



Identification of seven haplotype-specific *SFBs* in European pear (*Pyrus communis*) and their use as molecular markers

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ABSTRACT

The European pear (*Pyrus communis*) carries the *S*-RNase-mediated gametophytic self-incompatibility (GSI) system. The *S*-haplotype is conferred by an *S*-locus, which contains the style-specific expressed *S*-RNase, and the pollen-specific expressed *F*-box genes (*SFB*). Both the *S*-RNase and the *SFB* genes are multi-allelic and each is characteristic of one of the *S*-haplotypes. Therefore, they are ideal markers for molecular *S*-genotyping. In this work, for the first time, seven haplotype-specific *SFBs* were isolated from European pears. Particular primers for each of these *SFBs* were generated, thus providing an additional tool for *S*-genotyping of European pear cultivars.

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1. Introduction

The European pear (*Pyrus communis*) belongs to the Rosaceae family, which carries the *S*-RNase-mediated gametophytic self-incompatibility (GSI) fertilization system (Sassa et al., 1992). In this system, compatibility among cultivars is determined by the *S*-locus, which harbors an RNase (*S*-RNase) and an *F*-box gene termed *SLF* (*S*-locus *F*-box) or *SFB* (*S*-haplotype-specific *F*-box) (Entani et al., 2003; Ushijima et al., 2003). The *S*-RNase is presumed to be involved in the pistil-maternal part of the system, and the *SLF/SFB* in the pollen-paternal part (Kao and Tsukamoto, 2004). The *F*-box genes are components of the SCF complex that leads to poly-ubiquitination of the selected protein and its degradation by the 26S proteasome (Hershko and Ciechanover, 1998). However, the exact role of *SLF/SFB* has yet to be determined (Goldraij et al., 2006; Hua et al., 2007).

Both the *S*-RNase and the *SLF/SFB* genes are multi-allelic and are individually characteristic for each haplotype (Lai et al., 2002; Entani et al., 2003; Ushijima et al., 2003; Yamane et al., 2003; Goldway et al., 2007). Thus, each of the alleles can serve as a molecular marker for its respective haplotype. Eighteen European pear *S*-RNase alleles were cloned and sequenced, and more than 130 cultivars were molecularly *S*-genotyped on the basis of their *S*-RNase genes (Zuccherelli et al., 2002; Zisovich et al., 2004; Sanzol et al., 2006; Takasaki et al., 2006; Goldway et al., 2009; Sanzol and Robbins, 2008). The *SLF/SFB* gene has been cloned from a few

members of the Rosaceae family, including almond (*Prunus dulcis*) from the sub-family Amygdaloideae (Ushijima et al., 2003), apricot (*Prunus mume*) from the sub-family Prunodeae (Entani et al., 2003), and also apple (*Malus domestica*) and Japanese pear (*Pyrus pyrifolia* Nakai) from the Maloideae (Sassa et al., 2007). Here we present, for the first time, seven European pear (*P. communis* L.) haplotype-specific *SFB* alleles, and the PCR-based identification of each of these *SFB* genes.

2. Materials and methods

2.1. Plant materials

One-month-old pear leaves were collected during the spring of 2007 and were stored at -80°C pending use.

2.2. DNA extraction

DNA was extracted from the leaves according to Doyle and Doyle (1987). Briefly, 700 μl of extraction buffer (2% hexadecyltrimethylammonium bromide [CTAB], 100 mM of Tris pH 8, 20 mM of ethylenediamine tetraacetic acid [EDTA] pH 8, 1.4 M of NaCl, 1% polyvinylpyrrolidone [PVP] MW 40,000, and 1% β -mercaptoethanol) were added to 100–200 mg of leaves, which had been powdered under liquid nitrogen with a pestle and mortar. This mixture was incubated for 30 min at 65°C , with occasional mixing. After it had cooled to room temperature, two extractions were performed with chloroform:octanol (24:1). The DNA was pelleted with ethanol and dissolved in DDW. The DNA extract was kept at -20°C pending use.

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2.3. PCR amplification

The universal primers used for the PCR amplification of the *SFB* alleles were FjbFB1 (CCAAGTCTCTGATGMGRITCAAATG) and RjbFB1 (SRGTTAGKWGTTTTGTCCATGAAC), as described by Sassa et al. (2007). FjbFB1 is from the F-box motif, about 60 nucleotides into the open reading frame (ORF), and RjbFB1 is from the hyper-variable region A (Hva), about 200 nucleotides prior to the end of the ORF. The PCR was used to extract DNA from 13 European pear cultivars (the *S*-genotype is presented according to the new numeration, Goldway et al., 2009): 'Spadona' (S101 S103), 'Coscia' (S103 S104), 'Gentile' (S101 S106), 'Spadonchina' (S102 S103), 'Dagan' (S101 S104), 'Etrusca' (S103 S7), 'Red Clapp' (S101 S108), 'Cascade' (S101 S104), 'Lawson' (S115 S117), 'Delbard première' (S101 S109), 'Forelle' (S101 S116), 'Rosemarie' (S101 S116) and 'Red Druz' (S103 S107). From each cultivar between 4 and 20 PCR products were cloned. Each of the clones was sequenced and aligned with the gene bank in the NCBI.

For each specific European pear *SFB* allele, a unique pair of primers was designed, based on the genomic DNA sequences; they are listed in Table 1.

The PCR tube contained about 20 ng of DNA, 5 µl of 10× Ex Taq PCR buffer (Takara Bio, Shiga Japan), 0.2 mM dNTP mixture, 20 pmol of each primer and 0.25 µl of TaKaRa Ex Taq (Takara Bio, Inc., Japan) at 5 units/µl, in 50 µl of reaction mixture.

Amplification was performed in a MyCycler PCR apparatus (Bio Rad, Hercules, CA, USA). The PCR conditions were: an initial cycle of 2 min at 94 °C, 10 cycles of 15 s at 94 °C, 30 s at the annealing temperature, which depended on the primer pair (Table 1) and 2 min at 70 °C; then 20 cycles of 15 s at 94 °C, 30 s at the appropriate annealing temperature (Table 1) and 2.5 min at 70 °C; with a final step of 7 min at 72 °C.

2.4. Cloning and DNA sequencing of PCR products

PCR products were cloned into pGEM-T plasmid (Promega, Madison, WI, USA). Each clone was sequenced in both directions at least twice, on an ABI PRISM 377 DNA sequencer (PE Bio Systems, USA).

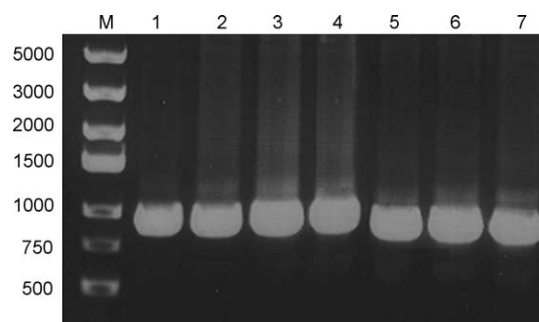


Fig. 1. *SFB* PCR products from a reaction performed with universal primers 'FjbFB1' and 'RjbFB1' and with DNA extracted from European pear cultivars (1% agarose gel, stained with ethidium bromide). M-size marker, GeneRuler™ Express DNA Ladder (Fermentas). Lane: (1) Spadona; (2) Coscia; (3) Gentile; (4) Spadonchina; (5) Red Clapp; (6) Cascade; (7) Lawson.

2.5. DNA sequence analysis

The DNA sequence data were analyzed and the protein sequence was estimated with the BLAST of NCBI Clustal W software, at the EMBL BoxShade server at <http://www.ebi.ac.uk/clustalw/index.html>, and with the DNASTAR-Lasergene 6-SeqMan II.

3. Results

3.1. Cloning of *SFBs* from European pear cultivars

The PCR for amplifying European pear *SFB* alleles was performed with FjbFB1 as forward primers and RjbFB1 as reverse primer; these had first been generated by Sassa et al. (2007) for cloning apple and Japanese pear *SFB* alleles. The PCR was used to extract DNA from 13 European pear cultivars.

A single band of about 900 bp was obtained from all of the cultivars (Fig. 1). We suspected that this band contained a sequence of more than one *SFB* gene, because the cultivars are heterozygous at their *S*-locus and, moreover, the PCR primers that were applied amplified three *SFB* alleles from each *S*-locus in Japanese pear (Sassa et al., 2007).

Table 1
Primer pairs and the PCR conditions.

Allele	Primers		Annealing temp. (°C)	Comments
	F-sense (forward), R-anti-sense (reverse)	Sequence		
<i>SFB</i> general	FjbFB1 RjbFB1	CCAAGTCTCTGATGMGRITCAAATG SRGTTAGKWGTTTTGTCCATGAAC	62	Sassa, 2007
<i>SFB</i> 101	F101 fbox R101 fbox	CAGGAAAGGTACTT GCAACTGTGGAGTAT	45	25 cycles in stage B
<i>SFB</i> 103	F103 fbox R103 fbox	ATGCACGTTTTCCCGGACCAG TCCCTTCAAGTATTGTGAACC	62	25 cycles in stage B
<i>SFB</i> 104	F104 fbox R104 fbox	CAGCCGTCTCAGATGCCGG ACAGAGATTGTCTCCAATTG	57	25 cycles at stage B
<i>SFB</i> 106	F106 fbox R106 fbox	GTAGGGATGACCATAAGCCCTT CTCAAGTACACAGAAAAAGGATA	60	
<i>SFB</i> 107	F107 fbox R107 fbox	CCTCACATTTTCCCGGACCAGAA AAGTAAACCGAACAAGACCAG	60	
<i>SFB</i> 108	F108 fbox	GCGAACATTTTCCAGACCAGAG	58–60	Stage A—10 cycles with annealing at 60 °C and at stage B annealing at 58 °C
	R108 fbox	AAGTACACTGAACAAGACAT		
<i>SFB</i> 115	F115 fbox R115 fbox	CTCGTGTTTTCCAGACAAT CCGAAGACCGTTTCCAATTGG	62	

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