SELF-INCOMPATIBILITY IN BRASSICA NAPUS

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ABSTRACT AND S-NOMENCLATURE

There are two S-loci in *B. napus*, the ancestral *B. rapa* S-locus (^{R}S) and the ancestral *B. oleracea* S-locus (^{O}S). There is potential for allelic variation at the ^{O}S and ^{R}S loci including both defined *B. oleracea* ($^{O}S_{22}$, $^{O}S_{25}$, $^{O}S_{29}$ etc) and *B. rapa* ($^{R}S_{A1}$) S-alleles introduced into Oil Seed Rape (OSR) via resynthesised *B. napus* lines with known S-alleles and undefined *B. oleracea* and *B. rapa* S-alleles present in existing OSR varieties (e.g. $^{O}S_{Tap}$ and $^{R}S_{Tap}$ from the cultivar "Tapidor").

In addition there is a suppressor locus (P) which is not linked to the S-loci. OSR allele(s) at the P-locus (P_2) have a dominant epistatic interaction over normal resident OSR S-alleles and over "recessive" S-alleles introduced from *B. oleracea* and *B. rapa* causing the suppression of the SI activity. The allele(s) at the P-locus in *B. oleracea* or *B. rapa* (P_1) are normally dominant to P_2 and "dominant" *B. oleracea* S-alleles have a dominant epistatic effect over P_2. Rare P-alleles (P_3), that are recessive to P_2 are also found in cultivars of *B. oleracea* or *B. rapa*.

INTRODUCTION

Sporophytic self-incompatibility (SI) has been characterised genetically in *B. oleracea* and *B. rapa* (Ockendon, 1974). Recently the cloning of the specific determinant at the S-locus has allowed analysis of SI at the molecular level (Trick, 1990). SI is more complex in the economically important amphidiploid *B. napus* which contains S-loci and S-related recognition and signal transduction mechanisms from both the *B. oleracea* and *B. rapa* ancestors. While the vast majority of resynthesised *B. napus* lines are SI almost all OSR varieties are self-compatible (SC). A breeding strategy for using SI to produce F_1 hybrid varieties of OSR were formulated by Thompson and Hughes (1986) and has exhibited some success (P. Werner, personal communication). However, the underlying genetic control of SI in *B. napus* has not been satisfactorily explained although the cloning and sequencing of a defective S-allele from OSR has been described (Goring *et al*,

1993). The availability of cloned S-alleles and their use as RFLP markers has allowed S-genotype to be determined separately from S-phenotype for the first time. This has allowed a thorough analysis of the genetic recognition of SI in OSR.

EXPERIMENTATION

S-genotype and S-phenotype

A range of resynthesised *B. napus* lines were generated from interspecific crosses between a range of *B. oleracea* lines with defined S-alleles and a constant inbred *B. rapa* line (A1). The doubled haploid (DH) resynthesised *B. napus* lines were each used to pollinate a DH line derived from the OSR variety "Tapidor" (Tap) to produce F_1 plants. The F_1 plants were used to pollinate; a range of OSR varieties (Table 1) to produce T_1 populations, Tap to produce B_1 populations and in turn self-pollinated to produce F_2 populations (Table 2).

The S-genotype of individual plants was determined on the basis of RFLP analysis using $^{O}S_{29}$ (Trick, 1990) and pW150 (D. Lydiate, personal communication) as probes. $^{O}S_{29}$ detects $^{R}S_{OSR}$ and $^{O}S_{22}$, $^{O}S_{23}$, $^{O}S_{25}$, $^{O}S_{29}$ and $^{O}S_{35}$. pW150 detects allelic series at loci closely linked to both ^{O}S and ^{R}S. The S-phenotype was determined essentially as described by Kho and Baer (1968).

Table 1 shows the effect of allelic variation at the *B. oleracea* S-locus and the P-loci in T_1 populations

S-genotype[a]		S-phenotype[b]		
$^{R}S'$ $^{O}S^{d}$		SI	INTER	SC
$^{O}S_{22}$	T- 22-	8	-	-
	T- T -	4	1	6
$^{O}S_{23}$	T- 23-	9	-	-
	T- T-	4	1	7
$^{O}S_{25}$	T- 25-	2	3	-
	T- T -	-	1	9
$^{O}S_{29}$	T- 29-	4	-	-
	T- T -	3	1	6
$^{O}S_{35}$	T- 35-	6	3	1
	T- T -	-	1	8

a - determined on the basis of inherited RFLP alleles. b - SI (self-incompatibility) is 0-5 pollen-tubes per pollinated flower, Inter (intermediate) is 6-30 pollen-tubes per fresh flower, SC (self-compatible) is > 30 pollen-tubes per fresh flower. Number are number of characterised individuals in each class. c - T- $^{R}S_{Tap}$ (resident Tapidor S-allele), $^{R}S_{CULTIVAR}$ where the cultivar were Apache, Apex, Bristol, Mandarin and Navajo
d - $^{O}S_{CULTIVAR}$ where cultivar were the same as above

$^{O}S_{22}$, $^{O}S_{23}$, $^{O}S_{29}$ - all plants carrying these alleles were SI, demonstrating epistatic dominance of these S-alleles over the cultivar suppressor allele (P_2) or dominance of P_1 over P_2

$^{O}S_{25}$ and $^{O}S_{35}$ - plants carrying these alleles were segregating for SI, demonstrating P_2 is exhibiting epistatic dominance over $^{O}S_{25}$ and $^{O}S_{35}$, but that P_3 is dominant over P_2 with regard to the suppression of $^{O}S_{25}$ and $^{O}S_{35}$ by P_2.

There is segregation for SI in lines derived from the $^{O}S_{22}$, $^{O}S_{23}$ and $^{O}S_{29}$ crosses but carrying only $^{O}S_{OSR}$ and/or $^{O}S_{Tap}$ S-alleles demonstrating that P_1 is dominant to P_2 and that "Tapidor and/or other OSR cultivars harbour a latent ^{O}S-allele

P_2 and P_3 - The lines derived from the $^{O}S_{25}$ and $^{O}S_{35}$ crosses but carrying only $^{O}S_{OSR}$ and/or $^{O}S_{Tap}$ S-alleles are SC indicating that P_3 is recessive to P_2 with regard to suppression of $^{O}S_{Tap}$ and $^{O}S_{OSR}$

Table 2. S-genotype and phenotype of F_2 and B_1 plants segregating for SI

	$^{O}S_{25/25}$			$^{O}S_{25/Tap}$			$^{O}S_{Tap/Tap}$		
	SI	INT	SC	SI	INT	SC	SI	INT	SC
$^{R}S_{AI/AI}$	1	-	-	6	-	-	5	-	-
$^{R}S_{AI/Tap}$	1	-	-	5	2	1	-	-	9
$^{R}S_{Tap/Tap}$	-	1	-	1	6	8	-	-	12

SI - (self-incompatibility) is 0-5 pollen-tubes per pollinated flower, INT - (intermediate) is 6-30 pollen-tubes per fresh flower, SC-(self-compatible) is > 30 pollen-tubes per fresh flower. Number are number of characterised individuals in each class.

Table 2 shows allelic variation at the *B. rapa* S-locus and the P-loci. Plants carrying $^{R}S_{AI/Tap}$ $^{O}S_{25/Tap}$ and $^{R}S_{Tap/Tap}$ $^{O}S_{25/Tap}$ alleles are segregating for SI, demonstrating the expression of P which is not linked to the S-locus.

$^{R}S_{AI/Tap}$ heterozygote is epistatically recessive to P_2. Plants with $^{R}S_{AI/AI}$ homozygote alleles are all SI irrespective of the allele combination at the *B. oleracea* S-locus. This demonstrates that there is an interaction between P_2 and $^{R}S_{Tap}$ and that $^{R}S_{Tap}$ is required for P_2 to suppress. This is supported by previous experiments carried out by Parkin and Lydiate (personal communication)

An individual with $^{R}S_{Tap/Tap}$ $^{O}S_{25/Tap}$ genotype has been used to pollinate Tapidor and the segregation for SI of this BC population of $^{O}S_{25/Tap}$ will be used to map the P-locus.

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