	Helios 322 (SH)
	1978—1979	Hemus (OPV), HB-451 (SH), Peredovik (OPV)
	1982—1983	HB-783 (SH)
France (INRA)	1976—1977	Airelle (SH), Relax (SH), Remil (SH) Issanka (OPV)
	1978—1979	Remil (SH), Luciole (SH), INRA-7702 (SH)
	1980—1981	Primasol (SH)
	1982—1983	H 9 P 1 (SH), H 9 P 2 (TH), H 9 P 4 (TH)
F. R. Germany (Giessen)	1978—1979	Sorex (SH), Olga II (SH)
	1980—1981	H-27-77 (SH), Marika (SH), Vera (SH)
	1982—1983	G 9-76 (SH), G 19-77 (SH), G 24-77 (SH)
Hungary (Iregszemcse and Szeged)	1978—1979	IH-10 (OPV), Iregi 816 B (OPV), Iregi Csikós (OPV)
	1980—1981	Gahib 6 (SH)
	1982—1983	HNK-81 (SH), HNK-84 (SH), Koflor 1 (SH), IH-56 (SH), IH-155 (SH), Gahib 7 (SH), Citosol 2 (SH), Citosol 3 (SH)
Italy	1978—1979	Argentario (OPV)
	1980—1981	Ala (OPV)
Poland (Poznan)	1976—1977	Wielkopolski (OPV)
Romania (Fundulea)	1976—1977	Romsun 52 (SH), Romsun 53 (SH), Romsun 59 (SH), Sorem 80 (SH), Sorem 82 (SH), Sorem HT-64 (TH) RO-18 (SH), RO-20 (SH), Romsun 301 (SH).
	1978—1979	Record (OPV), Romsun 59 (SH), Sorem HT-111 (TH), Sorem HT-116 (TH), Sorem HT-117 (TH), Romsun 90 (SH).
	1980—1981	RO-18 (SH), RO-19 (SH), RO-33 (SH), RO-26 (SH), RO-27 (TH), RO-34 (SH), RO-29 (TH), RO-40 (SH), RO-45 (SH), RO-46 (SH), RO-100 (SH), RO-130 (SH)
	1982—1983	RO-25 (SH), RO-36 (SH), RO-70 (SH), RO-44 (SH), RO-131 (SH), RO-134 (SH), RO-141 (TH), RO-150 (SH)
Spain (INTA)	1976—1977	H-23 (SH)
	1978—1979	Sepasol (OPV), HS-1161 (SH), HS-72 M (SH)
	1980—1981	Halcon (SH), Pinzon (SH), SH-S-690 (SH), SH-3000×2 (HT), SH-72 M×1161 (HT)
U.S.A.	1978—1979	P.O.I. 301 A (SH), H-894 (SH), H-241 (SH), Sungro 380 A (SH)
	1980—1981	Sunbred 265 (SH), Interst. 7775 (SH), DO-704 (SH)
	1982—1983	Sunbred 254 (SH), Cargill 205 (SH), Seedtec S-315 (SH), Stauffer 3101 (SH)
Yugoslavia (Novi Sad)	1976—1977	YU-NS-65 (SH), YU-NS-1 (SH)
	1978—1979	Novi Sad 20 (OPV), Novi Sad 61 (OPV), VNIIMK 8931 (OPV), NS-H-27 (SH), NS-H-34 (SH), NS-H-63 RM (SH)
	1980—1981	NS-H-10 (SH), NS-H-11 (SH), NS-H-13 (SH), NS-H-17 (SH), NS-H-33 (SH), NS-H-36 (SH),
	1982—1983	NS-H-3 (SH), NS-H-4 (SH), NS-H-5 (SH), NS-H-40 (SH), NS-H-42 (SH), NS-H-43 (SH).

a range of environments of their respective deviations from the mean yield of all genotypes in each environment.

Săulescu et al. (1981) used the coefficient of correlation (r) and the coefficient of determination (r^2) between the yields of each cultivar pair in two large sets of winter wheat yield tests. The coefficient of correlation has the advantage of indicating directly the pairs of genotypes with the highest yield stability. It is known that the mean variance of two variables depends not only on the variance of each of them but also on the magnitude of the coefficient of correlation between them : $S^2\left(\frac{x+y}{2}\right)=\frac{1}{4}S_x^2+\frac{1}{4}S_y^2+\frac{1}{2}r\cdot S_x\,S_y$. So, as smaller than 1 is the correlation coefficient (r) between the yields of two cultivars, the better is compensated their yield variation in different environments and the variance of the average yields is smaller.

In the present paper, the genetic resemblance of sunflower cultivars was estimated in accordance with their seed yields in different years and locations, using the square of the correlation coefficients between seed yields of each pair of cultivars, i.e. the coefficient of determination ($r^2\cdot 100$), which can be considered a weighted estimation for the percentage of identical alleles for all genes controlling the yield in the given set of environments.

Three replications of each trial were used in calculation and the assessment of the significance of differences between correlation coefficients and further between the coefficients of determination was performed by computing the value : $Z=\frac{1}{2}\ 1\ n\,(1+r)-1\ n\,(1-r)$, where 1 n is the natural logarithm and r the correlation coefficient.

RESULTS AND DISCUSSION

Data from Tables 1 to 8 give the coefficients of determination ($r^2 \cdot 100$) calculated for each of the eight biennial trials conducted co-operatively in the seasons 1976—1977, 1978—1979, 1980—1981 and 1982—1983. Taking into account the similarities in seed yields of each pair of cultivars under various environmental conditions (16—41 locations), one could observe a large amplitude of the estimations of genetic resemblance, going from 8—84% in the first biennial cycle to 52—98% in the fourth biennial cycle.

Both similar responses and therefore a greater genetic resemblance and uncorrelated responses and therefore great genetic differences among the pairs of cultivars can be established. An important number of cultivars falls into an intermediate group of a less striking resemblance.

It should be noted that almost all values of the coefficients of determination were significantly different from 100, meaning that any pair of cultivars will give more stable average yields than each cultivar taken individually.

Diagram representation of the coefficients of determination, in which their magnitude is conventionally marked by the thickness of the lines, allows to obtain a better image of the genetic relationships among the cultivars tested (Figures 1 to 8). Values of the coefficients of determination less than 75 were considered as indicating uncorrelated responses and therefore more or less distinct genotypes.

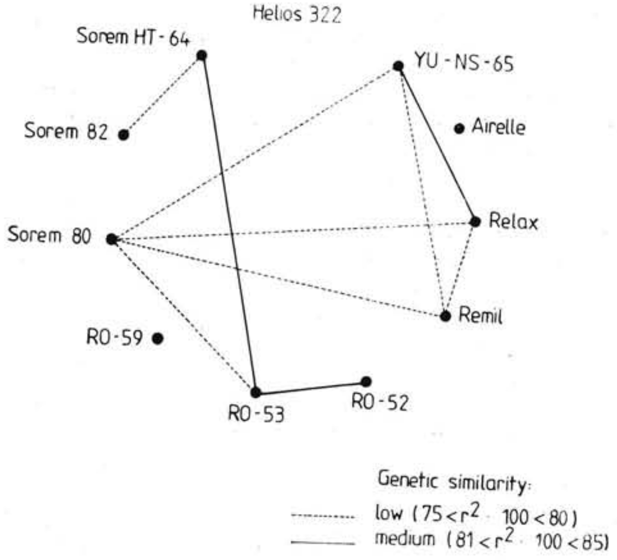

Fig. 1 — Diagram representation of genetic relationship of sunflower hybrids from Trial No. 1, 1976—1977

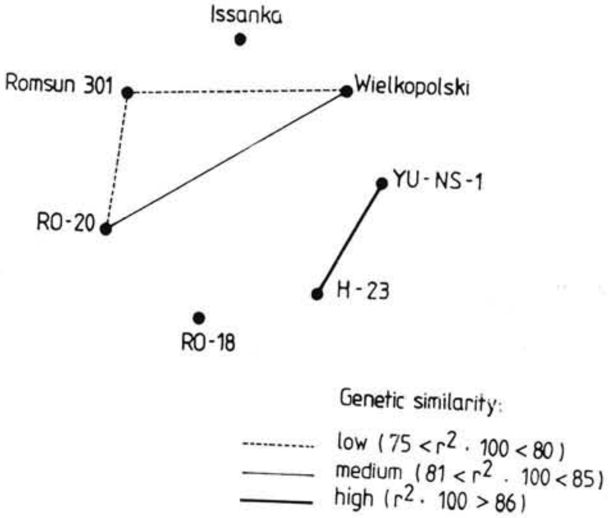

Fig. 2 — Diagram representation of genetic relationship of sunflower cultivars from Trial No. 2, 1976—1977

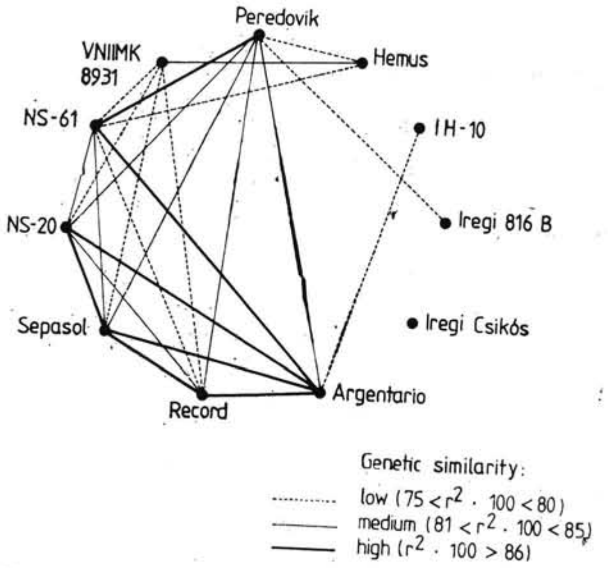

Fig. 3 — Diagram representation of genetic relationship of sunflower open pollinated varieties from Trial No. 1, 1978—1979

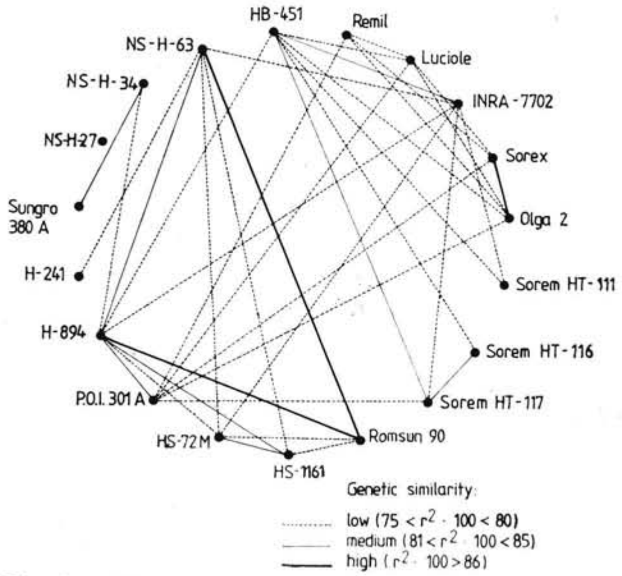

Fig. 4 — Diagram representation of genetic relationship of sunflower hybrids from Trial No. 1, 1978—1979

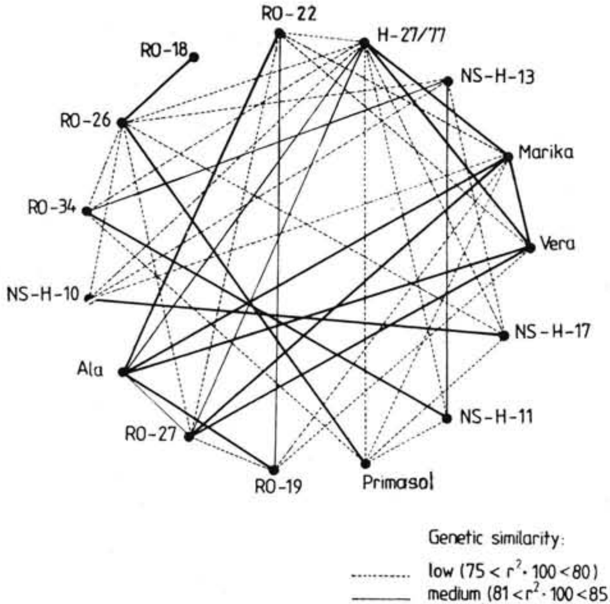

Fig. 5 — Diagram representation of genetic relationship of sunflower cultivars from Trial No. 1, 1980—1981

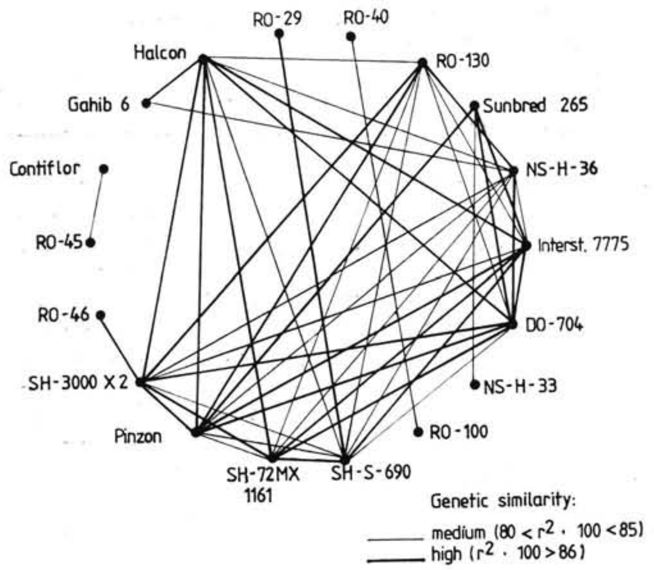

Fig. 6 — Diagram representation of genetic relationship of sunflower hybrids from Trial No. 2, 1980—1981

A similar response and therefore a greater genetic resemblance showed the following pairs and groups of cultivars :

Trial No. 1 (1976—1977) :
YU-NS-65/Relax, Romsun 52/Romsun 53, Romsun 53/Sorem HT-64 (Table 1).

Trial No. 2 (1976—1977) :
YU-NS-1/H-23, Wielkopolski/RO-30 (Table 2).

Trial No. 1 (1978—1979) :
Argentario/Sepasol/Record, NS-61/Peredovik/Argentario, NS-20/Argentario/Sepasol (Table 3).

Trial No. 2 (1978—1979) :
H-894/Romsun 90/NS-H-63/HS-1161/P.O.I. 301 A, Sorex/Olga II, Sorem HT-117/Sorem HT-116/HB-451, NS-H-34/Sungro-80 A (table 4).

Trial No. 1 (1980—1981) :
Marika/Vera/RO-27/Ala/H-27-77, NS-H-10/NS-H-17, NS-H-11/RO-34, RO-22/Ala/RO-19, RO-26/Primasol, RO-18/RO-26 (Table 5).

Trial No. 2 (1980—1981) :
IH-10/Iregi 816 B/Halcon/Gahib 6, Halcon/SH-3 000 × 2/Pinzon/SH-72 M × 1 161/SH-S-690/RO-130/DO-704/Interst. 7775, Sunbred 265/Pinzon/DO-704/Interst. 7775, RO-46/SH-3 000 × 2, RO-29/SH-S-690 (Table 6).

Trial No. 1 (1982—1983) :
H9-P2/Koflor 1/NS-H-4/NS-H-5/HNK-81, G9-76/G19-77/HNK-81/HNK-84, RO-36/G19-77/G 24-77, NS-H-3/Citosol 3/Koflor 1/NS-H-4/NS-H-5, RO-25/HNK-84 (Table 7).

Trial No. 2 (1982—1983) :
H 9 P 4/NS-H-42/NS-H-40/Cargill 205/Sunbred 254/Citosol 2, IH-56/Cargill 205/Gahib 7, HB-783/Seedtec S-315/Gahib 7, Seedtec S-315/IH-155 (Table 8).

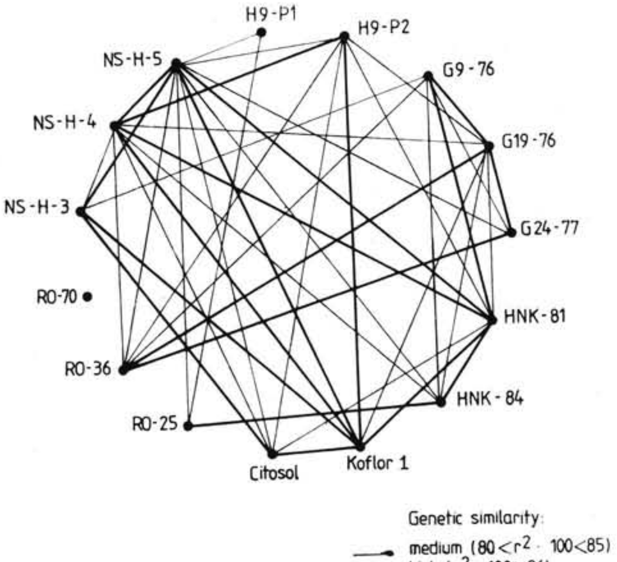

Fig. 7 — Diagram representation of genetic relationship of sunflower hybrids from Trial No. 1, 1982—1983

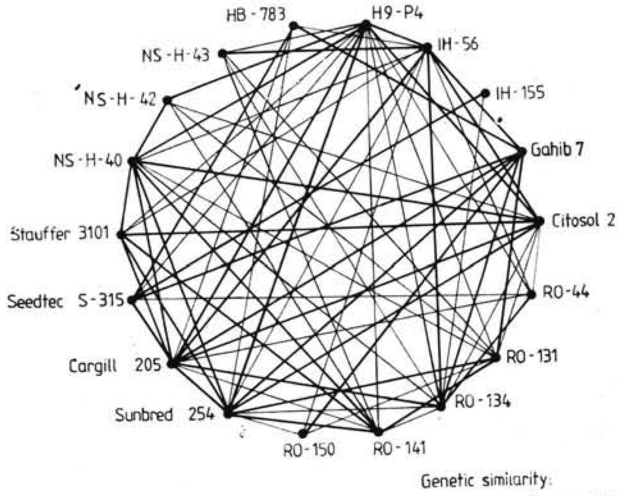

Fig. 8 — Diagram representation of genetic relationship of sunflower hybrids from Trial No. 2, 1982—1983

Table 1

Estimation of genetic resemblance ($r^2 \cdot 100$) among 11 sunflower medium-late hybrids (F.A.O. Trial No. 1, 1976—1977, 19 locations)

Cultivars (F_1)	1	2	3	4	5	6	7	8	9	10	11
1. Helios 322	100	47	63	47	38	15	35	62	33	37	33
2. YU-NS-65		100	16	84	78	42	66	49	78	50	71
3. Airelle			100	36	28	15	15	49	11	15	8
4. Relax				100	80	57	68	57	79	39	69
5. Remil					100	60	64	44	78	55	61
6. Romsun 52						100	82	48	59	56	54
7. Romsun 53							100	57	76	67	83
8. Romsun 59								100	53	47	47
9. Sorem 80									100	74	76
10. Sorem 82										100	60
11. Sorem HT-64											100

L.S.D. 0.05=7

Table 2

Estimation of genetic resemblance ($r^2 \cdot 100$) among 7 sunflower early cultivars (F.A.O. Trial No. 2, 1976—1977, 23 locations)

Cultivars (OPV+F_1)	1	2	3	4	5	6	7
1. Issanka	100	53	36	28	52	58	68
2. Wielkopolski		100	61	69	63	84	79
3. YU-NS-1			100	86	66	72	70
4. H-23				100	66	65	73
5. RO-18					100	62	66
6. RO-20						100	80
7. Romsun 301							100

L.S.D. 0.05=9

A general look over the diagrams of genetic relationships permits to appreciate that the genetic diversity of the present sunflower hybrids is quite limited and has even decreased in the last trials, indicating that many hybrids may have one inbred line in common or their parents could originate from the same or similar sources of germplasm such as high oil varieties or closely related pollen fertility restorers.

Making a connection between the correlations presented in this study and data on morpho-physiological traits of the respective sunflower cultivars published in HELIA, numbers 1, 2, 3, 5 and 7, one can observe that, contrary to expectation the similitude of reaction to environment was not always greater between genotypes with similar maturity and plant height, suggesting that other characteristics could play an equal important role in the response of sunflower cultivars to the variations of soil and climate factors.

Table 3

Estimation of genetic resemblance ($r^2 \cdot 100$) among 11 sunflower open pollinated varieties (F.A.O. Trial No 1, 1978—1979, 38 locations)

Cultivars (OPV)	1	2	3	4	5	6	7	8	9	10	11
1. Peredovik	100	77	72	76	63	84	83	85	84	89	74
2. Hemus		100	69	67	60	74	66	60	63	77	82
3. IH-10			100	71	68	75	71	71	65	53	58
4. Iregi 816 B				100	61	66	63	65	64	48	47
5. Iregi Csikós					100	67	66	60	63	40	66
6. Argentario						100	89	88	89	89	74
7. Record							100	91	82	80	76
8. Sepasol								100	88	82	76
9. Novi Sad 20									100	82	75
10. Novi Sad 61										100	77
11. VNIIMK 8931											100

L.S.D. 0.05=9

Table 4

Estimation of genetic resemblance ($r^2 \cdot 100$) among 19 sunflower medium-late hybrids (F.A.O. Trial No. 2, 1978—1979, 41 locations)

Cultivars (F₁)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1. HB-451	100	66	75	82	65	75	78	80	83	74	72	74	73	75	74	71	66	66	71
2. Remil		100	78	70	78	77	66	71	70	63	71	74	78	72	58	64	66	70	63
3. Luciole			100	69	76	75	65	63	68	64	73	71	78	72	65	63	49	63	66
4. INRA-7702				100	74	73	77	65	76	71	68	75	66	75	71	73	68	71	76
5. Sorex					100	86	67	71	65	47	54	56	77	54	52	37	47	50	55
6. Olga II						100	67	70	69	51	71	72	75	52	64	55	53	43	51
7. Sorem HT-111							100	72	63	15	47	59	54	58	49	49	48	49	66
8. Sorem HT-116								100	84	70	64	70	73	74	66	64	60	61	67
9. Sorem HT-117									100	74	66	59	76	70	73	69	70	59	68
10. Romsun 90										100	78	77	66	86	66	64	71	75	92
11. HS-1161											100	81	71	81	73	51	67	74	78
12. HS-72 M												100	72	79	61	58	63	67	78
13. P.O.I. 301 A													100	83	68	73	71	65	63
14. H-894														100	66	71	72	76	82
15. H-241															100	66	72	63	75
16. Sungro 380 A																100	71	83	68
17. NS-H-27																	100	65	63
18. NS-H-34																		100	64
19. NS-H-63 RM																			100

L.S.D. 0.05=8

Table 5

Estimation of genetic resemblance ($r^2 \cdot 100$) among 15 sunflower medium early cultivars (F.A.O. Trial No 1, 1980—1981, 16 locations)

Cultivars (F₁+OPV)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1. RO-22	100	79	48	77	78	74	49	61	84	79	88	71	41	62	37
2. H-27-77		100	69	87	90	76	77	79	58	84	84	76	76	77	49
3. NS-H-13			100	55	56	76	83	61	28	53	49	77	82	79	59
4. Marika				100	92	71	64	79	77	86	90	77	50	71	48
5. Vera					100	69	61	66	77	86	88	67	53	66	45
6. NS-H-17						100	69	77	55	67	67	85	64	76	48
7. NS-H-11							100	76	34	62	58	72	88	72	46
8. Primasol								100	41	64	64	69	79	85	50
9. RO-19									100	76	90	61	24	53	45
10. RO-27										100	86	71	61	78	66
11. Ala											100	74	45	67	46
12. NS-H-10												100	66	78	64
13. RO-34													100	77	58
14. RO-26														100	86
15. RO-18															100

L.S.D. 0.05=7

Table 6

Estimation of genetic resemblance among 18 sunflower medium-late hybrids (F.A.O. Trial No. 2, 1980—1981, 22 locations)

Cultivars (F₁)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1. RO-29	100	64	79	73	76	77	79	58	67	87	74	79	71	56	38	48	66	68
2. RO-40		100	69	62	67	69	66	66	84	61	58	76	72	71	74	76	70	74
3. RO-130			100	79	86	83	85	62	79	84	82	92	87	76	50	70	54	83
4. Sunbred 265				100	76	86	90	82	76	69	80	86	80	59	45	58	78	79
5. NS-H-36					100	83	86	61	78	82	81	85	88	72	56	72	84	85
6. Interst. 7775						100	92	79	77	85	88	88	85	66	49	68	72	88
7. DO-704							100	79	76	82	88	92	88	67	44	68	68	86
8. NS-H-33								100	74	62	71	79	77	59	56	66	74	74
9. RO-100									100	71	71	80	80	72	76	77	52	68
10. SH-S-690										100	90	81	85	62	34	70	78	84
11. SH-72 MX 1161											100	84	86	64	35	72	76	88
12. Pinzon												100	92	76	59	72	76	87
13. SH-3000×2													100	88	66	70	79	91
14. RO-46														100	71	63	63	80
15. RO-45															100	84	48	51
16. Contiflor																100	63	71
17. Gahib 6																	100	86
18. Halcon																		100

L.S.D. 0.05=8

Table 7

Estimation of genetic resemblance ($r^2 \cdot 100$) among 15 medium-early hybrids (F.A.O. Trial No. 1, 1982—1983, 36 locations)

Cultivars (F_1)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1. H 9 P 1	100	79	72	70	70	78	79	79	80	81	67	78	75	77	81
2. H 9 P 2		100	78	81	75	85	75	87	81	77	81	71	80	87	85
3. G 9-76			100	87	83	86	85	78	79	75	83	76	81	79	75
4. G 19-77				100	88	85	83	82	78	73	92	80	79	81	79
5. G 24-77					100	79	78	76	76	68	92	74	80	80	83
6. HNK-81						100	88	89	81	79	79	78	80	86	87
7. HNK-84							100	76	74	87	75	73	79	83	83
8. Koflor 1								100	88	74	78	76	88	87	86
9. Citosol 3									100	62	76	74	87	82	83
10. RO-25										100	72	69	77	79	81
11. RO-36											100	79	80	82	81
12. RO-70												100	59	66	70
13. NS-H-3													100	85	88
14. NS-H-4														100	86
15. NS-H-5															100

L.S.D. 0.05=6

Table 8

Estimation of genetic resemblance ($r^2 \cdot 100$) among 18 medium-late hybrids (F.A.O. Trial No. 2, 1982—1983, 39 locations)

Cultivars (F_1)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1. HB-783	100	80	82	70	92	75	62	80	80	74	80	82	85	92	73	77	71	77
2. H 9 P 4		100	94	79	80	91	83	82	84	83	52	94	90	81	83	90	87	83
3. IH-56			100	79	91	90	85	79	90	80	81	85	88	66	82	81	77	86
4. IH-155				100	67	74	74	73	83	69	67	80	80	88	73	70	71	79
5. Gahib 7					100	76	63	87	90	76	87	86	98	90	71	80	71	77
6. Citosol 2						100	81	83	81	77	78	91	94	74	93	94	82	80
7. RO-44							100	80	86	80	76	80	83	83	80	80	71	74
8. RO-131								100	85	93	83	97	76	68	78	83	81	84
9. RO-134									100	82	74	84	93	77	77	81	77	83
10. RO-141										100	77	93	82	69	94	91	83	82
11. RO-150											100	82	80	73	71	78	70	79
12. Sunbred 254												100	86	79	93	93	71	80
13. Cargill 205													100	90	90	94	78	68
14. Seedtec S-315														100	78	80	73	70
15. Stauffer 3101															100	92	78	74
16. NS-H-40																100	92	79
17. NS-H-42																	100	67
18. NS-H-43																		100

L.S.D. 0.05=8

CONCLUSIONS

Although some groups of sunflower cultivars differing genetically could be established from this study, the genetic diversity of the present cultivated hybrids seems to be quite limited to fit all environmental variations and to minimize the genetic vulnerability of sunflower crops. The limiting factors are connected primarily with the utilization of the same type of cytoplasmic male sterility, the genetic similarity of many of the female parents originating from high oil varieties and the reduced number of pollen fertility restorer lines.

In order to enlarge the genetic diversity of sunflower hybrids, breeders have to develop source-populations with various genetic background which would serve as selfing genepools and to identify new *cms* and *Rf* sources from interspecific crosses.

The significant variability existing among various pairs of hybrids from the standpoint of the magnitude of the coefficients of determination allows to choose those couples of hybrids with the best reciprocal compensation of the yield variations and so to achieve an appropriate structure of hybrids which might assure a better stability of high average yield levels.

As it becomes apparent, beside high yielding capacity, sunflower hybrids should also be improved for their different reaction to the environmental factors.

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LA SIMILITUDE GÉNÉTIQUE DES CULTIVARS DE TOURNESOL EXPÉRIMENTÉS DANS LES ESSAIS INTERNATIONAUX

Résumé

La similitude génétique de 101 hybrides et 13 cultivars de tournesol a été étudiée, ceux-ci étant testés dans le cadre du Réseau de recherches de la F.A.O. pour le tournesol pendant 1976—1983, dans un grand nombre de localités d'Europe et hors Europe. La similitude génétique a été estimée en utilisant le carré des coefficients de corrélation entre les rendements en graines de chaque paire de cultivars, c'est-à-dire le coefficient de détermination ($r^2 \cdot 100$). En considérant la similitude des rendements de chaque paire de cultivars en conditions très variées de milieu (16—41 localités), une large amplitude des coefficients de détermination a été observée, allant de 8 à 98%.

Bien que certaines groupes de cultivars différant génotypiquement peuvent être établies, la diversité génétique des hybrides actuels de tournesol est assez limitée, pour correspondre à toutes les variations du milieu et pour réduire au minimum la vulnerabilité génétique des cultures de tournesol. Les facteurs limitatifs sont liés à l'utilisation du même type de stérilité mâle cytoplasmique, ainsi qu'à la similitude génétique de beaucoup de formes parentales femelles, provenant des cultivars à teneur élevée d'huile et au nombre réduit de lignées restauratrices de la fertilité du pollen.

Afin d'élargir la diversité génétique des hybrides de tournesol, il est nécessaire de créer des sources-populations à base génétique différente, pour servir comme matériel initiel pour l'autofécondation, et d'identifier des nouvelles sources de stérilité mâle cytoplasmique et de restauration de la fertilité du pollen, lors des croisements interspécifiques.

SEMEJANZA GENÉTICA DE LOS CULTIVARES DE GIRASOL TESTADOS EN LOS CULTIVOS COMPARATIVOS INTERNACIONALES

Resúmen

Se ha estudiado la semejanza genética de un número de 101 híbridos y 13 variedades de girasol testados en la Red de investigaciones F.A.O. para el girasol en el período 1976—1983 en gran número de localidades de Europa y fuera de Europa. La semejanza genética fue estimada empleándose el cuadrado de los coeficientes de correlación entre las producciones de semillas de cada pareja de cultivares, esto es el coeficiente de determinación ($r^2 \cdot 100$). Tomando en consideración la similitud de las producciones de cada pareja de cultivares en condiciones variadas de medio, se nota una gran amplitud de los coeficientes de determinación comprendida entre 8 y 98 por ciento.

A pesar de que se pueden establecer algunos grupos de cultivares que difieren genotipicamente, la diversidad genética de los híbridos actuales de girasol es bastante limitada para corresponder a todas la variaciones de medio y para minimalizar la vulnerabilidad genética de los cultivos de girasol. Los factores limitativos están relacionados al empleo de un mismo tipo de androesterilidad citoplasmática, así como a la similitud genética de muchas formas parentales femelas provinientes de las variedades con contenido elevado de aceite y del número reducido de líneas restauradoras de la fertilidad del poleno.

Para ampliar la diversidad genética de los híbridos de girasol hace falta crearse fuentes-poblaciones con base genética diferente que sirvan como material inicial para autofecundación y que identifiquen nuevas fuentas de androesterilidad citoplasmática y restauración de la fertilidad del poleno dentro de los cruces interspecíficos.