HELIA, 17, Nr. 21, p.p. 93-102 (1994)

UDC 633.854.78:631.527.56

REPORT ON THE PAST ACTIVITIES OF THE F.A.O. WORKING GROUP: "IDENTIFICATION, STUDY AND UTILIZATION IN BREEDING PROGRAMS OF NEW CMS SOURCES", FOR THE PERIOD 1991-1993

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SUMMARY

Due to particularly active work developed in the CMS working group by most of the participants, interesting results have been got. The most significant contributions were:

- The discovery of the CMS sources.
- The finding of restorer genes for "difficult to restore" CMS.
- The analysis of the genetic determinism of the fertility restoration of new CMS.
- The comparison of the CMS by genetical, molecular or agronomical ways.

Therefore, evidence is that a lot of studies are still necessary to differentiate the CMS sources. Likely, some of the 42 CMS sources reported may be identical. It is clear that complementary genetical studies have to be performed. Molecular studies on Mt DNA, proved to be powerful tools and fast technics, either to separate the CMS or to explain the mechanisms of the cytoplasmic male sterility.

Another aspect to be studied is the identification of the specific Rf genes in the different CMS. With this object, several participants have already started crosses between restorer genotypes to prepare allelism tests. This could be one of the proposals of the W. G., for the next period.

SYNTHESIS OF THE RESULTS

Cytoplasmic male sterility (CMS) and associated restorer genes (Rf) have been the major promoters for the development of commercial hybrids in the world. Now, more than 90% of the hybrids are made on the unique CMS-PET1 cytoplasm discovered by Leclercq in the progeny of a cross between *H. petiolaris* and the sunflower. The recent research programs have attempted to find new CMS sources in order to broaden the genetic base and reduce the vulnerability of the cultivated crop. The diversification of CMS sources may also be useful to optimise the utilisation of genetic resources in breeding programs by "changing" the restorer status of an inbred line (a restorer genotype for a cytoplasm may be a male sterility maintainer of another cytoplasm). Another application is linked to the "agronomic" value of the new CMS sources. This may be, for the breeder, a way to improve the hybrid performances. Finally, the availability of different CMS sources constitutes a powerful tool for genetics and molecular biology to understand the mechanisms of the CMS.

During 1987-1990 an important structured work was undertaken in the CMS working group. The main goals were to: (1) identify all new CMS sources, so as to define a catalogue and propose a codification for all the CMS, (2) compare 13 CMS sources by crossing with a sample of 18 inbred sunflower lines (provided by the coordination center

Table 1: List of the known CMS sources (15/06/94).

Common denomination	Species	Acc-code	Year obs.	Author, report	FAO code
KOUBAN	*H. annuus lenticularis*			ANASCHENKO, 1974	ANL1
INDIANA 1	*H. annuus lenticularis*			HEISER, 1982	ANL2
VIR 126	*H. lenticularis*			ANASCHENKO, 1974	ANL3
397	*H. annuus wild*	INRA-397	81	SERIEYS, 1984	ANN1
517	*H. annuus wild*	INRA-517	81	SERIEYS, 1984	ANN2
519	*H. annuus wild*	INRA-519	81	SERIEYS, 1984	ANN3
521	*H. annuus wild*	INRA-521	81	SERIEYS, 1984	ANN4
NS-ANN-81	*H. annuus wild*			MARINKOVIC, 1986	ANN5
NS-ANN-2	*H. annuus wild*			SKORIC, 1987	ANN6
	H. annuus wild	PI 413024	88	JAN, 1988	ANN7
	H. annuus wild	PI 413043	88	JAN, 1988	ANN8
	H. annuus wild	PI 413158	88	JAN, 1994	ANN9
AN-67	*H. annuus*	E-067	86	CHRISTOV, 1992	ANN10
AN-58	*H. annuus*	E-058	88	CHRISTOV, 1994	ANN11
AN-2-91	*H. annuus*	E-002	91	CHRISTOV, 1991	ANN12
AN-2-92	*H. annuus*	E-002	92	CHRISTOV, 1992	ANN13
FUNDULEA 1	*H. annuus texanis*			VRANCEANU, 1986	ANT1
ANOMALUS	*H. anomalus*	INRA-525	87	SERIEYS, 1994	ANO1
ARGOPHYLLUS	*H. argophyllus*	E-006	84	CHRISTOV, 1990	ARG1
ARGOPHYLLUS	*H. argophyllus*	E-007	87	CHRISTOV, 1990	ARG2
ARGOPHYLLUS	*H. argophyllus*	E-006	85	CHRISTOV, 1985	ARG3
BOLANDERI	*H. bolanderi*	INRA-255	80	SERIEYS, 1984	BOL1
DV-10	*H. debilis*	E-010	90	CHRISTOV, 1994	DEB1
EXILIS	*H. exilis*	INRA-130	82	SERIEYS, 1987	EXI1
EX12	*H. exilis*	INRA-331	88	SERIEYS, 1994	EXI2
CMG2	*H. giganteus*			WHELAN, 1981	GIG1
CMG3	*H. maximiliani*			WHELAN, 1980	MAX1
	H. maximiliani		83	JAN, 1994	MAX2
NEGLECTUS	*H. neglectus*	INRA-201	83	SERIEYS, 1994	NEG1
CANESCENS	*H. niveus canescens*	INRA-197	82	SERIEYS, 1987	NIC1
FALLAX	*H. petiolaris fallax*	INRA-200	80	SERIEYS, 1984	PEF1
PET/PET	*H. petiolaris petiol.*	INRA-737	87	SERIEYS, 1994	PEP1
CLASSIC CMS	*H. petiolaris Nutt*			LECLERCQ, 1969	PET1
CMG1	*H. petiolaris Nutt*			WHELAN, 1980	PET2
PETIOLARIS BIS	*H. petiolaris Nutt*			LECLERCQ, 1983	PET3
PET34	*H. petiolaris*	E-034	91	CHRISTOV, 1991	PET4
PHIR-27	*H. praecox*	E-027	90	CHRISTOV, 1990	PRH1
PRAECOX	*H. praecox praecox*	INRA-678	88	SERIEYS, 1994	PRP1
RUN-29	*H. praecox*	E-029	89	CHRISTOV, 1989	PRR1
RIG. RUSSIAN	*H. rigidus*			JAN, 1994	RIG0
VULPE	*H. rigidus*			VULPE, 1972	RIG1
RIG-M-28	*H. rigidus*	M-002	91	CHRISTOV, 1991	RIG2

of Montpellier), (3) search for restorer genes through F1 combinations, (4) study the stability of the CMS in different environments, and (5) study the genetic determinism of the restoration of the CMS. This important work, involving a cooperation between 9 countries, lead to interesting results on the stability and the comparison of the CMS; it was presented in a detailed report at the last F.A.O. consultation (Pisa, 1991).

The work done in the recent period (1991-1993) was a continuation of the studies initiated on 1988. The following aspects were particularly developed:

- identification of new CMS;
- search for new restorer genes;
- studies on the genetics of restoration;
- preparation of the allelism test to identify Rf genes;
- comparison of the CMS sources by genetic and molecular approaches. Several CMS have been genetically and molecularly differentiated, but separation is still not clearly established for all of them. So, complementary studies are necessary.

1) IDENTIFICATION OF NEW CMS SOURCES IN THE WORKING GROUP

The number of new cytoplasmic male sterilities (CMS) reported up to date increased significantly. More than 40 sources have been described. For all of them, demonstration has been made that origin of the androsterility results from nucleocytoplasmic interactions. The list of the known CMS, with indication of author and the species from which they originated, is reported here after. The denomination according to F.A.O. codification is also proposed.

Nineteen additional CMS sources have been discovered recently:

- seven in the *H. annuus* species: cms-ANN7, ANN8, ANN9 (C. C. Jan) and cms-ANN10, ANN11, ANN12, ANN13 (Christov).
- three in the *H. praecox* ssp: cms-PRR1, cms-PRH1 (Christov) and cms-PRP1 (Serieys)
- two in *H. rigidus*: cms-RIG2 (Christov) and cms-RIG0 (Russian source, reported by Jan). In fact, this latter CMS could be similar to cms-RIG1 reported by Vulpe (the new restorers of RIG0 have to be tested on RIG1)
- two in *H. petiolaris* ssp: cms-PET3 (Christov) and cms-PEP1 (Serieys)
- the other five CMS were detected in different *Helianthus* species: cms-MAX2 (Jan); cms-DEB1 (Christov); and cms-ANO1, EXI2, and cms-NEG1 (Serieys).

If we consider the 42 cms sources listed, they come from 12 different *Helianthus* species, most of them (36) being issued from *Helianthus (ex annui)* section. The most "productive" species for CMS were: the wild *H. annuus* (17 CMS), *H. petiolaris* species (6), *H. argophyllus* (3); *H. praecox* species (3 CMS), *H. exilis* (2 CMS), *H. maximiliani* (2 CMS).

These results suggest the existence of both inter and intraspecific cytoplasmic diversities.

Table 2: Restoration response of some sunflower inbred lines (or populations) to different cytoplasmic backgrounds.

Common denomination of the CMS	FAO code	% of restorer lines among:		Restoration sources:
		Cms-PET1 maint. genotypes	Cms PET1 restorer genotypes	
KOUBAN	ANL1	61.5% (26)[1]	40.0% (20)	HA89, HA99, HA291, RCMG3
INDIANA 1	ANL2	55.6% (18)	27.7% (18)	PAH3, RHA273, HA291, RCMG3
397	ANN1	3.3% (30)	0% (19)	HA291*, PAH2*, HA822*, LYRA*
517	ANN2	3.7% (27)	0% (21)	P21, RMAX1, PI413178, PS231
519	ANN3	14.2% (21)	0% (19)	P21, RHA280, RPET2, RHA801, PI413180
521	ANN4	3.2% (31)	3.2% (31)	P21, RHA280, PI406647, R-ANN4
NS-ANN-81	ANN5	0% (2)	0% (2)	
NS-ANN-2	ANN6	–	–	
PI413024	ANN7	–	–	P21, RHA280, PI413024
PI413043	ANN8	–	–	HA89, RHA266, RHA274, RHA294, PI413043
PI413158	ANN9	–	–	P21, PI413058
AN-67	ANN10	0% (5)	100% (5)	RHA274, R3880, NS26R, R147
AN-58	ANN11	–	–	
AN-2-91	ANN12	–	–	
AN-2-92	ANN13	–	–	
ANOMALUS	ANO1	7.7% (13)	66.7% (9)	HAB, PAH3, RHA265, PAH2
FUNDULEA1	ANT1	0% (4)	8.3% (12)	RANT1, RCMG2
ARG1	ARG1	0% (5)	100% (6)	R147, R3840, RHA274, RHA280, NS26R
ARG2	ARG2	33.3% (3)	–	85B3, D34, R147, RHA274, NS26R
ARG3	ARG3	0% (6)	25.0% (4)	R147, R3840, NS26R
BOLANDER1	BOL1	69.2% (39)	82.1% (28)	HA291, HA89, RHA266, RHA279, RHA801
DV-10	DEB1	–	–	
EXILIS	EXI1	63.3% (30)	57.1% (21)	HA89, LA, RHA276, RHA298, RHA299
EXI2	EXI2	33.3% (3)	100% (4)	RHA274, RHA801, PAH3, PW1
CMG2	GIG1	8.0% (18)	25.0% (24)	RHA280, RHA801, PAH3, BZA2, RHA294
CMG3	MAX1	25.0% (20)	11.1% (18)	HA291, PAH3, RHA801, XH
	MAX2	–	–	Hopi dye, Seneca, RHA294, RHA266
NEGLECTUS	NEG1	26.3% (19)	94.1% (17)	WG, FJ, HAB, RHA265, RHA266, RHA274
CANESCENS	NIC1(**)	30.4% (23)	11.7% (17)	RHA265, RHA274, CAC, D34
FALLAX	PEF1	15.2% (46)	16.6% (36)	CP3.1, LA, PAH3, RHA298
PET/PET	PEP1	27.3% (11)	20.0% (10)	CP3.1, LA, PAH2, PAH3
CMG1	PET2	8.0% (25)	28.0% (25)	RCMG1, CP3.1, RHA280, 82HR38, RHA294
PET34	PET4	–	–	
PHIR-27	PRH1	0% (2)	–	
PRAECOX	PRP1	0% (7)	100% (7)	PAH3, RHA278, RHA274
RUN-29	PRR1	0% (2)		
RIG. RUSSIAN	RIG			Luch, RPET2
VULPE	RIG1	0% (3)	0% (2)	none
RIG-M-28	RIG3			

(1) number of lines tested. (*) partial restoration. (**) NIC1: incomplete malesterility.

Underlined restorer lines = 100% restoration in the progeny.
PAH2, PAH3, 85B3, D34, PW1, FJ, CP3.1, BZA2, XH, WG, FJ, HAB, CAC, LA; 82HR38, R-ANN4 = INRA inbred lines. R3880, NS26R, R147 are I. W. S. inbred lines.
RANT1 is a line from ICCPT, the other lines are from USDA.

2) SEARCH FOR CMS RESTORERS GENES

Important results were obtained in the working group for isolation of Rf restorer genes. In most of the reported CMS sources, they have been found either among the wild parents donors of the CMS, interspecific progenies or cultivated inbred lines.

In Table 2, the restoration response is reported from 39 CMS. This was measured by the restoration status of the F1 plants issued from crosses between malesterile plants and different fertile genotypes. Due to the activity of the working group, we have identified restorer genes for most of the CMS sources.

According to the CMS, the frequency of the restoration responses varies from 0% to more than 80% of the genotypes tested. Rf genes have not been reported in seven CMS, either because the CMS were still not studied, or because these genes are very rare in the *Helianthus* germplasm.

Interesting results were reported by C. C. Jan who found restorer genes related to three CMS (for which an efficient Rf gene has not been detected): cms-ANN2 (restored by P21, RMAX1 and the wild parent), cms-ANN3 (restored by P21, RHA 280, RPET2, RHA801, and the wild parent), and cms-ANN4 (restored by P21, RHA280, and the wild parent). For the last source, INRA Montpellier has also fixed an inbred restorer line, R-ANN4, in the progeny of a cross with the wild donor parent. Similarly, M. Iuoras has reported efficient restorer genes in the wild *H. annuus ssp. lenticularis* and other two wild species, for cms-ANT1.

Another attractive result is the discovery of Rf genes for the cms-RIG sterility. Indeed, J. Miller (1991) found Rf genes in the genotypes Luch and RPET2. We wonder if the two cms, RIG0 and RIG1, are similar in that they are derived from the same *H. rigidus* species, difficult to restore, and come from Russia or Romania. Complementary crosses and molecular studies are needed to check this hypothesis.

Table 2 shows that Rf genes are common for cms-ANL1, ANL2, BOL1, EXI1, EXI2, NEG1 and particularly scarse for cms-ANN1, 2, 3, 4, 5, ANT1 and RIG1.

The stability of the CMS – estimated as the phenotypic expression of male fertility restoration in different locations – shows a variability for this trait: different restoration levels were registered between locations, due to either different appreciation of the male-sterile phenotype and/or CMS-location interactions.

This variability makes difficult a global comparison between the CMS sources. In spite of these difficulties, we found stable restorers for most of the CMS sources. Such restorers are reported (underlined) in Table 2.

Table 3: Frequency of Rf genes in the *Helianthus* germplasm, related to CMS sources. (Expressed as % of genotypes containing Rf genes)

High > 50%	Intermediate 25-50%	Low < 25%
ANL1, ANL2, BOL1, EXI1, EXI2, NEG1, PET1	ANN10, ANO1, ARG1, ARG2, NIC1, PRP1	ANN1, ANN2, ANN3, ANN4, ANN5, ANT1, ARG3, GIG1, MAX1, PEF1, PEP1, PRH1, RIG0, RIG1

The CMS sources may be classified in three groups according to the frequency of restorer genes found in the *Helianthus* germplasm (Table 3).

3) GENETIC DETERMINISM OF RESTORATION

During the last three years, interesting results were reported by Jan on the heredity of cms-ANN2 and ANN3, where restoration is controlled respectively by a single dominant Rf gene and 2 dominant complementary genes. The variation in pollen stainability in some crosses suggests the presence of modifier genes. Interesting studies were also performed on the genetics of the Rf genes in the cms-RIG source. The data agree with the hypothesis of two dominant complementary genes involved in the restoration of cms-RIG.

Another important study was performed at I. F. V. C. Novi Sad, where multiple nuclear combinations (involving 11 inbred lines) were studied on cms-ANN2, ANN3, ANN4 and BOL1.

The results exhibit the lack of restorer genes in the crosses with cms-ANN2, ANN3 and MAX1. Interesting results were found in cms-BOL1, for which the frequency of good maintainer lines is low. The following nuclear combinations lead either to complete male sterile hybrids (RCMG1 X RCMG2, RCMG1 X RHA276, RHA271 X RHA278, RHA271 X RCMG3) or to male fertile: male sterile segregations (RHA265 X RCMG3 or RHA279; RCMG3 X RHA266). In other respects, most of the F2 segregations already studied on cms-BOL1 agree with the hypothesis of male sterility controlled by two independent recessive Rf genes. The explanation of the restoration responses observed in this work is complex and probably involves more than 2 Rf genes.

The genetics of restoration was analysed at Montpellier for cms-NEG1, ANO1, PRP1, EXI1 and PEP1 sources. The F2 segregations studied clearly indicate that the restoration of the first three CMS were governed by a single Rf gene and that two complementary dominant Rf genes were involved in EXI1 and PEP1 sources.

The data shown in Table 4 indicate that restoration in sunflower is generally controlled by single Rf genes or series of 2 independent complementary genes. Therefore, the restoration of some sources (particularly BOL1) remain difficult to explain by a simple hypothesis.

An important work is now in progress at Fargo (allelism tests between restorer lines), to identify the Rf genes involved in cms-BOL1 and cms-ANL1 sources.

A summary of the inheritance studies of restoration is reported in Table 4.

4) COMPARISON OF CMS SOURCES

Genetic and molecular approaches

Both genetic and molecular studies involving mitochondrial DNA RFLP and transcript products were undertaken on several CMS sources. The objectives were to compare the CMS and to explain the mechanisms of the CMS.

Interesting work was performed at Giessen on the comparison of cms-PET1 and fertile normal cytoplasms (Horn, 1990; Kohler, 1991). Cytoplasmic male sterile lines cms-PET1-89 and cms-PET1-Baso differ from the male fertile analogue lines in a mitochondrial sequence (open reading frame *orfH522*) in the vicinity of the *atp*A gene.

Table 4: Genetic determinism of male fertility restoration.

Common denomination	FAO code	Genetic control of restoration	Reference
KOUBAN	ANL1	2 complementary dominant genes	Leclercq, 1984; FAO report 1991
INDIANA1	ANL2	no clearcut segregation. Possible 2 complementary dominant Rf genes	FAO report, 1991
397	ANN1	–	
517, PI	ANN2	one Rf dominant gene + modifiers	Jan, 1994
519, PI	ANN3	2 complementary dominant genes + modifiers	Jan, 1994
521, PI	ANN4	–	
NS-ANN-81	ANN5	–	
NS-ANN-2	ANN6	–	
	ANN7	–	
	ANN8	–	
	ANN9	–	
AN-67	ANN10	–	
AN-58	ANN11	–	
AN-2-91	ANN12	–	
AN-2-92	ANN13	–	
ANOMALUS	ANO1	single dominant Rf gene	Serieys, 1994
FUNDULEA1	ANT1	complex. At least two complementary dominant genes	Iuoras, 1991, 1994
ARGOPHYLLUS	ARG1	–	
ARGOPHYLLUS	ARG2	–	
ARGOPHYLLUS	ARG3	–	
BOLANDER1	BOL1	complex. 2 independent dominant Rf genes explain many segregations. Serieys, 1991 (FAO report)	
DV-10	DEB1	–	
EXILIS	EXI1	2 complementary dominant Rf genes	Serieys, 1987, 1994
EXI2	EXI2	–	
CMG2	GIG1	–	
CMG3	MAX1	2 or more complementary Rf genes	
	MAX2	no clearcut segregations	
NEGLECTUS	NEG1	one dominant Rf gene	Serieys, 1994
CANESCENS	NIC1	–	
FALLAX	PEF1	2 (or rare 3) complementary dominant independent genes.	Serieys, 1987, 1991
PET/PET	PEP1	2 independent complementary Rf genes	Serieys, 1994
CLASSICAL CMS	PET2	one dominant Rf gene	FAO report, 1991
PRAECOX	PRP1	one dominant Rf gene	Serieys, 1994
RUN-29	PRR1	–	
RIG. RUSSIAN	RIG	2 complementary dominant genes	Jan, 1994
VULPE	RIG1	–	
RIG-M-28	RIG3	–	

The transcription pattern of *atp*A is changed in male sterile lines as compared with fertile ones. A 16 kDa protein is expressed in male sterile lines carryng the *H. petiolaris* (PET1) cytoplasm as well as in the restored male fertile lines. This protein is not detectable in the wild *H. petiolaris* species. It is suggested that this polypeptide may play a role in the CMS.

Another work is reported by M. Iuoras (1992). The plasmide P1t (1.45 Kb) is a good probe to distinguish the cytoplasms from cms-PET1 since it is present in fertile maintainer lines but not in cms-PET1. No hybridization signal was detected between the plasmide P1t and the total DNA from cms-ANT1 or the wild *H. annuus ssp texanus*.

Besides, Spassova (1992) studied 6 new Bulgarian CMS, including PET1 and ANT1. She used atpA gene and showed that cms-ANT1 differed for mt genomic structure from both the fertile genotypes and all the 6 new CMS.

Molecular comparison of a large sample of CMS was also realized by Crouzillat (1991, 1994). The genetics of male fertility restoration and the RFLP of the mitochondrial DNA were studied for 16 sunflower cytoplasms. Male fertility restoration / male sterility maintainers patterns distinguished 12 cytotypes. Four cytoplasms completely unrestored were not genetically distinguished (ANN1, ANN2, ANN3, ANN4) as well as PEF1 and PEP1.

The RFLP of the mitochondrial DNA revealed specific differences between the cytotypes analysed and permitted the distinction of 13 cytotypes. It was shown that mt DNA diversity occurs both between and within the *Helianthus* species.

For genetical and mitochondrial RFLP studies, phenograms built according to similarity indexes show that most of the CMS groups defined by restoration patterns correspond with a restriction fragment pattern of the mt DNA. One exception occurred for cms-ANN4, but recently restorer genes were found in this CMS (Jan, 1994; Serieys, 1994) which now made possible the genetic separation from the other three CMS (ANN1, ANN2 and ANN3).

Agronomical approach

Field trials were undertaken at INRA to compare the agronomical effects of the CMS sources. The classical cms-PET1 was compared to 9 sunflower CMS (PEF1, BOL1, EXI1, PEP1, GIG1, PET2, ANL2, ANO1, NEG1) through isogenic alloplasmic hybrids. Results show significant, positive or negative, cytoplasmic effects for all the studied characters: seed yield, flowering date, plant height, oil content. Some cytoplasmic effects were also suggested for *Phomopsis* tolerance, but they have to be confirmed.

5) CONCLUSIONS

Due to particularly active work developed in the CMS working group by most of the participants, interesting results have been got. The most significant contributions were:

- the discovery of the CMS sources.
- the finding of restorer genes for "difficult to restore" CMS.
- the analysis of the genetic determinism of the fertility restoration of new CMS.
- the comparison of the CMS by genetical, molecular or agronomical ways.

Therefore, evidence is that a lot of studies are still necessary to differentiate the CMS sources. Likely, some of the 42 CMS sources reported may be identical. It is clear that complementary genetical studies have to be performed. Molecular studies on Mt DNA,

proved to be powerful tools and fast technics, either to separate the CMS or to explain the mechanisms of the cytoplasmic male sterility.

Another aspect to be studied is the identification of the specific Rf genes in the different CMS. With this object, several participants have already started crosses between restorer genotypes to prepare allelism tests. This could be one of the proposals of the W. G., for the next period.

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INFORME SOBRE ACTIVIDADES DEL GRUPO DE TRABAJO DE F.A.O. "IDENTIFICACION, ESTUDIO Y UTILIZACION EN PROGRAMAS DE GIRASOL DE NUEVAS FUENTES DE ANDROESTERILIDAD CITOPLASMICA" DURANTE EL PERIODO 1991-1993

RESUMEN

Debido particularmente al trabajo activo desarrollado en el grupo de trabajo de androestorilidad citoplásmica (CMS) por la mayor parte de los participantes, se han obtenido interesantes resultados. Las contribuciones mas interesantes fueron:

- El descubrimiento de nuevas fuentes de CMS.
- El encuentro de nuevos genes de restauración para CMS difíciles de restaurador.
- El análisis del determinismo genético de la restauración de la fertilidad de nuevas CMS.
- La comparación de CMS por medio de medios genéticos moleculares y agronómicos.

Por tanto, la evidencia es que muchos estudios son aún necesarios para diferenciar las fuentes de CMS. Igualmente alguna de las 42 fuentes de CMS encontrades pueden ser idén ticas. Está claro que estudios genéticos complementarios deben ser llevados a cabo. Estudios moleculares sobre Mt DNA constituyen la herramienta mas poderosa y rápida técnica bien para roparar las fuentes de CMS o para explicar los mecanismos de androesterilidad.

Otro aspecto a ser estudiado es la identificación de los genes Rf especificos en los diferentes CMS. Con este objetivo varioo partioipantos han omposade ya aruses centre genetipos restauradores par preparar test de alelismo. Este podria ser una de las propuestas del grupo de trabajo para el próximo periodo.

RAPPORT SUR LES ACTIVITES DU GROUPE DE TRAVAIL F.A.O. SUR L'IDENTIFICATION, L'ETUDE ET L'UTILISATION DANS LES PROGRAMMES DE SELECTION DE NOUVELLES SOURCES DE STERILITE MALE CYTOPLASMIQUE (CMS), POUR LA PERIODE 1991-1993.

RÉSUMÉ

Des résultats intéressants ont été obtenus, grâce au travail particulièrement aclif réalisé par la plupart des participants, dans ce groupe de travail. Les contributions les plus significatives concernent:

- La découverte de nouvelles sources de CMS
- La découverte de gènes de restauration pour les sources réputées difficiles à restaurer,
- L'analyse du déterminisme génétique de la restauration de fertilité chez les nouvelles CMS
- La comparaison des CMS par les approches génétique, moléculaire et agronomique.

Les résultats obtenus mettent en évidence que des études sont encore nécessaires pour différencier les sources de CMS. Il est vraisemblable que plusieurs des 42 sources répertoriées sont identiques et il est clair que des études génétiques complémentaires doivent être réalisées. Les études moléculaires sur le DNA mt constituent des outils puissants et offrent des techniques rapides, soit pour différencier les sources de CMS ou expliquer les mécanismes impliqués dans la stérilité mâle cytoplasmique.

Un autre aspect qui doit être étudié réside dans l'identification des gènes Rf spécifiques de ces diverses CMS. Dans ce but, plusieurs participants ont déjà initié les croisements entre génotypes restaurateurs pour préparer les tests d'allélisme. Ceci constituera une des propositions d'étude de la stérilité mâle du tournesol, pour la prochaine période.