Intronic T-DNA Insertion Renders Arabidopsis opr3 a Conditional Jasmonic Acid-Producing Mutant

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Jasmonic acid and its derived metabolites (JAs) orchestrate plant defense against insects and fungi. 12-Oxo-phytodienoic acid (OPDA), a JA precursor, has also been implicated in plant defense. We sought to define JAs and OPDA functions through comparative defense susceptibility characteristics of three Arabidopsis (Arabidopsis thaliana) genotypes: aos, lacking JAs and OPDA; opda reductase3 (opr3), deficient in JA production but can accumulate OPDA; and transgensics that overexpress opr3. opr3, like aos, is susceptible to cabbage loopers (Trichoplusia ni) but, relative to aos, opr3 has enhanced resistance to a necrotrophic fungus. Gas chromatography-mass spectrometry reveals that opr3 produces OPDA but no detectable JAs following wounding and looper infestation; unexpectedly, substantial levels of JAs accumulate in opr3. Full-length OPR3 transcripts accumulate in fungal-infected opr3, potentially through splicing of the T-DNA containing intron. Fungal resistance correlates with levels of JAs not OPDA; therefore, opr3 resistance to some pests is likely due to JA accumulation, and signaling activities ascribed to OPDA should be reassessed because opr3 can produce JAs. Together these data (1) reinforce the primary role JAs play in plant defense against insects and necrotrophic fungi, (2) argue for a reassessment of signaling activities ascribed to OPDA, and (3) provide evidence that mutants with intron insertions can retain gene function.

Plants are sessile organisms constantly challenged by diverse pests ranging from macroscopic insects to microbes. In response, plants have evolved an effective and diverse arsenal of toxic secondary metabolites to fight off and survive these challenges. For example, Arabidopsis (Arabidopsis thaliana) plants infested with cabbage loopers (Trichoplusia ni) or infected with necrotrophic pathogens, such as Botrytis cinerea, produce high levels of toxic glucosinolates and camalexin to resist its invaders (Jander et al., 2001; Lambrix et al., 2001; Kliebenstein et al., 2002; Sellam et al., 2007; Rowe et al., 2010). Production of such toxins involves signaling through the phytohormone jasmonic acid (JA) and several of its derivatives, including its biologically active form JA-Ile (Staswick and Tiryaki, 2004; Chen et al., 2005; Chehab et al., 2008; Suza and Staswick, 2008; Rowe et al., 2010). Here we refer to JA, JA-Ile, and other derivatives collectively as JAs, for simplicity.

JAs are important signaling molecules involved not only in plant defense (Albrecht et al., 1993; Howe et al., 1996; McConn and Browse, 1996; Creelman and Mullet, 1997; Staswick et al., 1998; Vijayan et al., 1998) but also in responses to abiotic stress (Parthier, 1990), mechanotransduction (Falkenstein et al., 1991), and reproduction (Creelman and Mullet, 1995; McConn and Browse, 1996; Hause et al., 2000; Ishiguro et al., 2001). JA synthesis is initiated by the oxidation of α-linolenic acid (18:3), released from chloroplast membranes, into 13-hydroperoxylinolenic acid. The latter is further dehydrated by ALLENE OXIDE SYNTHASE (AOS) and cyclized into (9S, 13S)-12-oxo-phytodienoic acid (OPDA) by allene oxide cyclase. OPDA REDUCTASE3 (OPR3) reduces OPDA to 3-oxo-2(2Z)-pentenyl cyclopentane-1-oxa-tocanic acid that undergoes three rounds of β-oxidation in the peroxisomes to yield JA. Subsequently, JA is converted into JA-Ile (Staswick and Tiryaki, 2004; Suza and Staswick, 2008). The F-box protein, CORONATINE INSENSITIVE1 (COI1), mediates JA action, as binding of JA-Ile to COI1 results in ubiquitination and degradation of JAZ proteins acting as transcriptional repressors of downstream gene targets (Chini et al., 2007; Thines et al., 2007; Yan et al., 2007; Katsir et al., 2008; Melotto et al., 2008).

Mutants defective in JA biosynthesis and response have revealed roles for JAs in defense. These mutants include the triple fad3 fad7 fad8 mutant, which lacks JA and its precursor metabolites (McConn and Browse, 1996), opr3, which contains a 17-kb T-DNA insertion in its second intron and is reported to block the JA biosynthesis pathway downstream of OPDA (Stintzi and Browse, 2000), and coi1, which produces normal levels of OPDA, JA, and its derived metabolites but is JA insensitive. All three mutants are male sterile; however, there are key differences in their resistance...
to various pathogens. In contrast to fad3 fad7 fad8 and coi1, which are highly susceptible to the necrotrophic fungus, Alternaria brassicicola, as well as to the soil gnat, Bradysia impatiens, opr3 is more resistant to these invaders (Stintzi et al., 2001; Zhang and Turner, 2008). fad3 fad7 fad8 and opr3 differ in that opr3 can synthesize OPDA. Therefore, the observed resistance of opr3 to A. brassicicola and B. impatiens has been attributed to the presence of OPDA. In addition, the susceptibility of coi1 to the same plant invaders implicated OPDA in playing a defense role through COI1, similarly to JA (Stintzi et al., 2001). However, to date there is no experimental evidence that OPDA promotes COI1 and JAZ interaction (Thines et al., 2007), although such interaction could still take place through unknown mechanism(s). Reports also suggest that some of the OPDA actions may be COI1 independent (Stintzi et al., 2001; Taki et al., 2005). Thus how OPDA might act to mediate defense in opr3 remains an open question. Alternatively, there might be an unidentified explanation for the resistance of opr3 to invaders.

With the aim toward gaining a better understanding of the potential role of OPDA in plant defense responses, we employed a set of Arabidopsis mutant genotypes differentially affected in the JA pathway and challenged them with B. cinerea or cabbage loopers. We demonstrate that upon B. cinerea infection, opr3 is capable of producing full-length OPR3 transcripts potentially through successful removal of the T-DNA-harborring intron and consequently accumulating JAs at substantial levels. Furthermore, resistance to B. cinerea and cabbage loopers in all examined genotypes correlates with accumulation levels of JAs. Therefore, previous interpretations about the sufficiency of OPDA in pathogen defense based on opr3 mutant resistance need to be reconsidered because opr3 can accumulate JAs. We conclude that JAs are most likely responsible for Arabidopsis resistance to B. cinerea and cabbage loopers.

RESULTS

Introgression of opr3 Mutation into Columbia-0 Background

We sought to elucidate and differentiate the functions and mechanisms of action of JAs and their precursor, OPDA, both of which have been implicated in insect and fungal defense responses. Toward this goal, we employed two mutants: aos, which lacks both OPDA and JA by loss of conversion of 13-hydroperoxylinolenic acid to 12,13-epoxyoctadecatrienoic acid, and opr3, reported to produce OPDA but be deficient in JA production due to a failure to convert OPDA to 3-oxo-2(2′Z)-pentenyl)cyclopentane-1-octanoic acid (Stintzi and Browse, 2000; Stintzi et al., 2001). These two mutant lines have two different genetic backgrounds. Therefore, for comparative analyses, we repeatedly backcrossed opr3, originally in the Wassilewskija (Ws) background, eight times with the genetic background of the aos mutant, gl-1 (Columbia-0 [Col-0]), and employed gl-1 as the control background in all subsequent experiments. It should be noted that there are no significant detectable differences in AOS-derived metabolites between gl-1 and Col-0 wild type (Chehab et al., 2008). The aos mutant as well as the resultant opr3 are conditionally male sterile, rescued by exogenous methyl jasmonate (MeJA) application (Fig. 1A). In addition, like aos, opr3 failed to accumulate JA and MeJA (referred to here as JAs for simplicity), even in response to wounding, which leads to increased accumulation of JAs in the control (gl-1; Fig. 1B). In contrast, opr3 and gl-1 lines accumulated statistically similar levels of OPDA before and after wounding, whereas aos had no detectable OPDA (Fig. 1C). These data obtained for opr3 in the gl-1 (Col-0) background are similar to that reported for Ws-background plants harboring the same opr3 mutation (Stintzi and Browse, 2000). Stintzi et al. (2001) reported that wounded opr3 accumulates JAs to less than 4% the levels observed in wild type. Growth conditions may account for the lower levels we observe for JAs and OPDA in wounded gl-1 plants compared to some previously published reports.

Figure 1. JA rescue of male fertility, and accumulation of JAs and OPDA in mechanically wounded Arabidopsis. A, Male fertility is restored in aos and opr3 by the exogenous application of JA. B, Levels of JAs in untreated leaves (CR) and wounded leaves 2 h after mechanical damage (W). C, Levels of OPDA in untreated leaves (CR) and wounded leaves 2 h after mechanical damage (W). Means ± se are shown. n = 3. [See online article for color version of this figure.]
**opr3 Mutants Have Increased Susceptibility to Cabbage Loopers**

The apparent ability of *opr3* to accumulate only OPDA but not JA provides a potentially powerful tool to uncouple the roles of these two metabolites in plant defense responses. JAs play an important role in plant defense against the cabbage looper, a chewing generalist lepidopteran (Jander et al., 2001; Lambrix et al., 2001; Kliebenstein et al., 2002; Chehab et al., 2008). We therefore first examined whether OPR3 is necessary for enhanced resistance to cabbage loopers. No-choice bioassays were employed to assess the susceptibility of *opr3* to the cabbage looper. Loopers reared on *gl-1* had approximately 45% lower final weight than larvae feeding on *aos* or *opr3* (Fig. 2A). No statistical differences in looper weights were found between those reared on *aos* or *opr3* (Fig. 2A). Increased susceptibility of *opr3* and *aos* to looper attack was also evident by the remaining shoot mass of the plants following infestation; while *gl-1* retains relatively abundant shoot mass, both mutants are nearly devoid of rosette leaves 12 d after looper release (Fig. 2B). These results indicate that OPR3 is essential for plant resistance to loopers and suggest that OPDA produced in *opr3* is not sufficient to confer looper resistance.

**Figure 2.** *opr3* has increased susceptibility to cabbage loopers. A, Looper weights 12 d after release of a newly hatched larva in an arena containing five plants of indicated genotype. Means ± SEM of two independent experiments, each with approximately 15 arenas per genotype, are shown. B, Representative photos of *gl-1*, *opr3*, and *aos* showing tissue damage. C, Levels of JAs in control (CR) and looper-infested (L) leaves 72 h post infestation. Means ± SD are shown, n = 3. D, Levels of OPDA in control (CR) and looper-infested (L) leaves 72 h post infestation. Means ± SD are shown, n = 3. [See online article for color version of this figure.]

To verify whether OPDA, and not JAs, accumulate in *opr3* upon looper infestation, we measured levels of JAs and OPDA in tissues from looper-challenged plants (Fig. 2, C and D). *gl-1* plants produced inducible levels of JAs upon looper infestation, whereas *opr3* and *aos* had no detectable JAs (Fig. 2C). *gl-1* and *opr3* accumulated OPDA, but *aos* had none (Fig. 2D). These results confirm that OPDA is not sufficient for cabbage looper resistance and that the JA-related metabolites produced upon looper infestation (Fig. 2) are comparable to those produced after mechanical wounding (Fig. 1). Together these data indicate that OPR3 function and the ability to accumulate JAs are necessary for Arabidopsis resistance to loopers.

**opr3 Has Partial Resistance to B. cinerea and Produces Camalexin**

The JA signaling pathway is also implicated in necrotrophic pathogen responses, therefore we next addressed whether OPDA accumulation in *opr3* is sufficient for fungal resistance. *B. cinerea* conidia were applied to *gl-1*, *opr3*, and *aos* leaves. The mean diameters of the necrotic area are similar for *gl-1* and *opr3* at 48 h post inoculation (hpi) but are 30% larger for *aos* (Fig. 3A). At 72 hpi, *opr3* lesions were 30% larger than those on *gl-1*. In contrast, *aos* lesions were nearly 400% larger than *gl-1* (Fig. 3A). Therefore, *opr3* is more resistant than *aos* to the fungus, although it is less resistant than *gl-1*. Stintzi et al. (2001) previously reported enhanced resistance of *opr3* against a different necrotrophic pathogen, *A. brassicicola*. Camalexin, a primary Arabidopsis phytoalexin important for pathogen growth inhibition, accumulates in *opr3* to nearly 75% the levels of that found in *gl-1* (Fig. 3B). In contrast, *aos* lacks detectable camalexin (Fig. 3B; Chehab et al., 2008). Depending on the invading pathogen, JA may be required for camalexin biosynthesis (Rowe et al., 2010). Together, these data appear to be consistent with the possible interpretation that OPR3 function is not necessary for enhanced resistance to necrotrophic fungi. However, this interpretation is likely false as the following results indicate.

**JA Accumulates in opr3 Infected with B. cinerea**

To examine whether the partial resistance of *opr3* to *B. cinerea* is evidence for JA-independent defense, we measured levels of JA and OPDA in *B. cinerea*-infected leaves at 48 and 72 hpi. As expected, *gl-1* accumulated high levels of both OPDA and JA in infected leaves, whereas neither metabolite is detectable in *aos* (Fig. 3. C and D). *opr3* also had higher levels of OPDA than *gl-1* (Fig. 3D). However, an unexpected and critically important finding is that *opr3* leaves produced substantial levels of JAs, approximately 30% of the total JAs produced by *gl-1* at both recorded time points (Fig. 3C). Thus, *opr3* can accumulate substantial amounts of JAs at least under specific conditions. This finding indicates that *opr3* phenotypes, such as
enhanced resistance to *B. cinerea* and camalexin accumulation, may be consequences of JA production rather than OPDA accumulation. The interpretation that JAs are the active metabolites conferring these phenotypes is consistent with the observation that *opr3* accumulates less JAs, has less camalexin, and has lower *B. cinerea* resistance compared to *gl-1* that accumulates higher levels of JAs and camalexin and has superior *B. cinerea* resistance (Fig. 3, A–C).

**opr3** Is Not a Loss-of-Function Mutant

The *opr3* mutation is a 17-kb T-DNA insertion within the second OPR3 intron. Previous findings identified *opr3* as a likely null mutant, given the large DNA insertion, the lack of detectable OPR3 transcripts, the JA-dependent male fertility phenotype, and an apparent deficiency in JA accumulation (Stintzi and Browse, 2000; Stintzi et al., 2001). The discovery of easily detectable levels of JA in *opr3* in response to *B. cinerea* (Fig. 3C) led us to investigate the molecular basis of the finding by examining the OPR3 transcript levels in plants subjected to mechanical wounding, cabbage loopers, or *B. cinerea* infection. In *gl-1*, full-length mature OPR3 transcripts were detectable by semi-quantitative reverse transcription (RT)-PCR, using primers targeted to sequences including the start and stop translational codons, in untreated plants and increased approximately 2-fold 2 h after wounding and 72 h post infestation with cabbage loopers, and 8-fold 72 hpi with *B. cinerea* (Fig. 4A, left section). In contrast, *opr3* lacked detectable full-length OPR3 transcripts when subjected to wounding or cabbage loopers (Fig. 4A, right section). However, full-length OPR3 transcripts were detected in *opr3* subjected to fungal infection (Fig. 4A, right section). These full-length RT-PCR products from *opr3* were confirmed to be derived from the OPR3 locus by restriction digests and DNA sequencing that indicated that the second intron was precisely excised. These results were corroborated by quantitative RT-PCR using primers that flank the T-DNA-harboring second intron (Fig. 4, B and C). Note that *aos* lacks detectable OPR3 transcripts under all treatment conditions (Fig. 4, B

![Figure 3](image-url)  
**Figure 3.** *opr3* has increased resistance to *B. cinerea* relative to *aos* and accumulates camalexin and JAs. A, *aos*, *opr3*, and *gl-1* leaf lesion diameters at 48 and 72 hpi with fungal conidia. Mean lesion diameters ± sd are shown. n = 40. Photographs of representative leaves of each genotype 72 hpi. Bar = 1 cm. B, Leaf camalexin levels at 72 hpi. Means ± sd, n = 30. C, Levels of leaf JAs at 48 and 72 hpi with fungal conidia. Means ± sd. n = 8. D, Levels of leaf OPDA at 48 and 72 hpi with fungal conidia. Means ± sd. n = 8. Within any given treatment, letters indicate significant differences (P < 0.005, Tukey’s test).

![Figure 4](image-url)  
**Figure 4.** OPR3 transcript levels. A, Semiquantitative RT-PCR of full-length OPR3 and ACTIN transcripts in *gl-1* and *opr3* that were not treated (CR), wounded (W), looper infested for 72 h (L), or *B. cinerea* infected 72 hpi (B). Primers used to generate the full open reading frame from the start codon to the stop codon. B, Quantitative RT-PCR of OPR3 transcripts relative to *TUB4* transcripts in *gl-1* and *opr3* that were not treated (CR), wounded (W), looper infested for 72 h (L), or *B. cinerea* infected 72 hpi (B). Means ± sd. n = 6. C, Quantitative RT-PCR analysis of OPR3 transcripts relative to *TUB4* transcripts in *gl-1*, *opr3*, and *aos* at 48 and 72 hpi with *B. cinerea*. Means ± sd. n = 6.
and C), confirming the dependence on JAs for OPR3 expression. OPR3 transcript accumulation was detected in opr3 at 48 hpi, and the transcript level increased 4-fold in abundance by 72 hpi with B. cinerea (Fig. 4C). Furthermore, OPR3 transcript abundance in infected opr3 (Fig. 4C) correlated with JA accumulation and B. cinerea resistance: JAs and evidence of B. cinerea resistance were also detected in opr3 at 48 hpi and increased at 72 hpi (Fig. 3, A and C). Finally to rule out the possibility of opr3 seed stock contamination, similar analyses were performed on individual opr3 plants. Three individual opr3 plants each showed (1) the expected male-sterile phenotype, (2) an absence of detectable wild-type OPR3 gene, (3) the presence of the mutant allele, and (4) detectable accumulation of full-length OPR3 transcripts by RT-PCR (Supplemental Fig. S1). Furthermore, JAs were detected in extracts from the pooled infected leaves from these three plants (Supplemental Fig. S1). Overall these results demonstrate that opr3 is not a null mutant but instead is able to produce full-length mature OPR3 transcripts under certain conditions, likely through splicing out the intron harboring the 17-kb T-DNA insertion, albeit with low efficiency.

The Arabidopsis genome contains five other OPR-encoding genes. Although biochemical studies established that OPR3 is the reductase responsible for converting OPDA to OPC:8, the involvement of the other OPRs in JA production has not been ruled out (Schaller et al., 2000). We examined transcript levels of the other five OPRs upon fungal infection and found that only OPR2 showed an increase in transcript level in response to infection (Supplemental Fig. S2). Although it is unlikely that reductases other than OPR3 convert OPDA to OPC:8 (Breithaupt et al., 2001, 2006; Malone et al., 2005; Hall et al., 2007, 2008; Beynon, et al., 2009; Schaller and Stintzi, 2009), whether OPR2 or other OPRs are involved in the production of JAs and thus play a role in fungal resistance remains to be determined.

The data presented strengthen the hypothesis that JAs may be necessary for defense against necrotrophic fungi resistance and that OPDA is not sufficient to confer resistance. To further investigate the potential role for JAs in resistance against B. cinerea, we supplied aos with exogenous JA and monitored fungal growth. Because aos lacks both OPDA and JAs (Fig. 2, C and D; Chehab et al., 2008), the effects of exogenous JA, without potential interference by endogenous OPDA, could be assessed. Fungal spores were spotted on gl-1 and aos leaves, and the leaves were subsequently sprayed with water or JA. Lesion diameters were measured at 72 hpi. B. cinerea-infected gl-1 leaves did not show statistically significant differences in the lesion diameters whether sprayed with water or increasing concentrations of JA (Fig. 5, A and B). This indicates that exogenous JA application was neither toxic to the fungus nor inhibitory to fungal infectivity. Furthermore, these data suggest that the endogenously produced JAs in gl-1 are likely accumulating to a maximally beneficial level. In contrast, the mean lesion diameters on aos leaves decreased relative to the increased JA concentrations applied (Fig. 5, A and B). aos leaves sprayed with 0.5 mM JA had a mean lesion diameter not significantly different than that measured on gl-1 (Fig. 5, A and B). These results indicate that JA treatment is sufficient to confer B. cinerea resistance to aos.

To verify whether JAs, and not OPDA, were responsible for aos fungal resistance, we measured OPDA levels in fungal-infected aos and gl-1 leaves treated with 0.5 mM JA. OPDA was absent in aos but present in gl-1 (Fig. 5C). Thus, JAs, in the absence of OPDA, can induce at least some defense mechanisms against B. cinerea. These results suggest that OPDA may have no
direct role in fungal defense but acts only as a JA precursor.

**Overexpression of OPR3 Reduces OPDA Levels**

The previously described experiment demonstrates that the exogenous application of JA is sufficient to elicit defense against *B. cinerea*. However, exogenous application of metabolites can fail to induce responses comparable to those produced in vivo (Chehab et al., 2008). Furthermore, to examine whether OPDA itself may also have a role in fungal resistance, we generated plants that overexpress OPR3 in an attempt to reduce levels of OPDA and increase endogenous levels of JAs relative to wild type. All lines examined had altered levels of OPDA and JAs (Supplemental Fig. S3, A and B). The representative line, which we denote here as OPR3-OE, had approximately 35% higher basal and wound-induced JAs and approximately 40% lower basal and wound-induced OPDA as compared to wild type.

**OPR3-OE Is Resistant to B. cinerea, and OPDA Levels Do Not Correlate with Resistance**

As expected, fungal-infected OPR3-OE accumulated 45% less OPDA and 30% more JAs as compared to Col-0 (Fig. 6, B and C). At 72 hpi, OPR3-OE lesions were 25% smaller in diameter than those of Col-0 (Fig. 6A). Independent OPR3 overexpressing lines behaved similarly to OPR3-OE (Supplemental Fig. S4). These experimental results support a lack of correlation between OPDA accumulation and fungal resistance. Instead, there is a strong inverse correlation between mean fungal lesion diameter and accumulation of JAs, thus further supporting the central functional role for JAs in fungal resistance.

**DISCUSSION**

Plant defense against necrotic fungi and chewing insects depends upon the JA response pathway. Elucidation of downstream responses requires the identification of the active compounds. JA-Ile action has been defined; JA-Ile binds COI1 and mediates destruction of the JAZ repressor proteins (Chini et al., 2007; Thines et al., 2007; Yan et al., 2007; Katsir et al., 2008; Melotto et al., 2008). In contrast, although OPDA had been implicated as an active oxylipin, its mechanism of action remained unclear. OPDA, unlike JA-Ile, does not bind COI1; yet COI1 is thought to be required for some, but not all putative OPDA actions (Ribot et al., 2008). Much of the evidence that OPDA has defense activity comes from previous characterization of the mutant opr3, with a 17-kb T-DNA insertion in an OPR3 intron, manifests resistance to *A. brassicicola* and *B. impatiens* comparable to wild type (Stintzi et al., 2001). The interpretation that such an observed resistance results from a direct role for OPDA needs to be reevaluated in the light of the data presented here indicating that opr3 can accumulate JAs upon *B. cinerea* infection (Fig. 3C). Our discovery that opr3 is a not a null mutant, capable of generating mature full-length OPR3 transcripts (Fig. 4) and accumulating JA (Fig. 3C) indicates that JA and its derived metabolites are likely necessary for necrotrophic fungal defense.

Furthermore, because opr3 accumulates OPDA but is sensitive to cabbage loopers, we conclude that OPDA is not sufficient for defense against this insect and that JAs are also likely the primary metabolites involved in looper resistance (Fig. 2). Similarly, tomato (*Solanum lycopersicum*) plants able to produce OPDA but not JAs due to a mutation in ACX1A, essential for β-oxidation steps of JA biosynthesis, are susceptible to *Manduca sexta* (Li et al., 2005). Together, these data, in addition to recently published reports (Kang et al., 2006), support the conclusion that JAs are required for plant defense against chewing lepidopterans.

Our data also present a strong correlation between *B. cinerea* resistance and levels of JAs. Wild type is most resistant to *B. cinerea* infection with the highest accumulation of JAs, whereas opr3 is moderately resistant and accumulates moderate levels of JAs. *aos* is highly susceptible to the fungus and generates no JAs (Fig. 3, A–D). Furthermore, transgenic plants that overexpress OPR3 accumulate more JAs than wild type and exhibit...
greater fungal resistance (Fig. 6). OPDA levels, in contrast, are higher in opr3 mutants and lower in OPR3-OE as compared to wild type, inversely correlated with relative fungal defense. Indeed, B. cinerea-induced lesions on aos leaves were reduced in diameter by treatment with exogenous JA (Fig. 5, A and B). This increased JA-induced resistance was independent of OPDA, confirming the central role for JAs in mediating fungal defense.

Recently, Schilmiller et al. (2007) reported that JA-deficient Arabidopsis acx1/5 mutants, defective in genes involved in β-oxidation steps of JA biosynthesis, accumulate JA upon fungal infection and are resistant to A. brassicicola. These mutants fail to produce JA in response to looper infestation or mechanical wounding. One possible conclusion was that the observed JA accumulation in fungal-treated acx1/5 leaves might be from JA or JA precursor production by the fungus. Although this might also be a possible explanation for the results presented here, we believe it is unlikely because aos remains highly susceptible to B. cinerea infection (Fig. 3A) and JAs are undetectable in B. cinerea-infected aos (Fig. 3C). The demonstration that OPR3 transcripts are generated in opr3 is strong evidence that JAs are most likely produced by the plant; we therefore conclude that the observed increased resistance of opr3 is most likely due to its ability to produce JAs.

OPR3 expression is progressively increased in wild-type plants that are wounded, looper infested, or fungal infected, respectively. However, only fungal-infected opr3 plants accumulated detectable levels of intact full-length OPR3 transcripts (Fig. 4A). We propose that proper splicing of the OPR3 RNA in opr3 is inefficient due to the presence of the 17-kb T-DNA insert, with only less than 4% of primary transcript being successfully spliced upon B. cinerea infection as compared to wild type (Fig. 4). Thus, we hypothesize that only under certain conditions, such as B. cinerea infection, when OPR3 primary transcripts accumulate to very high levels does such inefficient splicing produce detectable properly processed mRNA. An alternative possibility is that fungal infection somehow promotes productive OPR3 transcript splicing. The second OPR3 intron also contains a nonautonomous transposable element, TnAt1, which could also potentially play a role in intron removal. Verification of the mechanism by which full-length mature OPR3 transcripts are generated upon specific stimuli is a focus of our current studies. The unexpected finding that intronic insertions may be removed, albeit at low efficiency, to generate functional transcripts should promote caution among researchers working with insertional mutants, especially those mutants with insertions within introns. Perhaps even very large insertions can be tolerated, and the mutated gene can thereby retain at least partial function.

MATERIALS AND METHODS

Plant Growth Conditions, and Generation and Molecular Characterization of Transgenic and Mutant Lines

Transgenic and mutant Arabidopsis (Arabidopsis thaliana) plants were grown as previously described (Chehab et al., 2006). Experiments were performed with 5-week-old plants. aos seeds (CS6149) were purchased from the Arabidopsis Biological Resource Center (Columbus, OH). PCR analyses confirmed the presence of the T-DNA insertion within AIAOS, as previously described (Park et al., 2002). To generate OPR3-OE and Line X, the OPR3 cDNA clone, purchased from the Arabidopsis Biological Resource Center, was amplified by PCR with oligonucleotides designed for Gateway cloning. Primers used for amplification were: forward: 5'-CACATGACCGCGCA-CACAAGG-3' and reverse: 5'-TCAGGCGGGGAAAAAGGA3-3'. PCR amplification was conducted in 25 μL of 10× Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl2, 100 μM of each dNTP, 500 μM each of forward and reverse primer, 0.625 units of Taq DNA polymerase, and 50 ng of DNA template. Amplification was conducted at 94°C for 1 min, 94°C for 30 s, 54°C for 1 min, 72°C for 90 s, with a 10-min extension step at 72°C. The amplified product was cloned into the pENTR/D-TOPO vector and subcloned into the Gateway destination vector pB2GW7.0 (Karimi et al., 2002). The plasmid was sequenced and transformed into the EHA101 Agrobacterium strain. Col-0 transformation was performed by the floral-dip method (Clough and Bent, 1998). T1 transgenics were selected with 1:1,000 finale (equivalent to 5.78% glutosamine ammonium) twice a week starting at 10 to 12 d of age. Single-insert transgenic lines were propagated and the genomic DNA was isolated using the CTAB method for amplification. The PCR profile was 30 cycles, each 1 min; for the final step, the temperature was held at 72°C. The PCR products were electrophoresed on 1.5% agarose gel and visualized under UV light.

Genomic DNA Isolation and Genomic DNA PCR

Leaves from individual Arabidopsis plants were ground in liquid nitrogen, and the genomic DNA was isolated using the CTAB method for amplification by PCR. The genomic DNA (g-OPR3) flanking the T-DNA insert was amplified by PCR using Takara Ex Taq DNA polymerase and the following primers (forward primer 5'-AGCGGAACACTCCCGGGCGTTTC-3' and reverse primer 5'-CTGTAAGCTGTTTCCACACCTT-3') according to manufacturer’s instructions. The interactive PCR round was performed exactly as in the primary PCR reaction but using 2 μL from the 20 μL primary PCR reaction as template. The presence of the T-DNA insertion was confirmed using the following primers (forward primer 5'-AGCACGTGCCGGCACTCTTGC-3' and reverse primer 5'-GGCGCTGGAACAGCATTCT-3'). The annealing temperature for the primer pairs was 56°C. The PCR profile was 30 cycles, each consisting of 94°C for 2 min, annealing temperature for 1 min, and 72°C for 1 min; for the final step, the temperature was held at 72°C for 10 min.
Quantitative RT-PCR

Leaves were ground in liquid nitrogen, and RNA was extracted using the Tri reagent (Molecular Research Center) according to the manufacturer’s instructions. Extracted RNA was quantified using NanoDrop 100 spectrophotometer (Thermo Fisher Scientific), and 1 μg was reverse transcribed into cDNA using a poly (dT) reverse primer and Superscript III reverse transcriptase as instructed by the manufacturer (Invitrogen) after DNase treatment (Roche Diagnostics). Quantitative real-time PCR was performed with Taqman SYBR green PCR master mix (Applied Biosystems) in an ABI PRISM 7000 (Applied Biosystems) system cycled 40 times with primers designed for OPR1 (AT1G76680), OPR2 (AT1G76690), OPR3 (AT2G06050), OPR4 (AT1G7990) (ATIG18020), and OPR6 (ATIG04904). Primers used for OPR4 are forward primer 5'-ACGGACACTCCCGCGCGTTTC-3', reverse primer 5'-GCTGAAACCTTCCACAACT-3'. Primers used for OPR1, OPR2, OPR4, and OPR6 are the same ones reported in Beynon et al. (2009).

Semiquantitative RT-PCR

Two microtiter of cDNA produced as described above was used for semiquantitative RT-PCR performed in 25 μL of buffer containing 1.5 mm MgCl2, 100 μM of each dNTP, 500 nm of each forward and reverse primer, 0.625 units of Taq DNA polymerase. PCR conditions used were as described above. The 5′ OPR3 primer was specific for sequences containing the translational start codon (forward: 5′-CATCATGCGCCGGCAACAAGG-3′) and the 3′ OPR3 primer was specific for sequences containing the stop codon (reverse: 5′-TCAGAGGCGGGAAAAAGGA-3′). ACTIN-specific primers (forward primer 5′-GATCTAACCAGCGCTGTACAG-3′, reverse primer 5′-GACTGACTCTGACTACATCGG-3′) were used as a control to normalize gene expression in each sample. Quantification was conducted as previously described (Tsai et al., 2007).

B. cinerea Assays and Camalexin Measurements

B. cinerea isolate ‘Grape’ was obtained from the laboratory of Melanie Vivier (University of Capetown, South Africa; Denby et al., 2004). The grape (Vitis vinifera) isolate has previously been shown to be sensitive to JA-dependent defenses as well as camalexin (Rowe et al., 2010). Rosette leaves from 5-week-old Arabidopsis were excised and placed in 145 × 20 mm plastic petri dishes with 1% agar. Each dish contained a single genotype. Each experiment used at least four dishes per genotype, containing 10 leaves per dish. Leaves were inoculated with 4 μL droplets of 2.5 × 10^6 conidia/mL in half-strength-filtered grape juice and incubated at room temperature. Lesion area (cm^2) was digitally measured from images (118 pixels/cm) of infected leaves using Image J (Abramoff et al., 2004) with scale objects included in each image. Camalexin was extracted from individual infected leaves and quantified as described (Kliebenstein et al., 2005).

Cabbage Looper Development Assay

Eggs of the cabbage looper (Trichoplusia ni) were purchased from Benzon Research, Inc. One newly hatched larva was transferred with a fine brush to a 32 mm plastic petri dish. Each dish contained a single genotype. Each pot was confined in a screened cage. After 12 d, the fresh weights of loopers were individually determined. Student’s t-tests were performed to compare larval weights.

Quantification of OPDA and Jasmonates

MeJA, JA, and 12-OPDA were extracted as described (Chehab et al., 2008). The produced methyl ester volatiles were captured on HaySep-Q (Grace Davison Discovery Sciences) columns by vapor-phase extraction as described (Engelberth et al., 2003). The trapped metabolites were then eluted with 150 μL of dichloromethane and analyzed by gas chromatography-mass spectrometry using a Hewlett and Packard 6890 series gas chromatograph coupled to an Agilent Technologies 5973 network mass selective detector operated in electronic ionization mode. One microliter of sample was injected in splitless mode at 250°C and separated using an Restek Rtx-35ms column (30 m x 0.25 mm x 0.1 μm) held at 40°C for 1 min after injection, and then at increasing temperatures programmed to ramp at 15°C/min to 250°C (10 min), with helium as the carrier gas (constant flow rate 0.7 mL/min). Measurements were carried out in selected ion monitoring (Sellam et al., 2007) mode with retention times and M+ mass-to-charge ratio ions as follows: JA-OPD (trans 11.98 min, cis 12.28 min, 224) and 12-OPDA-OPD (trans 17.82 min, cis 18.31 min, 306).

Sequence data from this article can be found in the GenBank/EMBL database libraries under accession numbers OPR1, NM_202428; OPR2, NM_106319; OPR3 (Ws), AF293653; OPR3 (Col-0), NM_201702; OPR4, AF344314; OPR5, NM_179352; and OPR6, NM_100810.

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. Phenotypic and molecular analysis of individual opr3 mutant plants.

Supplemental Figure S2. OPR transcript levels.

Supplemental Figure S3. Comparisons of accumulation of JAs and OPDA in mechanically wounded Col-0 (wild type) and OPR3 overexpression lines [OPR3-OE, Line X, Line Y].

Supplemental Figure S4. OPR3 overexpression lines are resistant to B. cinerea.

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