Arabidopsis sfd Mutants Affect Plastidic Lipid Composition and Suppress Dwarfing, Cell Death, and the Enhanced Disease Resistance Phenotypes Resulting from the Deficiency of a Fatty Acid Desaturase

Ashis Nandi,a Kartikeya Krothapalli,a,b Christen M. Buseman,a Maoyin Li,a,1 Ruth Welti,a,b Alexander Enyedi,c and Jyoti Shaha,b,2

a Division of Biology, Kansas State University, Manhattan, Kansas 66506
b Molecular, Cellular, and Developmental Biology Program, Kansas State University, Manhattan, Kansas 66506
c Department of Biological Sciences, Western Michigan University, Kalamazoo, Michigan 49008

A loss-of-function mutation in the Arabidopsis SSII2/FAB2 gene, which encodes a plastidic stearoyl-acyl-carrier protein desaturase, has pleiotropic effects. The ssii2 mutant plant is dwarf, spontaneously develops lesions containing dead cells, accumulates increased salicylic acid (SA) levels, and constitutively expresses SA-mediated, NPR1-dependent and -independent defense responses. In parallel, jasmonic acid–regulated signaling is compromised in the ssii2 mutant. In an effort to discern the involvement of lipids in the ssii2-confferred developmental and defense phenotypes, we identified suppressors of fatty acid (stearyl) desaturase deficiency (sfd) mutants. The sfd1, sfd2, and sfd4 mutant alleles suppress the ssii2-conferring dwarfing and lesion development, the NPR1-independent expression of the PATHOGENESIS-RELATED1 (PR1) gene, and resistance to Pseudomonas syringae pv maculicola. The sfd1 and sfd4 mutant alleles also depress ssii2-conferring PR1 expression in NPR1-containing sfd1 ssii2 and sfd4 ssii2 plants. By contrast, the sfd2 ssii2 plant retains the ssii2-conferrered high-level expression of PR1. In parallel with the loss of ssii2-conferring constitutive SA signaling, the ability of jasmonic acid to activate PDF1.2 expression is reinstated in the sfd1 ssii2 npr1 plant. sfd4 is a mutation in the FAD6 gene that encodes a plastidic ω-6-desaturase that is involved in the synthesis of polyunsaturated fatty acid–containing lipids. Because the levels of plastid complex lipid species containing hexadecatrienoic acid are depressed in all of the sfd ssii2 npr1 plants, we propose that these lipids are involved in the manifestation of the ssii2-conferrered phenotypes.

INTRODUCTION

Lipids are important structural components of biological membranes. In addition, lipid-derived second messengers participate in signal transduction mechanisms to influence plant growth, development, and responses to environmental cues (Munnik et al., 1982; Somerville et al., 2000; Wallis and Browse, 2002). Some PC species, or fragments thereof, are returned to the plastid, where an acyl-glycerol component is incorporated into complex plastid lipids (Browse et al., 1996; Mongrand et al., 2000). Differences in the enzymes present in the two compartments result in differences in the positions at which 16- and 18-C acyl species are esterified to glycerol, the extent of 16- and 18-C acyl desaturation, and the lipid head group classes formed in the cytoplasm and plastid. The desaturation of 16:0 and 18:1 occurs on 16-C and 18-C fatty acids incorporated into complex lipids. In Arabidopsis, the desaturation of 16:0 to hexadecatrienoic acid (16:3) occurs primarily on plastid-localized complex lipids. Hence, 16:3-containing lipids are found predominantly in the plastid lipid, MGDG (Wallis and Browse, 2002). Polyunsaturated fatty acids (PUFAs) released from membrane lipids are precursors for the synthesis of oxylipins, a large family of oxidized lipids. For example, jasmonic acid (JA) and its methyl ester (MeJA) are synthesized from linolenic acid (18:3) via the octadecanoid pathway. In addition, a parallel hexadecanoid pathway in Arabidopsis synthesizes JA-related compounds from 16:3 (Weber, 2002). Oxylipins are important signaling molecules in plant development and defense against...
wounding, insect feeding, and pathogen infection (Reymond and Farmer, 1998; Weber, 2002). For example, JA is required for pollen development, and several Arabidopsis mutants blocked in JA synthesis or signaling are male sterile as a result of improper pollen development (Feys et al., 1994; McConn and Browse, 1996; Stinzi and Browse, 2000). In addition, JA biosynthesis and signaling mutants exhibit increased susceptibility to fungal pathogens and insects (Penniset et al., 1996; Staswick et al., 1998; Vijayan et al., 1998). By contrast, JA application activates the expression of the antifungal protein defensin gene PDF1.2 (Penniset et al., 1998). Moreover, high-level expression of PDF1.2 correlates with increased resistance to the necrotrophic fungus Botrytis cinerea (Berrocal-Lobo et al., 2002).

Salicylic acid (SA) is another important signaling molecule in plants, influencing plant development and defense responses (Shah and Klessig, 1999). The involvement of SA in plant defense has been studied extensively. SA levels are increased in plants resisting pathogen attack, and these increases correlate with the activation of PATHOGENESIS-RELATED (PR) gene expression and resistance (Durner et al., 1997; Shah and Klessig, 1999). In addition, the application of SA activates PR gene expression and disease resistance. Several PR proteins have proven antimicrobial activities, and their expression serves as a molecular marker for the activation of defense responses (Klessig and Malamy, 1994; Hammond-Kosack and Jones, 1996; Sali et al., 1996; Ryals et al., 1996). Blocking SA biosynthesis in the Arabidopsis eds5 (sid1) and sid2 (eds16) mutants decreases PR expression in pathogen-infected plants and enhances susceptibility to pathogens (Navrath and Metraux, 1999; Dewdney et al., 2002). Likewise, preventing SA accumulation by expressing the SA-degrading salicylate hydroxylase, which is encoded by the bacterial nahG gene, suppresses the expression of PR genes and confers enhanced susceptibility to pathogens (Gaffney et al., 1993; Delaney et al., 1994). The NPR1 gene is an important regulator of the SA-dependent expression of PR genes and resistance in Arabidopsis. The loss of NPR1 activity affects the SA-inducible expression of PR genes and resistance in npr1/nim1 mutants (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 2001). However, SA signaling also occurs via NPR1-independent mechanism(s) in addition to the NPR1-dependent pathway (Shah et al., 1999, 2001; Clarke et al., 2000).

The ssi (suppressor of SA insensitivity) mutants were identified in a screen for mutants that restore SA signaling in the npr1 genetic background (Shah et al., 1999, 2001; Shirano et al., 2002). SA signaling through the NPR1-dependent and -independent pathways is constitutively active in the ssi2 mutant (Shah et al., 2001). PR genes are expressed at increased levels, and resistance to Peronospora parasitica is enhanced in ssi2 and ssi2 npr1 plants (Shah et al., 2001). In addition, enhanced resistance to an avirulent strain of Pseudomonas syringae pv tomato is observed in the ssi2 mutant. The ssi2-conferred PR expression and resistance phenotypes are associated with the accumulation of increased levels of SA. Moreover, increased SA levels are required for the ssi2-conferred PR expression and enhanced disease resistance; PR1 expression and resistance to P. parasitica and P. syringae are depressed in the ssi2 nahG plant (Shah et al., 2001). Crosstalk between SA and JA signaling pathways is important for the fine-tuning of plant defense responses. Both synergistic and antagonistic interactions between SA and JA signaling have been reported (Reymond and Farmer, 1998; Kunkel and Brooks, 2002). Similarly, in the ssi2 mutant, the constitutive activation of SA-dependent defense responses is paralleled by the inability of JA to activate PDF1.2 expression and enhanced susceptibility to B. cinerea (Kachroo et al., 2001). In addition to altering defense responses, ssi2 and the allelic fab2 mutant are dwarf and develop lesions that contain dead cells (Lightner et al., 1994a, 1994b; Shah et al., 2001). Figure 1 summarizes the impact of ssi2 on Arabidopsis defense signaling. The ssi2 phenotypes are caused by a deficiency in a plastidic stearoyl-ACP desaturase activity (Kachroo et al., 2001), sug-

![Figure 1. Impact of the ssi2 Mutant on Defense Signaling in Arabidopsis.](image-url)
gusting the involvement of lipids and lipid signaling in plant development and in modulating SA- and JA-dependent defense mechanisms. The FAB2 (SSI2)-encoded stearoyl-ACP desaturase preferentially desaturates 18:0-ACP to yield 18:1-ACP (Shanklin and Somerville, 1991; Shanklin and Cahoon, 1998). Compared with those in wild-type plants, 18:0 levels were increased and 18:1 levels were depressed in the ssi2 mutant. Moreover, coapplication of 18:1 restored JA-activated PDF1.2 expression in the ssi2 mutant, suggesting that 18:1 deficiency, rather than the increased 18:0 level, was responsible for the inability of the ssi2 mutant to express PDF1.2 (Kachroo et al., 2001). However, the role of altered lipid composition in other ssi2-conferred phenotypes was unclear.

To further elucidate the role of lipids in the ssi2-conferred growth and developmental phenotypes and defense responses, we conducted a suppressor screen in the ssi2 npr1 genetic background for mutants that lack ssi2-conferred dwarfing and PR1 expression. The sfd1, sfd2, and sfd4 mutant alleles suppress the ssi2-conferred dwarfing and lesion development, the NPR1-independent expression of PR1, and resistance to Pseudomonas syringae pv maculicola (Psm). In addition, sfd1 overcomes the ssi2-conferred block on MeJA activation of PDF1.2 expression. sfd4 contains a mutation in the 16:1/18:1 Δ6 desaturase gene FAD6. Moreover, levels of the PUFA 16:3 were depressed in all sfd ssi2 npr1 plants, suggesting a role for PUFA-derived signals in promoting the ssi2-conferred plant developmental and defense response phenotypes.

RESULTS

sfd Mutant Alleles Suppress the ssi2-Conferred Dwarfing and Lesion Development and the NPR1-Independent Expression of the PR1 Gene

To isolate suppressors of the stearoyl-ACP desaturase-deficient ssi2 mutation, seeds from ssi2 npr1 plants were mutagenized with ethyl methanesulfonate as described previously (Shah et al., 1997). Four-week-old M2 progeny of these ethyl methanesulfonate–mutagenized M1 seeds were screened for large plants and for the loss of ssi2-conferred constitutive PR1 expression. Seven sfd mutants were identified among the 4000 M2 plants screened. These sfd mutants define four complementation groups: sfd1 (two alleles: sfd1-1 and sfd1-2), sfd2 (three alleles: sfd2-1, sfd2-2, and sfd2-3), sfd3, and sfd4. Mutants in the sfd1, sfd2, and sfd4 complementation groups were characterized further. As shown in Figures 2A and 3A, mutants in the sfd1, sfd2, and sfd4 complementation groups ameliorate the ssi2-conferred dwarf phenotype and depress the ssi2-conferred NPR1-independent expression of the PR1 gene. The suppressive effect of these sfd alleles on the ssi2-conferred BGL2 expression was less pronounced.

Compared with the wild type and npr1, leaves of all sfd ssi2 npr1 plants were lighter green. Leaves of the ssi2 and ssi2 npr1 mutant plants develop macroscopic lesions containing dead cells (Shah et al., 2001). However, leaves of all sfd1 ssi2 npr1 and sfd2 ssi2 npr1 plants and the sfd4 ssi2 npr1 plant do not exhibit macroscopic lesions. We examined trypan blue–stained leaves from the sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants to determine whether they had microscopic lesions containing dead cells. Trypan blue stains dead cells dark blue. As shown in Figure 2B, unlike the ssi2 npr1 plant, but like the npr1 control, leaves of the sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants lacked intensely stained dead cells.

sfd1 and sfd4 Suppress the ssi2-Conferred SA Accumulation

Previously, we had shown that the ssi2-conferred accumulation of increased SA is not required for cell death and dwarfing (Shah et al., 2001). Dwarfing, cell death, and SA accumulation may be activated independently by ssi2. Alternatively, dwarfing and/or the activation of cell death in the ssi2 mutant may stimulate SA accumulation. Therefore, we measured the total SA plus SA-glucoside levels in leaves of sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants. As shown in Table 1, the total SA content of sfd1-1 ssi2 npr1 and sfd4 ssi2 npr1 plants was comparable to the total SA level in wild-type and npr1 plants and 25- to 50-fold lower than the total SA level in the ssi2 npr1 plant. By contrast, the total SA content in the sfd2-1 ssi2 npr1 plant was ~13-fold higher than the total SA level in wild-type and npr1 plants and one-quarter of that in the ssi2 npr1 plant.

To determine if the loss of ssi2-conferred NPR1-independent PR1 expression in sfd1-1 ssi2 npr1 is attributable to the lack of SA accumulation, we examined PR1 expression in leaves of the SA-treated sfd1-1 ssi2 npr1 plant. SA-treated wild-type, ssi2, and ssi2 npr1 plants served as positive controls for monitoring the efficacy of SA application in this experiment, and the npr1 mutant served as a negative control. As shown in Figure 3B, SA was ineffective at restoring ssi2-conferred PR1 expression in the sfd1-1 ssi2 npr1 plant. Likewise, SA application was ineffective at restoring PR1 expression in the sfd2-1 ssi2 npr1 plant (Figure 3B) and sfd4 ssi2 npr1 plants (data not shown). By contrast, the SA-treated wild-type and ssi2 control plants expressed high levels of PR1. Similar results were obtained with the application of benzothiadiazole, a functional analog of SA (data not shown). Hence, another ssi2-modulated factor(s), in addition to SA, is required for the NPR1-independent PR1 expression observed in the ssi2 mutant.

sfd1, sfd2, and sfd4 Suppress the ssi2-Conferred NPR1-Independent Resistance to Psm

We had shown previously that the activation of SA signaling in the ssi2 npr1 plant confers enhanced resistance to P. syringae pv tomato DC3000 containing the avirulence gene avrRpt2 and the oomycete Peronospora parasitica Emco5 (Shah et al., 2001). Similarly, as shown in Figure 4A, compared with wild-type and npr1 plants, the ssi2 npr1 double mutant plant exhibited enhanced resistance to Psm. Bacterial numbers at 3 days after inoculation in the ssi2 npr1 plant were 20-fold lower than those in the npr1 plant. Therefore, we tested if the sfd1, sfd2, and sfd4 mutant alleles could suppress the ssi2-conferred NPR1-independent resistance to Psm. Bacterial numbers were monitored in sfd1-1 ssi2 npr1, sfd1-2 ssi2 npr1, sfd2-1 ssi2 npr1, sfd2-2 ssi2 npr1, sfd2-3 ssi2 npr1, and sfd4 ssi2 npr1 plants. As shown in Figure 4A, bacterial numbers in sfd1-1 ssi2
npr1, sfd1-2 ssi2 npr1, sfd2-1 ssi2 npr1, sfd2-2 ssi2 npr1, sfd2-3 ssi2 npr1, and sfd4 ssi2 npr1 plants at 3 days after inoculation were 8- to 10-fold higher than those in the ssi2 npr1 plant.

**sfd2 Does Not Suppress the ssi2-Conferred NPR1-Dependent Expression of PR1**

The ssi2 mutant activates SA signaling through the NPR1-dependent pathway in addition to via the NPR1-independent mechanism (Shah et al., 2001). Therefore, we tested if the sfd1-1 and sfd2-1 mutant alleles could suppress ssi2-conferred PR1 expression in the wild-type NPR1-containing sfd1-1 ssi2 and sfd2-1 ssi2 plants. As shown in Figure 3C, the sfd1-1 allele effectively suppressed ssi2-conferred constitutive PR1 expression in the sfd1-1 ssi2 plant. By contrast, the sfd2-1 allele was not very effective at blocking ssi2-conferred PR1 expression in the sfd2-1 ssi2 double mutant (Figure 3A). Compared with the PR1 transcript levels in the ssi2 mutant plant, only a slight reduction in the accumulation of PR1 transcript, probably as a result of the suppression of the NPR1-independent pathway, was observed in the sfd2-1 ssi2 plant, suggesting that sfd2 specifically affects NPR1-independent signaling.

**sfd1 Bypasses the ssi2-Conferred Block on the JA-Activated Expression of PDF1.2**

The loss of SSI2 activity in the ssi2 mutant prevents the JA-activated expression of the PDF1.2 gene (Kachroo et al., 2001).

Figure 2. Comparison of Morphological and Cell Death Phenotypes of the sfd ssi2 npr1 Mutants.

(A) Comparison of the morphology of 4-week-old npr1, ssi2 npr1, sfd1-1 ssi2 npr1, sfd1-2 ssi2 npr1, sfd2-1 ssi2 npr1, sfd2-1/- ssi2 npr1, sfd2-2 ssi2 npr1, and sfd4 ssi2 npr1 plants. The sfd2-1/- ssi2 npr1 plant is heterozygous for the sfd2-1 mutant allele. All plants were photographed from the same distance.

(B) Light microscopy of trypan blue–stained leaves from npr1, ssi2 npr1, sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants. The arrows mark areas containing intensely stained dead cells in ssi2 npr1. All photographs were taken at the same magnification.
The Plant Cell

Kloek et al. (2001) have shown that JA signaling antagonizes SA signaling in plant defense, including the expression of PR1 and resistance to P. syringae. The lack of ssi2-conferred PR1 expression in the sfd1 ssi2 npr1, sfd2 ssi2 npr1, and sfd4 ssi2 npr1 plants could result from the restoration of JA signaling. Therefore, we examined the expression of the PDF1.2 gene in MeJA-treated leaves of the sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants. MeJA-treated leaves of wild-type and npr1 plants served as positive controls for this experiment, and ssi2, ssi2 npr1, and ssi2 npr1 nahG plants served as negative controls. As shown previously (Kachroo et al., 2001), MeJA application conferred high-level expression of the PDF1.2 gene in leaves of wild-type and npr1 plants but not in ssi2, ssi2 npr1, and ssi2 npr1 nahG plants (Figure 3E). The presence of the sfd1-1 allele restored PDF1.2 expression in MeJA-treated leaves of the sfd1-1 ssi2 npr1 plant (Figure 3E). However, MeJA was unable to activate PDF1.2 expression in the leaves of sfd2-1 ssi2 npr1 and sfd4 ssi2 npr1. As expected, control plants treated with ethanol, which was used to dilute the MeJA, did not activate the expression of PDF1.2 (data not shown).

**ssi2-Conferred Susceptibility to B. cinerea Is Unaffected by sfd1, sfd2, and sfd4**

An increased susceptibility to B. cinerea parallels the inability of the ssi2 mutant to express the PDF1.2 gene in response to JA application (Kachroo et al., 2001). Therefore, we tested whether the restoration of JA-inducible PDF1.2 expression in the sfd1-1 ssi2 npr1 plant is associated with the reestablishment of resistance to B. cinerea. As shown in Figure 4B, compared with the wild-type plant, the sfd1-1 ssi2 npr1 plant retained the ssi2-conferred enhanced susceptibility to infection with B. cinerea. The relative infection rating of sfd1-1 ssi2 npr1 was comparable to those of ssi2 npr1 and ssi2 plants. Similarly, the sfd1-2 ssi2 npr1 plant retained the ssi2-conferred enhanced susceptibility to B. cinerea. The relative infection ratings for sfd2-1 ssi2 npr1, sfd2-2 ssi2 npr1, and sfd4 ssi2 npr1 plants were comparable to that of the ssi2 npr1 plant as well.

**sfd1, sfd2, and sfd4 Modify the Lipid Profile of the ssi2 Mutant**

It was hypothesized previously that decreased levels of 18:1 contribute directly or indirectly to the ssi2 phenotypes (Kachroo et al., 2001). Alternatively, high levels of 18:0 in membrane lipids of the ssi2 mutant might activate one or more ssi2-con-
ferred phenotypes. The *sfd*-mediated suppression of the *ssi2*-conferring phenotypes could result from restoration or other alterations in the lipid composition of the mutant plants. Therefore, we compared the fatty acid composition of polar lipids from *sfd1-1 ssi2 npr1*, *sfd2-1 ssi2 npr1*, and *sfd4 ssi2 npr1* plants with those of wild-type, *npr1*, and *ssi2 npr1* plants. As shown previously (Kachroo et al., 2001), the mol % of 18:0 in *ssi2 npr1* was sixfold higher and that of 18:1 was one-third of the level in the *npr1* plant (Table 2). The mol % of 18:0 in *sfd1-1 ssi2 npr1* was comparable to that in *ssi2 npr1*, whereas the mol % of 18:0 in the *sfd2-1 ssi2 npr1* and *sfd4 ssi2 npr1* plants were slightly lower than that in *ssi2 npr1*. However, these levels still were fivefold higher than the mol % of 18:0 in the *npr1* plant. Hence, it seems unlikely that increased 18:0 mol % is responsible for the *ssi2* phenotypes.

By contrast, the mol % of 18:1 in *sfd1-1 ssi2 npr1* was 2.5-fold higher and that in *sfd2-1 ssi2 npr1* was 2-fold higher than that in the *ssi2 npr1* plant. The mol % of 18:1 in the *sfd4 ssi2 npr1* plant was ~18-fold higher than in the *ssi2 npr1* plant and 6-fold higher than that in *npr1*. This increase in the mol % of 18:1 in *sfd4 ssi2 npr1* was paralleled by a corresponding reduction in the mol % of 18:3. One striking and consistent alteration in the fatty acid compositions of all of the *sfd ssi2 npr1* plants was the decrease in the mol % of hexadecatetraenoic acid (16:3). 16:3 mol % in the *sfd1-1 ssi2 npr1* mutant was 40% lower than that in the *ssi2 npr1* plant, whereas 16:3 mol % in *sfd2-1 ssi2 npr1* and *sfd4 ssi2 npr1* were 82 and 90% lower, respectively, than that in *ssi2 npr1*. The decreased mol % of 16:3 in *sfd4 ssi2 npr1* was paralleled by an increase in the mol % of 16:1.

The lipid compositions were examined in more detail by comparing the molecular species of the membrane lipids in the leaves of *ssi2, ssi2 npr1*, *sfd1-1 ssi2 npr1*, *sfd2-1 ssi2 npr1*, and *sfd4 ssi2 npr1* plants. Wild-type and *npr1* plants served as controls for this experiment. Compared with the wild-type (214 nmol diacyl species/mg dry weight) and the *npr1* mutant (213 nmol diacyl species/mg dry weight), the *ssi2* and *ssi2 npr1* plants contained lower amounts of lipid (147 and 155 nmol diacyl species/mg dry weight, respectively). As shown in Figure 5A, the lower lipid levels in *ssi2* and *ssi2 npr1* were attributable to a lower content of the lipids that are primarily plastid synthesized and localized: PG and MGDG species decreased by ~40%, whereas DGDG levels decreased by ~50%. The total lipid content was increased somewhat in the *sfd1-1 ssi2 npr1* (191 nmol diacyl species/mg dry weight) and *sfd2-1 ssi2 npr1* (166 nmol diacyl species/mg dry weight) plants, compared with

### Table 1. Total SA Content in *sfd* Plants

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Total SA ± SD (µg/g FW)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild type</td>
<td>0.5 ± 0.2</td>
</tr>
<tr>
<td><em>npr1</em></td>
<td>0.5 ± 0.1</td>
</tr>
<tr>
<td><em>ssi2 npr1</em></td>
<td>24.0 ± 1.8</td>
</tr>
<tr>
<td><em>sfd1-1 ssi2 npr1</em></td>
<td>0.5 ± 0.1</td>
</tr>
<tr>
<td><em>sfd2-1 ssi2 npr1</em></td>
<td>6.6 ± 1.3</td>
</tr>
<tr>
<td><em>sfd4 ssi2 npr1</em></td>
<td>0.9 ± 0.3</td>
</tr>
</tbody>
</table>

Total SA values for each line are averages of five samples ± SD. All values are corrected based on a 73% recovery. FW, fresh weight.
Table 2. Fatty Acyl Profile of Polar Lipids in sfd Plants

<table>
<thead>
<tr>
<th>Genotype</th>
<th>16:0</th>
<th>16:1</th>
<th>16:2</th>
<th>16:3</th>
<th>18:0</th>
<th>18:1</th>
<th>18:2</th>
<th>18:3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild type</td>
<td>15.7</td>
<td>4.3</td>
<td>0.8</td>
<td>15.5</td>
<td>1.4</td>
<td>2.5</td>
<td>14.1</td>
<td>45.3</td>
</tr>
<tr>
<td>npr1</td>
<td>18.4</td>
<td>5.6</td>
<td>1.0</td>
<td>14.0</td>
<td>1.9</td>
<td>2.7</td>
<td>14.5</td>
<td>41.1</td>
</tr>
<tr>
<td>sfd2-1 ssi2 npr1</td>
<td>13.9</td>
<td>3.4</td>
<td>0.6</td>
<td>12.4</td>
<td>1.2</td>
<td>1.0</td>
<td>15.5</td>
<td>40.4</td>
</tr>
<tr>
<td>sfd4 ssi2 npr1</td>
<td>16.0</td>
<td>15.9</td>
<td>0.3</td>
<td>1.3</td>
<td>9.6</td>
<td>17.7</td>
<td>14.6</td>
<td>24.3</td>
</tr>
<tr>
<td>sfd2-1 ssi2 npr1</td>
<td>19.3</td>
<td>4.0</td>
<td>0.3</td>
<td>2.7</td>
<td>8.4</td>
<td>2.0</td>
<td>14.4</td>
<td>48.5</td>
</tr>
</tbody>
</table>

All values are given as mol % of fatty acids. The value for each line is the average of five samples ± SD. Values for 14:0 are not listed.

155 nmol diacyl species/mg dry weight for ssi2 npr1. This increase was primarily the result of an increase in the content of 36:6-MGDG (18:3-18:3 acyl combination) in sfd1-1 ssi2 npr1 and sfd2-1 ssi2 npr1 (Figure 5A). Total lipid in the sfd4 ssi2 npr1 mutant plant (153 nmol diacyl species/mg dry weight) was not increased. The large reduction in 16:3 levels in sfd2-1 ssi2 npr1 and sfd4 ssi2 npr1 were reflected in a >80% reduction in the level of 34:6-MGDG (16:3-18:3 acyl combination) (Figure 5A). 34:6 levels in sfd1-1 ssi2 npr1 were only 17% lower than those in ssi2 npr1. However, the ratio of 34:6-MGDG to 36:6-MGDG was low in all the mutants, with ratios of 0.8 in sfd1-1 ssi2 npr1, 0.2 in sfd2-1 ssi2 npr1, and 0.3 in sfd4 ssi2 npr1, compared with 2.6 in the wild type and 2.3 in ssi2 npr1.

In addition, there were considerable differences in the molecular species within the phospholipid classes of ssi2 and ssi2 npr1 plants compared with those in wild-type and npr1 plants. For example, ssi2 and ssi2 npr1 plants contained higher proportions of PE, PC, and PI containing either a 36:2 or 36:3 acyl composition (Figure 5B). Analysis of the acyl fragments of these 36:2 and 36:3 molecular species in ssi2 npr1 plants indicated that they represent primarily the 18:2-18:2 and 18:3-18:3 combinations, respectively. The levels of 34:2-PC, 34:2-PE, and 34:2-PI were lower in the ssi2 and ssi2 npr1 plants than in wild-type or npr1 plants, whereas 34:3-PC, 34:3-PE, and 34:3-PI were similar or slightly higher in ssi2 and ssi2 npr1 (Figure 5B). Acyl fragment analysis showed that 34:2 species in npr1 and ssi2 npr1 represented mainly a combination of 18:2 and 16:0, whereas 34:3 species were mainly a 16:3-18:0 combination, but lower amounts of 16:1-18:2 and 18:0-16:3 combinations were detected. Interestingly, the trace amounts of 18:0-16:3 in phospholipids were higher in ssi2 npr1 plants than in npr1 plants. For example, in npr1 plants, 16:3-18:0 represents 0.3% of the 34:3-PE species, whereas in ssi2 npr1, 16:3-18:0 represents 1.4% of the 34:3-PE species. Levels of the 34:2-, 36:2-, and 36:3 PC, PE, and PI species in sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 were comparable to the levels of these species in ssi2 npr1 (Figure 5B). However, compared with the levels in wild-type, npr1, and ssi2 npr1 plants, the levels of 34:3-PC, 34:3-PE, and 34:3-PI species were lower in the sfd1-1 ssi2 npr1 and sfd4 ssi2 npr1 plants.

Genetic Characterization of the sfd1 and sfd2 Mutants

The genetic basis of the sfd1 and sfd2 phenotypes was characterized in detail. F1 plants resulting from a cross between sfd1-1 ssi2 npr1 and the ssi2 npr1 parent exhibited the typical small-plant phenotype associated with the ssi2 mutant, suggesting that sfd1-1 is recessive to the wild-type SFD1 allele (Table 3). These F1 plants also developed lesions containing dead cells and expressed the PR1 gene at high levels (data not shown). The F2 progeny of these F1 plants segregated wild-type and ssi2-like plants in a nearly 1:3 ratio. Moreover, only the ssi2-like dwarf segregants expressed PR1, confirming that sfd1-1 is a recessive mutation at a single genetic locus. Likewise, the sfd1-2 phenotype also was confirmed to be a monogenic recessive trait (data not shown). The F1 plants generated by crossing the sfd1-1 ssi2 npr1 plant with the sfd1-2 ssi2 npr1 plant were large, devoid of lesions, and lacked PR1 expression. Moreover, none of the F2 F2 progeny derived from these F1 plants exhibited the dwarf and lesion-bearing phenotypes associated with ssi2, confirming that sfd1-1 and sfd1-2 are allelic (Table 3).

F1 plants (sfd2-1/+ ssi2 npr1) generated by crossing the sfd2-1 ssi2 npr1 plant with a ssi2 npr1 plant were intermediate in size compared with the parents (Figure 2A). In addition, the level of PR1 transcript in these sfd2-1/+ ssi2 npr1 plants was intermediate to levels of PR1 transcript in the ssi2 npr1 and homozygous sfd2-1 ssi2 npr1 plants (Figure 3D), suggesting that sfd2-1 is semidominant. Likewise, in contrast to the sfd2-1 ssi2 npr1 plant, the sfd2-1-mediated suppression of ssi2 conferring resistance to Psm was less pronounced in the sfd2-1/+ ssi2 npr1 plant (A. Nandi and J. Shah, unpublished data). The semidominance of sfd2-1 was confirmed in the F2 progeny, which segregated large, intermediate, and dwarf plants in a nearly 1:2:1 ratio (Table 3). Negligible levels of PR1 transcript were observed in the large F2 progeny plants, whereas moderate and high levels of constitutive PR1 expression were observed in the intermediate and dwarf plants, respectively (data not shown). F3 progeny of the intermediate F2 plants segregated large, intermediate, and dwarf plants, confirming that these F2 plants were heterozygous at the sfd2 locus. Similarly, the sfd2-1 and sfd2-3 alleles also exhibited a semidominant phenotype (data not shown). Crosses between sfd2-1 ssi2 npr1 and sfd2-2 ssi2 npr1, sfd2-1 ssi2 npr1 and sfd2-3 ssi2 npr1, and sfd2-2 ssi2 npr1 and sfd2-3 ssi2 npr1 suggested that sfd2-1, sfd2-2, and sfd2-3 are allelic. All F1 plants from these crosses retained the large sfd2 phenotype. Furthermore, none of them segregated dwarf ssi2-like F2 progeny plants. Further support for allelism among sfd2-1, sfd2-2, and sfd2-3 is provided by the identical lipid profiles of these mutants (A. Nandi, C. Buseman, M. Li, R. Welti, and J. Shah, unpublished data).
In our attempts to outcross $sfd1$ away from the $ssi2$ mutant allele, we discovered that $sfd1$ was linked to the $ssi2$ locus on chromosome 2. As shown in Table 3, of the 146 F2 progeny of an F1 plant obtained from a cross between $sfd1$-2 $ssi2$ $npr1$ and a wild-type plant, only two morphologically $ssi2$-like segregants were observed. Mapping populations composed of large and lesionless ($sfd1$/$sfd1$) F2 progeny of F1 plants derived from a cross between $sfd1$-1 $ssi2$ $npr1$ and the $fab2$ (allelic with $ssi2$) mutant in ecotype Nössen and the $f2d2$ (allelic with $ssi2$) mutant in ecotype Columbia confirmed that $sfd1$ maps in the vicinity of $SSI2$. Likewise, mapping populations generated by crossing the $sfd1$-2 $ssi2$ $npr1$ plant with the $fab2$ mutant also localized $sfd1$-2 on chromosome 2, near $SSID$. Cleaved amplified polymorphic sequence (Konieczny and Ausubel, 1993) and simple sequence length polymorphism (Bell and Ecker, 1994) analyses performed on 29 $sfd1$-1/$sfd1$-1 and 26 $sfd1$-2/$sfd1$-2 F2 progeny plants mapped the $sfd1$ locus between the SSLP markers F27D4 and the $SSI2$ gene, 20 centi-morgan (cM) from F27D4 and 3 cM from $SSI2$. The size of the mapping population was increased subsequently to 301 F2 $sfd1$/$sfd1$ plants to map $sfd1$ between the SSLP marker nga168 (2.1 cM; 13 recombinant chromosomes) and the $SSI2$ gene (2.6 cM; 16 recombinant chromosomes).

Mapping populations generated by crossing $sfd2$-1 $ssi2$ $npr1$ with $fab2$ were used to map $sfd2$. Analysis of 20 large $sfd2$-1/$sfd2$-1 F2 progeny plants mapped the $sfd2$ locus to a 27-cM interval on chromosome 3, between the cleaved amplified polymorphic sequence marker T6H20 and the SSLP nga6, 20 cM from T6H20 and 7 cM from nga6.

Figure 5. Lipid Profiles of the $sfd$ Mutants.

(A) Electrospray ionization–tandem mass spectrometry–generated profiles of the plastidic glycerolipids PG, DGDG, and MGDG in wild-type (WT), $npr1$, $ssi2$, $ssi2$ $npr1$, $sfd1$-1 $ssi2$ $npr1$, $sfd2$-1 $ssi2$ $npr1$, and $sfd4$ $ssi2$ $npr1$ plants.

(B) Electrospray ionization–tandem mass spectrometry–generated profiles of the extraplastidic glycerolipids PC, PE, and PI in wild-type (WT), $npr1$, $ssi2$, $ssi2$ $npr1$, $sfd1$-1 $ssi2$ $npr1$, $sfd2$-1 $ssi2$ $npr1$, and $sfd4$ $ssi2$ $npr1$ plants.
**sfd4 Contains a Mutation in the FAD6 Gene**

The fatty acid composition of polar lipids in sfd4 ssi2 npr1 showed a decrease in content of the trienoic acids 16:3 and 18:3 and a corresponding increase in the concentrations of 16:1 and 18:1 (Table 2), suggesting that it is blocked in the desaturation of 16:1 and 18:1. This is similar to the defect in the fad6 mutant, which is deficient in a plastidic 16:1/18:1 ω6 desaturase activity (Browse et al., 1989). Therefore, we sequenced the FAD6 locus from wild-type Nössen and sfd4 ssi2 npr1 plants. Indeed, the sfd4 ssi2 npr1 plant contained a single nucleotide change (C→T transition) in the FAD6 gene (Falcone et al., 1994), which is expected to result in a Ser-133→Phe-133 change in the corresponding protein. Ser-133 is highly conserved among FAD6 homologs from various plant and cyanobacterial species (Figure 6A). This C→T transition mutation in the sfd4 ssi2 npr1 plant resulted in an EcoRV restriction polymorphism (Figure 6B), thus confirming the presence of a mutation in the FAD6 gene. To confirm that FAD6 is required for the manifestation of the ssi2-conferring development and defense phenotypes, we generated the ssi2 fad6 double mutant. As shown in Figures 6D and 6E, the fad6 mutant allele suppressed the ssi2-conferring dwarfing and spontaneous cell death phenotypes. In addition, the ssi2-conferring constitutive PR1 expression also was suppressed by the fad6 allele (Figure 6C). These effects of the fad6 allele on the ssi2 phenotype were recessive to the wild-type FAD6 allele, and the ssi2 fad6/+ plant retained all of the ssi2-conferring phenotypes.

**DISCUSSION**

The sfd1, sfd2, and sfd4 mutations suppress key phenotypes of the ssi2 mutation, including dwarfing, lesion development, the NPR1-independent expression of the PR1 gene, and resistance to Psm. The high mol % of 18:0 in leaves of sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants imply that increased 18:0 levels are not sufficient to cause the ssi2 phenotypes. The
increases in mol % of 18:1 in the leaves of the *sfd1-1 ssi2 npr1*, *sfd2-1 ssi2 npr1*, and *sfd4 ssi2 npr1* plants could account for the suppression of some *ssi2*-conferred phenotypes. However, pharmacological experiments argue against this increase in 18:1 mol % suppressing the *ssi2*-conferred *PR1* expression. To the contrary, the application of 18:1 free fatty acid to leaves of the wild-type plant activates *PR1* expression (A. Nandi and J. Shah, unpublished data), further suggesting that *gly1* and *sfd1* contain mutations in the same gene.

The *sfd4* mutation is predicted to alter the highly conserved Ser-133 to Phe-133 in the FAD6 protein. *FAD6* encodes a 16:1/18:1 ω6 desaturase that catalyzes the desaturation of plastid-localized 16:1 and 18:1 to 16:2 and 18:2, respectively (Browse et al., 1989; Falcone et al., 1994). In wild-type plants, 16:2 and 18:2 can be converted further to 16:3 and 18:3, respectively, by other desaturases. Like the *fad6* mutant, *sfd4 ssi2 npr1* contains higher levels of the monounsaturated 16:1 and 18:1 fatty acids at the expense of the trienoic fatty acids 16:3 and 18:3, the two predominant PUFAs in Arabidopsis (Wallis and Browse, 2002). Mutations in the *FAD5* gene also affect the synthesis of 16:3 (Kunst et al., 1989). However, unlike the *fad6* mutation, mutations in *fad5* do not affect 18:3 levels. *FAD5* encodes a plastidic palmitoyl desaturase (Mekhedov et al., 2000). Compared with *ssi2 npr1* and *npr1*, 16:3 levels are very low in leaves of the *sfd2 ssi2 npr1* plant, and no decrease in the level of 18:3 was observed (Table 2). These data suggest that *SFD2*, like *FAD5*, might affect the synthesis or accumulation of 16:3. However, *sfd2* does not map to the *FAD5* locus; thus, it identifies a novel gene that affects 16:3 biosynthesis or accumulation. Therefore, our results suggest an important role for 16:3, or complex lipids containing it, in the manifestation of one or more *ssi2*-conferred phenotypes.

**SA Signaling in the *sfd* Mutants**

The activation of JA signaling can antagonize SA signaling in Arabidopsis (Kloeck et al., 2001). It is possible that the *ssi2*-conferred *PR1* expression is the result of the loss of this inhibitory effect of JA. Indeed, the loss of *ssi2*-conferred *PR1* expression in *sfd1 ssi2 npr1* plants correlates with the restoration of JA-activated *PDF1.2* expression. However, JA responses are not restored in the *sfd2 ssi2 npr1* and *sfd4 ssi2 npr1* mutants, yet *ssi2*-conferred NPR1-independent *PR1* expression is sup-

---

**Table 3. Genetic Analysis of the *sfd1* and *sfd2* Mutants**

<table>
<thead>
<tr>
<th>Cross</th>
<th>F1 Phenotype</th>
<th>F2 Progeny</th>
<th>Mendelian Ratio</th>
<th>Hypothesis</th>
<th>χ²</th>
<th>P²</th>
<th>Fit?/Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>sfd1-1 ssi2 npr1 × ssi2 npr1</em></td>
<td>Large</td>
<td>11</td>
<td>0</td>
<td>1:2:9</td>
<td>0.05</td>
<td>0.9 &gt; P &gt; 0.5</td>
<td>Yes</td>
</tr>
<tr>
<td><em>sfd1-1 ssi2 npr1 × sfd1-2 ssi2 npr1</em></td>
<td>Intermediate</td>
<td>72</td>
<td>0</td>
<td>alinked to sfd2</td>
<td>1:1:9:1:1</td>
<td>Monogenic recessive</td>
<td>0.17</td>
</tr>
<tr>
<td><em>sfd1-2 ssi2 npr1 × SFD1 SSI2 NPR1</em></td>
<td>Intermediate</td>
<td>144</td>
<td>2</td>
<td>Linked to ssi2</td>
<td>2</td>
<td>0.9 &gt; P &gt; 0.5</td>
<td>Yes</td>
</tr>
<tr>
<td><em>sfd2-1 ssi2 npr1 × ssi2 npr1</em></td>
<td>Dwarf</td>
<td>9</td>
<td>17</td>
<td>10</td>
<td>1</td>
<td>1.9:1.1</td>
<td>Yes</td>
</tr>
</tbody>
</table>

---

*a* Plants were scored for the presence/absence of the dwarf phenotype associated with *ssi2*.

*b* Degrees of freedom used to calculate probability: *sfd1-1 ssi2 npr1 × ssi2 npr1* (df = 1); *sfd2-1 ssi2 npr1 × ssi2 npr1* (df = 2). The Plant Cell
pressed in these plants, arguing against JA signaling per se affecting PR1 expression in the ssi2 mutant. However, we cannot exclude the possibility that the sfd2 and sfd4 mutants affect a step after the point of this crosstalk between the JA and SA pathways.

The simultaneous absence of ssi2-conferring cell death, dwarfism, SA and PR1 transcript accumulation, and enhanced resistance to Psm in the sfd1 ssi2 npr1 and sfd4 ssi2 npr1 plants suggests that SFD1 and SFD4 target a step common to the expression of these ssi2 phenotypes (Figure 7). The sfd1-1 and sfd4/fad6 mutants blocked the ssi2-conferring PR1 expression equally well in wild-type NPR1 and npr1 mutant backgrounds (Figures 3C and 6C). The lack of an increased SA level could account for the absence of ssi2-conferring PR1 expression in the sfd1-1 ssi2 and sfd4/fad6 ssi2 plants. However, unlike the sfd1 ssi2 npr1 and sfd4 ssi2 npr1 plants, the sfd2-1 ssi2 npr1 plant accumulates increased SA levels. Furthermore, in contrast to the sfd2-1 ssi2 npr1 plant, PR1 was expressed constitutively in sfd2-1 ssi2, which contains the wild-type NPR1 gene. Thus, SFD2 is required only for the ssi2-conferring cell death, dwarfing, and for the functioning of the NPR1-independent defense pathway. The fatty acid composition in sfd2-1 ssi2 was comparable to that in sfd2-1 ssi2 npr1 (Table 2). Hence, the inability of sfd2-1 to suppress the NPR1-dependent PR1 expression is not caused by differences in lipid composition between the sfd2-1 ssi2 and sfd2-1 ssi2 npr1 plants. Instead, the high SA content may suffice to activate PR1 expression through the NPR1-regulated pathway in the sfd2-1 ssi2 plant.

The inability of applied SA to restore PR1 expression in the sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants (Figure 3B and data not shown) suggests the requirement for an additional factor, in addition to SA, for the activation of NPR1-independent PR1 expression. A 16:3-derived product and/or regulated activity could be this second factor required for the activation of SA signaling. Lipid signaling was shown by Anderson et al. (1998) to be an important factor in modulating the SA-activated expression of the PR1 gene in tobacco. Alternatively, this second factor could be made available by the cell death and/or dwarfing that occurs in the ssi2 mutant.

JA Signaling in sfd Mutants

Lack of an 18:1-derived signal/factor was suggested to be responsible for the inability of JA to activate PDF1.2 expression in the ssi2 mutant (Kachroo et al., 2001). The restoration of wild-type levels of 18:1 (Table 2) could account for the establishment of JA-activated PDF1.2 expression in the sfd1-1 ssi2 npr1 plant (Figure 3E). However, comparable levels of 18:1 in the sfd2-1 ssi2 npr1 plant and the eightfold higher levels of 18:1 in sfd4 ssi2 npr1 were not sufficient to restore JA-activated expression in the sfd Mutants.

(E) Light microscopy of trypan blue-stained leaves of 4-week-old soil-grown ssi2 plants that are homozygous for the wild-type FAD6 allele (ssi2), heterozygous for the fad6-1 mutant allele (ssi2 fad6/+) and homozygous for the fad6-1 mutant allele (ssi2 fad6). All plants were photographed from the same distance.
This model is a refinement of Figure 1. The sfd1, sfd2, and sfd4 mutant alleles suppress (−) the ssi2-confounded dwarfing, spontaneous development of lesions containing dead cells, NPR1-independent expression of PR1, and enhanced resistance to Psm. In addition, sfd1 and sfd4 also suppress the ssi2-confounded accumulation of high SA levels. However, SA application is ineffective in restoring PR1 expression in sfd1 ssi2 npr1, sfd2 ssi2 npr1, and sfd4 ssi2 npr1 plants, implicating the involvement of another ssi2-contributed factor in the activation of the NPR1-independent pathway leading to the expression of PR1 and enhanced resistance to Psm. The absence of SA accumulation in the ssi2 nahG and ssi2 eds5 plants does not ameliorate the ssi2-confounded cell death phenotype, suggesting that high levels of SA do not have a causal role in the cell death phenotype. The sfd2 ssi2 npr1 plants accumulate increased SA levels despite the lack of spontaneous cell death, suggesting that cell death is not the primary factor that promotes SA accumulation in the ssi2 mutant. Hence, ssi2-confounded cell death and SA accumulation are shown to be independent of each other. The sfd1 mutant alleles restore JA-inducible PDF1.2 expression in sfd1 ssi2 npr1 plants. sfd1 is shown to impinge on a step that is common to the activation of cell death, SA accumulation, the activation of the NPR1-independent defense pathway, and the repression of JA signaling in the ssi2 mutant. However, because sfd1 does not restore resistance to B. cinerea, despite restoring PDF1.2 expression in the sfd1 ssi2 npr1 plants, an additional ssi2-modulated mechanism is shown to suppress (−) the defense against B. cinerea. sfd4 does not restore JA-inducible PDF1.2 expression in sfd4 ssi2 npr1. Hence, sfd4 is shown to suppress (−) a step that is common to the activation of cell death and dwarfing, SA accumulation, and the activation of the NPR1-independent defense pathway. sfd2 is shown to interfere with (−) a step common to the activation of ssi2-confounded cell death and the activation of NPR1-independent signaling.

suggests that an SFD1-dependent signal may be an inhibitor of PDF1.2 expression in the ssi2 plant (Figure 7). In wild-type plants, the 18:1-derived signal may antagonize this inhibitory activity, allowing JA to activate PDF1.2 expression.

JA application activates PDF1.2 expression and confers protection against the necrotrophic pathogen B. cinerea (Penninckx et al., 1996, 1998; Thomma et al., 1999). In addition, enhancing PDF1.2 expression by the overexpression of ETHYLENE RESPONSE FACTOR1, a regulator of PDF1.2 expression in Arabidopsis, enhances resistance to B. cinerea (Berrocal-Lobo et al., 2002). An increased susceptibility to B. cinerea parallels the inability of the ssi2 mutant to express the PDF1.2 gene in response to JA application (Kachroo et al., 2001). However, the restoration of MeJA-activated PDF1.2 expression in the sfd1-1 ssi2 npr1 plant (Figure 3E) was not sufficient to restore resistance to B. cinerea (Figure 4B). Therefore, we cannot exclude the possibility that the sfd1-1 ssi2 npr1 plant, although responsive to MeJA, may not be very sensitive to it or to other factors that activate PDF1.2. For example, although exogenously applied MeJA activated PDF1.2 expression in sfd1-1 ssi2 npr1 plants, the PDF1.2 gene transcript accumulated to lower levels than in the MeJA-treated control npr1 plant (Figure 3E). In addition, application of 1-aminocyclopropane-1-carboxylic acid was ineffective at activating PDF1.2 expression in sfd1-1 ssi2 npr1 plants (A. Nandi and J. Shah, unpublished data).

Govrin and Levine (2000) have shown that hypersensitive response-associated cell death in Arabidopsis enhances susceptibility to B. cinerea. It is likely that cell death in ssi2 predisposes the mutant plant to infection by B. cinerea. However, the prevalence of the ssi2-confounded enhanced susceptibility to B. cinerea in the sfd1-1 ssi2 npr1, sfd2-1 ssi2 npr1, and sfd4 ssi2 npr1 plants (Figure 4B), despite the absence of ssi2-confounded cell death (Figure 2B), argues against cell death being an important factor in the susceptibility of the ssi2 mutant to B. cinerea. The loss of ssi2-activated high-level SA accumulation in the sfd1-1 ssi2 npr1 and sfd4 ssi2 npr1 plants also excludes any involvement of SA in the susceptibility of the ssi2 mutant to B. cinerea.

In conclusion, we show here that the mere increase in 18:0 level resulting from the deficiency of a plastid fatty acid desaturase activity is not sufficient to cause the development defects and the altered defense phenotypes observed in the ssi2 mutant. Instead, the signals/factors derived from the PUFA 16:3 may be involved in the activation of one or more of the ssi2-confounded phenotypes. Although the exact identity of these signaling molecules and the mechanism by which they exert their effects on plant development and defense responses are unclear, the genetic dissection of these signaling mechanisms in concert with lipid compositional analysis in mutants should facilitate our understanding of how plants generate and decipher complex information involving lipids.

**METHODS**

**Cultivation of Plants and Pathogens**

Arabidopsis thaliana seeds were germinated at 22°C in a tissue culture chamber exposed to a 14-h-light (80 µE·m⁻²·s⁻¹)/10-h-dark cycle on
Infections with Bacterial and Fungal Pathogens

Infections with *Psm* ES4326 were performed on 4-week-old soil-grown plants as described previously (Nandi et al., 2003). For every set of infections, 25 (five replications of five leaves in each sample) leaf discs (0.15 cm²) were harvested at 3 days after infection and placed in preweighed tubes. After the weight of each sample was determined, bacterial counts were determined as described previously (Shah et al., 1997). Bacterial counts were expressed as colony-forming units per milligram of leaf tissue.

*Botrytis cinerea* infections were performed on 4-week-old soil-grown plants as described previously (Nandi et al., 2003). Three leaves per plant were pricked with a needle. Infection was initiated by placing a 10-μL drop of freshly harvested spore suspension (5 × 10⁵ spores/mL) on each needle prick. The inoculum was allowed to air dry. Thereafter, plants were covered with a transparent plastic dome and cultivated at 22°C in a growth chamber programmed for a 14-h-light (80 μE·m⁻²·s⁻¹)/10-h-dark cycle. Spores were harvested and infections performed as described previously (Nandi et al., 2003).

Chemical Treatment of Plants

For methyl jasmonate treatment, leaves from 4-week-old plants, excised at the base of the petioles, were floated on 5 mL of a methyl jasmonate solution (5 μM in 0.1% ethanol; Bedoukian Research, Danbury, CT) on tissue culture plates. As the control, leaves from the same plants were floated simultaneously on 5 mL of 0.1% ethanol solution. Leaves were harvested 48 h later, quick frozen in liquid nitrogen, and stored at -80°C until RNA extraction.

Salicylic acid (SA; 500 μM) treatment of 4-week-old soil-grown plants was performed as described previously (Shah et al., 1997). As controls, plants were treated similarly with water. Leaves were harvested 48 h after treatment and quick-frozen in liquid nitrogen. Leaf samples were stored at -80°C until RNA extraction.

RNA Extraction and RNA Gel Blot Analyses

Leaf tissue was ground under liquid nitrogen, and RNA was extracted using acid guanidinium thiocyanate-phenol-chloroform as described by Chomczynski and Sacchi (1987). RNA gel blot analysis and the synthesis of random primed probes for *PR1*, *BGL2*, and *PDF1.2* were performed as described previously (Shah et al., 1997, 1999).

DNA Extraction and PCR Analyses

Arabidopsis genomic DNA from leaf tissue was isolated by the method of Konieczny and Ausubel (1993). PCR analyses to distinguish between the wild-type NPR1 and the npr1-5 mutant alleles were performed as described previously (Shah et al., 1999). A cleaved amplified polymorphic sequence (CAPS) marker was used to distinguish between the ssi2-1 and SSI2 alleles (Kachroo et al., 2001). For studies with *sf4*, the primers FAD6-F1 (5'-GTGCGCTTCTTCTCGATTTTC-3') and FAD6-R1 (5'-TGA-TGACTCAAACTCCTCTG-3') were used for PCR. Thirty cycles of PCR were performed. Each cycle consisted of incubation at 95°C for 45 s followed by 56°C for 30 s and 72°C for 2 min. The PCR products were digested with EcoRV to distinguish the *sf4* mutant allele from the wild-type *SF4* allele. PCR amplification of the other CAPS and simple sequence length polymorphism markers used in this study were performed as described at http://www.arabidopsis.org.

Histochemistry and Microscopy

Leaves from 4-week-old soil-grown plants were used for trypan blue staining of dead cells. Samples were processed and analyzed as described by Rate et al. (1999).

SA Quantitation

Total SA (SA plus SA-glucoside) in 0.25 to 0.5 g (fresh weight) of leaf tissue was extracted in methanol. The methanol extracts were dried and resuspended in 1.25 mL of 100 mM sodium acetate buffer, pH 5.5, containing 20 units of β-glucosidase (EC 3.2.1.21; almond). After 1.5 h of incubation at 37°C, extracts were acidified to pH 1.0 with 10% (w/v) trichloroacetic acid and subjected to SA extraction and quantification by spectrophotofluorescence HPLC as described previously (Enyedi, 1999).

Fatty Acid and Lipid Profiling

For fatty acid analysis, leaves from two to three plants were cut and immediately transferred to 3 mL of isopropanol containing 0.01% butylated hydroxytoluene at 75°C. After 15 min, 1.5 mL of chloroform plus 0.6 mL of water were added. The tubes were shaken for 1 h, followed by removal of the extract. The leaves were reextracted five times with chloroform:methanol (2:1) containing 0.01% butylated hydroxytoluene. During each extraction, the tubes were agitated for 30 min. The extracted leaf tissue was heated overnight at 105°C and weighed. The weight of the dried and extracted tissue was the “dry weight” of the sample. Dry weights ranged from 14 to 78 mg. The combined extracts were washed once with 1 mL of 1 M KCl and once with 2 mL of water. The solvent was evaporated under nitrogen, and the lipid extract was dissolved in 1 mL of chloroform.

For analysis of the fatty acyl species in complex lipids, 200 μL of the sample was applied to a silicic acid (0.3 g) column in chloroform. Neutral lipids were eluted with 10 mL of chloroform, and complex lipids were eluted with 10 mL of methanol. The solvent was evaporated from the methanol fraction, and fatty acid methyl esters were formed from 4% of each sample in duplicate by derivatization in 1.5 M methanolic HCl. After heating at 78°C for 90 min, 2 volumes of water was added to the reaction mixture. Each mixture was extracted twice with pentane and dried with sodium sulfate. The solvent was evaporated, and each sample was dissolved in carbon disulfide and analyzed by gas-liquid chromatography with a Supelco 30-meter Omegawax 250 capillary column (Sigma-Aldrich) at 155°C. The temperature of the injector was 220°C, and the flame ionization detector was also at 220°C. The fatty acyl composition for each sample was an average of the two analyses. The fatty acyl composition of each Arabidopsis line is the average ± SD of five samples.

An automated electrospray ionization–tandem mass spectrometry approach was used to profile lipid composition in Arabidopsis leaves. Sample preparation, processing, data acquisition and analysis, and acyl group identification were as described previously (Welti et al., 2002).

Mutagenesis and Selection of the *sf4* Mutants

Four thousand ssi2 npr1-5 seeds (ecotype Nössen) were mutagenized with 0.3% ethyl methanesulfonate (Sigma-Aldrich) as described previ-
ous (Shah et al., 1997). M2 seeds were harvested as pools; each pool contained M2 seeds derived from \( \sim 150 \) ethyl methanesulfonate–mutagenized M1 seeds. The M2 seeds were germinated in soil, in parallel with seeds of \( \text{ssi2} \text{npr1} \) and wild-type plants. Large plants were identified, and RNA was extracted from the leaves. RNA was analyzed by RNA gel blot analysis for \( PR1 \) expression. RNA extracted from wild-type and \( \text{ssi2} \text{npr1} \) plants served as negative and positive controls, respectively. Individual plants were allowed to set seeds. \( sfd \) phenotypes were confirmed in M3 progeny.

**Genetic Analysis**

Backcrosses were performed by pollinating flowers of the \( sfd \) mutant lines with pollen from the \( \text{ssi2} \text{npr1} \) parental line (Shah et al., 2001). This line contains the \( \text{npr1}-5 \) allele (Shah et al., 1999). A backcrossed homozygous line was used for all other genetic analyses. To generate the \( \text{ssf2}-1 \text{ssi2} \) line, flowers of a \( \text{ssf2}-1 \text{ssi2} \text{npr1} \) plant were crossed with pollen from a wild-type plant. The success of the cross was confirmed by CAPS analysis of F1 plants for heterozygosity at the \( \text{npr1} \) and \( \text{ssi2} \) loci. The genotype of the F1 generation was \( \text{ssf2}-1 \text{ssi2} \text{npr1} \). Large plants segregating in the F2 generation were screened using PCR to identify plants that were homozygous for the \( \text{ssi2} \) mutant allele. Because of their large stature, these plants were presumed to be homozygous for the \( \text{ssf2}-1 \) allele. These plants then were tested by PCR to identify those that were homozygous for the wild-type \( \text{NPR1} \) allele. The F2 lines that did not segregate any dwarf plants were confirmed to be \( \text{ssf2}-1 \text{ssi2} \).

The \( \text{ssf1}-1 \text{ssi2} \) line was generated from a cross involving the \( \text{ssf1}-1 \text{ssi2} \text{npr1} \) and \( \text{ssi2} \) plants. The genotype of these dwarf and lesion-bearing F1 plants was \( \text{ssf1}-1 \text{ssi2} \text{ssi2} \text{npr1} \). Large plants segregating in the F2 generation were analyzed using PCR for plants that are homozygous for the \( \text{NPR1} \) allele. F3 seeds from these \( \text{ssf1}-1 \text{ssi2} \) plants were used in experiments.

Mapping populations for \( sfd1 \) were generated by crossing the \( \text{ssf1}-1 \text{ssi2} \text{npr1} \) plant in ecotype Nössen with the \( \text{fab2} \) mutant in ecotype Colombia. The resulting F1 plants were dwarf and expressed the \( \text{PR1} \) gene at increased levels. The large F2 progeny plants were used to map \( sfd1-1 \). Similarly, F2 progeny plants from a cross between \( sfd1-2 \text{ssi2} \text{npr1} \) and \( \text{fab2} \) were used to map \( sfd1-2 \). F2 progeny from a cross of a \( sfd1-2 \text{ssi2} \text{npr1} \) plant (ecotype Nössen) and the \( \text{fab2} \) mutant (ecotype Colombia) were used to map \( sfd2-1 \). F2 progeny homozygous for \( sfd2-1 \), identified as large plants, were used for mapping.

A cross between the \( \text{ssi2} \) and \( \text{fad6}-1 \) (ecotype Colombia) plants was used to generate the \( \text{ssi2} \text{fad6} \) double mutant. F2 progeny plants from this cross were analyzed for the presence of the \( \text{ssi2} \) mutant allele by PCR (Kachroo et al., 2001). One-quarter of the plants that were homozygous for the \( \text{ssi2} \) mutant allele lacked the \( \text{ssi2} \)-conferred dwarf phenotype, suggesting recessive epistasis, with \( \text{fad6}-1 \) epistatic to \( \text{ssi2} \). The presence of the \( \text{fad6} \) or wild-type \( \text{FAD6} \) allele was monitored by PCR for the AAG and AtHDT1 markers, which flank the FAD6 locus and exhibit polymorphism between ecotypes Colombia and Nössen. All of the \( \text{ssi2}/ \text{ssi2} \) F2 plants that did not exhibit the \( \text{ssi2} \)-conferred dwarf phenotype were homozygous for the Columbia pattern at these two markers, confirming that they were homozygous for the \( \text{fad6}-1 \) mutant allele.

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 Jyoti Shah, shah@ksu.edu.

**ACKNOWLEDGMENTS**

We thank Ethan Baughman for his help in interpreting the lipid molecular species acyl fragmentation data and William Broekaert for providing a culture of *B. cinerea* IMI169558. We are grateful to Todd Williams for acquiring MS data and to Xuemin Wang for his suggestions and comments on this work. This material is based on work supported by the Cooperative State Research, Education, and Extension Service, U.S. Department of Agriculture, under Agreement 2002-35319-11655 and Grant MCB-0110979 from the National Science Foundation (to J.S. and R.W.). A Research Experience for Undergraduates supplement to National Science Foundation Grant MCB-0110979 and a fellowship from the Kansas Biomedical Research Infrastructure Network provided support for (C.M.B.). J.S. also acknowledges the National Science Foundation for Major Research Instrumentation Grant DBI-0079539, which provided for plant growth chambers to perform this work. This is Kansas Agricultural Experimental Station contribution 03–132–J.

Received July 15, 2003; accepted August 3, 2003.

**REFERENCES**


The Plant Cell


Correction


On page 2389, the fifth sentence of the first full paragraph contains an error. The sentence should read as follows: “Acyl fragment analysis showed that 34:2 species in npr1 and ssi2 npr1 represented mainly a combination of 18:2 and 16:0, whereas 34:3 species were mainly a 16:0-18:3 combination, but lower amounts of 16:1-18:2 and 16:3-18:0 combinations were detected.”
Arabidopsis sfd Mutants Affect Plastidic Lipid Composition and Suppress Dwarfing, Cell Death, and the Enhanced Disease Resistance Phenotypes Resulting from the Deficiency of a Fatty Acid Desaturase

Ashis Nandi, Kartikeya Krothapalli, Christen M. Buseman, Maoyin Li, Ruth Welti, Alexander Enyedi and Jyoti Shah

Plant Cell 2003;15;2383-2398; originally published online September 24, 2003;
DOI 10.1105/tpc.015529

This information is current as of July 12, 2017

References
This article cites 60 articles, 31 of which can be accessed free at:
/content/15/10/2383.full.html#ref-list-1

Permissions

eTOCs
Sign up for eTOCs at:
http://www.plantcell.org/cgi/alerts/ctmain

CiteTrack Alerts
Sign up for CiteTrack Alerts at:
http://www.plantcell.org/cgi/alerts/ctmain

Subscription Information
Subscription Information for The Plant Cell and Plant Physiology is available at:
http://www.aspb.org/publications/subscriptions.cfm

Errata
An erratum has been published regarding this article. It is appended to this PDF and can also be accessed at:
/content/15/12/3051.full.pdf