

DEVELOPMENT AND CHARACTERIZATION OF TOURNEFORTII CMS SYSTEM IN BRASSICA NAPUS L.

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ABSTRACT

Backcross substitution of *B. napus* genome in *B. tournefortii* cytoplasm via *B. juncea* bridge resulted in a stable CMS (*tour*) system, which is not associated with any yield penalty. Male fertility restorers were also identified. Genetic analysis revealed monogenic dominant inheritance of male fertility restoration by TFR 88-26, TFR 88-51 and TFR 9. A hybrid PGSH 51, based on this system, was released for general cultivation in Punjab during 1994. The hybrid outyielded the varietal check GSL-1 by about 18 per cent.

INTRODUCTION

Several cytoplasmic male sterility systems are available in *Brassica napus* but excepting *pol* CMS, no other system could be commercially exploited until now. In the present communication we describe the successful development F₁ hybrids based on *tournefortii* (*tour*) CMS system.

The male sterility was developed by substituting *B. napus* genome into a sterilizing cytoplasm which was originally discovered in an unknown population of *B. juncea* (Rawat and Anand, 1979). The evidence from mt DNA profiles later suggested that this CMS cytoplasm came from *B. tournefortii* (Pradhan *et al.*, 1991).

MATERIAL AND METHODS

As many as 66 CMS lines based on *tour* cytoplasm were developed through backcross substitution of nuclear genome of 66 Indian and exotic accessions of *B. napus* into the sterilizing cytoplasm. A total of 520 F₁ hybrids involving ten CMS lines and 52 *B. napus* genotypes were scored for the male fertility restoration. Each F₁ hybrid was scored using a male fertility index (MFI) based on visual observations and anther to stigma ratio (ASR). Male fertility index ranged from 0-4, with 0 indicating complete sterility and 4 indicating complete fertility. Any F₁ hybrid having all plants with MFI of 4 and ASR of more than 1 was categorized as fertile hybrid. Acetocarmine staining was subsequently used to test pollen grain fertility in the fertile hybrids.

The F₂ and backcross generations were studied to understand the inheritance of male fertility restoration. Chi-square analysis was used to test the goodness of fit to the null hypothesis. Selected F₁ hybrids were tested in large scale replicated yield evaluation trials conducted over four locations in Punjab from 1991-92 to 1993-94. Pre-release adaptive trials were conducted only for hybrid PGSH 51 vs varietal check GSL 1 in Punjab state during 1993-94.

RESULTS AND DISCUSSION

Male sterility was characterized by the presence of rudimentary anthers with little or no fertile pollen grains. In a majority of the CMS lines studied, the nectary size and female fertility was normal. In 12, out of the 66 CMS lines evaluated, impaired male fertility and a reduced nectary size was observed. The male sterile plants, however, had smaller flowers and narrow petals as compared to their euplasmic male fertile parent.

The biological penalty associated with the tour CMS was calculated by comparing the biological cost assessment of isonuclear alloplasmic and euplasmic lines. In a majority of the cases studied, the CMS conversion did not require any significant enhancement in photosynthetic requirement. There was some indication of little higher susceptibility to alternaria blight of CMS lines as compared to respective maintainer parents.

Of the 520 hybrids tested, male fertility restoration was observed in F₁ crosses involving TFR 88-26, TFR 88-51, TFR 88-53, TFR 9 and TFR 90 as male parents. The pollen grain fertility and anther-stigma ratio in completely restored F₁ hybrids was almost perfect. The RF gene source(s) of TFR 88-26, TFR 88-51 and TFR 9 restored pollen grain fertility in all the female genotypes used in crosses. The male fertility restoring ability of TFR 90 and TFR 89-53 was, however, influenced by the genotype of the maternal parent used in cross combinations.

This showed an interaction of certain fertility enhancer minor gene(s) in female nuclear background and gene(s) for male fertility restoration present in TFR 90 and TFR 89-53.

Inheritance of fertility restoration

The genetic analysis revealed monogenic dominant inheritance of male fertility restoration by TFR 88-26, TFR 88-51 and TFR 9 (Table 1).

TABLE 1: Genetics of male fertility restoration in *tour* cytoplasm

Cross and generation	Plants observed	Segregation			
		Pt.	St.	Exp.	χ^2
PRO-05 x TFR 88-26					
F ₂	467	358	109	3:1	0.71
BC ₁	126	70	56	1:1	1.65
PRO-05 x TFR 88-51					
F ₂	354	258	96	3:1	0.84
BC ₁	260	136	124	1:1	0.56
PRO-05 x TFR 9					
F ₂	412	298	114	3:1	1.56

Yield evaluation of F₁ hybrids

In 56 F₁ hybrids evaluated the yield superiority ranged from 16.9 to 29 per cent over the varietal check, GSL-1. One of the hybrids PGSH 51 was extensively tested. The summary results of the evaluation of PGSH 51 are presented in table 2.

TABLE 2. Yield performance of PGSH 51 vs GSL 1

Trials	Yield (kg/ha)		Per cent inc. over GSL-1
	PGSH 51	GSL 1	
Research(14)	2142	1772	+20.8
Adaptive(29)	1912	1641	+16.5

Figure in parenthesis indicates number of trials.

The hybrid PGSH 51 recorded an average yield increase of 20.8% and 16.5 per cent in research and adaptive trials respectively. The hybrid yielded a maximum of 2800 kg/ha under real form conditions. PGSH 51 was later released for general cultivation in Punjab state during 1994. This is the first ever hybrid of *B. napus* in India.

REFERENCES

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