Self-Incompatibility in the Brassicaceae: Receptor–Ligand Signaling and Cell-to-Cell Communication

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INTRODUCTION

Cell–cell interactions in plants are expected to occur between adjoining cells that share a common developmental history. One exception is the interaction of the pollen or pollen tube with cells of the pistil. As a result, pollen–pistil interactions have emerged as models for the study of cell-to-cell signaling, particularly in the context of genetic self-incompatibility (SI). SI is an intraspecific mating barrier found in a large number of species distributed among many plant families that allows cells of the pistil to recognize and reject self-related pollen (De Nettancourt, 2001). Many SI systems are controlled genetically by a single highly polymorphic locus, the S locus, and pollen inhibition occurs when pollen and pistil are derived from plants that express the same S locus variant(s).

Molecular studies performed during the last two decades have demonstrated that the term “self-incompatibility” does not represent one mechanism of self-recognition and that the S loci of different families are not homologous. Rather, the term encompasses a collection of disparate systems that have distinct evolutionary histories and are based on mechanistically different strategies for the inhibition of self-related pollen. One strategy used by members of the Solanaceae (McClure et al., 1989), Rosaceae (Sassa et al., 1993), Scrophulariaceae (Xue et al., 1996), and Campanulaceae (Stephenson et al., 2000) is directed at inhibiting pollen tubes after they have grown into the style and is based on the cytotoxic activity of stylar-secreted S-RNases, which act inside the pollen tube to inhibit its growth.

Other strategies, such as those used by the Brassicaceae and Papavaceae, are directed at preventing pollen germination or pollen tube ingress into the pistil; in this strategy, self pollen is inhibited at the stigma surface within minutes of pollen–stigma contact. It is in these two families that SI relies on the perception and transduction of specific signals, albeit using distinct molecular determinants and fundamentally different mechanisms, for the inhibition of self pollen. In the Brassicaceae, a signal is carried by the pollen grain, which is perceived and transduced into a cellular response within the stigma epidermis. In Papaver, the signal is produced by stigmatic cells and perceived by pollen, resulting in a transduction cascade within the pollen tube (Rudd and Franklin-Tong, 2001). Here, we review our understanding of cell-to-cell signaling in the SI system of the Brassicaceae, which is currently the only system for which the stigma and pollen recognition components are known.

SIGNAL PERCEPTION AT THE POLLEN–STIGMA INTERFACE IN THE BRASSICACEAE

The recognition of self-related pollen in the Brassicaceae occurs during the interaction of a pollen grain with an epidermal (papillar) cell of the stigma surface (Figure 1). An incompatible response interrupts the very early events of this interaction, namely, hydration and metabolic activation of the pollen grain, and subsequent elaboration of a pollen tube and its ingress into the papillar cell wall (Heslop-Harrison, 1975). The surface inhibition of self pollen and the rapidity of the response had suggested early on that this SI system likely would be based on the activity of specific cell surface molecules. Indeed, molecular studies performed at several laboratories during the last two decades in Brassica species, as well as more recent studies in Arabidopsis lyrata, have demonstrated that two S locus–encoded and highly polymorphic proteins function as receptor–ligand pairs that determine specificity in the stigma epidermis and pollen.

Identification of these receptor–ligand pairs was accomplished in Brassica as a result of molecular cloning, first of S locus–encoded genes whose products are expressed specifically in the stigma epidermis, and then of the SI specificity–determining region of the S locus. This endeavor was both aided and hampered by the highly polymorphic nature of S locus variants or haplotypes, of which >50 are known in Brassica oleracea (Ockendon, 1974). On the one hand, the sequence polymorphism expected for recognition genes was an invaluable criterion for identifying candidate SI specificity genes. On the other hand, the structural heteromorphism of S haplotypes, manifested by scrambled gene order...
and variable intergenic distances (Boyes et al., 1997; Suzuki et al., 1999; Cui et al., 2000; Nasrallah, 2000), did not allow straightforward transfer of physical and genetic mapping data between populations segregating for different pairs of S haplotypes. Figure 2A shows the organization of a Brassica S haplotype and the S locus gene products that function in SI.

### Stigma Receptors and Pollen Ligands for SI Specificity

The determinant of SI specificity in the stigma epidermis is the S locus receptor protein kinase (SRK) gene. The SRK nucleotide sequence predicts a protein with an extracellular domain, a single-pass transmembrane domain, and a cytoplasmic kinase domain (Figure 2A) (Stein et al., 1991) that exhibits Ser/Thr kinase activity (Goring and Rothstein, 1992; Stein and Nasrallah, 1993). SRK is the prototype of a ubiquitous class of plant receptor-like protein kinases (Shiu and Bleecker, 2001). These proteins share similar predicted extracellular domains, referred to as S domains, because they exhibit sequence similarity to the S locus glycoprotein (SLG), the first S locus–encoded gene isolated (Figure 2A) by Nasrallah et al. (1985). As expected for a receptor protein, SRK is an integral component of the plasma membrane (Stein et al., 1996; Dixit et al., 2000; Giranton et al., 2000), where it is displayed with its S domain on the outside of the cell and its kinase domain within the cytoplasm (Letham et al., 1999). At least one SRK allele (and possibly others) also produces soluble truncated forms of the SRK ectodomain, designated eSRKs (Giranton et al., 1995) (Figure 2A), apparently encoded by short transcripts that terminate within the first intron of the gene (Stein et al., 1991).

The SRK protein is expressed specifically in the stigma epidermis, SRK transcripts accumulate concomitantly with the attainment of SI by mature stigmas (Stein et al., 1991, 1996), and SRK alleles can exhibit as much as 35% overall amino acid sequence divergence (Stein et al., 1991; Nishio and Kusaba, 2000; Kusaba et al., 2001a). Moreover, transformation with an SRK transgene resulted in the acquisition by transgenic stigmas of the corresponding SI specificity and the ability to reject pollen expressing the same S haplotype as that of the transgene (Takasaki et al., 2000). Significantly, the pollen of these transgenic plants did not acquire new SI specificity. This result confirmed previous data that suggested the existence of distinct S locus genes for pollen and stigma specificity. Self-compatible mutants of Brassica were known that exhibited defects in stigma SI function alone (Nasrallah, 1974; Hinata and Okazaki, 1986; Nasrallah et al., 1992, 1994) or in pollen SI function alone (Nasrallah et al., 2000). Moreover, both homology-dependent silencing of SRK (Conner et al., 1997) and expression of a dominant-negative form of SRK in transgenic plants (Stahl et al., 1998) had led to the stigma-specific breakdown of SI.

The molecular cloning of SRK was facilitated by the previous isolation of SLG (Nasrallah et al., 1985), another highly polymorphic S locus gene that shares a high degree of sequence identity with the SRK ectodomain (Figure 2A) and is expressed at much higher levels than SRK. The SLG glycoprotein is an abundant component of the papillar cell wall (Kandasamy et al., 1989), which does not determine specificity in the SI response but appears to have an accessory role in SI. SLG<sub>28</sub> enhanced the SI phenotype determined by the SRK<sub>28</sub> transgene (Takasaki et al., 2000), and SLG was shown to facilitate the proper maturation of SRK and its accumulation to physiologically relevant levels in the stigma epidermis (Dixit et al., 2000). However, SLG is not absolutely required for a robust SI response. SLG<sub>90</sub> did not enhance the strength of the SI response in transgenic plants expressing the SRK<sub>90</sub> transgene (Silva et al., 2001). Furthermore, at least two Brassica S haplotypes (Suzuki et al., 2000) and the two A. lyrata S haplotypes analyzed to date (Kusaba et al., 2001a) do not contain an SLG gene. In these cases, the SRK isoforms might be inherently stable or might be stabilized by the corresponding eSRK molecules (Figure 2A).

SRK’s partner in recognition is the S locus Cys-rich protein SCR (Schopfer et al., 1999; Schopfer and Nasrallah, 2000), also designated SP-11 (Suzuki et al., 1999; Takayama et al., 2000; Shiba et al., 2001). The SCR gene is maintained in tight genetic linkage with SRK, probably as a result of the structural heteromorphism of S haplotypes and a reduced frequency of recombination at the S locus (Casselman et al., 2000). The SCR gene exhibits extensive S haplotype-associated polymorphism, is expressed exclusively in anthers, and encodes a small basic peptide of 50 to 59 amino acids.

The SCR gene is necessary and sufficient for SI in pollen. SCR transcripts are undetectable in a self-compatible mutant of Brassica that exhibits a pollen-specific breakdown of SI (Schopfer et al., 1999). Transformation of Brassica plants homozygous for one S haplotype with an SCR allele derived from another haplotype results in the acquisition by transgenic pollen of the SI specificity encoded by the transgene.
Self-Incompatibility in the Brassicaceae (Schopfer et al., 1999; Shiba et al., 2001). Furthermore, pre-treatment of stigma papillar cells with recombinant bacterially expressed “self” SCR inhibits the hydration of cross-pollen in pollination bioassays (Takayama et al., 2000, 2001; Kachroo et al., 2001).

The SCR protein has been shown to be localized to the pollen coat by immunocytochemistry (Shiba et al., 2001) and by biochemical fractionation (Kachroo et al., 2001). Such a localization had been predicted previously based on the SCR expression pattern (Schopfer et al., 1999; Schoepfer and Nasrallah, 2000; Takayama et al., 2000) and on a pollination bioassay that determined the pollen SI factor to be a component of the pollen coat (Stephenson et al., 1997). The site of SCR synthesis has not been resolved conclusively, however. Pollen coat proteins may be synthesized in the tapetum (i.e., sporophytically) or in microspores (i.e., gametophytically). All Brassica SCR alleles reported to date exhibit sporophytic and gametophytic expression, as evident from the accumulation of SCR transcripts in the anther tapetum and in microspores, respectively (Schopfer et al., 1999; Schoepfer and Nasrallah, 2000; Takayama et al., 2000; Shiba et al., 2001). In A. lyrata, the SCRb allele is expressed in tapetum and microspores, but the SCRa allele is expressed only in the tapetum of Ss homozygotes (Kusaba et al., 2001b). Therefore, sporophytic expression of SCR in the tapetum is sufficient for SI, and expression of two SCR alleles in the tapetum is an adequate explanation for the sporophytic control of pollen SI specificity in crucifers. The additional gametophytic expression exhibited by another A. lyrata allele, SCRb, and all reported Brassica SCR alleles might be redundant or serve to increase SCR levels in individual pollen grains.

Like SRK, SCR is a member of a large gene family that includes some 28 members in Arabidopsis thaliana (Vanoosthuyse et al., 2001). A distantly related family is the PCP-A1 gene family, which includes genes encoding pollen

![Figure 2. The S-Locus Genes of Crucifers, Receptor–Ligand Interactions, and Signal Transduction in the SI Response.](image)

(A) Arrangement of SI genes in the Brassica S8 haplotype and structures of their protein products. Arrows above the genes indicate the 5′→3′ orientations of the genes. The extracellular S domains are shown in red, and the kinase domain of SRK is shown in yellow. White bars in the S domains represent 12 conserved Cys residues, and circles indicate glycosylation sites. Black and gray boxes represent the signal sequences in SRK/SLG and SCR, respectively. The blue box represents the SRK transmembrane domain.

(B) A model of signal perception and response in the SI response. Molecules that have been shown conclusively to function in SI are shown as closed shapes. SRK is shown spanning the plasma membrane (orange bar) of the stigmatic epidermal cell, with its kinase (red circle) in the cytoplasm and its ectodomain (red crescent) extending into the cell wall (stippled area). SLG and eSRK are shown as crescents in the papillar cell wall. SCR molecules are shown as dimeric molecules in the papillar cell wall, to which they are transferred from the pollen coat of pollen. “Self” SCR (green circles) interacts with the SRK ectodomain and triggers a signaling cascade, whereas “nonself” SCR (purple triangles) does not. ARC1 is shown by a gray box, with red bars indicating arm repeats and a yellow bar indicating the U box. Phosphorylation is indicated by “P” enclosed by a circle. Less-well-defined associations are indicated by a question mark.

(C) Mutations that lead to loss of the SI response in stigmas. The diagram shows mutations in SRK, ARC1, and SLG and their consequences.

eSRK, soluble form of the SRK ectodomain; SCR, S-locus Cys-rich protein; SLG, S-locus glycoprotein; SRK, S-locus receptor protein kinase.
Receptor–Ligand Interactions

The sequences and localization of SRK and SCR, as well as the transgenic experiments summarized above, support the conclusion that they act as a receptor–ligand pair in the SI response. The current model of SI is that SCR is a diffusible signal carried in the pollen coat that functions as a ligand for the plasma membrane–localized SRK. Upon self-pollination, the SCR protein would be delivered to the stigmatic surface via the adhesion zone formed by the pollen coat. The papillogram of the SCR would be delivered to the stigmatic surface. It should be noted, however, that attempts to resolve the evolutionary relationships betweenSCR and the SCR gene. Indeed, only seven Cys residues and one Gly residue are conserved among the 22 SCR sequences identified to date in Brassica and A. lyrata (Schopfer and Nasrallah, 2000; Watanabe et al., 2001). In addition, SCR sequences cannot be aligned unambiguously because of the variable numbers of residues between the Cys residues.

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levels exceed those of SRK by 2 orders of magnitude (Stein et al., 1991), and even low affinities for SCR might be significant. Interestingly, and despite this large excess of SLG over SRK, these two proteins apparently occurred in an equal local molar concentration at the papillar cell surface, when differences in the volumes of the cell wall and plasma membrane were considered (Stein et al., 1996). Both SLG and eSRK may play regulatory roles, possibly by facilitating the interaction of SCR with SRK, as has been shown for “soluble” receptors in animal models (Flickinger et al., 1992).

**MECHANISM OF RECEPTOR ACTIVATION**

The SRK protein is one of only four plant single-pass receptor-like kinases whose ligands have been identified. The three other receptor–ligand systems belong to the Leu-rich repeat class of receptor-like kinases. These include the brassinolide-insensitive 1 (BR11) protein and its ligand brassinolide (Wang et al., 2001); the CLAVATA1 (CLV1) protein, which, together with its ligand, the CLAVATA3 (CLV3) peptide (Trotchaud et al., 2000), is required for the regulation of meristem development in *A. thaliana* (Clark et al., 1996); and the flagellin receptor FLS2, which binds the bacterial elicitor flagellin (Gómez-Gómez and Boller, 2000). Biochemical studies of these receptor–ligand systems have been initiated only recently, and mechanisms of plant receptor activation are still poorly understood.

**Lessons from Other Receptor–Ligand Systems**

Two major issues in receptor activation relate to the mechanisms of ligand binding and receptor activation. In mammalian systems, ligand binding is known to induce the dimerization of most receptors, resulting in transphosphorylation of the kinase domains (Heldin, 1995). Phosphorylated residues then act as binding sites for specific substrates. Different ligands use different strategies to induce dimerization of the receptor. For example, cytokines, such as growth hormone and erythropoietin, are bivalent, and one ligand binds two receptor molecules (Kossiakoff and De Vos, 1998; Jiang and Hunter, 1999). Several other growth factors, such as vascular endothelial growth factor (Wiesmann et al., 1997) and platelet-derived growth factor (Heldin et al., 1989), are homodimers themselves and induce dimerization of their receptors.

Mechanisms of receptor activation in plants are likely to be as varied as those in mammalian systems. Comparisons between the SRK–SCR and CLV1–CLV3 receptor–ligand pairs reveal similarities but also some differences. Just as the accumulation and maturation of some SRK isoforms require SLG, the proper accumulation of the CLV1 receptor complex requires CLV2, a receptor-like protein that, like CLV1, contains a Leu-rich repeat extracellular domain and a transmembrane domain but, unlike CLV1, lacks a kinase domain (Jeong et al., 1999). Furthermore, both SCR and CLV3 occur in higher order complexes in planta. The functional CLV3 ligand forms a multimeric complex in vivo (Trotchaud et al., 1999). SCR was detected as an ~16-kD dimer in pollen coat preparations (Kachroo et al., 2001), although it is not known if these dimers represent the native state of SCR and if this state is necessary for binding to SRK. An important difference, however, is that CLV3 binds only the active CLV1 complex, whereas SCR binds the purified extracellular domain of SRK lacking a functional kinase domain (Kachroo et al., 2001). In this respect, the SRK–SCR interaction is more similar to the binding of Brassinolide to its BRI1 receptor, which does not require a functional kinase domain (He et al., 2000), whereas both CLV1 and FLS2 do (Trotchaud et al., 2000; Gómez-Gómez et al., 2001).

**Ligand-Induced Phosphorylation of SRK**

Does SCR binding to the SRK ectodomain translate into oligomerization of the receptor, and does this binding result in transphosphorylation of the SRK kinase? The addition of a synthetic form of the ligand to stigma membrane fractions resulted in the autophosphorylation of SRK (Takayama et al., 2000). Furthermore, SRK was shown to autophosphorylate within 60 min after self-pollination (Cabrillac et al., 2001), apparently by transphosphorylation of the kinase chains (Giranton et al., 2000). However, the data are ambiguous regarding how SRK is activated upon ligand binding and how it is maintained in an inactive state in the absence of ligand. The activation of SRK has been suggested to involve oligomerization, because recombinant SRK was phosphorylated in a dose-dependent and saturable manner by antibodies to the N terminus of the SRK protein (Cabrillac et al., 2001). It also has been suggested, however, that SRK signaling may be initiated by the binding of SCR to preformed SRK oligomers and interaction with a coreceptor, because SRK oligomers were detected in unpollinated stigmas (i.e., in the absence of SCR) (Giranton et al., 2000).

In one study, recombinant SRK was found to be phosphorylated constitutively in vitro (Giranton et al., 2000). This phosphorylation was inhibited by soluble proteins from stigma extracts or by purified thioredoxin, a protein that interacts with the SRK kinase domain (Bower et al., 1996; Mazzurco et al., 2001) and is known to regulate the activity of several kinases in mammalian systems (Liu et al., 2000). The inhibition of SRK phosphorylation by thioredoxin was relieved by the addition of pollen coat proteins from *S. pleno*. These results suggest that thioredoxin may bind the SRK kinase domain to prevent the constitutive activation of the SI pathway (Cabrillac et al., 2001), thus allowing cross-pollination to proceed. The relationship of thioredoxins to SRK activation must await further studies, however, in view of other results that did not reveal any involvement of inhibitory factors (Takayama et al., 2001).
Regulation of SRK Activation

Receptor activation is usually regulated by the stoichiometry of the interacting partners and by the availability of ligand to the receptor. For example, CLV1 activation is restricted to cells within the domain of CLV3 diffusion (Clark, 2001). In the case of SI, SRK activation in the papillar cell is even more restricted and likely to be limited to a small subcellular region subtending the zone of contact with a self pollen grain. It has been shown that the successful germination of a compatible pollen grain is not disrupted by the presence of an incompatible pollen grain on the same papillar cell (Dickinson, 1995). Therefore, the pollen inhibitory reaction stemming from SRK activation is thought to result not from global modifications of the surface of the stigma epidermal cell but from localized alterations restricted to the site of contact with an individual pollen grain.

Within the microscopic zone of pollen–papillar cell contact and SRK activation, the stoichiometry of receptor and ligand appears to be critical for determining the magnitude of the response. We found a positive quantitative correlation between the levels of SCR transcripts (and presumably SCR protein) and the strength of the SI response. In an analysis of Brassica mutant strains generated by γ-irradiation of B. oleracea plants carrying the S_{13} haplotype, we identified two mutant strains exhibiting pollen-specific defects in SI phenotype (Nasrallah et al., 2000). One strain, m1600, did not produce detectable levels of SCR_{13} transcripts (Figure 3) (Schofer et al., 1999), and its pollen was fully compatible with S_{13}S_{13} stigmas. Another strain, m2134, showed a fourfold reduction in SCR_{13} transcripts (Figure 3), and its pollen exhibited partial compatibility with S_{13}S_{13} stigmas.

One interpretation of these results is that the mounting of an effective barrier to self pollen requires the activation of several SRK molecules and the recruitment of their downstream targets at the site of pollen–stigma contact. The magnitude of the response then would depend on the concentration of SCR molecules delivered to this site by a pollen grain. In the m2134 strain, the number of SCR molecules released from the tapetum into the anther locule would be reduced and would be incorporated unevenly into the coat of individual pollen grains. As a result, in self-pollinations, those pollen grains that display adequate levels of SCR would be inhibited and those that carry no or little SCR protein would escape inhibition. Similarly, the inherently “weak” SI response, or pseudocompatibility, specified by some S haplotypes might be associated with a relatively poorly expressed SCR allele.

Dominance–Recessiveness Interactions: Molecular Interference between Allelic SRK–SCR Pairs or Differential Expression of SI Genes?

An intriguing feature of SI in the Brassicaceae is that genetic interactions between S haplotypes influence the expression of SI specificity in stigmas and pollen, a feature that has far-reaching implications for the mechanism of SI as well as for

<table>
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<th>Stigma parent</th>
<th>S_{13}^{+}S_{13}^{+}</th>
<th>m1600</th>
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<tr>
<td>S_{13}S_{13}</td>
<td>&lt;10</td>
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<td>SI</td>
<td>SC</td>
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Figure 3. Expression of SCR and Strength of the SI Response.

Gel blot analysis of anther poly(A)^+ RNA (2 μg/lane) isolated from a self-incompatible wild-type strain of B. oleracea expressing the S_{13} haplotype and from the m1600 and m2134 self-compatible mutants. The blot was probed with SCR_{13} cDNA and with actin as a loading control. The table below the blots shows data from pollinations of S_{13}S_{13} stigmas with pollen from wild-type S_{13}S_{13}, m1600, and m2134 plants. Wild-type expression of SCR determines a robust self-incompatible (SI) phenotype. The absence of SCR transcripts in m1600 anthers is correlated with full self-compatibility (SC) in pollen (>300 pollen tubes produced per stigma), and a fourfold reduction in SCR mRNA levels in m2134 anthers results in partial self-compatibility (PSC; 50 to 75 pollen tubes produced per stigma).
the evolution and maintenance of S haplotypes in a population. Allelic interactions of codominance, dominance, incomplete dominance, or mutual weakening have been reported, and these interactions can differ in stigma and pollen, consistent with the activity of distinct stigma and pollen determinants of SI specificity. These allelic interactions suggest that SRK and SCR allelic pairs or SRK-SCR complexes do not always function independently of other SRK-SCR allelic pairs. Until recently, however, data on the molecular basis for S haplotypic interactions were lacking.

Recently, Hatakeyama et al. (2001) showed that dominance relationships in the Brassica stigma are a characteristic of the SRK gene and that recessiveness or dominance was not correlated with differences in SRK transcript levels. Similarly, in a study of SI in A. lyrata, the weakening of S8 activity in heterozygous S8S8 stigmas was not related to differences in SRK expression levels (Kusaba et al., 2001b). Although these studies did not exclude the possibility that dominance/recessiveness is related to differences in SRK protein levels, it is possible that these genetic interactions reflect interference between receptor or ligand isoforms either in the SRK-SCR interaction or in the recruitment of downstream effectors of the SI response.

More insight has been gained regarding the interactions of S haplotypes in pollen. In A. lyrata, the S8 haplotype is recessive to the S8 haplotype in pollen, and pollen grains from S8S8 plants exhibit S8 specificity (Kusaba et al., 2001a). Intriguingly, SRKa transcripts, which are expressed exclusively in the tapetum, were reduced by as much as 80-fold in S8S8 heterozygotes relative to S8 homozygotes (Kusaba et al., 2001b). The underlying mechanism of this reduction is not understood. Nevertheless, the recessive-dominant interaction exhibited by the SCRa and SRKb alleles in pollen is explained by monoallelic expression of the dominant SCRa allele in S8S8 heterozygotes resulting from severe downregulation of the recessive SCRb allele in the tapetum and the lack of SCRb expression in microspores.

The A. lyrata SCRb allele is the only “pollen-recessive” allele reported to date, and it remains to be determined how general this mechanism of dominance/recessiveness will prove to be. Nevertheless, it is likely that the features of exclusive tapetal expression of the recessive SCR allele and monoallelic expression of the dominant SCR allele will combine to explain many cases of dominant/recessive S haplotypic interactions in the pollen of A. lyrata, Brassica, and other self-incompatible crucifers.

**SIGNAL TRANSDUCTION IN THE SI RESPONSE**

**Molecular Analysis of SRK-Mediated Signal Transduction**

How SRK–SCR binding and SRK activation are transduced into the inhibition of self-related pollen is not understood. To date, only the arm repeat-containing protein ARC1 (Gu et al., 1998) (Figure 2B) has been identified conclusively as a component of the SRK signal transduction pathway. Another putative candidate signaling component, the MOD locus–associated aquaporin (MOD-AQP), was identified by virtue of its tight genetic linkage to a modifier of SI and by the fact that it was not expressed in self-compatible plants homozygous for the recessive mod mutation (Ikedo et al., 1997). However, analysis of two additional mod alleles generated by γ-irradiation of self-incompatible plants and of natural MOD-AQP variants subsequently showed that the aquaporin gene was unlikely to represent the MOD locus (Fukai et al., 2001).

ARC1 was identified in a yeast two-hybrid screen as a protein that interacted with the cytoplasmic domain of SRK (Gu et al., 1998). This interaction, which is mediated by the arm repeats in the C terminus of ARC1, requires an active SRK kinase domain and results in the phosphorylation of ARC1 in vitro (Gu et al., 1998). ARC1 transcripts are detected specifically in the stigma, supporting a role for ARC1 in pollination. Significantly, transgenic plants in which ARC1 transcripts were downregulated by the expression of an antisense ARC1 transgene showed a partial breakdown of SI in the stigma and were not affected in pollen SI function (Stone et al., 1999) (Figure 2C). That the breakdown of SI was only partial might be attributable to residual ARC1 expression in transgenic stigmas or might indicate that ARC1 is not the only substrate for SRK. Nevertheless, these results establish a role for ARC1 in SI.

How ARC1 functions is not understood. Some clues may be offered by the recent finding that ARC1 contains a U box (Azevedo et al., 2001), a motif identified initially in the yeast E4 polyubiquitination factor UFD2 (Koegl et al., 1999). Ubiquitination has been shown to play several roles in the regulation of signal transduction pathways, including the modulation of receptor signaling and receptor internalization and degradation. Therefore, the presence of a U box in ARC1 suggests a role for protein ubiquitination in SI. Because ARC1 is a positive effector of SI, it is possible that ARC1 phosphorylation by activated SRK triggers its interaction with components of the ubiquitination machinery and leads to the degradation of an inhibitor of the SI response (Figure 2B). Other scenarios are possible, however, because ubiquitination has been shown to have functions unrelated to protein degradation, such as subcellular targeting of proteins and their recruitment to molecular complexes (Wilkinson, 1999).

Isolation of self-compatible mutants carrying mutations in loci unlinked to the S locus and expressing functional ARC1 protein (Nasrallah et al., 2000) indicates that other as yet unidentified components are involved in the SI signal transduction pathway. The likely complexity of this pathway is underscored by cytological observations of the SI response, which show that the arrest of self pollen can occur at any of several stages, including pollen hydration, germination, or pollen tube ingress into the papillar cell wall (Dickinson, 1995). These observations suggest that the SCR–SRK-triggered signaling pathway has more than one molecular
outcome in the papillar cell and may proceed through more than one intermediate.

**Clues from the Physiology and Cell Biology of SI**

Over the years, clues to the identity of signaling components activated by self-recognition and to the immediate cause of pollen inhibition have been sought through physiological and cell biological studies of pollen tube development in incompatible and compatible pollination. Several factors are known to break down SI in *Brassica*, including high humidity, high temperature, increased CO$_2$ levels, and treatment of the stigma with sodium chloride, cycloheximide, and tunicamycin. However, none of these factors has provided any significant clues regarding the mechanism of pollen inhibition.

Several studies have focused on the potential role of calcium in SI. Calcium is known to play a crucial role in pollen germination and pollen tube growth (Bednarska and Butowt, 1994; Pierson et al., 1994; Franklin-Tong et al., 1995). Calcium, which probably is released by a regulated Ca$^{2+}$-ATPase in the papillar cells, is actively taken up by pollen grains (Bednarska, 1993). It may be sensed and sequestered by calcium binding proteins, such as the novel calcium binding protein 1 (*BPC1*), which is expressed specifically during pollen maturation (Rozwadowski et al., 1999). BCP1 is of particular interest, because it is localized in the cytosol of mature pollen grains, it leaks into the pollen wall after pollen hydration, and it concentrates near the surface of the elongating pollen tube. Ratio imaging has demonstrated that the elongating pollen tube maintains cytosolic free calcium in a gradient of descending concentration from the tip and that this gradient is established before germination (Bednarska and Butowt, 1994; Pierson et al., 1994; Franklin-Tong et al., 1995).

Germination and elongation of the pollen tube are exquisitely sensitive to changes in this calcium gradient, and it has been suggested that an increase in calcium in the pollen grain may be one of the early events triggered by self-pollination. Indeed, in the SI response of the poppy (*Papaver rhoesas*), the arrest of pollen tube growth is associated with increased calcium levels and the generation of a calcium wave subapically within the shank of the pollen tube (Franklin-Tong et al., 1995, 1997). In *Brassica* SI, a role for calcium in pollen arrest was suggested by an early study in which a 65% increase in calcium was observed in pollen during an incompatible pollination (Singh et al., 1989). Whether this result can be repeated using modern ratio imaging methods is not known.

A role for calcium in the stigma SI response also has been suggested. Cytological responses in the stigma include the deposition of callose (β-1,3-glucan) at the site of pollen contact (Dickinson, 1995). This deposition is calcium dependent (Kauss, 1987) and is triggered by the application of pollen grains, pollen coat proteins, and latex beads to the stigma (Deemaley et al., 1997; Elleman and Dickinson, 1999). However, treatment of stigmas with an inhibitor of callose synthesis prevented callose deposition but did not affect the ability of these stigmas to reject self pollen (Singh and Paolillo, 1990). In addition, the degradation of callose in the papillae of transgenic *Brassica* expressing β-1,3-glucanase did not affect the SI response (Sulaman et al., 1997). Thus, it is unlikely that callose deposition acts as a physical barrier to pollen tube ingress. Rather, it may represent a secondary effect of increased calcium levels within the papillar cell.

In *B. napus*, Ca$^{2+}$ peaks appeared to be required for pollen hydration (Deemaley et al., 1997). However, no differences between compatible and incompatible pollinations were observed in the magnitude of Ca$^{2+}$ increase, although the frequency of Ca$^{2+}$ peaks was higher in papillar cells exposed to compatible pollen relative to those exposed to incompatible pollen. In addition, both compatible and incompatible pollinations were equally effective at inducing increases in average membrane conductance and membrane permeability (Deemaley et al., 1997).

**Analogies to Other Plant Signal Transduction Pathways**

There is often convergence between different signaling pathways, and this convergence often suggests likely signaling intermediates. The inhibition of pollen tube development in SI responses has been compared with the inhibition of fungal pathogens in host disease resistance (Hodgkin et al., 1988; Elleman and Dickinson, 1999). However, there is as yet no evidence for molecular overlap between the SRK-mediated signal pathway and signaling in host–pathogen interactions. Nor is there experimental support for the sharing of signaling intermediates with other plant receptor–ligand signaling systems, the CLV1–CLV3 system in particular. CLV1 associates with other proteins in a 450-kD functional complex that includes its ligand, CLV3 (Trotchaud et al., 2000), CLV2, kinase-associated protein phosphatase (KAPP), and a Rho GTPase-related protein that may be required for downstream signal transduction (Trotchaud et al., 1999). KAPP is a negative regulator of CLV1 (Williams et al., 1997; Stone et al., 1998) and FLS2 (Gómez-Gómez et al., 2001) signal transduction pathways, and the Rho-related protein is thought to function in the relay of signals downstream of receptor activation. SRK is not known to associate with a Rho-related protein, but at least one allele of SRK binds KAPP in vitro (Braun et al., 1997). However, the physiological significance of this binding has not been demonstrated.

**FUTURE DIRECTIONS**

The last 2 years have seen rapid progress in our understanding of cell-to-cell communication in the SI response...
...and of the specific receptor-ligand interactions responsible for the recognition of self pollen. The foundation has been laid for increasingly detailed studies of pollen-stigma signaling. Analysis of the SRK-SCR signaling system no doubt will be influenced by parallel studies of other plant receptor-ligand systems, such as CLV1–CLV3, BRI1–Brassinolide, and FLS2–flagellin. Another pressing issue is unraveling the evolutionary and functional relationships to members of the large gene families that are related to these prototypic receptors and ligands (Cock and McCormick, 2001; Shiue and Bleecker, 2001; Vanoosthuyse et al., 2001). Elucidating the biological functions of this multitude of genes will be daunting. Even associating a specific receptor with its cognate ligand will be difficult, but this task could be aided by a better understanding of how the polymorphic SRK–SCR pair of genes coevolved. Ultimately, the study of these receptor-ligand systems will identify plant-specific features of signal perception and response as well as commonalities with signaling in animal and yeast models.

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