

COMBINING ABILITIES OF SUNFLOWER GENE POOLS ISSUED FROM CROSSES BETWEEN POPULATIONS AND INBRED LINES

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ABSTRACT

A programme was designed by INRA and French sunflower breeding (GIE Protournesol) companies to widen the genetic basis to breed new sunflower cultivars. Populations were evaluated for yield, oil content and diseases, and were crossed with inbred lines with complementary behaviours, then F2 progenies were selected for their combining abilities with four testers and the best ones were used to build twenty nine gene pools. These pools were tested for their combining ability with four testers during three years. Significant gene pool effects, i.e. general combining abilities, and gene pool x tester effects, i.e. specific combining abilities, were observed. According to their combining abilities, the best pools for grain yield were 19 (early restorer populations), 14 (phomopsis resistant populations), 15 (French populations) and 7 (Russian and Argentine maintainer populations), and the pools 5 (Romanian maintainer populations), 11 (Russian early populations) and 12 (Russian populations well combining with HA89) for oil content. Ranking for oil yield indicated the interest of pools 14, 5 and 7 in the late material and the synthetics 1 (Romanian early maintainer populations) and 3 (Romanian restorer populations) in the early material. Mandel analysis of the pools x tester interaction provided a grouping of gene pools on specific combining abilities for grain yield and oil content which suggests the way to use them as source material for breeders.

RESUME

L'INRA et des entreprises semencières françaises (GIE Protournesol) ont conduit un programme ayant pour but l'élargissement de la base génétique des variétés cultivées en tournesol. Des populations ont été évaluées pour le rendement, la teneur en huile et les maladies, et ont été croisées avec des lignées possédant des caractéristiques complémentaires. Des descendance F2 ont été sélectionnées ensuite pour leur aptitude à la combinaison avec quatre testeurs et les meilleures ont été utilisées pour constituer 29 pools. Ces pools ont été eux-mêmes testés pour leur aptitude à la combinaison avec quatre testeurs pendant trois ans. Des effets pools significatifs (aptitudes générales à la combinaison) et des interactions pools x testeurs (aptitudes spécifiques à la combinaison) ont été observés. En fonction de leurs aptitudes à la combinaison, les meilleurs pools pour le rendement étaient le 19 (populations restauratrices précoces), le 14 (populations résistantes au phomopsis), le 15 (populations françaises) et le 7 (populations mainteneuses russes et argentines); Les pools 5 (populations mainteneuses roumaines), 11 (populations russes précoces) et 12 (populations restauratrices roumaines) donnaient la meilleur teneur en huile. Un classement pour le rendement en huile montrait l'intérêt des pools 14, 5 et 7 dans le matériel tardif et celui de la synthétique 1 (populations roumaines précoces et mainteneuses) et 3 (populations roumaines restauratrices) dans le matériel précoce. Une analyse de Mandel sur l'interaction pools x testeurs donnait un regroupement des pools sur leur aptitude spécifique à la combinaison pour le rendement et la teneur en huile qui donnent des indications sur leur utilisation dans les programmes de sélection.

INTRODUCTION

The selection of hybrid varieties of sunflower led to genetic erosion, the lines used being more and more related. This point was assessed by Vranceanu and Stoenescu (1985), who found similarities between cultivars and suggested to create new source-populations with enlarged genetic variability to breed parental lines out of them. Moreover, the extension of the cultivation area made even more necessary the search for adaptation factors (disease resistance or drought resistance) A programme called "Source-Population Programme" was designed by INRA and French sunflower breeding companies (GIE Protournesol) to widen the genetic basis to breed new sunflower cultivars.

MATERIAL AND METHODS

Constitution of 26 gene pools and 3 synthetic populations

The design of the Source-Population programme is shown in Figure 1. 160 populations of various origin were studied for their combining abilities. Tersac *et. al.* (1993) determined a relation

between the specific combining abilities of populations and their geographical origin. The best populations were then crossed with "correction" inbred lines with traits complementary to each population. F₂ families were produced out of each crosses with two generations of sib-crosses, These families were themselves crossed with four testers, and the best ones were used to constitute 26 gene pools and 3 synthetic populations organised by topic, geographical origin and combining abilities. Two generations of intercrossing were performed before the pools were distributed . Their list is given in Table 1.

Evaluation of the gene pools and synthetic populations for their combining abilities

The 26 gene pools (briefly "pools") and synthetic populations (briefly "synthetics") were crossed with four male sterile testers : PET1-HA89, PET1-2603, ANN1-RHA274 and ANN1-PA230. The hybrids PET1-HA89*RHA274, ANN1-RHA274*Ha89, PET1-2603*HA99 and PET1-HA89*83HR4 were introduced as controls into the trials, which made possible to compare the general combining abilities of the pools with those of lines HA89, RHA274, HA99 and 83HR4. The hybrids were experimented for 3 years, with 3 locations and 3 replications per location each year. Flowering date, plant height, grain yield, oil content and humidity at harvest were noted.

The general combining abilities (GCA, i.e. mean value of each pool) were estimated on all crosses with the four testers using the following model :

$$\text{Model 1 : } Y_{ijklm} = \mu + L_{i/j} + B_{k/i/j} + A_j + F_l + M_m + \varepsilon_{ijklm}$$

with μ : general mean, $L_{i/j}$ effect of the location i in year j , $B_{k/i/j}$ effect of the block k in location i and year j , A_j effect of the year j , F_l effect of the female parent l , M_m effect of the male parent m

General and specific combining abilities (SCA, i.e.; pool*tester interaction) with the tester HA89,2603 and RHA274 were estimated after Model 2 :

$$Y_{ijklm} = \mu + L_{i/j} + B_{k/i/j} + A_j + F_l + M_m + (FM)_{lm} + \varepsilon_{ijklm}$$

with $(FM)_{lm}$ interaction between the female parent l and the male parent m .

Then, the pool*tester interaction was analysed according the method of Mandel (1971), which divides the interaction into orthogonal components in a way similar to that of a principal component analysis.

RESULTS

General combining abilities

In the overall analysis with Model 1, all the parental effects were significant for all the variables (Table 2). Compared with HA89 and 83HR4, certain pools were equivalent to the controls in GCA for yield, pools 19, 14, 15 and 7 being the best (Table 4). For oil content, certain pools were equivalent to HA89: pools 5, 11 and 12 and the synthetics. Pool 5 was the only one being non-significantly different from HA89 both for grain yield and oil content. Although humidity presented highly significant parental effects, the tiny differences between means were not very informative. The pools give hybrids later in average than controls HA89 and 83HR4. However the early pools give also the shortest hybrids: pool 2, pool 26 and synthetic 1.

**TABLE 2 : ANALYSIS OF VARIANCE ON 3 YEARS WITH CONTROL LINES
GCA OF GENE POOLS : MODEL 1 WITHOUT POOL*TESTER INTERACTION**

Effect	Grain yield	Humidity	Oil content	flowering date	Plant height
Location /year	**	**	**	NS	**
Year	**	**	**	**	**
Male parent	**	**	**	**	**
Female parent	**	*	**	**	**
Mean	27.3q/ha	10.4%	46.6%	-1.6day	168.6cm
CV	17.1	21.2	4.2		6.5

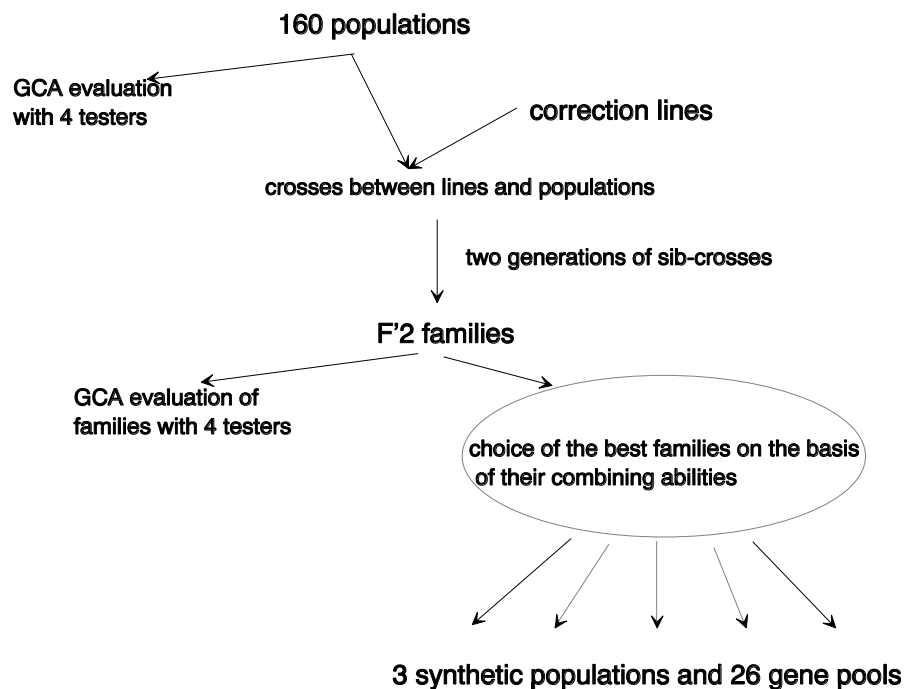
NS : non significant , * significant at $\alpha=0.05$; ** significant at $\alpha=0.01$

Flowering date : mean deviation from VIKI.

Specific combining abilities

Because some hybrid combinations were lacking, pools 17,19,21,24 and 26 were discarded from this study. The analysis of variance with Model 2 revealed highly significant pool * tester interaction for all traits (Table3).

**FIGURE 1 : CONSTITUTION OF SUNFLOWER GENE POOL
FRENCH SOURCE POPULATION PROGRAMME**



**TABLE 1 : GENE POOLS CREATED IN
THE FRENCH SOURCE-POPULATION PROGRAMME**

Year of creation :1985		
Code	Designation	Number of families
S1	Synthetic of early Romanian maintainer populations	9
S2	Synthetic of Romanian maintainer populations	10
S3	Synthetic of Romanian restorer populations	4
P1	Restorers from North American populations	12
P2	Maintainers from North American populations	44
P3	Maintainers from early Romanian populations	107
P4	Maintainers from late Romanian populations	83
P5	Restorers from Romanian populations	16
Year of creation :1986		
P6	Restorers from Moroccan populations	69
P7	Maintainer from Argentine x Russian populations	29
P8	Maintainers from Argentine populations	113
P9	Restorers from Argentine populations	8
P10	Russian populations resistant to downy mildew	60
P11	Early Russian populations	60
P12	Russian populations combining well with HA89	37
P13	Russian populations combining well with RHA274	71
P14	Phomopsis resistant populations	8
P15	French populations	32
Year of creation :1987		
P16	Restorers from Australian populations	53
P17	Maintainer from Hungarian and Syrian populations	84
P18	Restorers from Asian populations	56
P19	Early restorers	51
P20	Late restorers	64
Year of creation :1988		
P21	Restorers from Iranian, Argentine, Italian, Israeli and French "Clappiers" populations	32
P22	Maintainers from Iranian, Argentine, Italian, Israeli and French "Clappiers" populations	102
P23	Maintainers from Yugoslavian populations	145
P24	Maintainers from Giza and "Gabbes B" populations	17
P25	Maintainers from Bulgarian populations	102
P26	Maintainers from French populations like Issanka	16

TABLE 3 : GCA AND SCA OF GENE POOLS WITH THE TESTERS HA89, 2603 AND RHA274, ANALYSIS OF VARIANCE WITH MODEL 2

effect	Grain yield	Humidity	Oil content	Flowering date	Plant height
Location /year	**	**	**	NS	**
year	**	**	**	**	**
Pool	**	**	**	**	**
Tester	**	**	NS	**	**
Pool*tester	**	*	**	**	**
mean	27.4	10.3	46.7	-1.8	170
CV	16.4	23.1	3.9		6.1

NS : non significant , * significant at $\alpha=0.05$; ** significant at $\alpha=0.01$

Flowering date : mean deviation from VIKI.

We studied the structure of the interaction by a Mandel analysis on yield and oil content. We represented the two main axes for each trait. Pools combine well with testers drawn in the same direction: for each cross, the interaction term is the scalar product of the pool and the tester considered as vectors. Below, the terms "maintainer" and "restorer" are used in relation to the PET1 male sterility.

Concerning yield (fig. 2), the first axis constructed from the Mandel analysis opposes the maintainer testers to RHA274 and accounts for 76.5% of the variation. If we suppose that combining groups are related to PET1 restoration, we can regard the pools on the left of the figure as having the behaviour of " maintainers" and those on the right as having the behaviour of "restorers". The pools which contribute most to the interaction are pools 2 and 13 combining well with 2603, pool 6 combining well with HA89 and pools 4 and 16 combining well with RHA274. Pools 7 and 12, which combined well with HA89 and 2603, behaved as restorers. Axis 2 is mainly determined by interactions with HA89, primarily a positive SCA for HA89 * Pool 6.

For oil content (fig. 3), the structure of the interactions also opposed HA89 and 2603, on one hand to RHA274 on the other hand. but to a lesser extent than for yield (Axis 1, 56% of the variation). The most marked behaviours are those of the pools combining well with RHA274: pools 1, 9, 16, 20 and 25. The synthetics 1 and 3, the pools 2,3 and 8 presented positive SCA with the testers HA89 and 2603. Pool 6 presented a positive specific combining ability with HA89 for both oil and yield.

DISCUSSION

The best gene pools and synthetic populations provided by the Source-Population programme were comparable to elite lines HA89 and 83HR4 for their general combining abilities. Results related to the mean values of pools. It may be suggested that some families within the outstanding pools, but also within the medium ones can be good sources for breeding.

In addition, the pools can be classified according their SCA towards testers. Restorer families from Moroccan populations provided the pool 6, which combined well with the maintainer line HA89. Maintainer families of Rumanian populations entered pool 4 that combined well with RHA274. However, no strict coincidence occurred between the combining groups and the status of gene pools towards the PET1 cytoplasm. For example, pool 7, made out of maintainer families presented a negative SCA with RHA274 for yield (Figure 2). Pool 16 (restorers from Australian populations), combined well with RHA274. We found also that most of gene pools having good SCA for oil content with RHA274 were classified as restorers (figure 3). However, gene pools called restorers were not fixed for Rf. It would be possible to select B lines from them. It may be noted that pools 12 (Russian populations combining well with Ha89) and 13 (Russian populations combining well with RHA274 express primarily favourable SCA for yield with 2603, a tester which was not used to select the pools.

Moreover, as crosses were performed on testers with ANN1 we supposed that nucleus*cytoplasm interactions were small in comparison to differences between nuclei, as observed by Serieys (1992).

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**TABLE 4 : MEANS OF THE GENE POOLS CROSSED WITH FOUR TESTERS COMPARED WITH MEANS OF CONTROL LINES
MODEL 2 WITHOUT POOL*TESTER INTERACTION EFFECTS**

Parent	Grain yield	Sign. /HA89	humidity	Oil content	Sign. /HA89	Flowering date	Plant height
Males							
HA89	29.5	*	10.4	48.2	*	2.1	164.3
HA99	27.2	NS	9.9	48.7	NS	0.6	158.0
RHA274	29.1	*	10.2	44.7	*	-2.1	165.3
83HR4	26.6	*	10.9	46.6	*	0.1	156.1
SYNTH.1	26.1	*	9.5	47.6	NS	-3.6	159.1
SYNTH.2	25.9	*	11.0	48.2	NS	-2.1	163.5
SYNTH.3	25.9	*	9.8	48.3	NS	-1.5	161.2
POOL 01	25.5	*	10.5	45.1	*	-1.9	168.5
POOL 02	24.8	*	9.9	45.8	*	-2.7	160.8
POOL 03	26.8	*	10.3	47.7	NS	-1.5	163.4
POOL 04	26.9	*	10.5	47.0	*	-2.3	161.8
POOL 05	27.8	NS	10.1	47.6	NS	-2.6	164.3
POOL 06	26.5	*	10.7	46.5	*	-1.3	168.6
POOL 07	28.3	NS	11.4	46.8	*	-0.2	167.6
POOL 08	27.9	NS	10.3	46.8	*	-0.7	171.8
POOL 09	27.2	NS	10.0	46.0	*	-0.9	166.7
POOL 10	26.9	*	10.0	47.1	*	-3.3	166.4
POOL 11	27.0	*	10.4	48.1	NS	-2.2	165.8
POOL 12	25.6	*	9.7	48.1	NS	-2.1	163.1
POOL 13	24.4	*	10.4	47.3	NS	0.3	169.2
POOL 14	28.7	*	10.0	47.0	*	-1.2	170.9
POOL 15	28.5	NS	11.0	45.4	*	-1.8	168.9
POOL 16	25.8	*	10.8	44.9	*	-0.8	170.6
POOL 17	27.1	*	10.9	45.3	*	-0.5	167.5
POOL 18	27.2	*	10.9	45.4	*	-0.5	171.8
POOL 19	28.7	NS	11.4	44.9	*	-1.1	170.5
POOL 20	28.8	NS	10.7	44.2	*	-2.5	171.1
POOL 21	27.9	NS	10.0	45.7	*	-2.7	158.6
POOL 22	25.4	*	10.0	45.6	*	-2.3	163.4
POOL 23	27.7	NS	11.2	46.8	*	-2.3	169.1
POOL 24	26.4	NS	10.1	46.3	*	-3.1	159.5
POOL 25	27.1	NS	11.2	46.7	*	-1.2	167.2
POOL 26	25.4	*	9.6	47.4	NS	-3.9	151.6
females							
2603	27.8	NS	10.2	46.1	*	-2.2	171.1
HA89	27.7		10.5	49.2		0.4	164.3
PA230	26.0	*	10.7	46.0	*	-1.5	161.2
RHA274	26.4	*	10.2	45.1	*	-3.0	163.6

FIGURE 2 : MANDEL ANALYSIS OF THE POOL*TESTER INTERACTION SCA FOR GRAIN YIELD

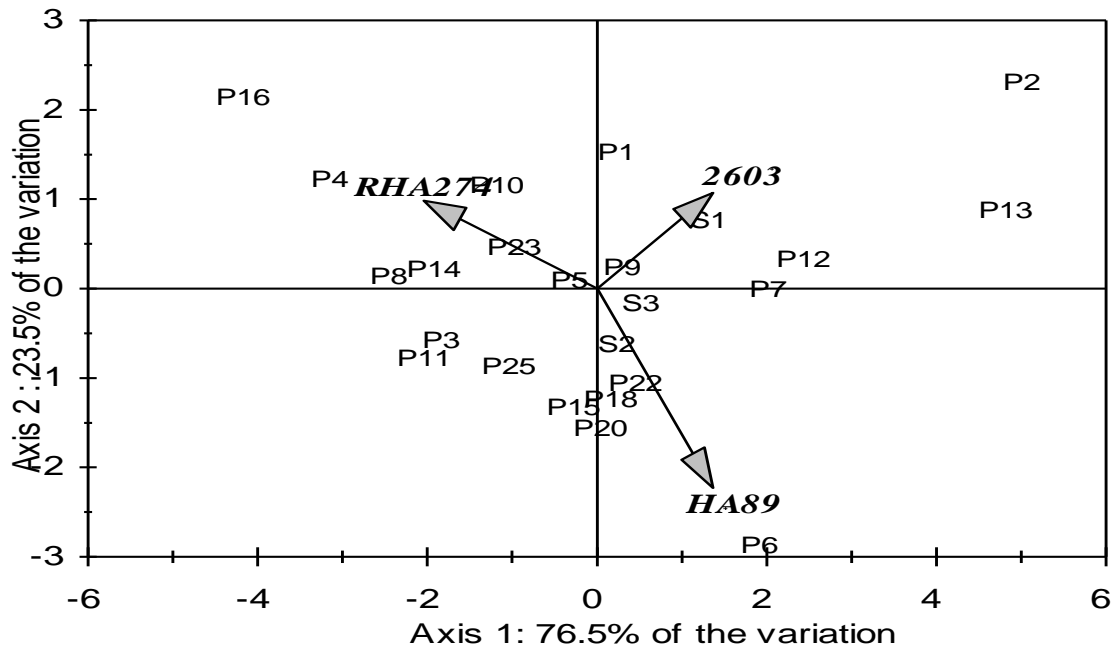


FIGURE 3 : MANDEL ANALYSIS OF THE POOL*TESTER INTERACTION SCA FOR OIL CONTENT

