

CYTOPLASMIC EFFECTS ON SOME AGRONOMICAL CHARACTERS IN SUNFLOWER.

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SUMMARY

The classical male sterile cytoplasm (*PET1*) was compared to ten other sunflower cytoplasmic (*PEF1*, *ANN1*, *ANN2*, *ANN3*, *ANN4*, *PET2*, *GIG1*, *EXI1*, *NEG1* and *ANL2*) through isogenic alloplasmic hybrids. Plant height, flowering date, seed yield and oil content were evaluated in field trials.

Results show occurrence of significant cytoplasmic effects for plant height flowering period, seed yield and oil content. *PEF1*, *ANN2*, *PET2*, *GIG1*, *ANL2* cytoplasmic induce later flowering date, while *PEF1*, *ANN2*, *ANN1*, *PET2*, *ANL2* sources produce taller plants. *EXI1* cytotypic acts positively on oil content (+4 %) while *PEF1* and *ANN2* decrease significantly mean seed yield.

Significant nucleocytoplasmic interactions were also identified in the agronomical characters tested, but the nuclear component remains prevailing on cytoplasmic effects.

INTRODUCTION

Studies on different species indicate that nuclear genetic material cannot be considered as the sole hereditary material of the cell. It is the total effect of the genetic and cytoplasmic materials interacting together that produces the phenotypic expression of a given individual. The cytoplasmic component was involved in characteristics as important as yield in maize (Hunter & al., 1968) or rice (Young & al., 1990). In sunflower, the most common cytoplasmic effect is related to the expression of male fertility. The new male sterile cytoplasmic (CMS) recently reported in the literature represent more than 25 sources. So, for the breeder, it is important to know the potential effects of the CMS on the agronomical traits, before using them in a selection program. The purpose of this paper was (1) to evaluate the effects of nuclear and cytoplasmic components on agronomical traits such as flowering period, plant height, seed yield and oil content and (2) to compare eleven different cytoplasmic to the classical *PET1* cytoplasm.

MATERIAL AND METHODS

Ten original cytoplasmic male sterile sources were compared to the classical *PET1** cytoplasm derived from *H. petiolaris* (Leclercq, 1969). (*) The acronyms used correspond to FAO codification.

The studied CMS descended from the following wild *Helianthus* species: *H. petiolaris* = *PET2** (Whelan, 1982); *H. giganteus* = *GIG1** (Whelan, 1980); *H. petiolaris fallax* = *PEF1**; *H.*

exilis = *EXII**; wild *H. annuus* species = *ANNI**, *ANN2**, *ANN3**, *ANN4** (Serieys & al., 1987); *H. annuus lenticularis* = *ANL2** (Heiser, 1982) and *H. neglectus* = *NEGI** (Serieys, unpublished).

These cytoplasms were compared through series of alloplasmic hybrids. In a first step, we convert public inbred lines (*HA89*, *RHA265*, *RHA274*) or INRA lines (*PAH3*, *B9*, *B16*) into the different cytoplasms by successive backcrosses (not less than five), to develop isogenic alloplasmic female lines. Yet, for a given cytoplasm, we only realize the conversion when the line behaved as sterility maintainer. Then, production of alloplasmic hybrids was realized by pollination of the former female isogenic lines by common male parents, in isolated plots. So, we got alloplasmic hybrids related to 9 different nuclear genotypes and 11 cytoplasms, as indicated in the following table.

List of nucleocytoplasmic combinations tested.

Cytoplasms	Hybrid nucleus								
	1	2	3	4	5	6	7	8	9
<i>PET1</i>	*			*	*	*	*	*	*
<i>PET2</i>	*	*	*	*	*		*	*	*
<i>PEF1</i>	*	*	*	*	*	*	*	*	*
<i>ANN1</i>	*	*	*	*	*	*	*	*	*
<i>ANN2</i>	*		*	*	*	*	*	*	*
<i>ANN3</i>				*	*	*	*	*	*
<i>ANN4</i>	*	*	*	*	*	*	*	*	*
<i>GIG1</i>	*	*	*	*			*		*
<i>EXII</i>	*								*
<i>ANL2</i>	*	*	*	*	*	*	*	*	
<i>NEGI</i>		*					*		

Nuclear genotypes: 1=(*RHA265* * *B16*); 2=(*RHA265* * *B9*); 3=(*RHA265* * *PAH3*); 4=(*RHA265* * *WG*); 5=(*WG* * *PAH3*); 6=(*HA89* * *PAH3*); 7=(*RHA274* * *HA89*); 8=(*HA89* * *WG*); 9=(*RHA274* * *B16*).

Three commercial hybrids (*PINTO*, *FRANKASOL*, *MIRASOL*) were included as controls. The experiments, using incomplete balanced blocs design, were laid out under 2 locations (Montpellier and Toulouse). The trials consisted of 4 replications (plots of 3 rows and 20 plants /row) in the first location and 3 replications (plots of 4 rows and 20 plants/row), in the second place. Flowering date, plant height, seed yield and oil content were evaluated in the two locations. Both nuclear, cytoplasmic, location, interaction effects and comparisons of the new CMS with the *PET1* classical cytoplasm, were analysed by the GLM procedure (SAS Institute Inc.).

RESULTS

1) Cytoplasmic and nuclear effects.

Analysis of the behaviour of 77 alloplasmic hybrids reveals highly significant nuclear effects ($p = 0.001$), for all considered traits. Similar cytoplasmic effects were also recorded for flowering date and plant height ($p = 0.001$). Therefore, the magnitude of effects, although statistically significant, was not so pronounced, respectively $p = 0.03$ and $p = 0.05$ with seed yield and oil content traits. Not any significant (nuclear * location) nor (cytoplasmic * location) interactions were detected, in the present study.

2) Comparison of the agronomical value of new cytoplasms with PET1.

Each cytoplasmic background was compared to *PET1* used here as reference cytoplasm. The statistical analysis take in account only the common nuclear genotypes (between 2 and 7) involved in the comparison of cytoplasm pairs (table 1).

Table 1: Comparison of new cytoplasms with CMS-PET1.
For each CMS, the values are ratio of the mean control (MIRASOL + FRANKASOL + PINTO)/3).

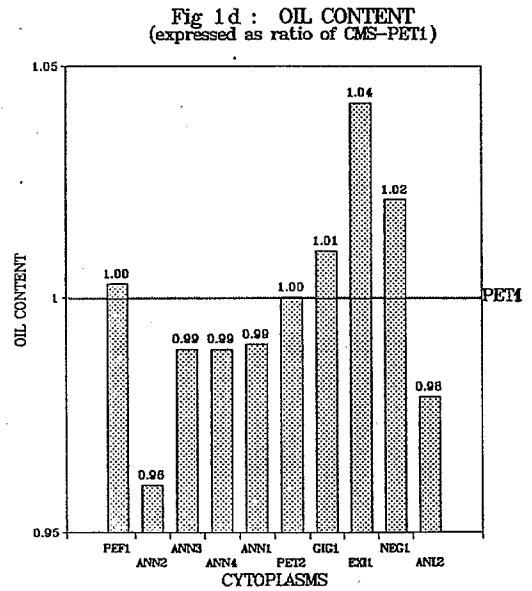
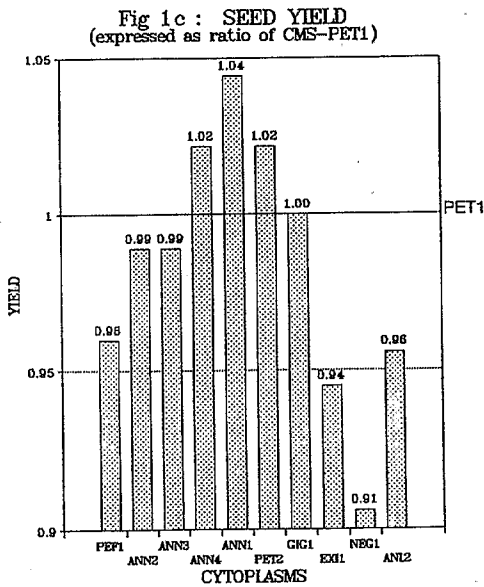
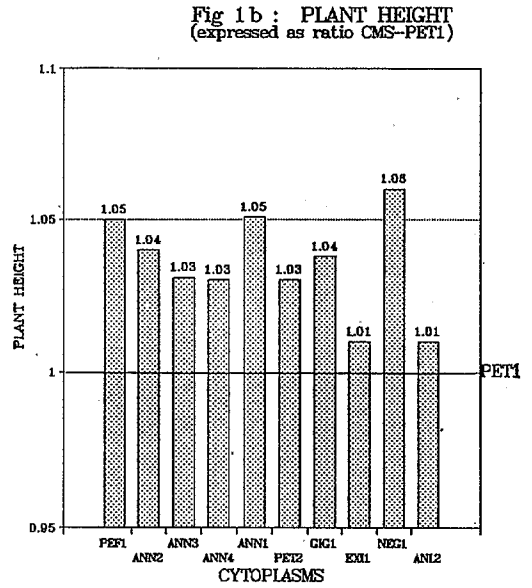
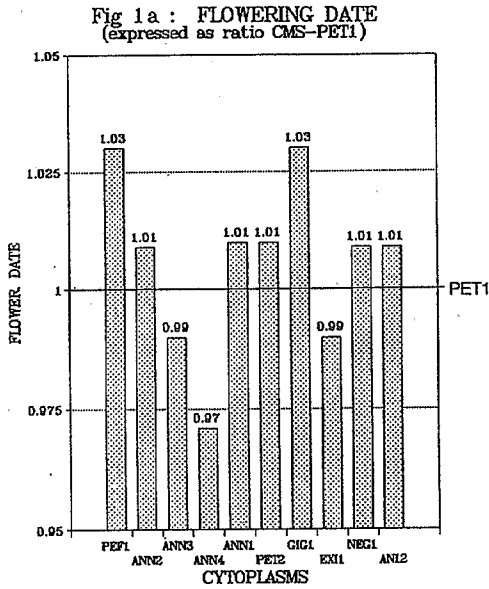
Cytoplasm	Seed yield	Flowering period	Plant height	Oil content	c_nb
PEF1 PET1 (N*C)	0.890 a 0.922 b	1.038 a 1.008 b *	1.051 a 1.002 b *	0.983 a 0.980 a *	6
ANN2 PET1 (N*C)	0.907 a 0.924 b *	1.022 a 1.010 b	1.037 a 1.002 b	0.967 a 1.005 b	6
ANN3 PET1 (N*C)	0.896 a 0.908 a	0.993 a 0.999 a *	0.987 a 0.961 a *	0.968 a 0.982 a	6
ANN4 PET1 (N*C)	0.940 a 0.910 a	0.990 a 1.010 b *	1.000 a 0.998 a *	0.974 a 0.979 a *	6
ANN1 PET1 (N*C)	0.950 a 0.910 b	1.010 a 1.000 a *	1.030 a 0.970 b *	0.974 a 0.979 a	7
PET2 PET1 (N*C)	0.929 a 0.912 a	1.010 a 1.000 b *	1.020 a 0.986 b *	0.967 a 0.970 a	6
GIG1 PET1 (N*C)	0.930 a 0.930 a	1.026 a 1.005 b	1.080 a 1.040 a	0.964 a 0.955 a	4
EXI1 PET1 (N*C)	0.928 a 0.875 a	0.999 a 0.992 a	1.036 a 1.000 a	0.977 a 0.944 b	2
NEG1 PET1 (N*C)	0.850 a 0.904 a	1.013 a 1.010 a	1.060 a 1.000 a	0.976 a 0.960 a	2
ANL2 PET1 (N*C)	0.871 a 0.911 a	1.020 a 1.008 b *	0.995 a 0.978 b *	0.969 a 0.988 a *	6

(a, b): cytoplasmic effects (F test, $p < 0.05$, when different letters).
(N*C): nucleocytoplasmic interaction, significant at 5 % when (*)
c_nb: number of hybrids in the comparison.

Flowering date (fig 1a)

PEF1, *ANN2*, *PET2*, *GIG1* and *ANL2* cytoplasms (except *ANN1*) induce significant lateness compared to the *PET1* reference. In contrast, *ANN4* shortens the number of days to flower (-3 %).

Fig 1 : COMPARISON OF AGRONOMICAL TRAITS OF NEW CMS, TO PET1 CYTOPLASM.



Plant height (fig 1b)

This trait is systematically increased in the 10 tested cytoplasmic backgrounds. Differences in plant height become significant in the following *PEF1*, *ANN1*, *ANN2*, *PET2* and *ANL2* cytotypes.

Grain yield (fig 1c):

As reported earlier, the cytoplasmic effect seems not so important as for previous traits. So, the reduction in grain yield was 4 % for *PEF1* and 1 % for *ANN2* cytoplasm (p = 0.01), while *ANN1* acts positively on this character (+ 4 %).

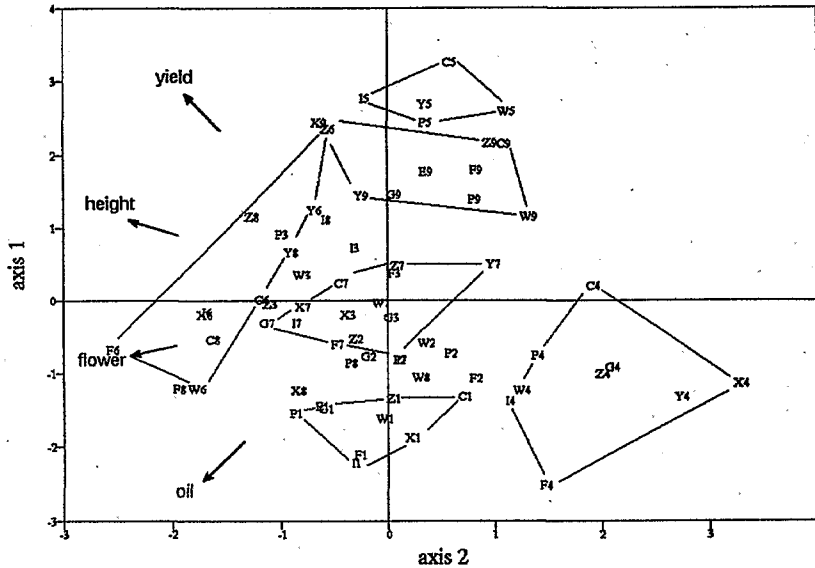
Oil content (fig 1d)

This character appears also less affected by cytoplasmic background than by nuclear genotype. Therefore, significant cytoplasmic effects were registered in 2 CMS sources, oil content being increased (+ 4 %) in *EX11* (but this evaluation is related to a limited hybrid sample) and reduced in *ANN4* cytoplasm.

As indicated in table 1 nucleocytoplasmic interactions occurred frequently in flowering date (6 significant effects on 10 tested), plant height (6/10), seed yield (1/10) and oil content (2/10).

The restoration status of the hybrids plays also an important role in grain and oil production levels. Indeed, these traits could be increased by 2 to 5 % in sterile plants, due to different allocation resources between fertile and sterile plants, as suggests Vear (1984). In our experiments, the hybrids on *ANN1*, *ANN2*, *ANN3*, *ANN4* and *PET2* cytoplasm were fully sterile. So, we can suppose that seed yield and oil content could benefit of this advantage.

Fig 2: Analysis of alloplasmic hybrids: structuration of nuclear and cytoplasmic effects by Principal Component Analysis.



CMS: PEF1 = X, ANN1 = W, ANN2 = X, ANN3 = Y, ANN4 = Z, PET2 = P, GIG1 = G, PET1 = C, ANL2 = I.
 NUCLEUS: 1, 2, 3, 4, 5, 6, 7, 8, 9.

3) Structuration of nuclear and cytoplasmic effects.

To separate nuclear from cytoplasmic effects, a principal component analysis was applied on seed yield, plant height, flowering date and oil content. Representation of the different hybrids is shown in fig 2. Hybrids appeared preferentially grouped according to their nuclear genotype rather than to their cytoplasmic origin. The relative position of the alloplasmic hybrids inside group (defined by the same nuclear genotype) differs strongly and underlines the importance of nucleocytoplasmic interactions.

CONCLUSIONS

In all considered traits, significant cytoplasmic effects were registered (3/10 for yield, 6/10 for flowering date, 5/10 for height of the plant and 2/10 for oil content). Similar results were also reported in early maize, where differences for yield and maturity have been related to the cytoplasmic components (Hunter & *al.*, 1968). In rice, both positive or negative cytoplasmic effects were also observed on days to flower, yield and plant height (Young & *al.*, 1990). In our experiments, new cytoplasmic reveal a general tendency to carry more negative than positive agronomical traits (increasing both the day number to flower, the size of the plant or lowering oil and seed yield). One explanation could be related to the origin of parental lines, bred (for *per se* value and combining ability) on *PET1* cytoplasm. We suggest that inbred lines developed in the *PET1* cytoplasmic background, has benefited of the long breeding work leading to optimum interactions between the nuclear genotypes and *H. petiolaris* Leclercq cytoplasm.

So, if new CMS sources have to be introduced in breeding programs, it seems preferable to select material on the related CMS sources, to isolate the most valuable agronomical nucleocytoplasmic interactions.

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