A Gain-of-Function Mutation in a Plant Disease Resistance Gene Leads to Constitutive Activation of Downstream Signal Transduction Pathways in *suppressor of npr1-1, constitutive 1*

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Plants have evolved sophisticated defense mechanisms against pathogen infections, during which resistance (*R*) genes play central roles in recognizing pathogens and initiating defense cascades. Most of the cloned *R* genes share two common domains: the central domain, which encodes a nucleotide binding adaptor shared by APAF-1, certain R proteins, and CED-4 (NB-ARC), plus a C-terminal region that encodes Leu-rich repeats (LRR). In Arabidopsis, a dominant mutant, *suppressor of npr1-1, constitutive 1* (*snc1*), was identified previously that constitutively expresses pathogenesis-related (*PR*) genes and resistance against both *Pseudomonas syringae* pv *maculicola* ES4326 and *Peronospora parasitica* Noco2. The *snc1* mutation was mapped to the *RPP4* cluster. In *snc1*, one of the TIR-NB-LRR–type *R* genes contains a point mutation that results in a single amino acid change from Glu to Lys in the region between NB-ARC and LRR. Deletions of this *R* gene in *snc1* reverted the plants to wild-type morphology and completely abolished constitutive *PR* gene expression and disease resistance. The constitutive activation of the defense responses was not the result of the overexpression of the *R* gene, because its expression level was not altered in *snc1*. Our data suggest that the point mutation in *snc1* renders the *R* gene constitutively active without interaction with pathogens. To analyze signal transduction pathways downstream of *snc1*, epistasis analyses between *snc1* and *pad4-1* or *eds5-3* were performed. Although the resistance signaling in *snc1* was fully dependent on *PAD4*, it was only partially affected by blocking salicylic acid (SA) synthesis, suggesting that *snc1* activates both SA-dependent and SA-independent resistance pathways.

INTRODUCTION

Plants use different mechanisms to fight against microbial pathogen infections. One of the main mechanisms is disease resistance mediated by plant resistance (*R*) genes (Staskawicz et al., 1995). Recognition of pathogens carrying *Avr* genes by the cognate *R* genes often leads to a localized hypersensitive response (HR) and restriction of pathogen spread (Hammond-Kosack and Jones, 1996). A number of *R* genes have been cloned from different species, and most of them encode proteins that contain nucleotide binding site (NB) and Leu-rich repeat (LRR) domains (Bent, 1996; Hammond-Kosack and Jones, 1997; Ellis et al., 2000). Some R proteins also contain a conserved ARC domain located between the NB and the LRR (van der Biezen and Jones, 1998a).

Because of the specificity of the genetic interactions between *R* genes and their cognate *Avr* genes, NB-LRR proteins have long been suggested to be the receptors of pathogen-derived ligands encoded by the *Avr* genes, and binding of the ligands to the NB-LRR proteins was believed to activate the downstream signal transduction cascade (Staskawicz et al., 1995; Baker et al., 1997). Recently, it was proposed that the interaction of the

NB-LRR and Avr proteins is indirect and may require a third host protein as a mediator (van der Biezen and Jones, 1998b; Dangl and Jones, 2001; Bonas and Lahaye, 2002). Activation of NB-LRR proteins results from the modification of host proteins by pathogen effectors rather than from direct interactions between NB-LRR and Avr proteins. This model is strongly supported by studies of RIN4, a protein that was identified in a yeast two-hybrid screen for plant proteins that interact with AvrB (Mackey et al., 2002), and its interaction with RPS2, an NB-LRR protein that recognizes bacterial pathogens that express AvrRpt2 (Innes et al., 1993; Bent et al., 1994; Mindrinos et al., 1994; Mackey et al., 2002, 2003; Axtell and Staskawicz, 2003). AvrRpt2 causes the elimination of RIN4 during the activation of the *RPS2* pathway. Suppression of *RIN4* by gene silencing activates defense responses constitutively. On the other hand, overexpression of *RIN4* inhibits *RPS2* function. The constitutive activation of defense responses caused by the loss of RIN4 function requires a functional RPS2. These data suggest that RPS2 senses the disappearance of RIN4 induced by AvrRpt2 and that the dissociation of RPS2 from RIN4 results in the activation of the downstream signal transduction cascade.

The localized HR that results from the recognition of pathogen *Avr* genes by the cognate plant *R* genes also triggers a secondary defense response termed systemic acquired resistance (SAR) in uninfected leaves (Ryals et al., 1996). Arabidopsis NPR1 is an essential regulator of SAR (Cao et al., 1997; Ryals et al., 1997). Mutations in *NPR1* abolish both pathogene-

sis-related (*PR*) gene expression and resistance induced by avirulent pathogens or SAR-inducing agents such as salicylic acid (SA) (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). *snc1* (*suppressor of npr1-1, constitutive1*) is an Arabidopsis mutant isolated from a screen for suppressors of *npr1-1* (Li et al., 2001). The *snc1* mutation results in constitutive *PR* gene expression and resistance to *Pseudomonas syringae* pv *maculicola* (*P.s.m.*) ES4326 and *Peronospora parasitica* Noco2 in the *npr1-1* background. *snc1* plants are smaller than wild-type plants, accumulate high levels of SA, and often have curly leaves. Although *snc1/SNC1* plants constitutively express *PR* genes, their morphology is indistinguishable from that of wild-type plants. It appears that both copies of *SNC1* must be mutated for the mutant morphological phenotypes to be visible.

Previously, the *snc1* mutation was mapped to a 120-kb region on chromosome 4. This region contains a cluster of *RPP5* orthologs, including the recently cloned *RPP4* (Parker et al., 1997; van der Biezen et al., 2002). The *snc1* mutant phenotypes are suppressed completely by *eds1*, but not by *ndr1*, suggesting that *SNC1* is located upstream of *EDS1* and that one of the *RPP5* homologs is activated constitutively in *snc1* (Li et al., 2001). Here, we report the identification of *snc1* and discuss the molecular mechanism by which this mutation affects *R* gene–mediated defense.

RESULTS

snc1 Contains a Mutation in *At4g16890*

To identify the molecular lesion in *snc1*, PCR fragments covering the entire 120-kb region to which *snc1* was mapped were amplified from *snc1* DNA and sequenced. The sequence then was compared with that of the wild type, and a single G-to-A mutation was found in the coding region of *At4g16890* (Figure 1), suggesting that *SNC1* is *At4g16890*. The cDNA sequence of the gene was obtained by sequencing reverse transcriptase–mediated (RT) PCR fragments and found to be consistent with the annotation of *At4g16890*. *At4g16890* encodes a putative protein of 1468 amino acids that is highly similar to *RPP4* (62% identical) and *RPP5* (68% identical), two closely related *R* genes of the Toll Interleukin1 Receptor (TIR)-NB-LRR class. As shown in Figure 1, the TIR and NB-ARC domains are encoded by exon 1 and 2, respectively. A stretch of 80 to 90 amino acids is encoded by exon 3. The *snc1* mutation is located in this region, which recently was named NL linker (Meyers et al., 2003). The remaining exons towards the 3′ end encode the LRRs. The *snc1* mutation converts the Glu at position 552 to a Lys in the NL linker.

To investigate the relationship between SNC1 and other TIR-NB-LRR–type R proteins, full-length amino acid sequences of R proteins that were shown previously to be functional were used to generate a phylogenetic tree (Figure 2A). Alignment of the amino acid sequences encoded by exon 3 of SNC1 and the corresponding sequences from other TIR-NB-LRR R proteins also was performed (Figure 2B). Although Glu-552 is conserved among SNC1, RPP4, and RPP5, other TIR-NB-LRR–type R proteins contain different residues at this position. However, closely related R proteins tend to have the same corresponding resi-

dues. Among the aligned R proteins, all except one have a charged amino acid at this position, suggesting potential functional conservation of these residues.

To compare the mutation in the snc1 protein with other gain-of-function R protein variants, the location of these mutations is summarized in Figure 2C. In the tomato Mi protein, there is an unusually long N-terminal extension. Replacing the N-terminal 161 amino acids with the corresponding region of a nonfunctional homolog causes localized HR when expressed transiently in *Nicotiana benthamiana* leaves (Hwang et al., 2000). Several *rx* mutations also were found to constitutively activate HR in transient assays (Bendahmane et al., 2002). These mutations are located in either the NB or the LRR region. Both *Mi* and *Rx* encode coiled-coil (CC)-NB-LRR–type R proteins. The lesion mimic *Rp1-D–21* mutant also contains a rearrangement in the LRR-encoding region of a *Rp1-D* haplotype, but it is unclear whether the lesion mimic phenotype is actually caused by this mutant haplotype (Sun et al., 2001). Recently, a mutation in the NB region of a TIR-NB-LRR–type R protein was found to cause spontaneous lesions in *ssi4* (Shirano et al., 2002). The mutation in *snc1* is the only one located in the NL linker region, and it is the only confirmed *R* gene mutation that causes constitutive disease resistance in the absence of cell death.

Deletions in *At4g16890* Revert the *snc1* Mutant to Wild Type

To confirm that the mutation in *At4g16890* is responsible for the *snc1* phenotypes, we performed a genetic screen to identify revertant mutations of the *snc1* gene that restored wild-type morphology. Seeds of *snc1 npr1-1* were mutagenized by fast neutron bombardment, and M2 plants were screened for mutants with wild-type morphology. M3 seeds from the candidate mutants were planted again to test for segregation of the wild-type and *snc1* morphologies. Because *snc1* is a dominant mutation and *snc1/SNC1* heterozygous plants have wild-type morphology, mutants that produce segregating progeny are likely to have defects in one copy of the *snc1* mutant gene.

Indeed, when nine such mutants were analyzed by PCR for mutations in *At4g16890*, eight had either large deletions or rearrangements detectable by agarose gel electrophoresis. All eight mutations affected at least part of the *At4g16890* coding region, with some also affecting neighboring genes. In one case, the entire exon 3 that contains the original *snc1* mutation was deleted (*snc1-r2*; Figure 1). In the only mutant with no large deletion detected, a small deletion of 8 bp (*snc1-r1*; Figure 1) was identified in the first exon by direct sequencing of *snc1-r1*.

We selected *snc1-r1 npr1-1* and *snc1-r2 npr1-1* for further characterization because the deletions in these two mutants were within *At4g16890*. As shown in Figure 3A, *snc1-r1 npr1-1* and *snc1-r2 npr1-1* plants were larger than *snc1 npr1-1* plants and no longer exhibited curly leaves. Both *snc1-r1 npr1-1* and *snc1-r2 npr1-1* had completely lost the constitutive expression of the *pBGL2*-β-glucuronidase (*GUS*) reporter gene (Figure 3B). RT-PCR analysis revealed that constitutive expression of the endogenous *BGL2* (*PR-2*) gene also was abolished in these plants (Figure 3C). In addition, both mutants exhibited enhanced
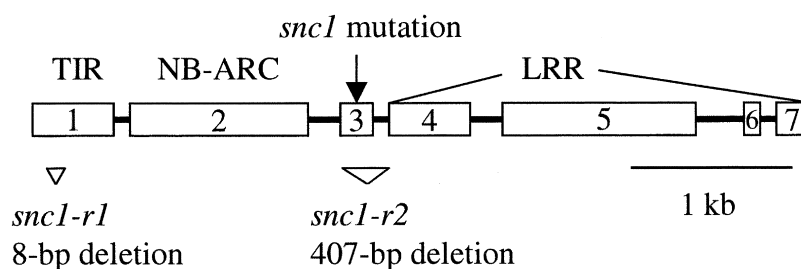
Figure 1. Gene Structure of *SNC1* (*At4g16890*).

Exons (rectangles) and introns (lines) are drawn in proportion to their lengths. Exons encoding the TIR (exon 1), NB-ARC (exon 2), and LRR (exons 4 to 7) domains are indicated. The position of the G-to-A mutation in *snc1* is indicated by the arrow. The two revertant mutations (*snc1-r1* and *snc1-r2*) are shown as triangles.

susceptibility to *P.s.m.* ES4326, a phenotype similar to that of *npr1-1* plants (Figure 3D). Overall, these data indicate that deletions in the mutated *At4g16890* reversed the phenotypes of the *snc1 npr1-1* mutant to those of *npr1-1*.

SNC1/snc1 heterozygous plants were shown previously to constitutively express the *pBGL2-GUS* reporter gene (Li et al., 2001). To determine whether *snc1* plants containing deletions in one copy of the *snc1* gene (referred to hereafter as *snc1/−*) still express *pBGL2-GUS*, seeds from heterozygous revertants were plated on MS medium (Murashige and Skoog, 1962) and the seedlings were stained for expression of the *GUS* reporter gene. We found that 36 of 47 plants from seeds of *snc1/snc1-r1* did not stain and 23 of 28 plants from seeds of *snc1/snc1-r2* did not stain, suggesting that *snc1/−* plants do not constitutively express *pBGL2-GUS*. This is consistent with the finding that no *pBGL2-GUS* expression was observed in the leaves of heterozygous *snc1* revertants (data not shown).

The *snc1* Phenotype Is Not Attributable to Overexpression of *At4g16890*

Previously, *bal* plants, as well as Arabidopsis transgenic plants overexpressing *At4g16890*, were shown to constitutively express *PR* genes (Stokes et al., 2002). Given this finding, we analyzed the expression level of *At4g16890* in *snc1 npr1-1*, *snc1*, and wild-type plants to determine whether the *snc1* mutant phenotype is caused by the overexpression of *At4g16890*. RT-PCR analysis showed that the expression level of *At4g16890* was not altered in the mutant plants (Figure 4). Similar results also were obtained using real-time quantitative RT-PCR (data not shown). Thus, the *snc1* phenotype is caused by the point mutation in *At4g16890* rather than by overexpression of the gene. It is unclear whether the snc1 mutant protein accumulates to a higher level than the wild-type protein.

To test whether the expression of *At4g16890* carrying the *snc1* mutation would confer the *snc1*-like phenotype to wild-type plants, genomic clones containing either wild-type *At4g16890* or a mutant *At4g16890* containing the *snc1* point mutation were transformed into wild-type plants. The *snc1*-like morphology was observed in 15 of 21 plants (>70%) transformed with the mutant *At4g16890*. On the other hand, only 5 of 23 plants (<25%) transformed with the wild-type gene developed *snc1*-

like morphology, which could be the result of the overexpression of the *At4g16890* transgene in these plants. Based on these data, we conclude that *SNC1* is *At4g16890* and that the Glu-552–to–Lys-552 mutation causes the constitutive activation of this R protein homolog.

The *snc1* Phenotype Is Fully Dependent on *PAD4*

Previously, we showed that the *snc1* mutant phenotype is suppressed completely by *eds1*. This finding is consistent with the fact that *SNC1* belongs to the TIR-NB-LRR class of *R* genes, which usually require EDS1 as a downstream signaling component (Aarts et al., 1998). PAD4 interacts with EDS1 in vivo (Feys et al., 2001). To determine whether *PAD4* also is required for the manifestation of the *snc1* phenotype, a double mutant was constructed between *snc1* and *pad4-1* (Glazebrook et al., 1996; Jirage et al., 1999). As shown in Figure 5A, *pad4-1* completely suppressed the morphological phenotypes of *snc1*. The double mutant also lost constitutive *pBGL2-GUS* expression (Figure 5B) and resistance to both *P.s.m.* ES4326 and *P. parasitica* Noco2 (Figures 5C and 5D). These data suggest that PAD4 is fully required for downstream signaling in *snc1*.

snc1 Activates Both SA-Dependent and SA-Independent Defense Pathways

To test whether the increased SA level in *snc1* is required for the activation of downstream defense pathways, a double mutant was constructed between *snc1* and *eds5-3*, a mutant defective in pathogen-induced SA synthesis (Nawrath and Métraux, 1999; Nawrath et al., 2002). As shown in Figures 6A and 6B, *snc1 eds5-3* had a similar amount of SA as *eds5-3*. *snc1 eds5-3* plants were slightly smaller than wild-type plants, and the leaves of *snc1 eds5-3* were still curly (Figure 6C). Constitutive expression of *pBGL2-GUS* in *snc1* was not affected by *eds5-3* (Figure 6D). RT-PCR analysis of *PR-2* (*BGL2*) expression confirmed that *eds5-3* did not affect the expression of *PR-2* in the double mutant (Figure 6E). To determine whether the resistance of *snc1* was affected by the decreased SA level, growth of the virulent bacterial pathogen *P.s.m.* ES4326 on *snc1 eds5-3* also was determined (Figure 6F). Although *snc1 npr1* was resistant to *P.s.m.* ES4326, *snc1 eds5-3* was more susceptible than wild-type

A

B

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                                                    E→K
                                                     *
RPP4     TVLGIRVPPTVLFSTRPLLVINEESFKGMRN--------------LQYLEIGH------ 558
RPP5     TLLGIRLPHPGYLTTR-SFLIDEKSFKGMRN--------------LQYLEIGY------ 559
SNC1     TLLGIRLPFEEYFSTR-PLLIDKESFKGMRN--------------LQYLEIGY------ 555
RPP1-WsA RFIGIHL---DLSKNEEELNISEKALERIHD--------------FQFVRIND------ 605
RPP1-WsB RFIGINL---DLYKNVEBELNISEKALERIHD--------------FQFVRING------ 637
RPP1-WsC RFIGINL---ELSNTEEELNISEBKVLERVHD--------------FHFVRIDASFQPER 644
SSI4     SVKGISF---DASNS-EEVSVGKGAFEGMPN--------------LQFLRIYR----EY 562
N        AMEAIWVS-----SYSSTLRFSNQAVKNMKR--------------LRVFNMGR------ 562
RPS4     KAANVRGIFLDLSEVEDETSLDRDHFINMGN--------------LRYLKFYNSHCPQE 597
L6       KVKAISIPWGVKYEFKSECFLNLSELRYLHAREAMLTGDFNNLLPNLKWLELPFYKHGED 641
RRS1-R   AQGSEEIEGLFLDTSNLRFDLQPSAFKNMLN--------------LRLLKIYCS---NP 536
                                                 .  :  . : .: ..:

RPP4     ---WSEIDLPQGLVYLPLKLKLLKWNYCPLKSLPSTFKAEYLVNLIMKYSKLEKLWEGTL 615
RPP5     ---WSDGVLPQSLVYFPRRKLKRLWWDNCPLKRLPSNFKAEYLVELRMVNSKLEKLWDGTQ 616
SNC1     ---YGD--LPQSLVYLPLKLRLLDWDDCPLKSLPSTFKAEYLVNLIMKYSKLEKLWEGTL 610
RPP1-WsA -KNHALHERLQDLICHSPKIRSLKWYSYQNICLPSTFNPBFLVELDMSFSKLQKLWEGTK 664
RPP1-WsB -KNHALHERLQGLIYQSPQIRSLHWKCYQNICLPSTFNSEFLVELDMSFSKLQKLWEGTK 696
RPP1-WsC LQPERLQLALQDLIYHSPKIRSLKWHRYQNICLPSTFNPEFLIBLDMRYSKLQKLWEGTK 704
SSI4     FNSEGTLQIPEDMKYLPP-VRLLHWENYPRKSLPQRFHPEHLVKIYMPRSKLKKLWGGIQ 621
N        ------SSTHYAIDYLPNNLRCFVCTNYPWESFPSTFELKMLVHLQLRHNSLRHLWTETK 616
RPS4     CKTNNKINIPDKLKLPLKEVRCLHWLKFPPLETLPNDFNPINLVDLKLPYSEMEQLWEGDK 657
L6       DPPLTNYTMKNLIIVILEHSHITADDWGGWRHMMKMAERLKVVRLASNYSLYGRRVRLSD 701
RRS1-R   EVHPVINFPTGSLHSLPNELRLLHWENYPLKSLPQNFDPRHLVEINMPYSQLQKLWGGTK 596
          :       :         :  . . :: :    .  :
```

C

Figure 2. Sequence Analysis of SNC1 and the *snc1* Mutation.

(A) Phylogenetic relationship of SNC1 and other TIR-NBS-LRR–type R proteins. The neighbor-joining tree was constructed with BIONJ (Gascuel, 1997) using proteins aligned with CLUSTAL W. Distances were calculated with TREE-PUZZLE 5.0 (Strimmer and von Haeseler, 1996) using the WAG substitution matrix.
(B) Amino acid sequence comparison of SNC1 exon 3 with other TIR-NBS-LRR proteins. The alignment was performed using CLUSTAL W. The predicted Glu-to-Lys (E→K) change in *snc1* is highlighted (asterisk). Colons indicate high amino acid identity, and dots indicate low identity. RPP4, Resistance to *Peronospora parasitica* 4 (van der Biezen et al., 2002); RPP5, Resistance to *P. parasitica* 5 (Parker et al., 1997); RPP1-WsA to RPP1-WsC, Resistance to *P. parasitica* 1, *Arabidopsis thaliana* accession Wassilewskija A to C (Botella et al., 1998); SSI4, suppressor of salicylic acid insensitivity of *npr1-5*, 4 (Shirano et al., 2002); N, *Nicotiana glutinosa* virus resistance gene (Whitham et al., 1994); RPS4, Resistance to *Pseudomonas syringae* 4 (Gassmann et al., 1999); L6, *Linum usitatissimum* rust resistance gene (Lawrence et al., 1995); RRS1-R, Resistance to *Ralstonia solanacearum* 1-recessive (Deslandes et al., 2002).
(C) Locations of the *snc1* mutation and amino acid changes in confirmed gain-of-function R protein variants that cause constitutive HR.

plants, suggesting that SA is required for the resistance of *snc1* to *P.s.m.* ES4326. Compared with *eds5-3*, *snc1 eds5-3* was slightly less susceptible, indicating that the SA-independent pathway also may contribute to resistance to the bacterial pathogen.

DISCUSSION

To identify the mutation that causes constitutive *PR* gene expression and pathogen resistance in *snc1* plants, we sequenced the complete region to which the *snc1* mutation was mapped and identified a single mutation in *At4g16890*, an NB-LRR–class *R* gene that is highly similar to *RPP4* and *RPP5*. We showed that deletions of this mutated *R* gene revert the mutant plants to the wild-type phenotype. In addition, we observed the *snc1*-like phenotype in >70% of wild-type plants transformed with a genomic clone containing the *snc1* mutation. These data indicate that *At4g16890* encodes SNC1 and that the point mutation we identified in SNC1 is a gain-of-function mutation that renders this R protein constitutively active. Unlike *bal* plants, *snc1* plants do not overexpress *At4g16890*. In addition, *snc1* is genetically stable but *bal* is metastable (Stokes et al., 2002). In our effort to identify revertants of *snc1*, we obtained nine revertants as well as a small number of recessive mutants (Y. Zhang and X. Li, unpublished data) by screening M2 plants from ~4000 M1 families. This is quite different from the results of the genetic screen that Stokes et al. (2002) performed to identify revertants of *bal*, in which a high frequency of revertants (~7% of the M2 plants) was observed in the progeny of mutagenized *bal* plants.

Mutational analysis of the NB-LRR class of *R* genes has suggested that both the NB and LRR domains are essential for the functions of these R proteins. A large number of mutations in both the NB and LRR domains have been found to inactivate the R proteins (Warren et al., 1998; Dinesh-Kumar et al., 2000; Tao et al., 2000, Axtell et al., 2001; Tornero et al., 2002), implying that the mutated residues are important for R protein function. Although negative regulation of this group of R proteins also may play a crucial role in *R* gene–mediated resistance, as suggested by the data that RPS2 can be activated constitutively by the elimination of its negative regulator RIN4 (Axtell and Staskawicz, 2003; Mackey et al., 2003), it is not known which regions of the *R* genes are important for this negative regulation. Here, we report that a single amino acid change in SNC1, located in the NL linker region, constitutively activates this R protein and that the NL linker region in SNC1 probably is involved in its negative regulation.

A model is proposed to explain how the mutation in *snc1* results in the constitutive activation of defense responses (Figure 7). In wild-type plants, SNC1 interacts with an R PROTEIN BINDING PROTEIN (RBP) equivalent to RIN4. This interaction involves the NL linker region in SNC1, and amino acid Glu-552 is one of the critical residues for this interaction. Changing the negatively charged Glu-552 to the positively charged Lys-552 results in reduced binding affinity between snc1 and the negative regulator and dissociation of snc1 from the complex, which then leads to the constitutive activation of the downstream resistance pathways.

A

snc1 npr1   *npr1*   *snc1-r1 npr1*   *snc1-r2 npr1*

B

snc1 npr1   *snc1-r1 npr1*   *snc1-r2 npr1*

C

PR-2

Actin 1

snc1 npr1   npr1   snc1-r1 npr1   snc1-r2 npr1

D

WT   *npr1*   *snc1 npr1*   *snc1-r1 npr1*   *snc1-r2 npr1*

Figure 3. Phenotypic Analysis of *snc1* Revertants.

(A) Morphological phenotypes of the *snc1* revertants. All plants were grown in parallel on soil and photographed when they were 4 weeks old.
(B) Suppression of *snc1*-induced *pBGL2-GUS* reporter gene expression in the revertants. Three-week-old seedlings grown on MS medium were stained for GUS activity from *pBGL2-GUS*.
(C) *PR-2* (*BGL2*) gene expression in *snc1* revertants. RNAs were prepared from 20-day-old plants grown on MS medium and reverse transcribed to obtain total cDNA. The cDNA samples were normalized by real-time PCR using an *Actin1* probe. *PR-2* and *Actin1* in different mutant plants then were amplified by 35 cycles of PCR using equal amounts of total cDNA, and the products were analyzed by agarose gel electrophoresis and ethidium bromide staining.
(D) Enhanced disease susceptibility of *snc1* revertants to *P.s.m.* ES4326. Leaves from 4-week-old plants were infiltrated with a *P.s.m.* ES4326 suspension in 10 mM MgCl₂ (OD₆₀₀ = 0.0001). Photographs were taken of representative leaves 4 days after infection. WT, wild type.

Our model explains the phenotypic differences between *snc1/SNC1*, *snc1/−*, and *snc1/snc1* plants. In *snc1/SNC1* plants, both the wild-type and mutant proteins bind to the negative regulator of SNC1. As a result of reduced binding affinity between snc1 and RBP, a portion of the snc1 protein dissociates from the negative regulator and partially activates the downstream signal transduction pathways. Because there is no wild-type protein in *snc1/−* plants, the excess amount of RBP sequesters all of the snc1 protein and blocks the activation of downstream defense responses. Because *snc1/snc1* plants most likely contain more snc1 protein than *snc1/SNC1* plants, the phenotype is more dramatic in *snc1/snc1* plants. The constitutive *PR* gene expression in transgenic plants overexpressing *SNC1* (*At4g16890*) also can be explained by the excess amount of SNC1 protein unbound to the negative regulator of SNC1. Furthermore, the existence of a negative regulator of SNC1 equivalent to RIN4 is supported by the finding that a loss-of-function mutation in *BON1/CPN1* (Hua et al., 2001; Jambunathan et al., 2001) leads to the constitutive activation of SNC1-dependent resistance pathways (J. Hua, personal communication).

How downstream signaling pathways are activated by snc1 protein dissociated from its negative regulator is unclear. Recently, different domains of Rx have been shown to interact with each other in vivo (Moffett et al., 2002). It was proposed that disruption of these intramolecular interactions leads to the activation of downstream pathways. It is possible that dissociation of the snc1 protein from its negative regulator also induces conformational changes of the protein, which subsequently triggers either the release or recruitment of active effectors, as suggested previously (Moffett et al., 2002).

Analysis of residues that correspond to Glu-552 in SNC1 revealed significant divergence of the residues among different TIR-NB-LRR–type R proteins (Figure 2B). RPS4 and RRS1-R

SNC1

Actin 1

snc1   WT   snc1 npr1-1
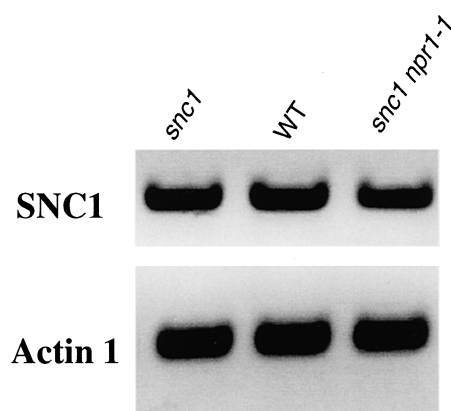
Figure 4. Analysis of *SNC1* Expression Levels in Wild-Type and Mutant Plants.

RNAs were prepared from 20-day-old plants grown on MS medium and reverse transcribed to obtain cDNA. The cDNA samples were first normalized by real-time PCR using an *Actin1* probe. *SNC1* and *Actin1* in wild-type (WT) and mutant plants then were amplified by 30 cycles of PCR using equal amounts of total cDNA, and the products were analyzed by agarose gel electrophoresis and ethidium bromide staining.

A

snc1   *snc1 pad4*

B

snc1   *snc1 pad4*

C

WT   *snc1*   *pad4*   *snc1 pad4*

D
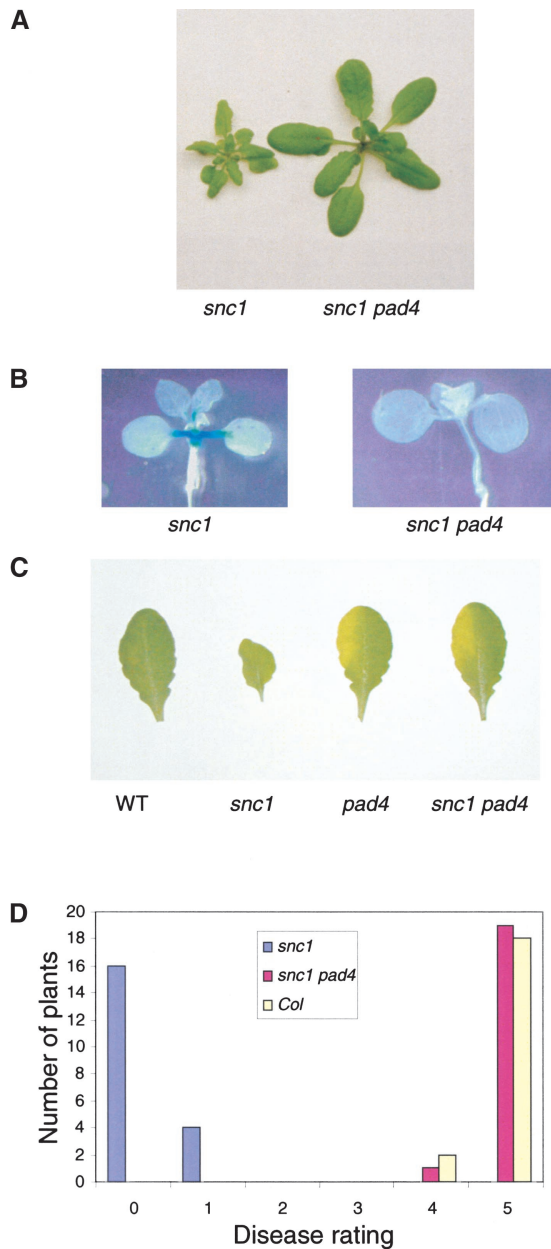
Figure 5. Analysis of *snc1 pad4-1*.

(A) Morphology of *snc1 pad4-1* plants. The photograph shows 4-week-old plants grown on soil.

(B) Suppression of constitutive *pBGL2-GUS* reporter gene expression in *snc1* by *pad4-1*. Twenty-day-old seedlings grown on MS medium were stained for GUS activity.

(C) Enhanced susceptibility of the *snc1 pad4-1* double mutant to *P.s.m.* ES4326. The leaves of 4-week-old soil-grown plants were infiltrated with a suspension of *P.s.m.* ES4326 in 10 mM $MgCl_2$ (OD_{600} = 0.00005). The photograph was taken 3 days after infection. At this dose, wild-type (WT) Arabidopsis normally is resistant to the bacterium.

(D) Susceptibility of *snc1 pad4-1* to *P. parasitica* Noco2. Two-week-old seedlings were sprayed with Noco2 spores at a conidiospore suspension concentration of 5×10^3 spores per milliliter of water. The infection was rated as follows on 20 plants at 6 days after infection by counting

actually contain a Lys at this position, indicating that the Glu-to-Lys difference at this position does not necessarily render other *R* genes constitutively active. The effects of this change may depend strictly on the nature of the interactions between the R proteins and their interacting partners. Compared with mutations in other constitutively active *R* gene variants, the mutation in *snc1* is unique. The region in which the *snc1* mutation is located is different from the regions of other R proteins in which HR-inducing mutations were found (Figure 2C). The chimeric Mi proteins that induce localized HR contain replacements in the N-terminal extension (Hwang et al., 2000), whereas mutations in *Rx* that lead to constitutive HR are localized either in the NB or the LRR (Bendahmane et al., 2002). In addition, both *Mi* and *Rx* are CC-NB-LRR–type *R* genes. The only reported TIR-NB-LRR–type *R* gene mutation that causes spontaneous lesion formation is *ssi4*, which also is found in the NB region (Shirano et al., 2002).

Unlike *ssi4*, *snc1* plants do not develop spontaneous lesions. *snc1* is the first confirmed *R* gene mutant that activates downstream resistance pathways in the absence of HR, suggesting that *R* gene–mediated resistance can be uncoupled from cell death. Transgenic plants overexpressing the *snc1* mutant gene do not have spontaneous lesions either (data not shown). The lack of HR-like lesions in *snc1* plants and the unique location of the *snc1* mutation suggest that the mutation may activate the R protein by a mechanism different from those in the constitutive HR-inducing mutants. We hypothesize that the activation of downstream defense pathways in *snc1* is attributable to the disruption of intermolecular interactions, whereas the HR induction by constitutively active *Rx*, *Mi*, and *SSI4* variants is caused by the disruption of intramolecular interactions by the mutations, as suggested previously (Hwang et al., 2000; Moffett et al., 2002).

The absence of spontaneous lesions in *snc1* also makes it a very useful tool for studying resistance pathways downstream of *R* genes without the interference of cell death. This is demonstrated by the analysis of the *snc1 pad4-1* and *snc1 eds5-3* double mutants. Because *SNC1* encodes an R protein belonging to the TIR-NB-LRR class and *EDS1* is required for resistance conferred by this group of *R* genes, it is not surprising that *eds1* completely suppressed the *snc1* mutant phenotypes. Resistance conferred by the TIR-NB-LRR class of *R* genes often is only partially dependent on *PAD4* (Glazebrook et al., 1996; Feys et al., 2001; van der Biezen et al., 2002). It is surprising that *pad4* completely suppressed the *snc1* mutant phenotype. One of the main differences between resistance in *snc1* and resistance conferred by other TIR-NB-LRR *R* genes such as *RPP4* and *RPP5* is that HR is not involved in the resistance

the number of conidiophores per infected leaf: 0, no conidiophores on the plants; 1, no more than 5 conidiophores per infected leaf; 2, 6 to 20 conidiophores on a few of the infected leaves; 3, 6 to 20 conidiophores on most of the infected leaves; 4, 5 or more conidiophores on all infected leaves; 5, 20 or more conidiophores on all infected leaves. Col, Columbia wild type.
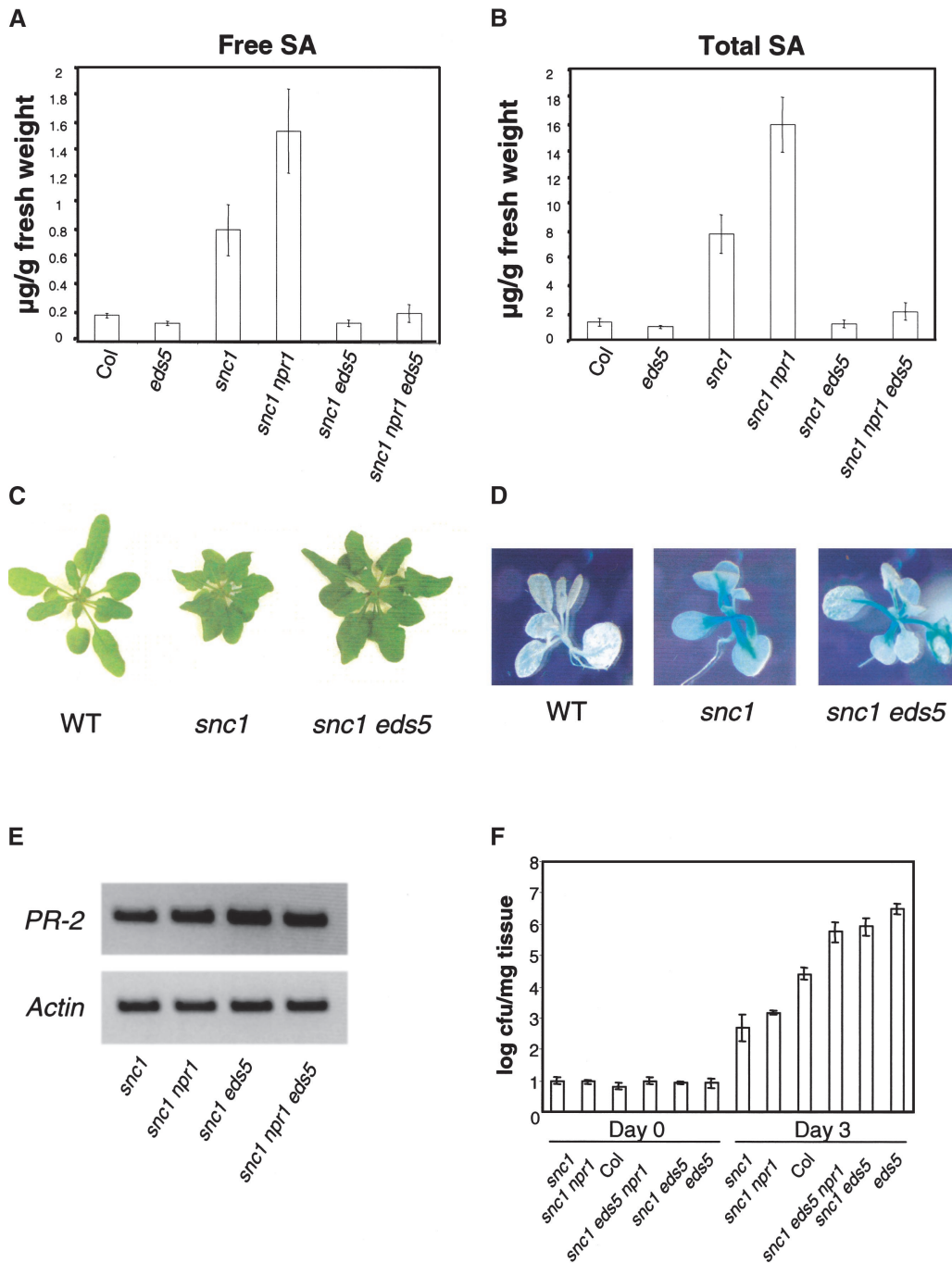
**Figure 6.** Epistasis Analysis of *snc1* and *eds5-3*.

(A) and **(B)** Free SA **(A)** and total SA **(B)** levels in the mutants. Leaf tissue was harvested 4 weeks after germination and used for SA extraction. Each treatment had four replicates. Col, Columbia wild type.

(C) Morphology of *snc1 eds5* compared with *snc1* and the wild type (WT).

(D) GUS staining of the *pBGL2-GUS* reporter gene in *snc1* and *snc1 eds5*. Staining was performed on 20-day-old plants grown on MS medium.

(E) *PR-2* expression in the mutants. RT-PCR was used to analyze the expression of *PR-2* as described for Figure 3.

(F) Bacterial growth of *P.s.m.* ES4326 in the mutants. Two leaves of each plant were infiltrated with the bacteria ($OD_{600} = 0.00005$). Leaf discs within the inoculated areas were taken after 0 and 3 days of infiltration. Four replicates were taken for each treatment. Error bars represent 95% confidence limits of log-transformed data. cfu, colony-forming units.

A RBP   SNC1/SNC1

B RBP   snc1/SNC1

C RBP   snc1/−

No activation

Activation
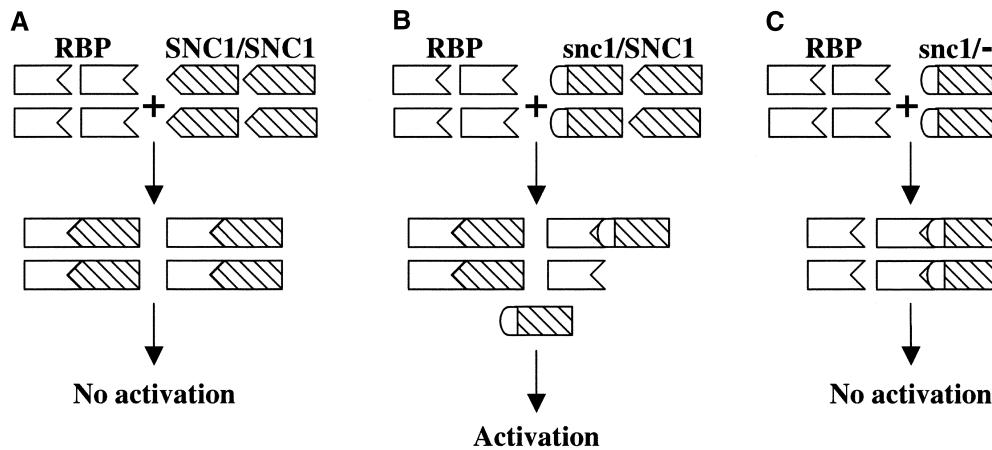
No activation

Figure 7. Model for the Activation of SNC1 by the *snc1* Mutation.

(A) In wild-type plants, SNC1 is sequestered by the proposed negative regulator RBP and is inactive.
(B) In *snc1/SNC1* plants, some snc1 protein dissociates from its negative regulator and activates downstream defense pathways.
(C) In heterozygous revertant *snc1/−* plants, all snc1 protein is sequestered as a result of the excess amount of the negative regulator.

in *snc1* because *snc1* plants do not form spontaneous lesions. As suggested previously by Feys et al. (2001), most likely, *EDS1* and *PAD4* both are fully required for the HR-independent resistance responses, whereas *EDS1* encodes additional functions for the generation of HR. Because the morphological phenotype of *snc1* is not nearly as dramatic as that of the transgenic plants overexpressing this gene (Stokes et al., 2002), *SNC1* probably is only partially activated by *snc1*. This effect also may contribute to the full dependence of the *snc1* phenotype on *PAD4*.

Another interesting observation is that *eds5-3* had no effect on constitutive *PR-2* expression in *snc1*, whereas the expression of the SA-degrading enzyme NahG in *snc1* suppressed the *pBGL2-GUS* reporter gene (Li et al., 2001). Because catechol, the product of NahG, induces disease susceptibility in plants (van Wees and Glazebrook, 2003), the suppression of *pBGL2-GUS* by NahG might be caused by the accumulation of catechol rather than by the reduction of SA. Alternatively, SA synthesized independent of *EDS5* might be required for constitutive *PR-2* expression, and the lack of *PR-2* expression in *snc1 NahG* might be the result of the hydrolysis of SA synthesized independent of *EDS5*.

A simplified model is proposed in Figure 8 to describe the resistance pathways activated by *snc1*. The activation of downstream pathways appears to require both *EDS1* and *PAD4*, because mutations in *EDS1* and *PAD4* completely suppressed the *snc1* phenotype. On the other hand, increased SA levels were only partially responsible for the *snc1* phenotypes, because *snc1 eds5-3* double mutants with wild-type levels of SA had intermediate sizes, curly leaves, and constitutive *PR-2* expression. Thus, both SA-dependent and SA-independent pathways exist downstream of *snc1*. Previously, it was shown that the induction of *PR-2* by avirulent pathogens was not affected in the inoculated leaves of *eds5* mutants (Nawrath and Métraux, 1999). The expression levels of *PR-2* in *cpr1* and *cpr5* also were not affected by *eds5* (Clarke et al., 2000). Thus, the constitu-

tive expression of *PR-2* appears to be a hallmark of the SA-independent resistance pathway.

Although *snc1 eds5-3* plants are susceptible, *snc1 npr1* plants are resistant to the bacterial pathogen *P.s.m.* ES4326, indicating that both NPR1-dependent and NPR1-independent pathways are activated downstream of SA. The SA-dependent and NPR1-independent pathway appears to be the major contributor to the resistance to *P.s.m.* ES4326 in *snc1 npr1* plants. On the other hand, SA alone cannot induce resistance to *P.s.m.*

snc1

EDS1/PAD4

EDS5

??

SA synthesis

??

NPR1

PR2   **Resistance**   **Resistance**
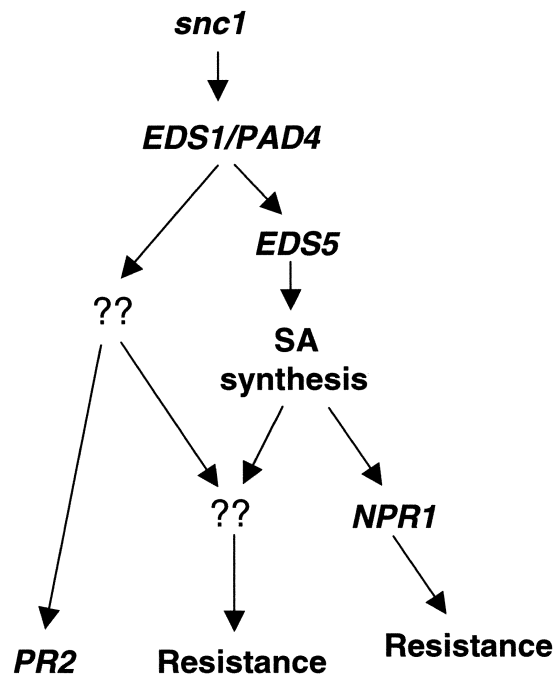
Figure 8. Model for Pathways Activated in *snc1* Plants.

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ES4326 in the *npr1* background (Cao et al., 1994), suggesting that the SA-independent pathway(s) also is required for resistance to the bacterial pathogen in *snc1 npr1* plants.

METHODS

Screening for *snc1* Revertants

The *snc1 npr1-1* mutant seeds of *Arabidopsis thaliana* were treated by fast-neutron bombardment at a dose of 60 Gray by Andrea Kodym (Agriculture and Biotechnology Laboratory, International Atomic Energy Agency, Vienna, Austria). M1 plants were grown on soil and allowed to self-pollinate. M2 seeds from 10 to 20 plants were pooled upon harvesting. M2 plants were grown on soil at 22°C under 16-h-light/8-h-dark cycles. Approximately 40,000 M2 plants from ∼4000 M1 families were screened for those with wild-type size and morphology. Seeds from putative mutants were collected and planted again. Lines producing progeny with both wild-type (approximately three-fourths) and *snc1* (approximately one-fourth) morphology were analyzed further for the presence of deletions in *At4g16890* by PCR and sequence analysis.

Mutant Characterization

To test *pBGL2-GUS* reporter gene expression, seeds were surface-sterilized and plated on MS medium (Murashige and Skoog, 1962). The plates were incubated in a TC16 plant growth chamber from Conviron (Winnipeg, Canada) at 22°C under 16-h-light/8-h-dark cycles. After 20 days, GUS staining was performed using a protocol described previously (Bowling et al., 1994). Infection of the plants with *Pseudomonas syringae* pv *maculicola* ES4326 and *Peronospora parasitica* Noco2 was performed as described previously (Li et al., 2001). Salicylic acid (SA) was extracted from fresh leaf tissue of 4-week-old plants and measured as described previously (Li et al., 1999).

Expression Analysis

To analyze the level of gene expression by reverse transcriptase–mediated PCR, total RNA samples were prepared from 20-day-old plants grown on MS medium using the Totally RNA kit from Ambion (Austin, TX). Reverse transcription was performed using the RT-for-PCR kit from Clontech (Palo Alto, CA). Real-time PCR was performed using the QuantiTect SYBR Green PCR kit from Qiagen (Valencia, CA). The primers used to amplify *Actin1* were 5′-CGATGAAGCTCAATCCAAACGA-3′ and 5′-CAGAGTCGAGCACAATACCG-3′. The primers used to amplify *PR-2* were 5′-GCTTCCTTCTTCAACCACACAGC-3′ and 5′-CGTTGATGT-ACCGGAATCTGAC-3′. The primers used to amplify *SNC1* were 5′-AGATGTCCCCGATGTCATCC-3′ and 5′-CCAAACATTTTCAGACTTACA-AGACTTG-3′. In each primer pair combination, one of the primers was designed to be cDNA specific according to the instructions of the QuantiTect SYBR Green PCR kit to avoid amplification of genomic DNA.

Reverse Complementation

A 7.2-kb PstI-BamHI genomic fragment containing the wild-type *At4g16890* gene was first cloned from BAC clone F5D3 to pGEM3Z (from Perkin-Elmer). The same fragment then was cloned from pGEM3Z to pGreen229 (Hellens et al., 2000) to obtain pG229-SNC1. A 1.2-kb KpnII-AvrII genomic fragment containing the *snc1* mutation was amplified by PCR from the genomic DNA of *snc1* plants and used to replace the wild-type fragment in pG229-SNC1. The resulting clone was named pG229-snc1. Both pG229-SNC1 and pG229-snc1 then were used to

transform the wild-type plants by the floral-dip method (Clough and Bent, 1998).

Creating the *snc1 pad4-1* Double Mutant

To create the *snc1 pad4-1* double mutant, the original *snc1 npr1-1* (as female) was crossed with *pad4-1*. The resulting F1 plants had wild-type morphology and were grown to set seeds. In the F2 population, 36 seedlings were grown on soil and 7 of the 36 plants showed the distinct *snc1* morphology of small stature and curly leaves. The F3 seeds of these seven *snc1*-like plants were collected and replanted. Among them, three had approximately one-quarter large wild-type plants segregating out. The plants with wild-type morphology were potential *snc1 pad4-1* double mutants. These lines were plated on MS plates with 0.2 mM SA to check for *NPR1* homozygosity, because *npr1* mutants bleach to death on high concentrations of SA that wild-type plants can survive (Cao et al., 1997). These lines also were plated on MS medium containing 50 µg/mL kanamycin to check for the presence of the *pBGL2-GUS* reporter gene. The lines that were both *NPR1* and *pBGL2-GUS* homozygous were used for further characterization. The resulting lines were backcrossed with *snc1* to confirm the presence of the *snc1* mutation, and as expected, the F1 plants had *snc1* morphology. The presence of *pad4-1* in the final mutant was confirmed by sequencing analysis of the *pad4-1* locus.

Creating the *snc1 eds5-3* Double Mutant

The strategy for obtaining the *snc1 eds5-3* double mutant was similar to that used to isolate *snc1 pad4-1*. The original *snc1 npr1-1* (as female) was crossed with *eds5-3*, and the resulting F1 plants had wild-type morphology and were grown to set seeds. In the F2 population, 72 seedlings were grown on soil and 19 of the 72 plants showed the distinct curly leaves of *snc1*. Among these 19 plants, 3 were larger, whereas the other 16 remained small. The F3 seeds of four small *snc1*-like plants were collected and replanted. Among them, two had approximately one-quarter large plants with curly leaves. The large plants with curly leaves were potential *snc1 eds5-3* double mutants. These lines were plated on MS plates with 0.2 mM SA to check for *NPR1* homozygosity. Lines that were *NPR1* or *npr1-1* homozygous were used for further characterization. The resulting lines were backcrossed with *snc1* to confirm the presence of the *snc1* mutation, and as expected, the F1 plants had *snc1* morphology. The presence of *eds5-3* in the final mutant lines was confirmed by sequencing analysis of the *eds5-3* locus.

Upon request, materials integral to the findings presented in this publication will be made available in a timely manner to all investigators on similar terms for noncommercial research purposes. To obtain materials, please contact Xin Li, xinli@interchange.ubc.ca.

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