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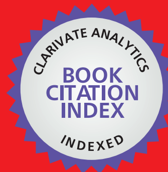

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Chapter 7

Evolutionary Analysis of Basic RNase Genes from Rosaceous Species — S-RNase and Non-SRNase Genes

Karim Sorkheh

Additional information is available at the end of the chapter

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Abstract

Over the past two and half decades there has been an explosion of progress in a growing number of model self incompatibility (SI) systems on our understanding of the molecular, biochemical and cellular processes underlying the recognition of self pollen and the initiation of a cascade of biochemical and cellular events that prevent self fertilization. These studies are unrevealing the complexity of a trait (SI) whose sole purpose, as far as we know, is to exert a strong influence on the breeding system of plants. Evolutionary interest in floral traits that influence the breeding system and in the forces that shape these traits began with Darwin who devoted one complete book to the subject (Darwin 1876) and significant portions of a second book. The evolution of plant breeding systems is often viewed as the interplay between the advantages and disadvantages of selfing. Evolutionary biologists have long noted that there are three primary advantages to selfing. First, there is an inherent genetic transmission advantage to selfing because a plant donates two haploid sets of chromosomes to each selfed seed and can still donate pollen to conspecifics. Second, selfing can provide reproductive assurance when pollinators are scarce or and third, it often costs less, in terms of energy and other resources, to produce selfed seed (e.g. fewer resources are expended to attract and reward pollinators. Some major questions remain unanswered concerning the evolution of stylar SRNases. Most pressing is the apparent disparity in patterns of diversification seen in the Solanaceae and Plantaginaceae relative to what is observed in the Rosaceae. Thus, we reviewing current publication regarding the evolutionary analysis basic RNases towards comprehensive view.

Keywords: S-ribonuclease, Transmitting tract specific glycoprotein, Evolutionary, Rosaceae

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1. Introduction

All angiosperms make indiscriminate bunches, and their regenerative organs are in close partition. This makes a genuine inclination toward inbreeding. Inbreeding often results to decreased offspring wellness (e.g. more susceptible to diseases). With advance blooming, plantsare not able to utilizephrase different systems to prevent self-fertilization and thereby to generate and maintain genetic diversity within a species thus, the profoundly genuine and distinct plant kingdom, which is composed of >80% angiosperms would not exist [102, 110, 118].

Self-incompatibility (SI) is among the most important techniques utilized by many flowering crops to counteract self-fertilization and thus, generate and support genetic range inside a species. Common ancestral reports argue that SI virtually in most species may be managed by a simple polymorphic locus, the true self-incompatibility S-locus. At present, at the very least, there are two gene loci: pistil S and pollen S, therefore, the term haplotype is used to describe variants of the S-locus. Pollen inhibition occurs if the same S-haplotype is expressed equally by pollen and pistil [18].

Most *Prunus* fruit trees exhibit homeomorphic gametophytic self-incompatibility (GSI) where self/non-self-recognition can be controlled by a single multi-allelic locus, termed the S locus. SI reaction is activated if the same ''S allele'' specificity can be expressed in the pollen and pistil (Fig. 1). Thus, the growth of pollen tube bearing either one of two ''S allele'' specificities carried with the recipient pistil can be arrested inside the style. Exactly the same type of GSI is found not only in other genera in Rosaceae, but also in *Malus*, *Pyrus*, Solanaceae and Plantaginaceae [18, 56, 86, 117, 141].

As fruit trees of the *Prunus* kind are not able to bear fruits parthenocarpically, fertilization and seed formation are important for excellent fruit generation in SI *Prunus* fruit trees. In industrial orchards, appropriate cross cultivars that are part of different pollen-incompatibility communities and that bloom simultaneously are inter-planted; and beehives are also often placed throughout orchards to make certain fruit set [135]. Hence, determination of pollen incompatibility groups and assignment of cultivars to these groups are fundamental. Expectedly, this has been proficient by controlled fertilizations and minute assessments of pollen tube development, which is tedious and affected by natural elements. To maintain a strategic distance from the downsides identified with SI, the formation of impeccable creation of self-good (SC) cultivars with extraordinary pomological qualities is among the critical expansion focuses on that identify with SI Prunus trees' natural items [52].

In the last two years, genes for those two proteins controlling the real allele specificity of GSI acknowledgement in *Prunus* have been actually identified. It is now known that two separate genes at the S locus handle male (pollen) and female (pistil) specificities (Fig. 1).

The advancement of vegetable reproducing frameworks is often seen as the exchange involving the focal items and hindrances of selfing. Evolutionary professionals have since noted three favorable and crucial outcomes of selfing. To start with, there is usually a characteristic genetic transmission place of attention to selfing throughout light that the a vegetable gives a couple

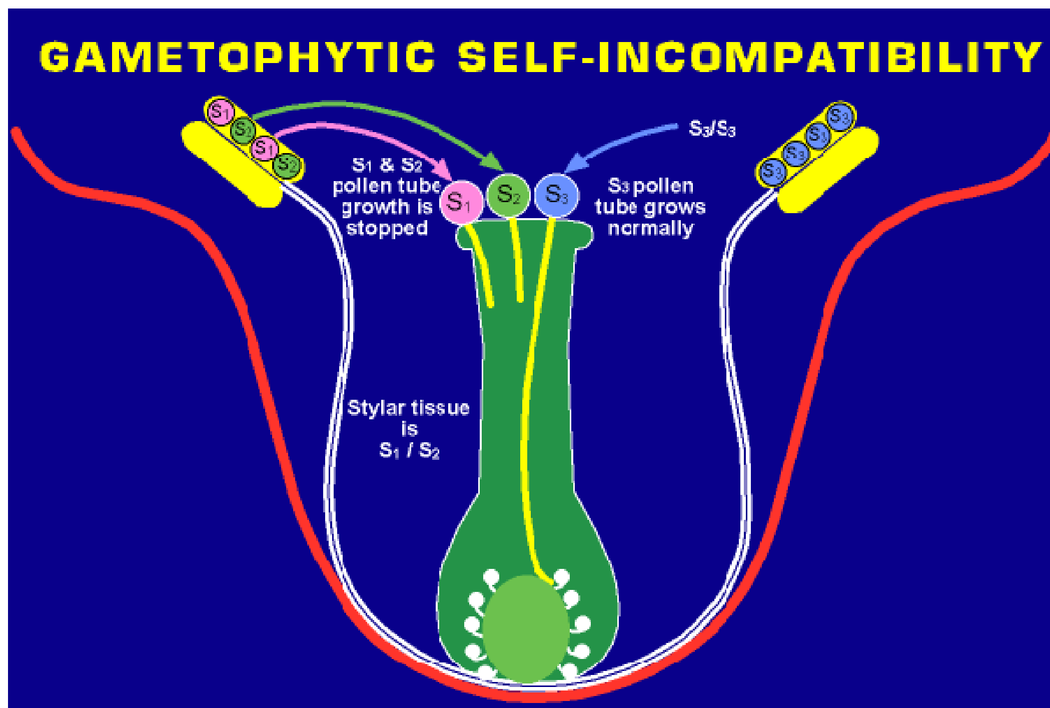

Figure 1. Genetic base gametophytic self-incompatibility

haploid sets of chromosomes to each one of these selfed seedling regardless may give dust to nonspecific [24]. Subsequently, selfing may cause regenerative affirmations when pollinators are rare (i.e. selfed descendants are better than no offspring) (e.g. Stebbins 1957; Schoen et al. 1996).Third, it often costs less, where vitality and various assets, to supply selfed seedling (e.g. less assets are utilized to pull and reward pollinators) [107, 108, 133].

Ribonuclease (RNase) and F-box genes were referred to as the pistil S and pollen S determinant genes, respectively (see review by [56]). Upon this discovery, the term 'S haplotype'is used to describe the real variants in the S locus, while the term 'allele'is used to describe the real variants in the S locus genes, pistil S and pollen S. On the real practical facet, these findings resulted to the advancement of new molecular approaches for S genotyping and SC screening process [120, 140, 141]. Molecular S genotyping and a number of marker-assisted SC offsprings are increasingly being successfully integrated in *Prunus* propagation programs worldwide.

Brewbaker (1959), in an expansive discussion of angiosperms, noted that SI has happened in no less than 71 families, and as of now, has been recorded all through around 250 to 600 genera that were explored; and the evaluation was that between 33% and another half off the blooming vegetation are self-contradictory. By and large, SI appears to have advanced no less than 21 exceptional times amid the development of blossoming vegetation [116] and a few one of a kind sorts may be recognized relying upon morphology, inherited genes, and molecular mechanism. In SI frameworks that are controlled by a single genetic locus, the locus has for every situation been termed the S-locus. It is obvious in any case, that various genes live inside of every S-locus, and the allelic complex of genes has been termed the S-haplotype.Nonethe-less, it is apparent that many genes dwell within just about every S-locus, as well as the

complicated allelic genes continue to be termed the real S-haplotype. Although in most of these methods, the ancestral locus has long been termed S, a variety of biochemically unique mechanisms are engaged, at very least at the degree of recognition of self- and non-self-pollen. Molecular information can be obtained for simply three types, the single-locus sporophytic and also two distinct types of single-locus gametophytic SI. In the actual sporophytic SI system of *Brassica*, both pollen and pistil S-genes are actually identified, and the stylar result is mediated by means of protein receptor kinases (for review, see [54]). The molecules mediating pistil S-specificity are actually identified and also cloned in two unique single-locus gametophytic methods. In the real Papaveraceae, SI consists of a complex number of events such as changes throughout calcium ion attentiveness, phosphorylation of specific meats, and transcription of pollen genes and DNA fragmentation of nuclei [53, 114],and the pistil S-gene has no significant homology to any gene of known purpose. In probably the most phylogenetically widespread way of gametophytic SI [116], the pistil S-gene product is usually a glycoprotein [59] together with ribonuclease action [83], and these molecules are actually termed S-RNases. The DNA sequences in the genes curbing SI systems can be quite a treasure chest of molecular data; and research of self-incompatibility gene sequences can offer data not just on the actual development in the systems themselves, but also the individual structure and demographic record of species [92]. Our emphasis with this particular article is going to be on solanaceous variety SI.

To date, some valid inquiries on the development of stylar SRNases remain unanswered. The most pressing may be the clear originality in degrees of expansion affecting the Solanaceae and also Plantaginaceae regarding what exactly is seen inside Rosaceae. We review data concerning the structure, functions, and molecular physiology of S-RNases; attempt to integrate these results with evolutionary studies, provide new analyses of domain structure and conservation; and present new analyses of selection/recombination in S-RNases.

2. Self-incompatibility

S-RNase-based SI genetically classified as gametophytic locus, the pistil differentiates between self and non-self-pollen based on the S-allele in the haploid pollen and meets either in the two S-alleles in the diploid pistil. The SI phenotype of pollen is determined by its own S-genotype. The rejection based on matching of S-alleles in pollen and pistil.

Pistil S-allele products were initially called basic polymorphic glycoproteins whose genetic abundance weight and isoelectric spot ranged from ~22 to 35 kDa and from ~8–10, respectively, and then further isolated together with S-alleles. These proteins are extracellular, largely confined to the upper third of the stylar transmitting tract-the site of self-pollen tube inhibition-and are developmentally correlated with the onset of SI, being absent 1 day prior to anthesis (immature pistil are self-compatible) and present at 1–10% of total protein at pollen release. S-RNase occurs at a truly high focus in completely created pistils and it has been approximated at 10–50 mg/ml inside the extracellular network of the stylar exchange tract with regard to the solanaceous type [51]. The primary quality encoding of one of these brilliant basic proteins has

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been cloned through *Nicotiana alata* by Anderson et al. in 1986 and more than 50 S-RNase arrangements have been reported since then. S-RNase arrangements are exceptionally disparate together with an amino p character from 38% to 98% sequence identities. Despite the fact that essential confirmation for that inclusion about S-RNases all through SI has been correlative, direct affirmation is attained by transgenic experimental tests similar to those done for *Petunia* and *Nicotiana* [67, 88]. Experiments showed that the S-specificity of pistils of transgenic plants can be altered through expression of a sense or antisense S-RNase transgene, leading to a gain or loss of S-specificity, respectively. These experimental tests likewise showed to some extent that high levels of S-RNase inside wild-type pistils are vital for pollen rejection to be complete. This information is once in a little while translated on the grounds that showing the genuine S-RNases is key and abundant for irregularity toward oneself inside pistil. It is not entirely genuine as different qualities less living at the S-locus has been demonstrated to influence the genuine SI result [85], subsequently, S-RNases are fundamental for SI and encode the genuine pistil S-specificity, yet are not general.

3. S-RNase function and structure

S-RNases are highly divergent, with allelic amino p sequence identities of about 30% to over 90% [125, 86]. Regardless of the excessive allelic string diversity, the real analysis of solanaceous S-RNase alleles exposed five conserved areas, from C1 to C5 (Fig. 2). C2 and C3 areas contain conserved catalytic histidine residues. Apart from C4, these regions are conserved throughout *Prunus* and also plantaginaceous S-RNases [127]. The 4th conserved rosaceous, called RC4, differs in placement and amino p sequence from C4 in the solanaceous S-RNase. There is a single (RHV) hypervariable region in rosaceous S-RNase, while a hypervariable couple (HVa and HVb) were within solanaceous and plantaginaceous SRNases [139]. Although hypervariable region(s) can be positively chosen and thought to play an essential role in self/non-self-recognition, recent conclusions suggested that other regions are important for that specificity in recognition [97, 133, 146].

Structural and phylogenetic analyses indicated that S-RNases in the three families share a typical origin, and so, the S-RNase-based GSI system evolved just once in eudicots [45, 131]. A single intron that is certainly common within the T2 form plant RNases is usually present inside the coding sequence in the hypervariable place of S-RNases of Solanaceae and *Pyrus* and *Malus* of Rosaceae (Fig. 2). With *Prunus*, also intron, there can be another intron inside the S-RNase code sequence at the junction involving the signal peptide and the start of the fully developed protein [45, 120]. It is intriguing that a stylar-expressed non-S-RNase within *Prunus*, that includes a single intron with no role in GSI, continues to be identified [5, 140]. Although biological and evolutionary significance in the other intron inside *Prunus* S-RNase can be unclear, the occurrence of a couple of introns varying in proportions has already been successfully useful in developing molecular solutions to distinguish one of several *Prunus* S-RNase alleles. A couple of PCRs are usually enough for S-RNase genotyping in *Prunus*, while allele-specific PCR as well as cleaved amplified polymorphic string (CAPS) markers are essential for genotyping in *Pyrus* and *Malus* [141].

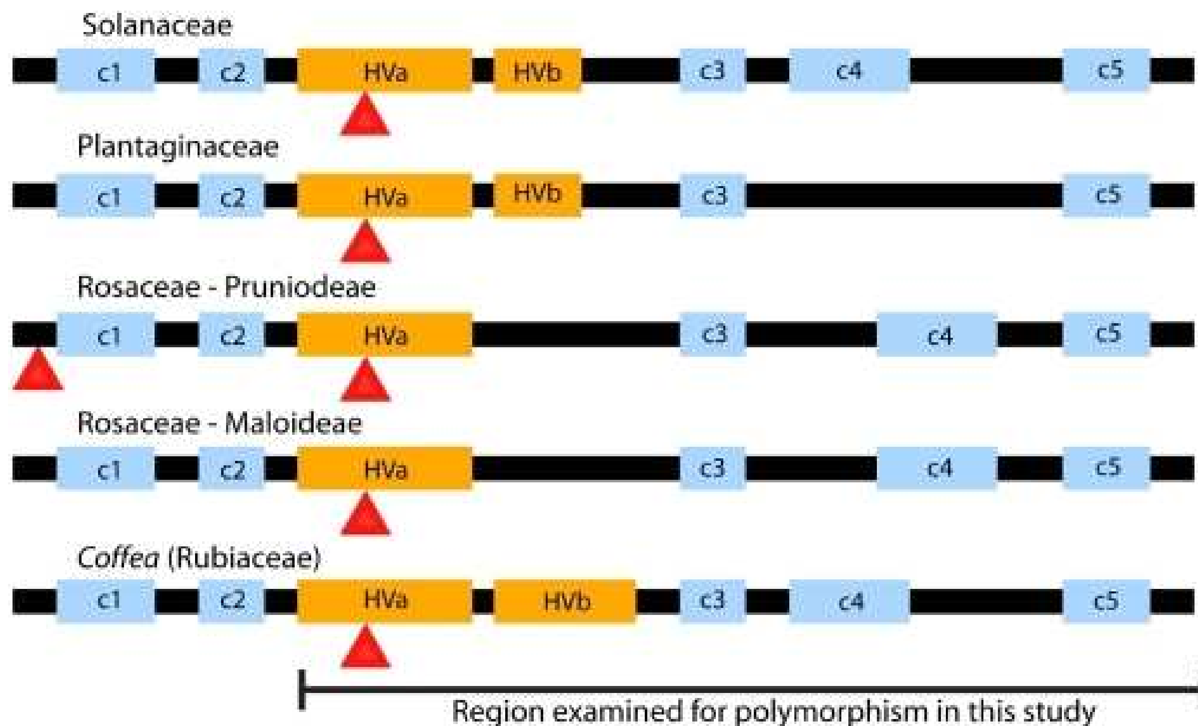

Figure 2. S-RNase structure and positions of intron groupings in S-RNase DNA succession. Solanaceous and rosaceous S-RNase structures are schematically represented. Intron arrangements are ordinarily found amid the coding successions for HVa and RHV of solanaceous and rosaceous S-RNases, separately. Notwithstanding this intron, there is another intron in Prunus S-RNase, yet not in *Malus* and *Pyrus* S-RNase. SP, signal peptide; C1 to C5, rationed locales 1–5; RC4, rosaceous preserved district 4; HVa and HVb, hypervariable areas a and b; RHV, rosaceous hypervariable area [119].

Several experiments of Solanaceae indicated that S-RNase exerts its cytotoxic effects inside the pollen tube through RNase action. Huang et al. (1994) confirmed that RNase action was essential for the pollen rejection response in *P. inflata*. Kowyama et al. (1994) looked into an SC *Lycopersicon peruvianum* variant and found that its SC lacks S-RNase action. Pollen rRNA was proved to be degraded right after SI, but not compatible pollination in *N. alata* [82]. Though every one of these fresh data was obtained with solanaceous vegetable species, it has been typically acknowledged that the RNase function is important for the real pollen rejection response in Rosaceae given that most functional S-RNases noted up to now have equally conserved catalytic histidine remains, which can be situated inside C2 and C3 areas. Gatekeeper and inhibitor types (Fig. 3) were proposed while using cytotoxicity in the S-RNase [86, 123].

The gatekeeper design assumed any recognition mechanism that helped only cognate S-RNase to enter the pollen tube to to exert its cytotoxicity, while the inhibitor design assumed the real presence of an inhibitor that inactivated the cognate S-RNase. Since immunocytochemical studies with Solanum chacoense showed that S11-RNase entered pollen tubes of both compatible and incompatible S haplotypes [73], the inhibitor model and its modification, the general inhibitor model, have been generally accepted [74]. Upon real identification, the pollen S encodes an F-box protein that could be involved in proteolysis; the cytotoxic effect of the S-RNase has been considered to be evaded due to S-RNase degradation rather than inhibition

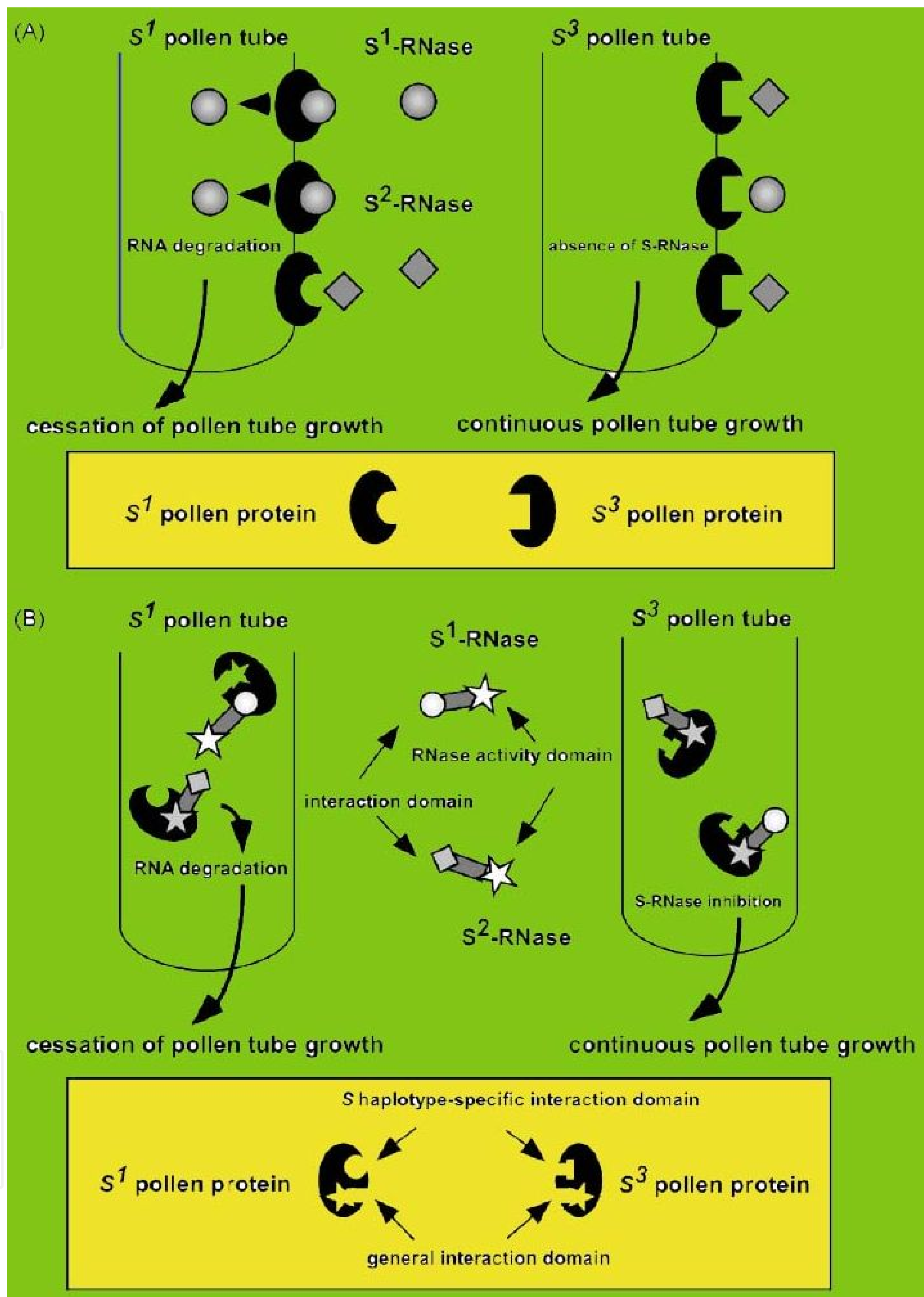

Figure 3. Gatekeeper and inhibitor models for the self-incompatibility reaction. The growth of S1 and S3 pollen tube in the S1S2 pistil is schematically described for the gatekeeper (A) and inhibitor (B) models [With permission of 118].

of S-RNase activity [39, 127-129, 143] (Fig. 5). Even though it remains to be seen whether or not both self- and non-self-S-RNases enter the pollen tube of Rosaceae, a degradation model has been offered for pollen-pistil acknowledgement. Although as mentioned previously, S-

RNases are highly polymorphic, sequence comparison in the 12 S-RNase sequences in 1991/1992 recognized five regions of conservation, known as C1 to C5 [123]. Of these, two (C2 and C3) share a high degree of sequence similarity while using corresponding regions of fungal RNases, RNase T2 [58], and RNase RH [38]. This similarity that led to the discovery that S-proteins are themselves RNases [83].

Discovery of a self-compatible S-allele in *Lycopersicon peruvianum*, in which one of the two catalytically essential histidine residues was mutated, provided a strong inference that RNase activity was necessary for SI function [104], but in the absence of same specificity, or identity of the pollen component of the interaction, this was not conclusive. Using a transgenic approach, where a mutant S-RNase gene with the codon for one of the two catalytically essential histidines replaced with an asparagine codon was introduced into plants, Huang et al. (1994) affirmed that the creation with this mutant SRNase was not ready to present an increment of S-capacity (dissimilar to the genuine wild-sort protein) so as a result of this, characteristic RNase activity is a bit of the reason behind S-RNases.

S-RNases are glycoproteins with one or more N-connected glycan structures, increasing the likelihood that allelic specificity may be encoded with the sugar moieties inside glycan structures. This question was addressed by engineering an S-RNase gene in which the asparagine codon of the only N-glycosylation site of the protein was replaced with an aspartic codon; however, N-glycosylation site in the protein has been supplanted with the aspartic codon. Investigation of transgenic vegetation communicating this sort of mutant S-RNase indicated that non-glycosylated S-RNase has the capacity to act similarly and effectively as wild-type S-RNase by releasing dust containing exactly the same S-allele [57]. Henceforth, the advancement of S-specificity is not found inside glycan feature chains in the protein spine of S-RNases.

A set of hypervariable regions, termed HVa and HVb, was additionally uncovered by Ioerger et al. (1991). These are the numerous hydrophilic locales of the S-RNase, realizing the speculation that HVa and HVb are the prime candidates for the determinant of S-RNAse specificity [49, 124]. The crystal structure of SF11-RNase has recently been determined by X-ray diffraction [44], confirming that both HVa and HVb regions are where they might play a role in determining allelic specificity. Ishimizu et al. (1998) found four regions of rosaceous S-RNases that demonstrate a crucial abundance of non-synonymous substitution around synonymous substitution and appear to be under positive selection, of which two overlap with HVa and HVb. In an investigation of Scrophulariaceae, extremely variable HVa and HVb ranges were discovered; however, but did not find evidence of diversifying selection [131]. It can be fascinating to see that a large proportion of these proteins are communicated at abnormal states in an exceedingly short period of time in the genuine procurement of SI. To date no codon usage studies have been carried out for S-RNases from any family but is an area of research that may provide interesting results.

There are several reports of experiments employing transgenic methods to identify regions and amino acid residues involved in the encoding of allelic specificity. Chimeric S-RNase genes have been created and presented in transgenic plant life intended of the S-specificity displayed

by hybrid S-RNases. Further, no gain of the new S-specificity of the donor allele was found, despite the fact that all hybrid S-RNases exhibited normal levels of RNase activity [55, 146].

A good but apparently contradictory result has been gained via a research employing a few very tightly related S-RNases (S11 and S13) of *Solanum chacoense* [80]. Both these S-RNases differ by a total of only 10 proteins, three that are within HVa and another of which in HVb. Substitution in the HVa and HVb regions of S11-RNase together with S13-RNase produced S-RNase found to exhibit S13- specificity; however, there was no S11 specificity in transgenic plant life.

These results seem to claim that HVa and HVb collectively are sufficient for S-haplotype specificity. However, any domain swapping experiment can only address the role of those amino acids which differ between the two proteins under study. If the outcomes of the specific three trials are obtained together, it would seem that proteins outside HVa and HVb (conserved S11-RNase and S13-RNase) are suitable to be engaged inside the allelic specificity of S-RNases [130]. Nevertheless, it is clear that the HVa and HVb areas play a vital role in encoding allelic specificity in S-RNases.

4. Pistil S determinant

4.1. Identification of S-RNase

The physiology and mechanisms of GSI are actually most substantially studied in solanaceous vegetable species. The development of cDNA glycoproteins co-segregated together with S alleles was first cloned via *Nicotiana alata* [2-3]. The deduced amino p sequence clearly implicated stylar RNase involvement in the recognition and rejection reaction inside the style. Along with other studies, it has been shown that in Solanaceae, the S allele product inside pistil is usually a highly simple glycoprotein comprising sequence motif characteristics in the active site in the fungal RNase T2 [58] and RH [38], termed S-RNase [83, 84].

At one point when transgenic analyses with *Petunia inflata* and *Nicotiana* proved that the S-RNase alone is enough for determining the specificity in the GSI pollen rejection response inside Solanaceae [67, 88], Sassa et al. (1996) and Broothaerts et al. (1995) reported that SRNases are associated together with GSI of *Pyrus* and *Malus* in Rosaceae. The finding that these families recruited the same molecule as the GSI pistil determinant has been unexpected because Solanaceae (*Asteridae*) and Rosaceae (*Rosidae*) are phylogenetically remote [12, 45]. Although deduced amino p sequences from cDNAs of S-RNases of *Pyrus* and *Malus* may be similar and support the active site of T2/S-type RNases, differences were clear involving the rosaceous and solanaceous S-RNases [105-108, 126]. Later, Xue et al. (1996) cloned the real S-RNase throughout *Antirrhinum* inside Plantaginaceae, a tightly related family of the Solanaceae.

As *Prunus* is one of the Rosaceae, it had been readily predicted that *Prunus* even offers an S-RNase-based GSI system. However, S-RNases remained unidentified for countless years after the real cloning in the *Pyrus* and *Malus* S-RNases, because polymerase chain reaction (PCR) cloning solutions for *Prunus* S-RNase were hindered by its fairly low DNA string, similar to

Pyrus and *Malus* SRNases as well as the presence of *Prunus* RNase genes which cannot involved with GSI. The first clue for the cloning of *Prunus* S-RNase was obtained when N-terminal sequences of almond (*Prunus dulcis*) SRNase were reported [120]. By the N-terminal amino p sequences, sweet cherry (*Prunus avium*) [120] and almond [125] S-RNases were cloned. Currently, sequences of over 100 *Prunus* S-RNase alleles are actually deposited in GenBank.

4.2. Pollen S determinant

4.2.1. Identification of F-box gene

The pollen S determinant in the S-RNase-based GSI in Rosaceae, Solanaceae, and Plantaginaceae was discovered decades after the real stylar determinant, S-RNase. The subcentromeric location in the solanaceous and plantaginaceous S locus experienced had long prevented chromosome walking [23, 142]. The first clue for the identification in the pollen S was from the S locus in the Plantaginaceae. Sequencing analysis in the *Antirrhinum hispanicum* S locus exposed the presence of the pollen-expressed F-box gene (AhSLF for a. *hispanicum* S locus F-box) located 9 kb downstream of S2-RNase [65].

Even though it was speculated that the F-box protein gene encoded the real pollen S, only one particular allele has been cloned. The S locus of *Prunus*, which is located right at the end of the linkage group 6 [20], was much more compact than those of Solanaceae and Plantaginaceae. Two separate groups in Japan successfully sequenced the real S locus of *Prunus* beginning from the S-RNase [22, 127]. Ushijima et al. (2003) did DNA sequencing and transcriptional analyses for the genomic areas that flank real almond (*P. dulcis*) S-RNase and identified polymorphic and non-polymorphic S locus F-box genes, called SFB of S haplotype-specific F-box gene and SLF for S locus F-box, respectively. At present, SLF continues to be referred to as SLFL1 [79] after the nomenclature of Entani et al. (2003). The options that come with SFB, including the high degree of allelic polymorphism, pollen-specific appearance, and the close physical distance to the S-RNase many supported that SFB may be the male determinant of GSI in almond. The same research group also found SFB in the cherry (*Prunus*) S locus in their attempt to compare the same S-RNase allele on SC and SI kinds of cherries, *R. cerasus* and *P. avium*, respectively [140]. Another study group in Japan reviewed the S locus place of a couple different S haplotypes in Japanese apricot (*Prunus mume*) and found some F-box genes [22]. Among them, SLF of S locus F-box, that includes a different name but can be orthologous to SFB throughout almond and cherries, shows a high level of allelic string diversity and was supposed to be a prospect of pollen S. The other F-box genes found, SLFL1, SLFL2, SLFL3 of SLF including gene 1, 2 and 3, respectively, showed far lower allelic string diversity. The pollen S candidate of Japanese apricot has been independently cloned in a study by Yamane et al. (2003d) and named differently as PmSFB. Since then, the *Prunus* pollen S was initially referred to by a couple of different words or terms such as ''SFB'' and also ''SLF''. We used ''SFB'' in this particular review to show the various features in *Prunus* SFB than the SLF in Solanacae and Plantaginaceae.

Direct evidence that S locus F-box gene adjustments of allele specificity in the pollen was from a transgenic research in *R. inflata* [109]. This kind of experiment employed a well-known

phenomenon termed ''competitive interaction'', where heteroallelic pollen which has two unique pollen S alleles work in pistils together with one as well as both cognate S haplotypes [18, 26-29].

Although transgenic analyses in *Prunus* are hindered by a long period and lacking a useful transformation system, molecular characterization in the S haplotypes throughout SC mutants supplied indirect but very good supporting facts for SFB staying the pollen S [125]. Later, multiple F-box genes, called SFB (SFBBs), were found in candidate pollen S genes in *Malus* and *Pyrus* [105-107]. Even though it has also been shown that the SFBB-gamma gene is not likely involved with the specificity determination of GSI reaction [131], it is still possible that just as with the other families and genera, one or a number of the SFBBs could be the pollen S.

4.3. Pollen S structure

SFB has just a single intron inside 50 untranslated places, where zero intron was within solanaceous and plantaginaceous SLFs. Although intron dimension varies together with different alleles, the difference inside the intron dimension is too small to be detected the intron length polymorphism for for S genotyping. Hence, fluorescent primers and an automatic sequencer were used to detect the real intron period polymorphism of S genotyping depending on SFB alleles [128]. Nonetheless, because fairly large-scale recombinational research using 1022 meioses confirmed no recombination involving the Prunus S-RNase and SFB [46] and S-RNase genotyping is often much easier, SFB genotyping can be used as a supplementary research for S haplotype determination. SFB research, on the contrary, is usually a powerful tool as well as the sole way to detect SC pollen-part mutant (PPM) S haplotypes, where only the real pollen S continues to be mutated [47-48, 126].

Another essential auxiliary examination of SFB uncovered the event of a few variables (V1 and V2) and two hypervariable (HVa and HVb) territories [47]. These hypervariable regions appeared to be hydrophilic or at least not strongly hydrophobic, which suggests that these regions may be exposed on the surface and function in the allele specificity of the recognition response. The fact that positively selected sites appear to concentrate in the variable and hypervariable regions further supports the possibility that these regions could play an important role in the SC/SI recognition.

Phylogenetic analyses with F-box genes inside *Arabidopsis thaliana* genome indicated that *Prunus* SFB, Petunia SLF, and Antirrhinum SLF might have a monophyletic beginning [134], as continues to be reported for that pistil S-RNase [45, 116]. Vieira et al. (2009) also concluded that there's no effective evidence to declare that the pollen S was independently recruited many times while in evolution. Nonetheless, phylogenetic reconstructions in the pollen S across all three families highlight numerous differences. As opposed to the phylogenetic tree of the S-RNase and S-like RNases of plants, the pollen-determinant F-box genes of a given family or genus are more closely related to its own S locus F-box genes that have no role in SI than to the pollen-determinants of the other families or genera [105, 126, 136, 79].

Another difference is available in the allelic string diversity in SFB of *Prunus* and SLF in the Solanaceae and also Plantaginaceae [92]. Deduced amino p sequences via SLF alleles prove as

extremely excessive high pairwise identities of over 90%. When it comes to plantaginaceous alleles, the actual pair wise identities about SLF alleles are 97% and 99% [144], while those of the respective S-RNase alleles are 30% and 60% [139]. On the contrary, the pair wise allelic string identities on Prunus SFB alleles is lower and a lot like those of S-RNase alleles; the degrees of divergence is comparable around 60–90% [45, 92]. Nonetheless, the phylogenetic associations among SFB are generally incongruent together with one of several S-RNases for the same S haplotype, regardless of the expectation of co-evolution in the pollen and pistil determinants [46, 92]. In Solanaceae and Plantaginaceae, it usually is plausible to consider that more allelic string identities can be achieved within SLF compared with SFB of *Prunus* and can show faster evolutionary heritage. Interestingly, the S-RNase of Solanaceae and also Plantaginaceae show higher degrees of allelic string diversity when compared with that of *Prunus*. Therefore, it is clear the *Prunus* S locus and also solanaceous and plantaginaceous S loci evolved in a variety of ways.

4.4. Pollen S-gene and function

The point that an acknowledgement event occurs involving the pollen and pistil inside operation of gametophytic self-incompatibility (GSI) dictates that recognition molecules have to be present in both tissues. For the real pistil and pollen components for being encoded by different body's genes raises many interesting conceptual issues both inside generation of new allelic specificities and inside maintenance in the genes to be a genetically associated unit. Therefore, many early types of the mechanism of gametophytic SI were relying on an individual gene, with inhibition occurring by using a dimerization event from the pollen tube or due to differential processing of a single gene as well as operon to create pistil and S-gene products [69]. There is a lot of evidence that pollen and pistil S-components are, in reality, separate body genes.

1. The expression of S-RNases throughout transgenic plants while using endogenous supporter causes a big difference in the pistil, but not pollen S-specificity [67].
2. The expression of S-RNases in transgenic plants employing a pollen particular promoter will not alter the real SI behavior in the pollen [21].
3. Through a phenomenon known as ''competitive connection,'' SI in time breaks down in pollen grains that carry a couple of different alleles. Plants holding duplication in the S-locus are actually generated by X-ray mutagenesis and these duplications are brought on the pollen to shed S specificity, presumably through the possession of two pollen S-specificities and in many of these self-compatible mutants, the real S-RNase is not present around the duplicated fragment [27-29].

A self-compatible mutant of *Pyrus serotina* (Rosaceae) has been identified in which the S-RNase has been deleted; this deletion affects the pistil, but not pollen S-function [104].

Major effort continues to be directed to the identification of the pollen S-gene and product. It must have a number of characteristics, such as ancestral linkage to S-RNase, allele particular polymorphism, and gene solution interaction in some way with S-RNases—either together with self-S-RNase, cross- S-RNases or both (but in many ways). Pollen meats that connect to

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S-RNases are actually identified such as calcium-dependent protein kinases, which phosphorylate S-RNases at the very least in vitro, however, not in an allele specific manner [63], and more recently, any protein comprising a RING-HC domain, which potentially may be mixed up in ubiquitin ligase-mediated protein degradation pathway, but again will not interact within an S-allele in a particular way [112].

Several studies have focused on mapping the position of the pollen S gene. Golz et al. (2001) determined the order of these marker genes for the S3-haplotype of *N. alata*, and placed the pollen S-gene between a marker (48A) and the S-RNase gene. Ushijima et al. (2001), in their study of a self-compatible cultivar of *Prunus dulcis* (Rosaceae), used a different approach to map the position of the pollen S-gene.

A study on this region via genomic the particular the southern part of subject of blotting prompted that 70 kb in the region quickly flanking the particular real S-RNase generally may seem to comprise sequences that demonstrate S-haplotype certain diversity. It will infer the particular plant pollen S-gene in this haplotype can be found by way of this kind of 70 kb place. It is actually established the real S-locus could be sub-contract centromeric interior Solanaceae with the knowledge that polymorphism of alleles generally appears to be improved with more than just one megabase in this relatives (see below). Certainly, polymorphism provides for just 70 kb through the*Prunus*, this resolves the dilemma about whether or not the real chromosomal site within the S-locus could be conserved among the Solanacaeae as well as the Rosaceae. Additional work would be likely essential to handle this kind of issue.

The latest focus of attempts to recognize the pollen S-gene that continues to be connected to the areas flanking S-RNase. Indeed, this repetitive nature of non-coding sequences flanking the real S-RNase gene, has, up to now, dissuaded attempts at chromosome walking in this area and string data via genomic clones (cloned throughout lambda phage) has been available only for a couple of kb upon each side in the S-RNase gene [14].

The latest technological advances, nonetheless, with unique advancement of the Bacterial Artificial Chromosome (BAC) local library, have greatly increased the size limit of genomic clones, increasing the number of sequence information per clone and rendering that more chromosome walking can be done. BAC clones containing S-RNase genes are actually identified throughout *Petunia inflata* [86-87] and *Antirrhinum hispanicum* [65]. BAC replicated from *Antirrhinum* encodes any 63.7 kb region in the S2-locus comprising the S-RNase and it has been sequenced [65]. Six putative body's genes were recognized whose deduced amino p sequences demonstrate homology together with known meats and of the four encode retrotransposons. The most significant finding has been a gene, known as SLF (S-locus F-box), encoding a great F-box comprising protein found about 9 kb downstream from S-RNase gene which can be expressed in the pollen as well as the tapetum [65]. Sequencing contig of 3 BAC clones, which signify a 328 kb region in the *P. inflata*S2-locus comprising the S-RNase, has shown a comparable abundance of retrotransposons and, interestingly, also has a gene a lot like SLF. SLF gene in *P. inflata* exhibits ~90% identity (at the real amino-acid level) concerning three haplotypes in support of ~30% personality to *Antirrhinum* SLF-S2. With both kinds, SLF genes look like the nearest pollen expressed gene for the S-RNase. Therefore, these represent very good candidates for the pollen S-gene. F-box comprising proteins are generally compo-

nents of ubiquitin–ligase processes, which, along with ubiquitin- initiating enzymes and ubiquitin-conjugating enzymes, mediate protein degradation with the 26S proteosome. Experiments are underway, making use of transgenic plants to discover if SLF is definitely the pollen S-gene.

Predicted amino acid sequences frompollen SFB and SLF from all functional SI S haplotypes conserve the F-box motif at the Nterminal, indicating that they function as F-box proteins. The F-box protein is known to be a component of a class of E3 ubiquitin ligases, the SCF complex, which regulates protein degradation in the ubiquitin/proteasome proteolytic pathway [19]. The F-box protein functions as a receptor to incorporate proteins targeted for polyubiquitination into the SCF complex. The polyubiquitinated targeted proteins are degraded by the 26S proteasome. It was, therefore, first proposed that the SCF complex that contains SFB (SCFSFB) and SLF (SCFSLF) might polyubiquitinate all nonself-SRNases for degradation but specifically interact with its cognate SRNase to leave it active, leading to the arrest of self-pollen tubes [56, 126-128].

Biochemical experimental results supporting this hypothesis have been obtained with Solanaceae and Plantaginaceae. Coimmunoprecipitation and yeast two hybrid analyses showed that *Antirrhinum* SLF (AhSLF) physically interacted with S-RNase in a nonallelic fashion and polyubiquitination of S-RNase was observed after incubating pollen proteins with compatible but not with incompatible stylar proteins [100]. Furthermore, AhSLF was shown to interact with ASK1 and CUL1-like proteins, suggesting that AhSLF makes an SCF complex. Later, AhSSK1 (*A. hispanicum* SLF-interacting SKP1-like1) that may work as an adaptor of the putative SCFSLF was cloned [42]. In contrast to AhSLF, *Petunia* SLF preferentially interacts using its nonself-S-RNase rather than its self-S-RNase [42]. This can be unexpected because the interactions of an allelic product in the pollen S using its self-S-RNase were long viewed as thermodynamically favored over the interactions using its nonself- S-RNase [56]. It would appear that *Petunia* SLF includes a domain that functions of S-RNase presenting (FD2) and two fields that control S-RNase-binding (FD1 and FD3) [41]. The FD1 and FD3 fields are shown to weaken the strong interaction involving FD2 and also S-RNase while in self-interactions, bringing about preferential connection and polyubiquitination of nonself-S-RNase.

The existence of different mechanisms of self-recognition in *Prunus* GSI can be suggested by means of molecular analyses of SC PPM S haplotypes as well as the SC/SI behavior in polyploids in *Prunus*. In contrast to the sign that the substrate of SCFSLF can be nonself-S-RNase in Solanaceae and Plantaginaceae, there are many indications that the substrate of SCFSFB might be a different molecule versus SRNase.

5. Genes that modulate the real SI reaction

Although the real S-locus encodes real determinants of S-haplotype specificity, there is evidence for the existence of other unlinked body's genes, termed modifier genes which can be required for SI result (reviewed in [16, 56, 81-84,], which is to be discussed in this article.

6. The pistil modifier variables

6.1. HT-B and glycoprotein

HT-B protein, a smaller asparagine-rich protein expressed late in style development, was initially identified by differential cDNA hybridization to screen fashion genes which were expressed in self-incompatible kinds such as *N. alata* however, but not in *N. plumbaginifolia*, any closely related self-compatible kinds [84]. Homologs of HT-B have also been recognized in other genera in the Solanaceae, *Lycopersicon* and *Solanum* [61, 94]. Down-regulation of HT-B appearance by anti-sense shift and RNAi was starving the transformants of the chance to reject self-pollen, suggesting that it is essential for SI [85, 94]. Within a comparative research of self-incompatible and self-compatible taxa of *Lycopersicon*, the appearance of HT-B gene had not been detected in all the self-compatible taxa [61]. Given that no direct interaction of HT-B and S-RNases has been detected, the complete role of HT-B of SI result was not yet determined until a newly released immunolocalization research [25].

This sort of revealed that in self-pollen pipes, HT-B was more likely to help S-RNase move from a great endomembrane compartment for the cytoplasm, where they might exert cytotoxicity, bringing about the arrest of pollen tube growth, when it is in compatible pollen pipes; the HT-B amount was appreciably down-regulated as well as the S-RNases were compartmentalized [25].

The 120 kDa glycoprotein (120K) is an abundant protein inside the stylar ECM and taken up by the real growing pollen pipes [71]. This 120K protein binds to S-RNase in vitro and, like HT-B, reductions of its expression by means of RNAi stopped self-pollen rejection [16, 33]. With recent immunolocalization trials, antibodies for the 120 kDa glycoprotein were found to label the real compartment tissue layer that enters the S-RNases inside the pollen pipes. However, given that S-RNase uptake is usual in 120K protein defective plant life; its specific role in SI continues to evade researchers [25].

7. Pollen modifier variables

7.1. SSK1

F-box proteins often serve as adaptors that bind specific substrate proteins to the SCF (Skp1-Cullin-F-box) E3 ubiquitin ligase complex [99]. This raised the possibility of whether the SLF involved in the SI also participates in an SCF complex, mediating S-RNase ubiquitination. Identification of other components in such a putative complex is obviously necessary to address this question. SSK1 (SLF-interacting SKP1-like1), a homolog of SKP1, was originally isolated in *A. hispanicum* through a yeast two-hybrid screening against a pollen cDNA library using AhSLF-S2 as bait [42] (Fig. 4.).

Pull-down assays encouraged that AhSSK1 could be an adaptor that connects SLF to CUL1 protein. Therefore, it can be thought that SLF and SSK1 will tend to be recruited to some anonical complicated SCF, which could be responsible for S-RNase ubiquitination.

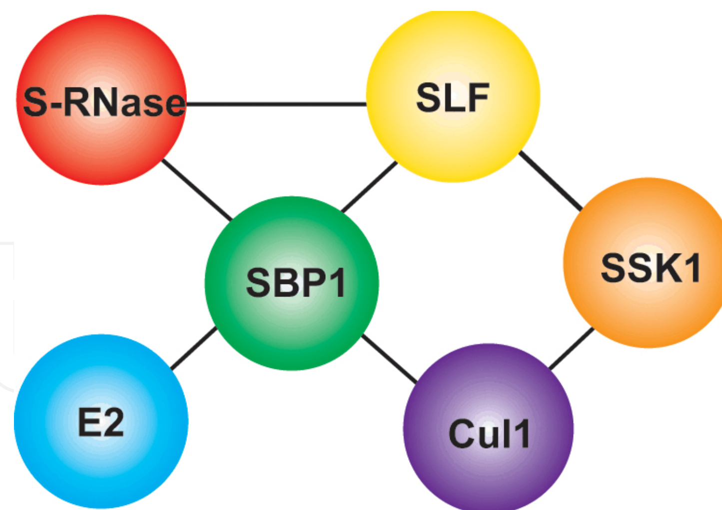

Figure 4. Protein interactions in gametophytic self-incompatibility [110]

7.2. SBP1

In trying to isolate the real pollen S, Sims and Ordanic (2001) screened a yeast twohybrid library from mature pollen of *P. hybrida* making use of *P. hybrida* S1-RNase because bait, and identified any gene known as PhSBP1 (S-RNase Presenting Protein1). Its homolog in *S. chacoense* was obtained depending on a comparable approach [95]. Nonetheless, the SBP1 gene displayed no haplotype polymorphismand was found to be expressed in almost all tissues. Additionally, it has been unlinked for the S-locus and so is unlikely to encode the real pollen S-determinant. Nonetheless, sequence research revealed that SBP1 has a RING-finger website, which can be characteristic of E3 ubiquitin ligases [60], indicating a possible role of SBP1 in S-RNase ubiquitination and degradation [95, 110-113]. Oddly enough, *P. inflata* SBP1 (PiSBP1) has recently been shown to interact together with PiSLFs, Pi CUL1 and an ubiquitin-conjugating enzyme, along with a novel E3 ligase complex continues to be suggested, with the possibility that PiSBP1 has a mixed role in SKP1 and RBX1 [111, 40].

8. S-like RNases in plants

Non-S RNases (syn. S-like RNases) in the T2/S-type are actually distinguished via different vegetable species. Non-S RNases are divided into two kinds, acidic and fundamental [127, 45]. A type of acidic non-SRNases is included in phosphate reuse as a result of phosphate confinement and tissue maturation [6, 121]. Other acidic non-S RNases can be up-controlled as a result of injury and vaccination together with pathogenic organisms. Albeit some essential non-S RNases are actually accounted of, for illustration, RNase Lc1 and Lc2 of *Luffa cylindrica*, RNase of *Momordica charantia* [46-48], and RNase X2 of *Petunia inflata* [68], their physiological capacities are not yet distinct.

Members of the real of category to which S-RNases fit in, exemplified with the fungal RNase T2, are actually identified creatures as varied as worms, bacteria, fungus, slime molds, Drosophila, and oysters [32]. In addition, plants are actually found to obtain T2 category RNases that are not involved with SI. Completion in the Arabidopsis genome string has revealed five T2 group RNases in this particular self-compatible kinds (GenBank Accession Nos.: NP_178399; NP_030524; NP_178399; NP_563940; NM_101288). With plants, the similarity of the T2 RNases to S-RNases has generated those S-like RNases. Although S-like RNases are closely related to S-RNases, there are important differences in their design, expression, and function [120] and they do not take part in the control of SI.

S-like RNases are actually found in all the plants examined and constitute an essential family of RNA-degrading meats in plant life. In distinction to S-RNases, their expression is not restricted for the pistil— they are expressed in a number of plant parts and caused by several unique stimuli. There is experimental evidence that S-like RNases are involved in phosphate starvation, senescence, wounding, programmed cell death, defense against pathogens, and light signaling (for review, see [6].

A particular class of S-like RNase has recently been given and called relic S-RNases. These are generally S-like RNases which can be expressed throughout pistils but are not S-linked and so are presumed not to be involved with SI. Relic SRNases are actually identified throughout both SI *Petunia* [68] and *Antirrhinum* and also SC *Nicotiana* [26, 64]. It has already been proposed that these relic SRNases include arisen by using a duplication process that takes place where a fragment in the S-locus, containing the real S-RNase that continues to be integrated elsewhere inside the genome and that has evolved independently [26]. This is founded on the fact that sequences of relic S-RNases are extremely closely linked to the S-RNases from the genus where they may have been found, unlike S-like S-RNases. Therefore, it is significant to make a distinction between relic S-RNases and S-like RNases when contemplating the evolution of this group because it seems likely that they may have very unique evolutionary histories. Whether relic SRNases have a new purpose or signify a non-functional similar gene is not yet determined. Nonetheless, it is clear that a number of processes that S-like RNases are actually involved in, in unique defense and senescence, are of significant importance in pistil tissue.

9. Evolutionary elements

S-RNases are actually involved in gametophytic SI in 3 distinct groups of eudicots, the real Solanaceae [2]; Rosaceae [105]; and also Scrophulariaceae [139]. This addresses the issue of whether or not primarily S-RNase-based SI includes a single beginning or whether they have arisen independently on multiple occasions. The Solanaceae and Scrophulariaceae are part of the subclass *Asteridae* in contrast to the Rosaceae that is part of the subclass *Rosidae*. A single origin in the S-RNases in these 3 families would suggest that primarily S-RNase-based SI was within the popular ancestor of its subclasses, which collectively form ~75% off dicot individuals. In improvement, it would suggest that there was extensive lack of primarily S-RNase- based SI and some gains of other forms of SI in higher dicots [45]. Even

though informative, estimating evolutionary relationship among S-RNases can be challenging for many reasons: the genes are fairly short long (~220AA residues), time since divergence can be long ~110 Mbps involving the *Asteridae* and *Rosidae*) along with a strongly adverse frequency-dependent assortment is likely to have generated extensive string divergence after the system comes [45].

A number of studies have attempted to discuss evolutionary associations among S-RNases and related S-like RNases [45, 101, 104-107, 116, 125, 139]. Preliminary studies found that solanaceous, rosaceous and scrophulariaceous S-RNases just about every formed monophyletic clade [105, 139], pointing to the idea that SRNases share a typical ancestor. Later studies, nonetheless, found simply very vulnerable bootstrap support for nodes uniting S-RNases [101, 125-128], but simply included a finite number about S-like RNases (7 and 14, respectively), limiting the chance to distinguish the single and also multiple beginnings of SRNase mediated SI. The two most up-to-date studies have taken advantage of the significant amount of completely new sequence information now available together with different phylogenetic approaches than those used previously to check phylogenetic associations among S-RNase sequences.

Igic and Kohn (2001) carried out a maximum likelihood analysis using 67 S-RNase and S-RNase-like DNA sequences, Steinbachs and Holsinger (2002) executed a Bayesian research of 72 DNA sequences. Together with maximum chance analysis, Igic and Kohn also analyzed intron presence/absence and position in 29 S-RNase and also S-RNase including genes, and found a high degree of congruence regarding relationships deduced by intron/exon structure as well as the tree extracted by utmost likelihood research. While not really unequivocal, the finest interpretation in the trees generated in similar studies is that S-RNases indeed carry out a kind ofmonophyletic clade (with the actual addition of one or two S-like RNases). Thus, primarily S-RNase-based GSI generally seems to have arisen from a popular ancestor, which covers three-quarters of dicot individuals, indicating that primarily S-RNase-based GSI has been the ancestors stated in nearly all dicots [45, 115].

10. Completely new perspectives

To address a number of unresolved difficulties surrounding the actual evolution of S-RNase-based SI systems, we analyzed the actual S-RNase information in two ways: (1) we explored the actual variation throughout S-RNase gene DNA and also amino p sequences, particularly in relation to structural and functional motifs described previously. (2) We also S-RNase string data of potential patterns of assortment and/or recombination. Previous works [44, 123] include suggested specific types of the structure in the S-RNase genes that we tested employing a broader phylogenetic test than previously used, as well as exploring the variation in gene sequence in a phylogenetic context. Some scientific tests have encouraged that recombination may play a role in the real diversification of alleles in S-RNase gene family, at very least within populations [134]. We explored an opportunity of assortment and/or recombination happening across many major S-RNases and S-like RNases. The gene structure of S-RNases has been

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previously described as including five conserved domains (C1–C5), two hypervariable regions (Hva and HVb), and several highly conserved amino acid residues including five cysteine residues, one leucine residue, and two tryptophan residues outside of the conserved domains and two histidine residues (one in C2 and one in C3) that are considered to be catalytic residues for RNase function [44, 123]. We first explored the real variation of proteins and nucleotides in S-RNase sequences employing a previously released dataset [116] by means of counting the amount of inferred changes on the phylogenetic tree using MacClade 4.03 [75]. During these evaluations, it has been noted the published alignment failed to align every one of the conserved fields previously identified [123]. The patterns seen together with nucleotide and amino p sequences suggested the same patterns; consequently, amino p variability was also evaluated.

Roalson et al. (2003) in this respect analyzed amino variety in SRNase position for 3 clades: (1) the whole S- and S-like RNases clade, (2) the real clade of Solanaceae and Scrophulariaceae S-RNases, and (3) the genuine clade of S-like II RNases. Comparative examples were essentially in different clades on the grounds that are alluded to here of these 3 clades. The examples of deviation for a large portion of these 3 clades are than the speculated monitored fields, hypervariable territories, and moderated amino p deposits.Amino p variety in the Solanaceae/ Scrophulariaceae clade is for the most part than the recommended basic components proposed by Ida et al. (2001). Altogether, there was substantially more amino p substitution surmised, even at hypothetically saved locales, than keeps on being beforehand recognized. At the point when numerous S- and S-like RNases are considered, in any event various amino acids in every one of the saved spaces may be variable, with upwards of 19 substitutions found at a few locales. In change, amino p positions outside the "hypervariable" zones show comparative degrees of amino p change inside a phylogenetic wording as is found inside HVa and HVb. Preserved amino p deposits (cysteine, leucine, tryptophan, and histidine) are several slightest variable amino p buildups, in spite of the fact that other amino p deposits were discovered which can be correspondingly saved. For example, the glycine deposit in C2 near the preserved histidine buildup, a tryptophan deposit in the middle of HVb and C3, the genuine lysine and glycine buildups all through C3 that encompass the genuine saved histidine deposit, and any tyrosine/phenylalanine set about halfway about C3 and C4. A couple of different positions appear to have minor variety, yet this is a result that does not have (crevice all through amino p arrangement) the amino p positions in numerous groupings. At the point when just probably utilitarian S-RNases are thought, for example, the S-RNases through Solanaceae and Scrophulariaceae, a comparable example of amino p variety is found, despite the fact that the aggregate number of changes at locales is lower. As a comparative example of variety is found in utilitarian S-RNases as is discovered when numerous S- furthermore S-like RNases are thought, it is not clear in the occasion the lower level of variety at positions is generally a capacity in the higher protection inside useful duplicates and additionally lower testing (26 versus 72 amino p successions). Since the discovery when numerous groupings were viewed, there is a huge level of variety inside all the moderated fields and there are heaps of amino acids outside the hypervariable fields that show comparative degrees of variety as is found in HVa also in HVb. As has been discovered, extreme S- and S-like RNases and the Solanaceae/ Scrophulariaceae S-RNases, huge degrees of a variety were discovered over the whole quality

if S-like RNase clade II alone is viewed as (Fig. 5). Just 16 groupings in this specific clade can be discovered, which can be reflected inside aggregate quantities of derived adjust at every amino p deposit, however, the genuine example of amino p substitutions over the quality takes after that inside alternate examinations. Also, most in the saved amino p buildups are correspondingly rationed inside S-like RNase II clade as theS-RNase clades (Fig. 5).

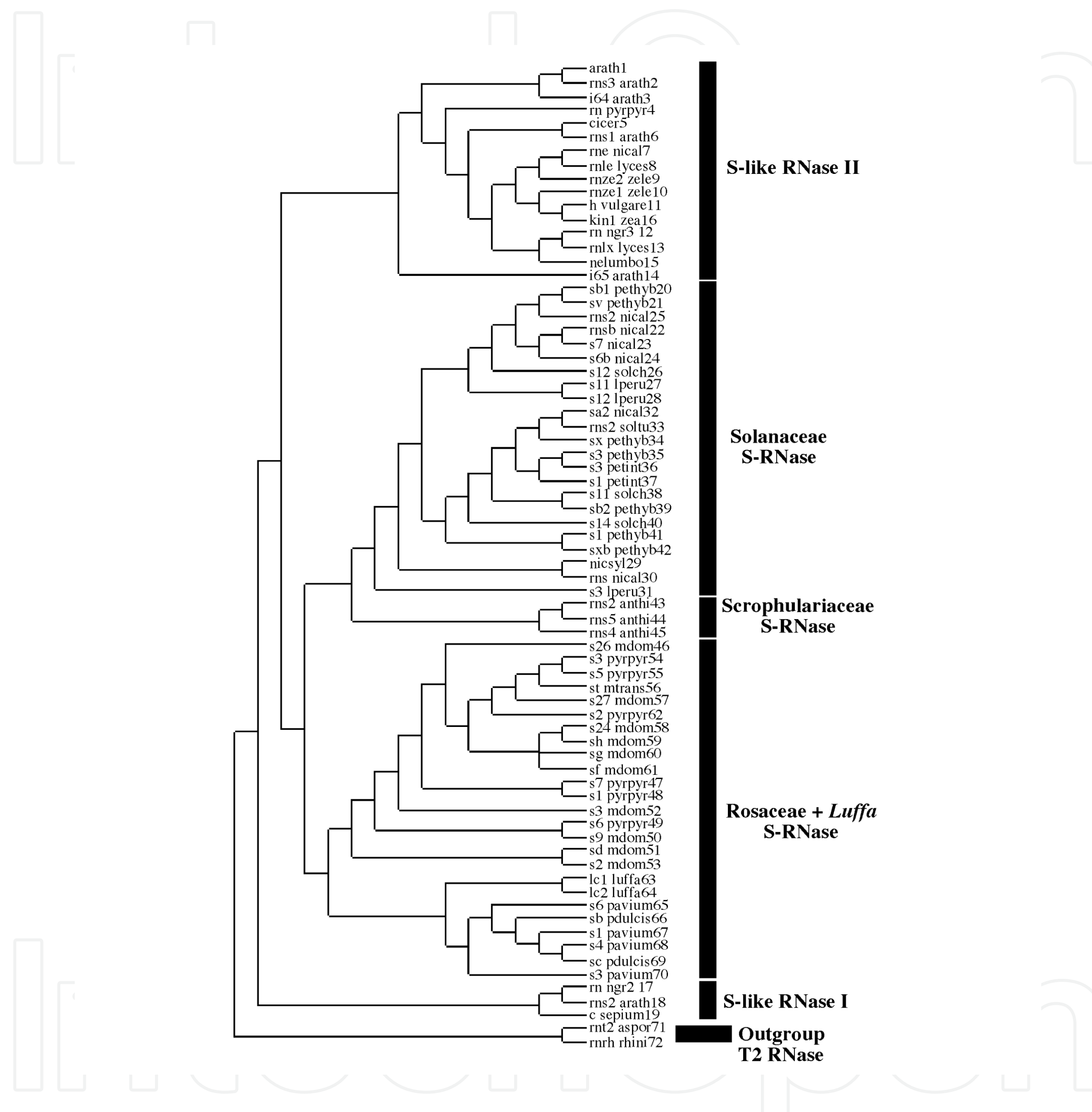

Figure 5. Phylogenetic hypothesis of relationships among S- and S-like RNase gene sequences with major clades labeled according to the plant family of origin and their inferred function (S- or S-like). Modified from Steinbachs and Holsinger (2002); Bayesian analysis of DNA sequence data [with permission from ref. 102].

In the analysis of S-RNase sequences via *P. inflata*, Wang et al. (2001) supplied evidence pertaining to recombination from the S-RNase gene. It has been determined that at the very least, now and again, homology between S-RNases varied from one end of the gene to the other, as an example, the 50 stop of S19-RNase has been closely linked to S2-RNase and 30 stop was closely linked to S8-RNase. Hence, while youwill find conceptual issues in accepting that recombination cannot only happen from the S-locus; however, within S-RNases themselves,

it is undoubtedly a probability that uncommon recombination functions have played a role in the actual evolution of the genes.

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Author details

Karim Sorkheh

Address all correspondence to: karimsorkheh@gmail.com

Department of Agronomy and Plant Breeding, Faculty of Agriculture, Shahid Chamran University of Ahvaz, Iran

References

[1] Ai, Y., Kron, E., Kao, T.-h., 1991. S-alleles are retained and expressed in a self-compatible cultivar of *Petunia hybrida*. Mol. Gen. Genet. 230, 353–358.

[2] Anderson, M.A., Cornish, E.C., Mau, S.-L., Williams, E.G., Hoggart, R., Atkinson, A., Bo° nig, I., Grego, B., Simpson, R., Roche, P.J., Haley, J.D., Penschow, J.D., Niall, H.D., Tregear, G.W., Coghlan, J.P., Crawford, R.J., Clarke, A.E., 1986a. Cloning of cDNA for a stylar glycoprotein associated with expression of self-incompatibility in *Nicotiana alata*. Nature 321, 38–44.

[3] Anderson, M.A., McGadden, G.I., Bernatzky, R., Atkinson, A., Orpin, T., Dedman, H., Tregear, G., Fernlyey, R., Clarke, A.E., 1989. Sequence variability of three alleles of the self-incompatibility gene of *Nicotiana alata*. Plant Cell 1, 483–491.

[4] Banovic, B., Surbanovski, N., Konstantinovic, M.,Maksimovic, V., 2009. Basic RNases of wild almond (*Prunus webbii*): cloning and characterization of six new SRNase and one ''non-S RNase'' genes. J. Plant Physiol. 166, 395–402.

[5] Bariola, P.A., Green, P.J., 1997. Plant ribonucleases. In: D_Alessio, G., Riordan, J.F. (Eds.), Ribonucleases: Structures and Functions. Academic Press, New York, pp. 163–190.

[6] Beecher, B., McClure, B.A., 2001. Effects of RNases on rejection of pollen from *Nicotiana tabacum* and *N. plumbaginifolia*. Sex. Plant Reprod. 14, 69–76.

[7] Bernacchi, D., Tanksley, S.D., 1997. An interspecific backcross of *Lycopersicon esculentum* L. hirsutum: linkage analysis and a QTL study of sexual compatibility factors and floral traits. Genetics 147, 861–877.

[8] Bernatzky, R., Glaven, R.H., Rivers, B.A., 1995. S-related protein can be recombined with self-compatibility in interspecific derivatives of *Lycopersicon*. Biochem. Genet. 33, 215–225.

[9] Brewbaker, J.L., 1959. Biology of the angiosperm pollen grain. Indian J. Genet. Plant Breed. 19, 121–133.

[10] Broothaerts, W., Janssens, G.A., Proost, P., Broekaert, W.F., 1995. cDNA cloning and molecular analysis of two self-incompatibility alleles from apple. Plant Mol. Biol. 27, 499–511.

[11] Chase, M.W., Soltis, D.E., Olmstead, R.G., Morgan, D., Less, D.H., Mishler, D., Duvall, M.R., Price, R.A., Hills, H.G., Qiu, Y.-L., Kron, K.A., Rettig, J.H., Conti, E., Palmer, J.D., Manhart, J.R., Sytma, K.J., Michels, H.J., Kress, W.J., Karol, K.G., Clake, W.D.,

[12] Chetelat, R.T., De Verna, J.W., 1991. Expression of unilateral incompatibility in pollen of *Lycopersicon pennellii* is determined by major loci on chromosomes 1, 6 and 10. Theo. Appl. Gene. 82, 704-712.

[13] Coleman, C.E., Kao, T.-h., 1992. The flanking regions of two *Petunia inflata* S-alleles are heterogeneous and contain repetitive sequences. Plant Mol. Biol. 18, 725–737.

[14] Craig, K.L., Tyers, M., 1999. The F-box: a new motif for ubiquitin dependent proteolysis in cell cycle regulation and signal transduction. Prog. Biophys. Mol. Biol. 72, 299–328.

[15] Cruz-Garcia, F., Hancock, C.N., McClure, B., 2003. S-RNase complexes and pollen rejection. J. Exp. Bot. 54, 123–130.

[16] de Nettancourt, D., 1977. Incompatibility in Angiosperms. Springer, Berlin.

[17] de Nettancourt, D., 2001. Incompatibility and Incongruity in Wild and Cultivated Plants. Springer, Berlin.

[18] Deshaies, R.J., 1999. SCF and cullin/RING H2-based ubiquitin ligases. Annu. Rev. Cell Dev. Biol. 15, 435–467.

[19] Dirlewanger, E., Graziano, E., Joobeur, T., Garriga-Calder´e, Cosson, P., Howad, W., Arus, P., 2004. Comparative mapping and marker-assisted selection in Rosaceae fruit crops. Proc. Natl. Acad. Sci. U.S.A. 101, 9891–9896.

[20] Dodds, P.N., Ferguson, C., Clarke, A.E., Newbigin, E., 1999. Pollen expressed S-RNases are not involved in self-incompatibility in *Lycopersicon peruvianum*. Sex. Plant Reprod. 12, 76–87.

[21] Entani, T., Iwano, M., Shiba, H., Che, F.-S., Isogai, A., Takayama, S., 2003. Comparative analysis of the self-incompatibility (S_) locus region of *Prunus mume*: identification of a pollen-expressed F-box gene with allelic diversity. Genes Cells 8, 203–213.

[22] Entani, T., Iwano, M., Shiba, H., Takayama, S., Fukui, K., Isogai, A., 1999a. Centromic localization of an S-RNase gene in *Petunia hybrida* Vilm. Theor. Appl. Genet. 99, 391–397.

[23] Fisher RA (1941) Average excess and average effect of a gene substitution. Ann Eugen 11:53–63.

[24] Goldraij, A., Kondo, K., Lee, C.B., Hancock, C.N., Sivaguru, M., Vazquez-Santana, S., Kim, S., Phillips, T.E., Cruz-Garcia, F., McClure, B., 2006. Compartmentalization of S-RNase and HT-B degradation in self-incompatible *Nicotina*. Nature 439, 805–810.

[25] Golz, J.F., Clarke, A.E., Newbigin, E., Anderson, M., 1998. A relic SRNase is expressed in the styles of self-compatible *Nicotiana sylvestris*. Plant J. 16, 591–599.

[26] Golz, J.F., Oh, H.-Y., Su, V., Kusaba, M., Newbigin, E., 2001. Genetic analysis of *Nicotiana* pollen-part mutants is consistent with the presence of an S-ribonuclease inhibitor at the S-locus. Proc. Natl. Acad. Sci. USA 98, 15372–15376.

[27] Golz, J.F., Oh, H.-Y., Su, V., Kusaba, M., Newbigin, E., 2001. Genetic analysis of *Nicotiana* pollen-part mutants is consistent with the presence of an S-ribonuclease inhibitor at the S locus. Proc. Natl. Acad. Sci. U.S.A. 98, 15372–15376.

[28] Golz, J.F., Su, V., Clarke, A.E., Newbigin, E., 1999. A molecular description of mutations affecting the pollen component of the *Nicotiana alata* S locus. Genetics 152, 1123–1135.

[29] Golz, J.F., Su, V., Clarke, A.E., Newbigin, E., 1999. A molecular description of mutations affecting the pollen component of the *Nicotiana alata* S locus. Genetics 152, 1123–1135.

[30] Grassly, N., Rambaut, A., 1998. PLATO 2.11—Partial likelihoods assessed through optimization. Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS.

[31] Green, P.J., 1994. The ribonucleases of higher plants. Annu. Rev. Plant Phys. Plant Mol. Biol. 45, 421–445.

[32] Hancock, C.N., Kent, L., McClure, B.A., 2005. The stylar 120 kDa glycoprotein is required for S-specific pollen rejection in *Nicotiana*. Plant J. 43, 716–723.

[33] Haring, V., Gray, J.E., McClure, B.A., Anderson, M.A., Clarke, A.E., 1990. Self-incompatibility: a self-recognition system in plants. Science 250, 937–941.

[34] Hedren, M., Gaul, B.S., Jansen, R.K., Kim, K.-J., Wimpee, C.F., Smith, J.F., Furnier, G.R., Stauss, S.H., Xiang, Q.-Y., Plunkett, G.M., Soltis, P.S., Swensen, S.M., Williams, S.E., Gadek, P.A., Quinn, C.J., Eguiarte, L.E., Golenberg, E., Learn Jr., G.H., Graham, S.W., Barett, S.C.H., Dayanandan, S., Albert, V.A., 1993. Phylogenetics of seed plants: an analysis of nucleotide sequences from the plastid gene rbcL. Ann. Missouri Bot. Gard. 80, 528–580.

[35] Hiscock, S.J., Dickinson, H.G., 1993. Unilateral incompatibility within the Brassicaceae: further evidence for the involvement of the self-incompatibility (S)-locus. Theor. Appl. Genet. 86, 744–753.

[36] Hogenboom, N.G., 1984. Incongruity: non-functioning of intercellular and intracellular partner relationships through non-matching information. In: Linskens, H.F., Heslop-Harrison, J. (Eds.), Encyclopedia of Plant Physiology. Springer, Berlin, pp. 640–654.

[37] Horiuchi, H., Yanai, K., Takagai, M., Yano, K., Wakabayashi, E., Sanda, A., Mine, S., Ohgi, K., Irie, M., 1988. Primary structure of base non-specific ribonucleases from Rhizopus niveus. J. Biochem. 103, 408–418.

[38] Hua, Z., Fields, A., Kao, T.-H., 2008. Biochemical models for S-RNase-based self-incompatibility. Mol. Plant 4, 575–585.

[39] Hua, Z., Kao, T.-H., 2006. Identification and characterization of components of a putative *Petunia* S-locus F-box-containing E ligase complex involved in SRNase-based self-incompatibility. Plant Cell 18, 2531–2553.

[40] Hua, Z., Meng, X., Kao, T.-H., 2007. Comparison of *Petunia inflata* S-locus F-box protein (Pi SLF) with Pi SLF-like proteins reveals its unique function in S-RNasebased self-incompatibility. Plant Cell 19, 3593–3609.

[41] Huang, J., Zhao, L., Yang, Q., Xue, Y., 2006. AhSSK1, a novel SKP1-like protein that interacts with the S-locus F-box preotein SLF. Plant J. 46, 780–793.

[42] Huang, S., Lee, H.-S., Karunandaa, B., Kao, T.-H., 1994. Ribonuclease activity of *Petunia inflata* S proteins is essential for rejection of self-pollen. Plant Cell 6, 1021–1028.

[43] Ida, K., Norioka, S., Yamamoto, M., Kumasaka, T., Yamashita, E., Newbigin, E., Clarke, A.E., Sakiyama, F., Sato, M., 2001. The 1.55 ºA a resolution structure of Nicotiana alata S(F11)-RNase associated with gametophytic self-incompatibility. J. Mol. Biol. 314, 103–112.

[44] Igic, B., Kohn, R., 2001. Evolutionary relationships among self-incompatibility RNases. Proc. Natl. Acad. Sci. U.S.A. 98, 13167–13171.

[45] Ikeda, K., Igic, B., Ushijima, K., Yamane, H., Hauck, N.R., Nakano, R., Sassa, H., Iezzoni, A.F., Kohn, J.R., Tao, R., 2004a. Primary structural features of the S haplotypespecific F-box protein, SFB, in Prunus. Sex. Plant Reprod. 16, 235–243.

[46] Ikeda, K., Ushijima, K., Yamane, H., Tao, R., Hauck, N.R., Sebolt, A.M., Iezzoni, A.F., 2005. Linkage and physical distances between the S-haplotype S-RNase and SFB genes in sweet cherry. Sex. Plant Reprod. 17, 289–296.

[47] Ikeda, K., Watari, A., Ushijima, K., Yamane, H., Hauck, N.R., Iezzoni, A.F., Tao, R., 2004b. Molecular markers for the self-compatible S40-haplotype, a pollen-part mutation in sweet cherrry (*Prunus avium* L.). J. Am. Soc. Hortic. Sci. 129, 724– 728.

[48] loerger, T.R., Gohlke, J.R., Xu, B., Kao, T.-H., 1991. Primary structural features of the self-incompatibility protein in Solanaceae. Sex. Plant Reprod. 4, 81–87.

[49] Ishimizu, T., Shinkawa, T., Sakiyama, F., Norioka, S., 1998. Primary structural features of rosaceous S-RNases associated with gametophytic self-incompatibility. Plant Mol. Biol. 37, 931–941.

[50] Jahnen, W., Lush, W.M., Clarke, A.E., 1989. Inhibition of in vitro pollen tube growth by isolated S-glycoproteins in *Nicotiana alata*. Plant Cell 1, 501–510.

[51] Janick, J., Moore, J., 1975. Advances in Fruit Breeding. Purdue Univ. Press, West Lafayette.

[52] Jordan, N.D., Franklin, F.C.H., Franklin-Tong, V.E., 2000. Evidence for DNA fragmentation triggered in the self-incompatibility response in pollen of Papaver rhoeas. Plant J. 23, 471–479.

[53] Kachroo, A., Nasrallah, M.E., Nasrallah, J.B., 2002. Self-incompatibility in the Brassicaceae: receptor-ligand signaling and cell–cell communication. Plant Cell 14 (Suppl.), S227–S238.

[54] Kao, T.-h., McCubbin, A.G., 1996. How flowering plants discriminate between self and non-self pollen to prevent inbreeding. Proc. Natl. Acad. Sci. USA 93, 12059–12065.

[55] Kao, T.-H., Tsukamoto, T., 2004. The molecular and genetic bases of S-RNase-based self-incompatibility. Plant Cell 16 (Suppl.), S72–S83.

[56] Karunanandaa, B., Huang, S., Kao, T.-h., 1994. Carbohydrate moiety of the *Petunia inflata* S3 protein is not required for self-incompatibility interactions between pollen and pistil. Plant Cell 6, 1933– 1940.

[57] Kawata, Y., Sakiyama, F., Tamakoi, H., 1988. Amino-acid sequence of ribonucleases T2 from *Aspergillus oryzae*. Eur. J. Biochem. 176, 683–697.

[58] Kehyr-Pour, A., Pernes, J., 1985. A new S-allele and specific S-proteins associated with two S-alleles in *Nicotiana alata*. In: Mulcahy, D.L., Mulcahy, G.B., Ottaviano, E. (Eds.), Biotechnology and Ecology of Pollen. Proceedings of the International Conference on the Biotechnology and Ecology of Pollen, 9–11 July, 1985, University of Massachusetts, Amherst. Springer, New York, pp. 191–196.

[59] Kerscher O, Felberbaum R, Hochstrasser M (2006) Modification of proteins by ubiquitin and ubiquitin-like proteins. Annu Rev Cell Dev Biol 22:159–180.

[60] Kondo, K., Yamamoto, M., Matton, D.P., Sato, T., Masashi, H., Norioka, S., Hattori, T., Kowyama, Y., 2002. Cultivated tomato has defects in both S-RNase and HT genes required for stylar function of self-incompatibility. Plant J. 29, 627–636.

[61] Kowyama, Y., Kunz, C., Newbigin, E., Clarke, A.E., Anderson, M.A., 1994. Selfcompatibility in a *Lycopersicon peruvianum* variant (LA2157) is associated with a lack of style S-RNase activity. Thor. Appl. Genet. 88, 859–864.

[62] Kunz, C., Chang, A., Faure, J.-D., Clarke, A.E., Polya, G., Anderson, M.A., 1996. Phosphorylation of style S-RNases by Ca2-dependent protein kinases from pollen tubes. Sex. Plant Reprod. 9, 25–34.

[63] Kuroda, S., Norioka, S., Mitta, M., Kato, I., Sakiyama, F., 1994. Primary structure of a novel stylar RNase unassociated with selfincompatibility in tobacco plant, *Nicotiana alata*. J. Protein Chem. 13, 438–439.

[64] Lai, Z., Ma, W., Han, B., Liang, L., Zhang, Y., Hong, G., Xue, Y., 2002. An F-box gene linked to the self-incompatibility (S) locus of *Antirrhinum* is expressed specifically in pollen and tapetum. Plant Mol. Biol. 50, 29–42.

[65] Lai, Z., Ma, W., Han, B., Liang, L., Zhang, Y., Hong, G., Xue, Y., 2002. An F-box gene linked to the self-incompatibility (S) locus of *Antirrhinum* is expressed specifically in pollen and tapetum. Plant Mol. Biol. 50, 29–42.

[66] Lee, H.-S., Huang, S., Kao, T.-H., 1994. S proteins control rejection of incompatible pollen in *Petunia inflata*. Nature 367, 560–563.

[67] Lee, H.-S., Singh, A., Kao, T.-h., 1992. RNase X2, a pistil-specific ribonuclease from *Petunia inflata*, shares sequence similarity with solanaceous S proteins. Plant Mol. Biol 20, 1131–1141.

[68] Lewis, D., 1954. Comparative incompatibility in angiosperms and fungi. Adv. Genet. 6, 235–285.

[69] Lewis, D., Crowe, L.K., 1958. Unilateral interspecific incompatibility in flowering plants. Heredity 12, 233–256.

[70] Lind, J.L., Bacic, A., Clarke, A.E., Anderson, M.A., 1994. A style-specific hydroxyproline- rich glycoprotein with properties of both extensins and arabinogalactan proteins. Plant J. 6, 491–502.

[71] Lush, W.M., Clarke, A.E., 1997. Observations of pollen tube growth in Nicotiana alata and their implications for the mechanism of selfincompatibility. Sex. Plant Reprod. 10, 27–35.

[72] Luu, D.T., Qin, X., Morse, D., Cappadocia, M., 2000. S-RNase uptake by compatible pollen tubes in gametophytic self-incompatibility. Nature 407, 649–651.

[73] Luu, D.T., Qin, X., Morse, D., Cappadocia, M., 2001. Rejection of S-heteroallelic pollen by a dual-specific S-RNase in *Solanum chaconse* predicts a multimeric SI pollen component. Genetics 159, 329–335.

[74] Maddison, D.R., Maddison, W.P., 2001. MacClade Version 4.02: Analysis of Phylogeny and Character Evolution. Sinauer Associates, Sunderland, MA. Mahtani, M.M., Willard, H.F., 1998. Physical and genetic mapping of the human X chromosome centromere: repression of recombination. Genome Res. 8, 100–110.

[75] Martin, F.W., 1967. The genetic control of unilateral incompatibility between two tomato species. Genetics 56, 391–398.

[76] Martin, F.W., 1968. The behavior of *Lycopersicon* incompatibility alleles in an alien genetic milieu. Genetics 60, 101–109.

[77] Mascarenhas, J.P., 1993. Molecular mechanisms of pollen tube growth and differentiation. Plant Cell 5, 1303–1314.

[78] Matsumoto, D., Yamane, H., Tao, R., 2008. Characterization of SLFL1, a pollen expressed F-box gene located in the *Prunus* S locus. Sex. Plant Reprod. 21, 113–121.

[79] Matton, D.P., Maes, O., Laublin, G., Xike, Q., Bertrand, C., Morse, D., Cappadocia, M., 1997. Hypervariable domains of self-incompatibility RNases mediate allele-specific pollen recognition. Plant Cell 9, 1757–1766.

[80] McClure, B.A., Cruz-Garcia, F., Beecher, B.S., Sulaman, W., 2000. Factors affecting inter- and intra-specific pollen rejection in in *Nicotiana*. Annals of Botany 85: 113-123.

[81] McClure, B.A., Gray, J.E., Anderson, M.A., Clarke, A.E., 1990. Self-incompatibility in *Nicotiana alata* involves degradation of pollen rRNA. Nature 347, 757–760.

[82] McClure, B.A., Haring, V., Ebert, P.R., Anderson, M.A., Simpson, R.J., Sakiyama, F., Clarke, A.E., 1989. Style self-incompatibility gene products of *Nicotiana alata* are ribonucleases. Nature 342, 955–957.

[83] McClure, B.A., Haring, V., Ebert, P.R., Anderson, M.A., Simpson, R.J., Sakiyama, F., Clarke, A.E., 1989a. Self-incompatibility in *Nicotiana alata* involves degradation of pollen rRNA. Nature 347, 757–760.

[84] McClure, B.A., Mou, B., Canevascini, S., Bernatzky, R., 1999. A small asparagine-rich protein required for S-allele-specific pollen rejection in *Nicotiana*. Proc. Natl. Acad. Sci. USA 96, 13548–13553.

[85] McCubbin, A.G., Kao, T.-H., 2000. Molecular recognition and response in pollen and pistil interactions. Annu. Rev. Cell Dev. Biol. 16, 333–364.

[86] McCubbin, A.G., Zuniga, C., Kao, T.-h., 2000b. Construction of a binary bacterial artificial chromosome library of *Petunia inflata* and the isolation of large genomic fragments linked to the selfincompatibility (S) locus. Genome 43, 820–826.

[87] Murfett, J., Atherton, T.L., Mou, B., Gasser, C.S., McClure, B.A., 1994. S-RNase expressed in transgenic *Nicotiana* causes S-allele-specific pollen rejection. Nature 367, 563–566.

[88] Murfett, J.M., Strabala, T.J., Zurek, D.M., Mou, B., Beecher, B., McClure, B.A., 1996. S-RNase and interspecific pollen rejection in the genus *Nicotiana*: multiple pollen rejection pathways contribute to unilateral incompatibility between self-incompatible and selfcompatible species. Plant Cell 8, 943–958.

[89] Mutschler, M.A., Liedl, B.E., 1994. Interspecific crossing barriers in *Lycopersicon* and their relationship to self-incompatibility. In: New Phytol. 172, 577–587

[90] Newbigin, E., 1996. The evolution of self-incompatibility: a molecular voyeur_s perspective. Sex. Plant Reprod. 9, 357–361.

[91] Newbigin, E., Paape, T., Kohn, J.R., 2008. RNase-based self-incompatibility: puzzled by pollen S. Plant Cell 20, 2286–2292.

[92] Nunes, M.D.S., Santos, R.A.M., Ferreira, S.M., Vieira, J., Vieira, C.P., 2006. Variability patterns and positively selected sites at the gametophytic self-incompatibility pollen SFB gene in a wild self-incompatible Prunus spinosa (Rosaceae) population.

[93] O'Brien M, Kapfer C, Major G, Laurin M, Bertrand C, Kondo K, Kowyama Y, Matton DP (2002) Molecular analysis of the stylar-expressed Solanum chacoense small asparagine-rich protein family related to the HT modifier of gametophytic self-incompatibility in *Nicotina*. Plant J 32:985–996

[94] O'Brien M, Major G, Chantha S-C, Matton DP (2004) Isolation of S-RNase binding proteins from Solanum chacoense:identification of an SBP1 (RING finger protein) ortholog. Sex Plant Reprod 17:81–87.

[95] Ortega, E., Bosˇkovic´, R.I., Sargent, D.J., Tobutt, K.R., 2006. Analysis of S-RNase alleles of almond (*Prunus dulcis*): characterization of new sequences, resolution of synonyms and evidence of intragenic recombination. Mol. Genet. Genomics 276, 413–426.

[96] Pandey, K.K., 1973. Phases in the S-gene expression, and S-allele interaction in the control of interspecific incompatibility. Heredity 31, 381–400.

[97] Pandey, K.K., 1981. Evolution of unilateral incompatibility in flowering plants: further evidence in favour of twin specificities controlling intra- and interspecific incompatibility. New Phytol. 89, 705–728.

[98] Petroski MD, Deshaies RJ (2005) Function and regulation of cullin-RING ubiquitin ligases. Nat Rev Mol Cell Biol 6:9–20.

[99] Qiao, H., Wang, H., Zhao, L., Zhou, J., Huang, J., Zhang, Y., Xue, Y., 2004. The F-box protein AhSLF-S2 physically interacts with S-RNases that may be inhibited by the

ubiquitin/26S proteasome pathway of protein degradation during compatible pollination in *Antirrhinum*. Plant Cell 16, 582–595.

[100] Richman, A.D., Broothaerts, W., Kohn, J.R., 1997. Self-incompatibility RNases from three plant families: homology or convergence? Am. J. Bot. 84, 912–917.

[101] Roalson E.H., McCubbin A. (2003) S-RNases and sexual incompatibility: structure, functions, and evolutionary perspectives. Molecular Phylogenetics and Evolution 29, 490–506.

[102] Royo, J., Kunz, C., Kowyama, Y., Anderson, M., Clarke, A.E., Newbigin, E., 1994. Loss of a histidine residue at the active site of S-locus ribonuclease is associated with self-compatibility in *Lycopersicon peruvianum*. Proc. Natl. Acad. Sci. USA 91, 6511–6514.

[103] Sassa, H., Hirano, H., Nishio, T., Koba, T., 1997. Style-specific self-compatible mutation caused by deletion of the S-RNase gene in Japanese pear (*Pyrus serotina*). Plant J. 12, 223–227.

[104] Sassa, H., Kakui, H., Miyamoto, M., Suzuki, Y., Hanada, T., Ushijima, K., Kusaba, M., Hirano, H., Koba, T., 2007. S locus F-box brothers: multiple and pollen-specific Fbox genes with S haplotype-specific polymorphisms in apple and Japanese pear. Genetics 175, 1869–1881.

[105] Sassa, H., Nishio, T., Kowyama, Y., Hirano, H., Koba, T., Ikehashi, H., 1996. Self-incompatibility (S) alleles of the Rosaceae encode members of a distinct class of the T2/S ribonuclease superfamily. Mol. Gen. Genet. 250, 547–557.

[106] Schemske DW (1978) Evolution of reproductive characteristics in Impatiens (Balsaminaceae): The significance of cleistogamy and chasmogamy. Ecology 59:596–613

[107] Schoen DJ, Morgan MT, Bataillon T (1996) How does self-pollination evolve? Inferences from floral ecology and molecular genetic variation. Phil Trans R Soc Lond B 351:1281–1290.

[108] Sijacic, P., Wang, X., Skirpan, A.L., Wang, Y., Dowd, P.E., McCubbin, A.G., Huang, S., Kao, T.-H., 2004. Identification of the pollen determinant of S-RNase-mediated self-incompatibility. Nature 429, 302–305.

[109] Sims T.L. (2012). Protein Interactions in S-RNase-Based Gametophytic Self-Incompatibility, Protein Interactions, Dr. Jianfeng Cai (Ed.), ISBN: 978-953-51-0244-1, InTech.

[110] Sims TL (2005) Pollen recognition and rejection in different self-incompatibility systems. Recent Research Developments in Plant Molecular Biology 2, 31-62.

[111] Sims, T.L., Ordanic, M., 2001. Identification of a S-ribonucleasebinding protein in Petunia hybrida. Plant Mol. Biol. 47, 771–783.

[112] Singh, A., Ai, Y., Kao, T.-h., 1991. Characterization of ribonuclease activity of three S-allele-associated proteins of *Petunia inflata*. Plant Physiol. 96, 61–68.

[113] Snowman, B.N., Geitman, A., Clarke, S.R., Staiger, C.J., Franklin, F.C.H., Emons, A.M.C., Franklin-Tong, V.E., 2000. Signaling and the cytoskeleton of pollen tubes of Papaver rhoeas. Ann. Bot. 85, 49–57.

[114] Stebbins GL (1957) Self-fertilization and population viability in the higher plants. Am Nat 91:337– 354.

[115] Steinbachs, J.E., Holsinger, K.E., 2002. S-RNase-mediated gametophytic self-incompatibility is ancestral in eudicots. Mol. Biol. Evol. 19, 825–829.

[116] Takayama, S., Isogai, A., 2005. Self-incompatibility in plants. Annu. Rev. Plant Biol. 56, 467–489.

[117] Tao R., Iezonni A. (2010) The S-RNase-based gametophytic self-incompatibility system in *Prunus* exhibits distinct genetic and molecular features. Scientia Horticulturae 124, 423–433

[118] Tao, R., Yamane, H., Sassa, H., Mori, H., Gradziel, T.M., Dandekar, A.M., Sugiura, A., 1997. Identification of stylar RNases associated with gametophytic self-incompatibility in almond (*Prunus dulcis*). Plant Cell Physiol. 38, 304–311.

[119] Tao, R., Yamane, H., Sugiura, A., Murayama, H., Sassa, H., Mori, H., 1999. Molecular typing of S-alleles through identification, characterization and cDNA cloning for S-RNases in sweet cherry. J. Am. Soc. Hortic. Sci. 124, 224–233.

[120] Taylor, C.B., Bariola, P.A., del Cardayre, S.B., Raines, R.T., Green, P.J., 1993. RNS2: a senescence-associated RNase of *Arabidopsis* that diverged from the S-RNases before speciation. Proc. Natl. Acad. Sci. USA 90, 5118–5122.

[121] Thompson, R.D., Kirch, H.H., 1992. The S locus of flowering plants: when self-rejection is self-interest. Trends Genet. 8, 381–387.

[122] Tsai, D.-S., Lee, H.-S., Post, L.C., Kreiling, K.M., Kao, T.-h., 1992. Sequence of an S-protein of *Lycopersicon peruvianum* and comparison with other solanaceous S-proteins. Sex. Plant Reprod. 5, 256–263.

[123] Tsukamoto, T., Ando, T., Kokubun, H., Watanabe, H., Masada, M., Zhu, X., Marchesi, E., Kao, T.-h., 1999. Breakdown of selfincompatibility in a natural population of *Petunia axillaris* (Solanaceae) in Uruguay containing both self-incompatible and self-compatible plants. Sex. Plant Reprod. 12, 6–13.

[124] Ushijima, K., Sassa, H., Dandekar, A.M., Gradziel, T.M., Tao, R., Hirano, H., 2003. Structural and transcriptional analysis of the self-incompatibility locus of almond: identification of a pollen-expressed F-box gene with haplotype-specific polymorphism. Plant Cell 15, 771–781.

[125] Ushijima, K., Sassa, H., Tamura, M., Kusaba, M., Tao, R., Gradziel, T.M., Dandekar, A.M., Hirano, H., 2001. Characterization of the S-locus region of almond (*Prunus dul-*

cis: analysis of a somaclona mutant and a cosmid contig for an S haplotype. Genetics 158, 379– 386.

[126] Ushijima, K., Sassa, H., Tao, R., Yamane, H., Dandekar, A.M., Gradziel, T.M., Hirano, H., 1998. Cloning and characterization of cDNAs encoding S-RNases from almond (*Prunus dulcis*): primary structural features and sequence diversity of the S-RNases in Rosaceae. Mol. Gen. Genet. 260, 261–268.

[127] Vaughan, S.P., Russell, K., Sargent, D.J., Tobutt, K.R., 2006. Isolation of S-locus F-box alleles in Prunus avium and their application in a novel method to determine self-incompatibility genotype. Theor. Appl. Genet. 112, 856–866.

[128] Verica, J.A., McCubbin, A.G., Kao, T.-h., 1998. Are the hypervariable regions of S RNases sufficient for allele-specific recognition of pollen? Plant Cell 10, 314–316.

[129] Vieira, C.P., Charlesworth, D., 2002. Molecular variation at the selfincompatibility locus in natural populations of the genera *Antirrhinum* and *Misopates*. Heredity 88, 172–181.

[130] Vieira, J., Fonseca, N.A., Vieira, C.P., 2008. An S-RNase-based gametophytic self-incompatibility system evolved only once in eudicots. J. Mol. Evol. 67, 179–190.

[131] Vieira, J., Morales-Hojas, R., Santos, R.A.M., Vieira, C.P., 2007. Different positively selected sites at the gametophytic self-incompatibility pistil S-RNase gene in the Solanaceae and Rosaceae (*Prunus, Pyrus*, and *Malus*). J. Mol. Evol. 65, 175–185.

[132] Waller DM (1979) The relative costs of self- and cross-fertilized seeds in *Impatiens capensis* (Balsaminaceae). Am J Bot 66:313–320.

[133] Wang, X., Hughes, A.L., Tsukamoto, T., Ando, T., Kao, T.-h., 2001. Evidence that intragenic recombination contributes to allelic diversity of the S-RNase gene at the self-incompatibility (S) locus in *Petunia inflata*. Plant Physiol. 125, 1012–1022.

[134] Westwood, M.N., 1993. Temperate-Zone Pomology. Physiology and Culture. Timber Press, Portland.

[135] Wheeler, D., Newbigin, E., 2007. Expression of 10 S-class SLF-like genes in Nicotiana alata pollen and its implications for understanding the pollen factor of the S locus. Genetics 177, 2171–2180.

[136] Wu, H.-m., Wang, H., Cheung, A.Y., 1995. A pollen tube growth stimulatory glycoprotein is deglycosylated by pollen tubes and displays a glycosylation gradient in the flower. Cell 83, 395–403.

[137] Wu, H.-m., Wong, E., Ogdahl, J., Chueung, A.Y., 2000. A pollen tube growth promoting arabinogalactan protein from *Nicotiana alata* is similar to the tobacco TTS protein. Plant J. 22, 165–176.

[138] Xue, Y., Carpenter, R., Dickinson, H.G., Coen, E.S., 1996. Origin of allelic diversity in *Antirrhinum* S locus RNases. Plant Cell 8, 805– 814.

[139] Yamane, H., Ikeda, K., Hauck, N.R., Iezzoni, A.F., Tao, R., 2003a. Self-incompatibility (S) locus region of the mutated S6-haplotype of sour cherry (*Prunus cerasus*) contains a functional pollen S allele and a non-functional pistil S allele. J. Exp. Bot. 54, 2431–2437.

[140] Yamane, H., Tao, R., 2009.Molecular basis of self-(in)compatibility and current status of S-genotyping in Rosaceous fruit trees. J. Jpn. Soc. Hortic. Sci. 78, 137–157.

[141] Yang, Q., Zhang, D., Li, Q., Cheng, Z., Xue, Y., 2007. Heterochromatic and genetic features are consistent with recombination suppression of the self-incompatibility locus in *Antirrhinum*. Plant J. 51, 140–151.

[142] Zhang, Y., Zhao, Z., Xue, Y., 2009. Roles of proteolysis in plant self-incompatibility. Annu. Rev. Plant Biol. 60, 21–42.

[143] Zhou J, Wang F, Ma W, Zhang Y, Han B, Xue Y (2003) Structural and transcriptional analysis of S-locus F-box (SLF) genes in *Antirrhinum*. Sex Plant Reprod 16:165–177.

[144] Zisovich, A.H., Stern, R.A., Sapir, G., Shafir, S., Goldway, M., 2004. The RHV region of S-RNase in the European pear (*Pyrus communis*) is not required for the determination of specific pollen rejection. Sex. Plant Reprod. 17, 151–156.