

# Structural and Transcriptional Analysis of the Self-Incompatibility Locus of Almond: Identification of a Pollen-Expressed F-Box Gene with Haplotype-Specific Polymorphism

Koichiro Ushijima,<sup>a,1</sup> Hidenori Sassa,<sup>b,1,2</sup> Abhaya M. Dandekar,<sup>c</sup> Thomas M. Gradziel,<sup>c</sup> Ryutaro Tao,<sup>a</sup> and Hisashi Hirano<sup>b</sup>

<sup>a</sup> Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan

<sup>b</sup> Kihara Institute for Biological Research and Graduate School of Integrated Science, Yokohama City University, Yokohama 244-0813, Japan

<sup>c</sup> Department of Pomology, University of California, Davis, California 95616

**Gametophytic self-incompatibility in Rosaceae, Solanaceae, and Scrophulariaceae is controlled by the S locus, which consists of an S-RNase gene and an unidentified “pollen S” gene. An ~70-kb segment of the S locus of the rosaceous species almond, the S haplotype-specific region containing the S-RNase gene, was sequenced completely. This region was found to contain two pollen-expressed F-box genes that are likely candidates for pollen S genes. One of them, named *SFB* (S haplotype-specific F-box protein), was expressed specifically in pollen and showed a high level of S haplotype-specific sequence polymorphism, comparable to that of the S-RNases. The other is unlikely to determine the S specificity of pollen because it showed little allelic sequence polymorphism and was expressed also in pistil. Three other S haplotypes were cloned, and the pollen-expressed genes were physically mapped. In all four cases, *SFBs* were linked physically to the S-RNase genes and were located at the S haplotype-specific region, where recombination is believed to be suppressed, suggesting that the two genes are inherited as a unit. These features are consistent with the hypothesis that *SFB* is the pollen S gene. This hypothesis predicts the involvement of the ubiquitin/26S proteasome proteolytic pathway in the RNase-based gametophytic self-incompatibility system.**

## INTRODUCTION

Self-incompatibility (SI) in flowering plants is a genetic system that prevents self-fertilization by enabling the pistil to reject pollen from genetically related individuals, thus promoting outcrossing. Genetic studies have shown that most SI systems are controlled by a single multiallele locus called the S locus. When an S allele of pollen matches that of the pistil, the pollen is recognized as “self” and rejected by the pistil (de Nettancourt, 2001). However, recent studies on pistil- or pollen-specific self-compatible mutants (Thompson et al., 1991; Sassa et al., 1997; Golz et al., 1999) and transformation experiments with solanaceous species (Lee et al., 1994; Murfett et al., 1994; Dodds et al., 1999) demonstrate that SI phenotypes of pistil and pollen are determined by different genes, called pistil S and pollen S genes, respectively. Based on the findings that the S locus is a multigene complex, the term “haplotype” has been adopted to denote variants of the locus, and the term “allele” is used to denote variants of a given polymorphic gene at the S locus (McCubbin and Kao, 2000).

The families Rosaceae, Solanaceae, and Scrophulariaceae

display gametophytic self-incompatibility (GSI) and share the same pistil S gene product, called the S-RNase (for review, see McCubbin and Kao, 2000). S-RNase is a basic glycoprotein with RNase activity (McClure et al., 1989). RNase activity of S-RNase is required for the pistil to reject self-pollen (Huang et al., 1994; Royo et al., 1994; McCubbin et al., 1997). The rRNA of incompatible pollen of *Nicotiana glauca* is degraded in the style, consistent with a model postulating that the S-RNases act as intracellular cytotoxins (McClure et al., 1990). On the other hand, the pollen S gene of the RNase-based GSI remains to be identified. Circumstantial evidence suggests two conceivable models for the action of pollen S product: the gatekeeper model and the inhibitor model (Thompson and Kirch, 1992; McCubbin and Kao, 2000). In the gatekeeper model, the pollen S product is assumed to be a gatekeeper located at the plasma membrane of the pollen tube. The gatekeeper interacts specifically with cognate S-RNase, assisting in its uptake into the pollen cytoplasm, leading to the degradation of pollen RNA and the arrest of self-pollen tube elongation. In the inhibitor model, all S-RNases enter the pollen tube regardless of their S haplotypes; however, the pollen S product inhibits the activity of all S-RNases except for the cognate S-RNase. As a consequence, the cognate S-RNase remains active in the pollen tube, leading to the degradation of self-pollen RNA. Golz et al. (1999, 2001) produced pollen-part self-compatible mutants of *N. glauca* by incompatible pollination with irradiated pollen and found that a deletion mutant for the pollen S gene could not be recovered

<sup>1</sup> These authors contributed equally to this work.

<sup>2</sup> To whom correspondence should be addressed. E-mail sassa@yokohama-cu.ac.jp; fax 81-45-820-1901.

Article, publication date, and citation information can be found at www.plantcell.org/cgi/doi/10.1105/tpc.009290.

by this screen. This finding suggests that the pollen *S* product is essential for pollen tube elongation, which is consistent with the inhibitor model but in conflict with the gatekeeper model. Immunocytological experiments showing the entry of the S-RNase into the compatible pollen tube support the inhibitor model (Luu et al., 2000).

The identification and characterization of the pollen *S* gene is essential to understanding the molecular mechanisms of the RNase-based GSI. The pollen *S* gene is expected to have the following features: first, tight linkage to the S-RNase gene; second, a high level of *S* haplotype-specific sequence polymorphism; third, pollen-specific expression. The tight genetic linkage between the pollen *S* gene and the S-RNase gene suggested that chromosome walking would be one of the feasible approaches for the identification of the pollen *S* gene. However, conventional chromosome walking in Solanaceae is difficult because the solanaceous *S* locus is located close to the centromere, a region abundant with repetitive sequences (Coleman and Kao, 1992; Matton et al., 1995; Bernacchi and Tanksley, 1997; Entani et al., 1999). McCubbin et al. (2000) screened a BAC library of the *Petunia inflata* genome with 13 molecular markers linked to the S-RNase gene and walked an *S* locus of *Petunia* from multiple starting points. Although they obtained 51 BAC clones spanning a >2-Mb region around the *S* locus region, they did not construct a contig encompassing the region that encodes *S* specificity, which is delimited by recombination breakpoints. Therefore, it is not clear whether the genomic clones contain the pollen *S* gene (McCubbin et al., 2000).

We previously conducted chromosome walking on the *S<sup>c</sup>* haplotype of almond, which belongs to the Rosaceae, and constructed the contigs covering an ~200-kb region around the *S<sup>c</sup>*-RNase gene (Ushijima et al., 2001). Genomic DNA gel blot analyses revealed that the nucleotide sequence of the ~70-kb region, which is defined by the two boundary markers NP79R and NP182F and contains the *S<sup>c</sup>*-RNase gene, was highly diverged and specific to each *S* haplotype. The regions outside of the boundary markers were relatively conserved among different *S* haplotypes. The structural heteromorphism is the distinctive feature of loci consisting of coadapted gene complexes in different genetic systems, including sporophytic SI of Brassicaceae (Ferris and Goodenough, 1994; Brown and Casselton, 2001; Kusaba et al., 2001). The heteromorphism of the region containing the *S* specificity genes is believed to maintain the tight association of the pistil *S* gene and the pollen *S* gene, suggesting that the pollen *S* gene of almond is located in the *S* haplotype-specific region (Ushijima et al., 2001).

Here, we sequenced the ~70-kb *S<sup>c</sup>* haplotype-specific region using a shotgun strategy. Based on the prediction of open reading frames (ORFs), two pollen-expressed genes were isolated. One of the two genes, named *SFB* (*S* haplotype-specific F-box protein), showed a high level of allelic polymorphism and pollen-specific expression. Comparative analysis of the four *S* haplotypes showed that all *SFB* alleles are located within ~30 kb of the S-RNase genes. Distances between genes and markers are highly variable among the *S* haplotypes, showing the heteromorphism of the region, which might ensure the tight association of *SFB* and the S-RNase gene. These features of *SFB*

are consistent with those of the expected pollen *S* gene. *SFB* encodes an F-box protein that is a component of a class of ubiquitin ligase (SCF complex) (Deshaies, 1999), raising the possibility that the ubiquitin/26S proteasome proteolytic system plays a central role in the discrimination of self/nonself pollen in the RNase-based GSI.

## RESULTS

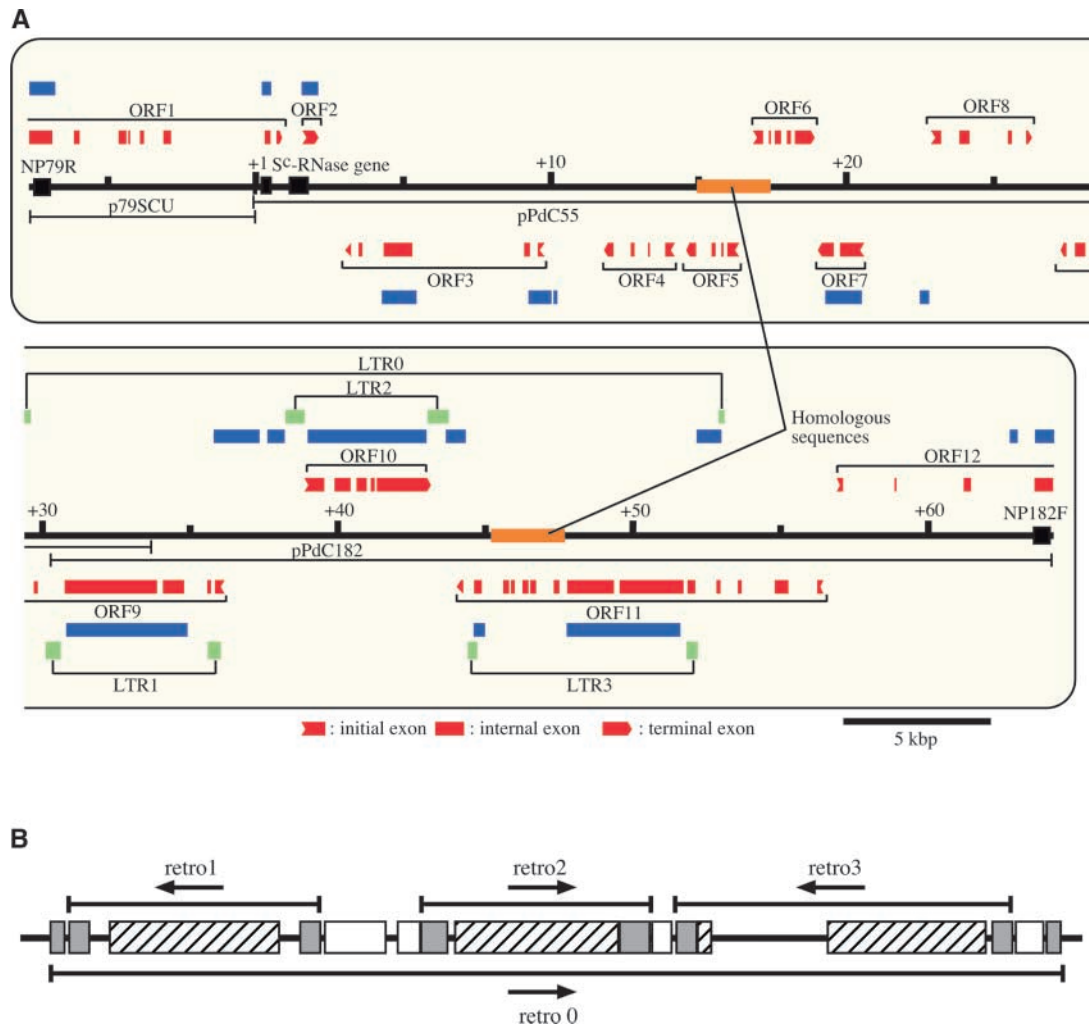
### Sequence Analysis of the ~70-kb *S<sup>c</sup>* Haplotype-Specific Region

We previously predicted the boundaries of the almond *S* locus and suggested that the pollen *S<sup>c</sup>* gene might be present in an ~70-kb area of the *S<sup>c</sup>* haplotype-specific region that also contains the *S<sup>c</sup>*-RNase gene (Ushijima et al., 2001). To identify the pollen *S* gene, the *S<sup>c</sup>* haplotype-specific region was sequenced completely using the shotgun strategy. Three genomic clones covering the region, p79SCU (~7 kb), pPdC55 (~35 kb), and pPdC182 (~36 kb), were used to construct the shotgun library (Figure 1A). A total of ~1000 sequences, which included PCR products filling gaps between the shotgun contigs, were assembled and gave a nucleotide sequence of 71,953 bp. The ~70-kb sequence was annotated by RiceGAAS (Rice Genome Automated Annotation System [Sakata et al., 2002]; <http://ricegaas.dna.affrc.go.jp/index.html>), which automatically analyzes large sequences using several programs for the prediction and analysis of protein-coding sequences: BLAST (Basic Local Alignment Search Tool [Altschul et al., 1990]), AutoPredLTR (Sakata et al., 2002), and GENSCAN (Burge and Karlin, 1997).

GENSCAN identified 12 ORFs (ORF1 to ORF12) in the sequenced region (Figure 1A). By this prediction, the three exons of the *S<sup>c</sup>*-RNase gene were misidentified as different genes, ORF1 and ORF2 (Table 1). AutoPredLTR search, which predicted a long terminal repeat (LTR) sequence, showed that the ~70-kb region contained four pairs of LTRs (Figure 1A). Sequences between the LTRs were found to be similar to retrotransposon-like sequences and were designated retro0 to retro3 (Figure 1B, Table 1). All four retrotransposon-like sequences included several mutations (insertion or deletion), causing their putative polyproteins to be truncated. Retro0 was found to be disrupted by the insertion of retro1 to retro3 (Figure 1B), implying that retro0 was first inserted into the *S<sup>c</sup>* haplotype. Retro3 also was disrupted by the insertion of a 2.5-kb DNA sequence. The inserted sequence showed high similarity to the region at +15 to +18 kb (Figure 1A) but displayed no significant homology with sequences in the public databases.

### cDNA Cloning of the Pollen-Expressed Genes Located at the *S<sup>c</sup>* Haplotype

To clone the pollen-expressed genes at the sequenced *S* locus region, we designed 17 forward and 11 reverse primers based on the prediction of ORFs. The primers were used for rapid amplification of cDNA ends (Frohman et al., 1988) with pollen cDNA. Pollen from almond cv Nonpareil (*S<sup>c</sup>S<sup>c</sup>*) was used, because an *S<sup>c</sup>* homozygous cultivar is not available. For most ORFs, sequences of isolated cDNA clones were not identical



**Figure 1.** Sequence Analyses of the  $S^c$  Haplotype-Specific Region.

**(A)** Scheme of the  $S^c$  haplotype-specific region. The nucleotide sequence of the  $\sim 70$ -kb  $S^c$  haplotype-specific region was characterized by GENSCAN, BLASTX, and AutoPredLTR search of RiceGAAS (Sakata et al., 2002). The A nucleotide of the putative initiation codon (ATG) of the  $S^c$ -RNase gene (Ushijima et al., 1998) is positioned as +1. Exons of the  $S^c$ -RNase gene and molecular markers NP79R and NP182F, which define the boundaries of the almond  $S$  locus (Ushijima et al., 2001), are represented by black boxes. Red, blue, and green boxes represent the results of GENSCAN, BLAST, and AutoPredLTR searches, respectively. Each pair of LTRs is linked by lines.

**(B)** Scheme of the retrotransposon-like sequence-rich region (+29 to +53 kb). Gray boxes represent LTR sequences. Hatched boxes represent the region encoding the polyprotein of retro1, retro2, and retro3. White boxes represent the region for the retro0 polyprotein, into which retro1, retro2, and retro3 were inserted.

to, but were similar to, those of the corresponding ORFs, suggesting that they constitute gene families and that those ORFs are not expressed in pollen. However, sequences of two of the cDNAs completely matched the corresponding ORF sequences (ORF1 and ORF3). The first exon of the predicted ORF1 was isolated as a pollen-expressed gene and is called ORF1 hereafter.

ORF1 was located 6.7 kb upstream of the  $S^c$ -RNase gene (Figure 1A). The transcriptional orientations of ORF1 and the  $S^c$ -RNase gene were the same. The deduced amino acid sequence of ORF1 showed 29.3% homology with that of *SLF* (*S*

locus F-box) of *Antirrhinum* (Figure 2A, Table 1). *SLF* is located at the *Antirrhinum S* locus region and encodes a protein with an F-box motif (Lai et al., 2002). We named ORF1 *PdSLF* for *S* locus F-box of *Prunus dulcis*. *PdSLF* of the  $S^c$  haplotype, designated *PdSLF<sup>c</sup>*, contained the sequence of the cosmid end probe NP79R, which defined the boundary of the  $S$  haplotype-specific region (Ushijima et al., 2001). NP79R sequence has been shown to be conserved in different  $S$  haplotypes of almond (Ushijima et al., 2001). *PdSLF* of the  $S^d$  haplotype, designated *PdSLF<sup>d</sup>*, was amplified by PCR from the cosmid clone of the  $S^d$  haplotype. The deduced amino acid sequences of

**Table 1.** Summary of Homology Search (BLASTX) Results for the ORFs Predicted by GENSCAN

| ORF                      | Homolog (Accession No.)                          | Expression |       |   |
|--------------------------|--|------------|-------|---|
|                          |  | Pollen     | Style | Description   |
| ORF1 (1st exon)          | <i>Antirrhinum SLF-S<sup>2</sup></i> (AJ297974)  | Yes        | Yes   | PdSLF ( <i>Prunus dulcis</i> S locus F-box protein) |
| ORF1 (7th exon)          | Almond S <sup>c</sup> -RNase (AB011470)          | No         | Yes   | N-terminal region of the S <sup>c</sup> -RNase      |
| ORF2                     | Almond S <sup>c</sup> -RNase (AB011470)          | No         | Yes   | C-terminal region of the S <sup>c</sup> -RNase      |
| ORF3 (1st and 2nd exons) | Arabidopsis putative protein (AL138652)          | No         |       |   |
| ORF3 (3rd exon)          | Arabidopsis putative F-box protein (AC018907)    | Yes        | No    | SFB (S haplotype-specific F-box protein)            |
| ORF4                     | Unknown  | No         |       |   |
| ORF5                     | Unknown  | No         |       |   |
| ORF6                     | Unknown  | No         |       |   |
| ORF7                     | <i>Oryza sativa</i> putative protein (AC084763)  | No         |       |   |
| ORF8                     | Unknown  | No         |       |   |
| ORF9                     | <i>Zea mays</i> retrotransposon (AF082133)       |            |       | Designated retro1 in Figure 1                       |
| ORF10                    | <i>Nicotiana</i> retrotransposon (CAA32025)      |            |       | Designated retro2 in Figure 1                       |
| ORF11                    | Arabidopsis retrotransposon (AC006248)           |            |       | Designated retro3 in Figure 1                       |
| ORF12                    | Arabidopsis Ser/Thr protein phosphatase (U80922) | No         |       |   |

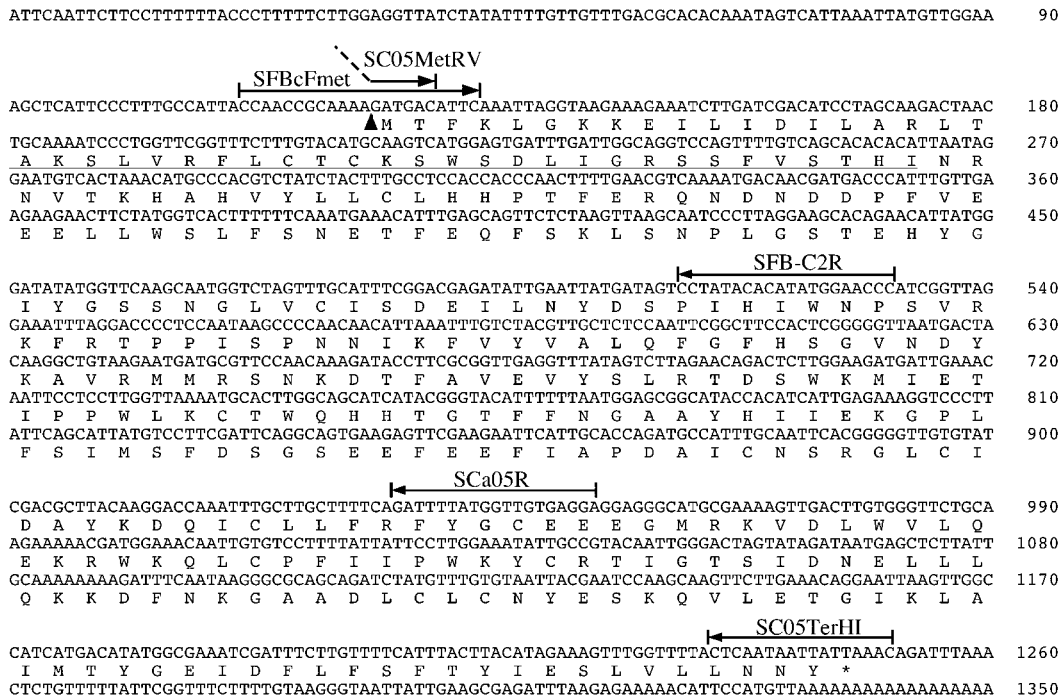
PdSLF<sup>c</sup> and PdSLF<sup>d</sup> were highly similar to each other (95.1% identity; Figure 2B), as were AhSLF-S<sub>2</sub> and AhSLF-S<sub>2</sub>L of *Antirrhinum* (97.9% identity; Lai et al., 2002), suggesting that they are unlikely to control the S specificity of pollen.

The ORF3 cDNA also encoded a protein with an F-box motif

(Figure 3). ORF3 and the S<sup>c</sup>-RNase gene were located in inverse orientation and separated by ~1.6 kb (Figure 1). ORF3 contained one intron at the 5' untranslated region (Figure 3). Except for the N-terminal region containing the F-box motif sequence, ORF3 showed no significant homology with known



**Figure 2.** Amino Acid Sequence Comparisons between SLFs. Deduced amino acid sequences were compared between PdSLF<sup>c</sup> and AhSLF-S<sub>2</sub> (A) and between PdSLF<sup>c</sup> and PdSLF<sup>d</sup> (B). Sites that are conserved or that have only conservative replacements (amino acid groups defined by Dayhoff et al. [1979]: C, STAPG, MILV, HRK, NDEQ, and FYW) are marked with asterisks or dots, respectively.



**Figure 3.** Nucleotide and Deduced Amino Acid Sequences of the cDNA for SFB<sup>c</sup> (ORF3).

The deduced amino acid sequence is shown under the nucleotide sequence of the cDNA. The arrowhead represents the position into which an 85-bp intron sequence was inserted. The amino acid sequence of the F-box motif is underlined. Arrows represent the positions and directions of primers that were used to amplify the alleles (see Figure 5) or to characterize organ-specific expression patterns (see Figure 6). The 5' region of primer SC05MetRV (5'-TGATATCATTTTCTACAGGATGAC-3') corresponds to the 3' end of the intron and is represented by a dotted line. Restriction sites for EcoRV and BamHI were added to the 5' regions of primers SC05MetRV and SC05TerHI (5'-TGGATCCGTTTAAATAATTATTGAG-3'), respectively.

proteins in the public databases. ORF3 has no known localization signal, suggesting that it is a cytoplasmic protein. Genomic DNA gel blot analysis with the ORF3 probe gave an S<sup>c</sup> haplotype-specific signal in all cultivars that contained the S<sup>c</sup>-RNase gene (Figure 4A). Based on this result, ORF3 was designated SFB (S haplotype-specific F-box protein). Phylogenetic analysis showed that SFB is a member of the A3 subfamily in the plant F-box superfamily defined by Gagne et al. (2002) (data not shown).

### S Haplotype-Specific Sequence Polymorphism of SFB

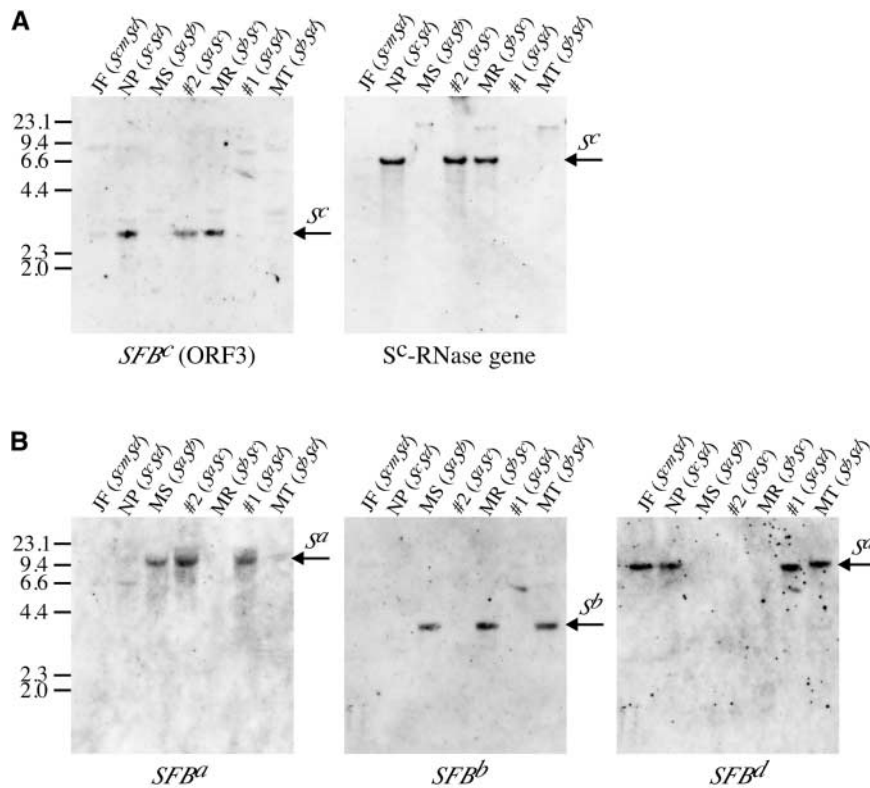
To clone the alleles of SFB, PCR was conducted with the primer pairs SC05MetRV/SCa05R or SC05MetRV/SFBTerHI (Figure 3). Three clones were isolated from genomic DNA of cv Mission (S<sup>a</sup>S<sup>b</sup>), Sauret No. 1 (S<sup>a</sup>S<sup>d</sup>), and Monterey (S<sup>b</sup>S<sup>d</sup>). Genomic DNA gel blot analyses of the three clones showed the S<sup>a</sup>, S<sup>b</sup>, and S<sup>d</sup> haplotype-specific signals (Figure 4B), suggesting that these SFB clones were derived from the respective S haplotypes.

Because the three clones lacked both ends of the coding region, rapid amplification of cDNA ends was conducted using pollen RNAs from different S haplotypes to obtain full-length cDNA sequences of SFB<sup>a</sup>, SFB<sup>b</sup>, and SFB<sup>d</sup>. Deduced amino

acid sequences of the SFB alleles were aligned and compared (Figure 5). The F-box motif was conserved at the N-terminal regions of all SFBs. Sequence identities among SFBs were 68.4 to 76.4% (Table 2), which were comparable to those of almond S-RNases (54.2 to 76.2%) (Ushijima et al., 1998; Tamura et al., 2000). Although variable sites are dispersed in the primary structure of the SFB, two regions at the C terminus are quite variable, as they are in the hypervariable region of the S-RNase (Ioerger et al., 1991; Ushijima et al., 1998).

### Organ-Specific Expression of the S Locus Genes

To investigate the expression pattern of SFB and PdSLF, we performed reverse transcriptase-mediated (RT) PCR analyses using RNA from leaf and floral organs of Nonpareil as templates. RT-PCR products for the S-RNase gene and the actin gene, which were used as controls, did not contain genomic DNA-derived PCR products, which are expected to contain introns and thus would be longer than the expected RT-PCR products, suggesting that the templates were not contaminated with genomic DNA. In addition, the forward primer for SFB was designed to include the junction of the two exons to prevent amplification from a genomic DNA template (Figure 3). The cDNA for S-RNase was amplified as expected from the



**Figure 4.** Genomic DNA Gel Blot Analyses for *SFB*.

Genomic DNAs from seven almond cultivars were digested with HindIII, separated on 0.8% agarose gels, and transferred to nylon membranes. The blot was probed with the  $S^c$  haplotype genes (*SFB<sup>c</sup>* and the  $S^c$ -RNase gene in **[A]**) and the homologs of *SFB<sup>c</sup>* (*SFB<sup>a</sup>*, *SFB<sup>b</sup>*, and *SFB<sup>d</sup>* in **[B]**). The arrows  $S^a$ ,  $S^b$ ,  $S^c$ , and  $S^d$  denote the respective *S* haplotype-specific signals. Abbreviations for almond cultivars are as follows: JF, Jeffries ( $S^mS^d$ ); NP, Nonpareil ( $S^cS^d$ ); MS, Mission ( $S^aS^b$ ); #2, Sauret No. 2 ( $S^aS^c$ ); MR, Merced ( $S^bS^c$ ); #1, Sauret No. 1 ( $S^aS^d$ ); MT, Monterey ( $S^bS^d$ ).

style and at low amounts from the ovary (Figure 6). The cDNA for *PdSLF* was amplified not only in the male organs (anther, pollen grain, and germinated pollen) but also in the style, where the pollen *S* gene is not expected to be expressed. On the other hand, *SFB<sup>c</sup>* was expressed only in the male organs. Signal intensities of pollen and germinated pollen were higher than that of anther, suggesting that *SFB* likely is expressed only in pollen.

#### Comparison of the Gene Organization of Four *S* Haplotypes

The cosmid or fosmid libraries were constructed from the genomic DNAs of almond cv Nonpareil ( $S^cS^d$ ), Sauret No. 1 ( $S^aS^c$ ), and Monterey ( $S^bS^d$ ). To construct the contigs encompassing the  $S^a$ ,  $S^b$ , and  $S^d$  haplotypes, we screened the libraries with probes for *SFBs*, the *S*-RNase genes, and the *S* locus boundary markers NP79R (= *PdSLF*) and NP182F (Ushijima et al., 2001). The order and orientations of the genes and markers were determined by long PCR. The *S*-RNase genes and *SFBs* of all *S* haplotypes were located in the region between the two

boundary markers NP79R and NP182F. The relative order and orientations of the genes and markers were conserved among the four *S* haplotypes (Figure 7). However, the physical distances between them were significantly different. The physical distance between *SFB* and the *S*-RNase gene was  $\sim 1.6$  kb in the  $S^c$  haplotype but was  $>10$  kb in the other three *S* haplotypes.

#### DISCUSSION

We previously scanned the *S* locus region of almond for sequence diversity by DNA gel blot analysis using probes located at varying distances from the *S*-RNase gene. The results showed that the region between two boundary markers, NP79R and NP182F, is highly diverged among the different *S* haplotypes, but the regions outside of the two markers are relatively well conserved (Ushijima et al., 2001). In this study, contigs encompassing the two markers were constructed for three additional *S* haplotypes. Comparative analysis of the contigs showed that the physical distances between genes and mark-



**Table 2.** Amino Acid Sequence Identities (%) among SFBs

|                  | SFB <sup>b</sup> | SFB <sup>c</sup> | SFB <sup>d</sup> |
|------------------|------------------|------------------|------------------|
| SFB <sup>a</sup> | 69.0             | 70.1             | 68.4             |
| SFB <sup>b</sup> |                  | 75.6             | 76.4             |
| SFB <sup>c</sup> |                  |                  | 75.8             |

S-RNase. Therefore, it seems unlikely that *PdSLF* is the pollen S gene.

In contrast to *PdSLF*, *SFB* showed distinctive features of a candidate for the pollen S gene: tight linkage to the S-RNase gene; a high level of sequence polymorphism; and pollen-specific expression. All *SFB*s were observed to be located at the S haplotype-specific region and to be linked physically (within ~30 kb) to the S-RNase gene. In addition, heteromorphism at the S haplotype-specific region also could maintain the linkage of the two genes by suppressing recombination at this region, suggesting that *SFB* and the S-RNase gene are inherited as a unit.

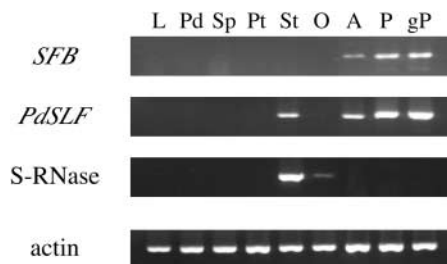
*SFB* showed a high level of the S haplotype-specific sequence polymorphism, comparable to that observed for the S-RNases of *Prunus* (Ushijima et al., 1998; Tamura et al., 2000). Amino acid sequence alignment showed that *SFB* contained two quite variable regions, as did S-RNase (Ioerger et al., 1991; Ushijima et al., 1998). The hypervariable region of S-RNase is exposed on the surface of the folded protein molecule and plays a pivotal role in the recognition of self-pollen (Matton et al., 1997, 1999; Ida et al., 2001; Matsuura et al., 2001). The two variable regions of *SFB* at the C terminus were found to be hydrophilic enough to be exposed on the surface (data not shown) and may have important recognition functions analogous to those of the S-RNase.

The pollen SI phenotype of Rosaceae and Solanaceae is controlled gametophytically, suggesting that the pollen S gene is expressed only in pollen. RT-PCR analysis revealed that *SFB* is expressed exclusively in the male reproductive organs and that expression in pollen grains and in germinated pollen is higher than that observed in whole anthers, suggesting that *SFB* is expressed only in pollen. This result is consistent with our finding that the 1.2-kb promoter region of *SFB<sup>c</sup>* directs the expression of a  $\beta$ -glucuronidase reporter gene in pollen but not in anther cells of transgenic tobacco (H. Sassa, K. Ushijima, R. Tao, and H. Hirano, unpublished results). Although we cannot exclude the possibility that the anther cell also expresses a small amount of *SFB*, it seems unlikely that the sporophytically expressed *SFB* affects the pollen SI phenotype, because it lacks signal peptide for secretion. In addition, the pollen tube rejection of the RNase-based GSI is a slow reaction that occurs inside the style tissue. This finding is in contrast to the sporophytic SI of *Brassica*, which is a quick response on the stigma surface, and suggests that exogenous *SFB* might have little effect on pollen. These findings suggest that *SFB* functions strictly in a gametophytic manner. All of the features of *SFB* discussed above are consistent with the hypothesis that *SFB* controls pollen S specificity in almond, representing the candidate for the pollen S gene of the RNase-based GSI systems.

Further analyses for physical interaction between *SFB* and the S-RNase, as well as functional analyses, will be required to clarify the role of *SFB* in the RNase-based GSI.

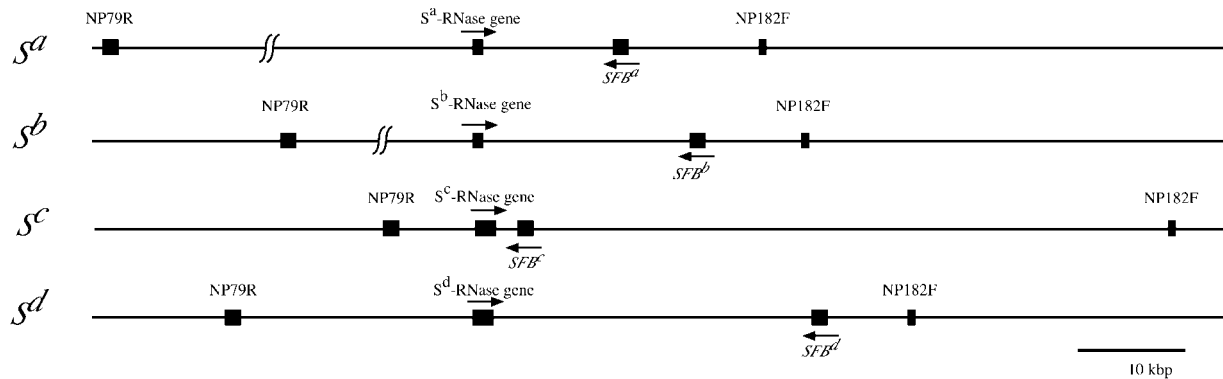
The F-box proteins are known to be a component of a class of ubiquitin ligase, the SCF complex (Deshaies, 1999). In the ubiquitin/26S proteasome pathway of protein degradation, target proteins destined for degradation become modified by covalent attachment of multiple ubiquitins. The polyubiquitinated proteins then are recognized by the 26S proteasome and degraded. The SCF complex catalyzes the final step of ubiquitination of target proteins. The F-box protein serves as a receptor to recruit appropriate target proteins to the core complex for ubiquitination. It associates with an SCF component, Skp1, through the F-box motif at the N terminus, and its C terminus binds specifically to the target (Bai et al., 1996). Our finding of the F-box protein *SFB* as a candidate for the pollen S gene product of the RNase-based GSI suggests that the likely target of the SCF complex containing the *SFB*, SCF<sup>*SFB*</sup>, is the S-RNase.

The idea that the S-RNase is degraded in pollen tubes through the ubiquitin/26S proteasome pathway seems to be compatible with a proposed model for SI, which hypothesizes that the pollen S gene product is an RNase inhibitor. Despite the apparent difficulty of accommodating the high degrees of structural diversity of the S-RNases, the inhibitor model is supported by recent findings on S haplotype-independent uptake of the S-RNase by the pollen tube (Luu et al., 2000) and the essential role of pollen S products for pollen tube elongation (Golz et al., 2001). As a possible interpretation of the peculiar nature of the pollen S product in the model, it was hypothesized that a pollen S protein contains an RNase inhibitor domain and an S haplotype specificity domain and that it interacts differently with self and nonself S-RNases (McCubbin and Kao, 2000). *SFB* might function as a component of SCF<sup>*SFB*</sup> and ubiquitinate all of the nonself S-RNases for degradation but interact specifically with the self S-RNase to leave it active, leading to the arrest of self pollen tube growth. Recently, it was reported that hnRNP-U functions as a pseudosubstrate that binds to the corresponding F-box protein but is not destined for degradation by the SCF complex (Davis et al., 2002). Based on this example, it is possible that self S-RNase serves as a pseudosubstrate for

**Figure 6.** Organ-Specific Expression of S Locus Genes.

RNAs were derived from leaf and floral organs of Nonpareil. cDNAs were synthesized from the RNAs and were used for RT-PCR with gene-specific primers. L, leaf; Pd, pedicel; Sp, sepal; Pt, petal; St, style; O, ovary; A, anther; P, pollen; gP, germinated pollen.





**Figure 7.** Gene Organization of Four S Haplotypes of Almond.

Boxes represent exons of the S-RNase genes, *SFBs*, and the S locus boundary markers NP79R and NP182F (Ushijima et al., 2001). NP79R is part of the PdSLF gene (see text). Arrows denote the orientations of the genes. In the  $S^a$  and  $S^b$  haplotypes, the physical distance between NP79R and the S-RNase gene was not determined accurately, although it is certain that NP79R links to the S-RNase gene.

SCF<sup>SFB</sup>. The two variable regions located at the C terminus of SFB are implicated in binding with the pseudosubstrate self S-RNase. In plants, the F-box gene family shows a substantial expansion relative to other eukaryotes (Gagne et al., 2002). Identification of almost 700 probable F-box genes in Arabidopsis suggests that the F-box gene family is one of the largest in plants and that the SCF complex-mediated ubiquitin/26S proteasome pathway is a major route for cellular regulation. The RNase-based GSI might represent one of the specialized roles of this highly divergent proteolytic pathway in plants.

## METHODS

### Plant Materials

Seven cultivars of almond (*Prunus dulcis*)—Nonpareil ( $S^cS^d$ ), Mission ( $S^aS^b$ ), Sauret No. 2 ( $S^aS^c$ ), Merced ( $S^bS^c$ ), Sauret No. 1 ( $S^cS^d$ ), Monterey ( $S^cS^d$ ), and Jeffries ( $S^{cm}S^d$ )—were used. Jeffries is a naturally occurring mutant found as a sport on a Nonpareil tree and lacks the  $S^c$  haplotype, and the mutated haplotype is designated  $S^{cm}$  (Kester et al., 1994; Tao et al., 1997; Ushijima et al., 2001). Pollen was germinated in vitro as described by Lush et al. (1997) with slight modifications.

### Shotgun Sequencing

Genomic clones (Figure 1A) were sheared physically by sonication, blunt-ended, and phosphorylated with T4 DNA polymerase and T4 nucleotide kinase (New England Biolabs, Beverly, MA). The resulting fragments were separated on a 1% agarose gel, and the 1.5- to 2.0-kb fragments were cloned into pBluescript II SK<sup>-</sup> (Stratagene, La Jolla, CA) or pGEM-3Zf(-) (Promega, Madison, WI). The lengths of the inserted fragments were confirmed by PCR. The PCR products were purified by Multiscreen PCR (Millipore, Bedford, MA) and sequenced with an autosequencer (model 4000L; Li-Cor, Lincoln, NE). Sequencing was continued until a minimum of approximately fourfold sequence coverage was achieved for each clone. Sequence alignments were generated using SeqMan II software (DNASTAR, Madison, WI). Gaps between shotgun contigs were amplified and filled by PCR with *Pyrobest* DNA polymerase (TaKaRa, Otsu, Japan).

### Isolation of Nucleic Acids

Freeze-dried leaves were ground into powder using a mortar and pestle. Genomic DNAs were isolated from the ground leaves as described by Ushijima et al. (2001). RNAs were isolated from leaves and floral organs of Nonpareil as described by McClure et al. (1990).

### Rapid Amplification of cDNA Ends

Total RNA from the pollen of Nonpareil was used for the synthesis of first-strand cDNA essentially as described for the SMART RACE (rapid amplification of cDNA ends) cDNA Amplification Kit (Clontech, Palo Alto, CA) and by Schmidt and Mueller (1999). The reaction mixture contained  $1 \times$  first-strand synthesis buffer (50 mM Tris-HCl, pH 8.3, 75 mM KCl, and 6 mM MgCl<sub>2</sub>), 1 mM deoxynucleotide triphosphates, 5 mM DTT, 2 mM MnCl<sub>2</sub>, 1  $\mu$ M RACE-N (5'-AAGGCTCCGTCGGCATCGATCGCGCGACTCTTTTTTTTTTTTTTTT-3'), 1  $\mu$ M SMART II (5'-AAGCAGTGGTAACAACGCAGAGTACGCGGG-3'), 4  $\mu$ g of total RNA, and 200 units of SuperScript II reverse transcriptase (Invitrogen, Carlsbad, CA) and was incubated at 42°C for 1.5 h. RACE-N and SMART II add the sequences for adapter primers to the cDNA at the 3' and 5' ends, respectively. 3' RACE used the resulting cDNA, *ExTaq* (TaKaRa), RACE II (5'-AAGGCTCCGTCGGCATCGATCGATC-3') as the adapter primer, and the gene-specific primers designed from *SFBs* or the putative open reading frames predicted by the GENSCAN program. 5' RACE used universal primer mixture (UPM) as the adapter primer instead of RACE II;  $1 \times$  UPM contains two primers, 0.1  $\mu$ M UPM short (5'-CTAATACGACTCACTATAGGGC-3') and 0.02  $\mu$ M UPM long (5'-CTAATACGACTCACTATAGGGCAAGCAGTGGTAACAACGCAGAGT-3'), and extends the 5' end of the cDNA for step-out PCR (Matz et al., 1999). If necessary, second-round PCR was conducted with gene-specific primers and adapter primers RACE III (5'-CGGCATCGATCGCGCGACTC-3') and NUP (5'-AAGCAGTGGTAACAACGCAGAGT-3') for 3' and 5' RACE, respectively.

RACE fragments were subjected to DNA gel blot analyses using the three genomic clones for the  $S^c$  haplotype-specific region (Figure 1A) as probes to detect cDNA species with low expression levels. The RACE fragments showing signal(s) were cloned into a plasmid vector. The positive clones for each RACE fragment were selected by colony hybridization with the probes of the genomic clones. For each open reading frame, 6 to 11 independent cDNA clones derived from different primer pairs were subjected to sequence analysis.

### Genomic DNA Gel Blot Analysis

Five micrograms of genomic DNAs digested with HindIII was separated and blotted onto a nylon membrane. The membrane was probed with digoxigenin-labeled cDNAs for genes expressed in pollen, washed, and visualized as described by Ushijima et al. (2001).

### Reverse Transcriptase-Mediated PCR for Characterization of the Gene Expression Pattern

RNAs from leaves and floral organs of Nonpareil were treated with DNaseI (Invitrogen). Their cDNAs were synthesized by PowerScript (Clontech) with oligo-d(T) primer. The resulting cDNAs were used as templates for PCR amplification with gene-specific primer sets SFB-cFmet (5'-CCAACCGCAAAGATGACATTC-3') and SFB-C2R (5'-GGG-TTCCATATKTGTATWGG-3') for *SFB<sup>c</sup>* (Figure 3), Sca01F (5'-GATTGG-TGGGGATGTGCTGTAG-3') and Sca01R (5'-CTTCGGTAACCATAA-GAATCTC-3') for *PdSLF*, AS1II and Amy-C5R for the S-RNase gene (Tamura et al., 2000), and ActF1 (5'-ATGGTGAGGATATCAACCC-3') and ActR1 (5'-CTTCCTGTGGACAATGGATGG-3') for the actin gene that was used as an internal control. PCR was performed with *ExTaq* (TaKaRa) using a program of 30 cycles at 94°C for 30 s, 53°C for 30 s, and 72°C for 45 s, an initial denaturing at 94°C for 2.5 min, and a final extension at 72°C for 7 min. PCR products were separated on a 1.5% agarose gel and stained with ethidium bromide.

### Construction and Screening of the Cosmid Library

Cosmid or fosmid libraries were constructed from three almond cultivars—Nonpareil (S<sup>c</sup>S<sup>c</sup>), Sauret No.1 (S<sup>a</sup>S<sup>c</sup>), and Monterey (S<sup>b</sup>S<sup>a</sup>)—using the pWEB::TNC Cosmid Cloning Kit or the CopyControl Fosmid Library Production Kit (Epicentre, Madison, WI). The libraries were screened with digoxigenin-labeled probes for the S-RNase gene *SFB*, NP79R and NP182F, as described by Ushijima et al. (2001). Long PCR with *ExTaq* or the Expand Long Template PCR System (Roche Diagnostics, Mannheim, Germany) was performed to determine the order and the orientations of the genes on the cosmid/fosmid clones.

Upon request, all novel materials described in this article will be made available in a timely manner for noncommercial research purposes.

### Accession Numbers

The accession numbers for the sequences mentioned in this article are as follows: AB081587 (S<sup>c</sup> haplotype-specific region), AB092966 (SFB<sup>a</sup>), AB092967 (SFB<sup>b</sup>), AB079776 (SFB<sup>c</sup>), AB081648 (SFB<sup>d</sup>). Other accession numbers are AJ297974 (SLF-S2 of *Antirrhinum hispanicum*), NM\_102834, AC005825, AF305597, and AF327430 (UFO, FBX8, ORE9, and TIR1 of *Arabidopsis thaliana*), S71192 (Fim of *Antirrhinum majus*), AF004843 (Stp of *Pisum sativum*), and AB050979 (Sklp2 of *Homo sapiens*).

### ACKNOWLEDGMENTS

We gratefully acknowledge S. Uratsu (University of California, Davis) for collecting and providing plant materials and M. Kusaba (Institute of Radiation Breeding, National Institute of Agrobiological Sciences, Ministry of Agriculture, Forestry, and Fisheries, Japan), for helpful comments. This work was supported by Grant-in-Aid 13660011 for Scientific Research (C) to H.S. and Grant-in-Aid 13460014 for Scientific Research (B) to R.T. from the Japan Society for the Promotion of Science and by grants to A.M.D. from the Almond Board of California.

Received November 14, 2002; accepted December 24, 2002.

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**Structural and Transcriptional Analysis of the Self-Incompatibility Locus of Almond:  
Identification of a Pollen-Expressed F-Box Gene with Haplotype-Specific Polymorphism**  
Koichiro Ushijima, Hidenori Sassa, Abhaya M. Dandekar, Thomas M. Gradziel, Ryutaro Tao and  
Hisashi Hirano  
*Plant Cell* 2003;15;771-781; originally published online February 21, 2003;  
DOI 10.1105/tpc.009290

This information is current as of July 9, 2017

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