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E-2-hexenal promotes susceptibility to Pseudomonas syringae by activating jasmonic acid pathways in Arabidopsis

Alessandra Scala1, Rossana Mirabella2, Cynthia Mug02, Kenji Matsui2, Michel A. Haring3 and Robert C. Schuurink1*

1 Department of Plant Physiology, Swammerdam Institute for Life Sciences, University of Amsterdam, Amsterdam, Netherlands
2 Department of Biological Chemistry, Faculty of Agriculture, Graduate School of Medicine, Yamaguchi University, Yamaguchi, Japan

INTRODUCTION

Plants produce green leaf volatiles (GLVs), C6-aldehydes, C6-alcohols, and their acetates, through the lipoxygenase (LOX) and hydroperoxide lyase (HPL) pathways. Linolenic and linoleic acid are the substrates for dioxygenation and subsequent cleavage to obtain C6-volatile aldehydes that can be further modified by alcohol dehydrogenases (ADH), an isomerization factor and an acetyltransferase leading to the formation of a bouquet of secondary metabolites (Bate and Rothstein, 1998; Arimura et al., 2000; Farag and Paré, 2002; Engelberth et al., 2004; Frost et al., 2007, 2008; Heil and Silva Bueno, 2007). Similarly, the E-2-hexenal released by rice upon planthopper infestation, induces expression of defense-related genes, increasing resistance to bacterial blight (Gomi et al., 2010). In some of these examples the effect of GLVs and jasmonic acid (JA) signaling have been linked (Engelberth et al., 2004; Halitschke et al., 2004; Kishimoto et al., 2006; Allmann et al., 2010; Tong et al., 2012).

Green leaf volatiles (GLVs) are C6-molecules – alcohols, aldehydes, and esters – produced by plants upon herbivory or during pathogen infection. Exposure to this blend of volatiles induces defense-related responses in neighboring undamaged plants, thus assigning a role to GLVs in regulating plant defenses. Here we compared Arabidopsis thaliana ecotype Landsberg erecta (Ler) with a hydroperoxide lyase line, hpl1, unable to synthesize GLVs, for susceptibility to Pseudomonas syringae pv. tomato (DC3000). We found that the growth of DC3000 was significantly reduced in the hpl1 mutant. This phenomenon correlated with lower jasmonic acid ( JA) levels and higher salicylic acid levels in the hpl1 mutant. Furthermore, upon infection, the JA-responsive genes VSP2 and LEC were only slightly or not induced, respectively, in hpl1. This suggests that the reduced growth of DC3000 in hpl1 plants is due to the constraint of JA-dependent responses. Treatment of hpl1 plants with E-2-hexenal, one of the more reactive GLVs, prior to infection with DC3000, resulted in increased growth of DC3000 in hpl1, thus complementing this mutant. Interestingly, the growth of DC3000 also increased in Ler plants treated with E-2-hexenal. This stronger growth was not dependent on the JA-signaling component MYC2, but on ORA59, an integrator of JA and ethylene signaling pathways, and on the production of coronatine by DC3000. GLVs may have multiple effects on plant-pathogen interactions, in this case reducing resistance to Pseudomonas syringae via JA and ORA59.

Keywords: green leaf volatiles, Pseudomonas syringae, jasmonate, coronatine, hormone crosstalk

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Finally, GLVs possess fungidical and bactericidal activity (Proost et al., 2005; Shiojiri et al., 2006b). Since GLVs are released after infection with pathogenic fungi and bacteria (Croft et al., 1993; Heiden et al., 2003; Shiojiri et al., 2006b), this testifies that a possible physiological role of these volatiles is to limit pathogen growth. Several observations support this hypothesis. For instance, upon infection with the pathogenic bacteria *Pseudomonas syringae, Phasmosus vulgaris* (lima bean) leaves release relatively high amounts of the C6-aldehyde 2-hexenal and the C6-alcohol Z-3-hexenol (Croft et al., 1993). Moreover, pre-treatment with the C6-aldehyde 2-hexenal as well as genetic manipulation to enhance C6-volatile production, resulted in increased resistance against the necrotrophic fungus *Botrytis cinerea* in Arabidopsis, most likely as a result of both activation of defense responses and direct inhibition of fungal growth (Kishimoto et al., 2005; Shiojiri et al., 2006b).

Since all this evidence indicates a role for GLVs in regulating plant responses to bacterial pathogens and GLV levels have been shown to increase in plants upon infection with *Pseudomonas syringae* (Croft et al., 1993; Heiden et al., 2003), we decided to further dissect the role of GLVs in the interaction of plants with this pathogen. Increased GLV levels could directly inhibit the pathogen and/or promote infection through downstream signaling favorable for the pathogen. *Pseudomonas syringae pv. tomato* DC3000 is a plant pathogen that enters leaves through stomata, multiplies in the apoplast, and produces necrotic lesions with chlorotic halos (Hirano and Upper, 2000). *Pseudomonas syringae pv. tomato* DC3000 (DC3000) causes bacterial speck on tomato (Cuppels, 1986), but also on A. thaliana (Whalen et al., 1991). DC3000 produces coronatine (COR), a toxin, responsible for chlorotic halos, which mimics the action of JA-iso-leucine (JA-Ile), the active form of JA. With this phytotoxin DC3000 exploits the antagonistic interaction between JA and salicylic acid (SA) in order to shut down SA-dependent defenses that plant triggers to fight against *Pseudomonas* infections (Bloxock, 2005; Glazebrook, 2005). We especially focused on the role of 2-hexenal during the *Arabidopsis-Pseudomonas* interaction. Although it is not the most abundant C6-volatile produced by HPL activity, 2-hexenal is emitted during *Pseudomonas* sp. infections in lima bean (Croft et al., 1993) and in tobacco (Heiden et al., 2003), and it has the highest bactericidal activity in vitro among oxylipins (Proost et al., 2005), likely because its α,β-unsaturated carbonyl moiety that can react with nucleophilic groups (Farmer and Davoine, 2007). Additionally, 2-hexenal has been shown to induce several responses in *Arabidopsis*, including induction of defenses, inhibition of root growth and enhancement of resistance against the necrotrophic fungus *B. cinerea* (Bate and Rothstein, 1998; Kishimoto et al., 2005; Misabilla et al., 2008). In order to determine the role of GLVs in the responses against *Pseudomonas*, we set out to study *Arabidopsis* plants with and without a functional HPL (Shiojiri et al., 2012) and did complementation studies with E-2-hexenal. Remarkably we found that the presence of a working copy of HPL increased susceptibility of *Arabidopsis* to DC3000. Treatment with E-2-hexenal also enhanced the susceptibility to this bacterial pathogen. We found evidence that this is mediated by the transcription factor ORA59, one of the main players in the JA-signaling pathways, and required the production of the bacterial toxin COR.

### Materials and Methods

#### Plant Lines

*Arabidopsis thaliana* ecotype Columbia-0 (Col-0) and Landsberg erecta (Ler) were used. The hpl mutant is an introgression line between Col-0 and Ler (Shiojiri et al., 2012). The mutant myc2 (jm11-7; Verhage et al., 2011), the transgenic lines RNAi:ORA59 and the 35S:GUS plants (Pré et al., 2008) were all in the Col-0 background. Plants were grown in soil in a growth chamber at 21°C, 70% relative humidity under an 11-h photoperiod with 100 μE m⁻² s⁻¹.

#### Bacterial Population Counts

Bacteria were grown overnight at 28°C in liquid King’s broth (KB) medium (King et al., 1954) containing rifampicin (50 μg/ml) for the *Pseudomonas syringae* pv. *tomato* DC3000 strain, and kanamycin (100 μg/ml) for the cor- DC3682 mutant strain, unable to produce COR (Ma et al., 1991). Plants were inoculated with either a low dose (OD₆₀₀ of 0.0007), for bacterial growth assays, or a high dose (OD₆₀₀ of 0.007), for qRT-PCR and hormone quantification, of the bacterial suspension, and bacteria (colony forming units, cfu) were counted as reported in Park et al. (2010).

#### Plant Hormones Extraction and Quantification

For JA and SA quantification, 12 leaves were harvested, in pools of 4, from 12 different mock-infiltrated (10 mM MgSO₄) or bacteria-infiltrated plants in two independent experiments. To extract JA and SA, frozen leaf material (50–150 mg) was ground and homogenized in 0.5 ml 70% methanol, spiked with 200 ng of D6-JA and D6-SA (internal standards for extraction efficiency; CDN Isotopes, Canada)¹, with a Precellys24 automated homogenizer (Bertin Technologies)². Samples were homogenized twice by shaking at 6,000 rpm for 40 s and centrifuged at 10,000 g for 20 min at 4°C. The supernatants of two extraction steps were pooled. JA and SA were quantified by liquid chromatography-mass spectrometry (LC-MS) analysis on Varian 320 Triple Quad LC/MS/MS. Ten microliters of each sample were injected onto a C18 Pursuit 5 (50 mm × 2.0 mm) column (Varian) coupled to a double mass spectrometer in tandem (Varian 320 MS-MS³). The mobile phase comprised solvent A (0.05% formic acid) and solvent B (0.05% formic acid in methanol) as follows: 85% solvent A for 1 min in negative mode. Molecular ions [M-H]⁻ at m/z 137 and 209 and 141 and 213 generated from endogenous SA and JA and their internal standards, respectively, were fragmented under 12 V collision energy. The ratios of ion intensities of their respective daughter ions, m/z 59 and 97 and m/z 59 and 63, were used to quantify endogenous SA and JA, respectively.

¹ www.cdnisotopes.com
³ www.agilent.com

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QUANTITATIVE RT-PCR

For analysis of transcript levels, total RNA was isolated using Tri-reagent (Ambion®) to remove DNA. cDNA was synthesized from 1 μg of total RNA using M-MuLV reverse transcriptase (Fermentas®), as described by the manufacturer, in a 20-μl reaction that was diluted to 50 μl prior to using it for the real-time PCR. This was performed in a 20-μl volume containing 2 μl of cDNA, 0.4 pmol of specific primer sets for each gene and 10 μl of iQ™ SYBR Green Supermix with ROX (Bio-Rad®). PCR conditions were as follows: 95°C for 2 min 30 s (first cycle), 95°C for 15 s and 60°C for 30 s (40 cycles). To ensure amplification of a single product during the qRT-PCR reactions, a dissociation protocol was performed in which samples were slowly heated from 55 to 95°C. qRT-PCR was performed using the ABI Prism 7300 real-time PCR detection system (Applied Biosystems) and the data were collected using software (ABI 7300 SDS version 1) provided by the supplier. Transcript levels were normalized to the levels of the SAND gene (At2g3990; Hong et al., 2010) and quantification was performed as described in previous work (Fuhl, 2001). Primer sequences were as reported in (Andersen and Badenhausen, 2004; Czechowski et al., 2005; Park et al., 2010) for PR1, VSP2, LEC, and SAND, respectively.

TRYPSAN BLUE AND ANILINE BLUE STAINING

Trypan blue staining solution was prepared as described by the manufacturer, in a 20-μl reaction that was diluted to 50 μl prior to using it for the real-time PCR. This was performed in a 20-μl volume containing 2 μl of cDNA, 0.4 pmol of specific primer sets for each gene and 10 μl of iQ™ SYBR Green Supermix with ROX (Bio-Rad®). PCR conditions were as follows: 95°C for 2 min 30 s (first cycle), 95°C for 15 s and 60°C for 30 s (40 cycles). To ensure amplification of a single product during the qRT-PCR reactions, a dissociation protocol was performed in which samples were slowly heated from 55 to 95°C. qRT-PCR was performed using the ABI Prism 7300 real-time PCR detection system (Applied Biosystems) and the data were collected using software (ABI 7300 SDS version 1) provided by the supplier. Transcript levels were normalized to the levels of the SAND gene (At2g3990; Hong et al., 2010) and quantification was performed as described in previous work (Fuhl, 2001). Primer sequences were as reported in (Andersen and Badenhausen, 2004; Czechowski et al., 2005; Park et al., 2010) for PR1, VSP2, LEC, and SAND, respectively.

CALLOSE QUANTIFICATION

Callose was quantified from digital photographs as the number of fluorescent callose-corresponding pixels, relative to the total number of pixels covering plant material (Liu et al., 2013).

E-2-HEXENAL TREATMENT

Plants were grown for 3 weeks under the conditions mentioned above before being exposed to volatiles. For the volatile treatment, 10 plants in single pots were placed into airtight glass desiccators (22 l). E-2-hexenal was diluted in methanol, and applied to a sterile cotton swab, placed in a Erlenmeyer flask, between the plants in the desiccators to give a final concentration of 3 μM. For the control treatment, only methanol was applied. Plants were incubated in the desiccators for 24 h and subsequently taken out to be placed under the growth conditions described above for 1 h, prior to infiltration with bacteria or mock solution as mentioned above. E-2-hexenal was purchased from Sigma-Aldrich.

RESULTS

hpl1 Influences Susceptibility to Pseudomonas syringae pv. tomato (DC3000)

In order to determine whether the ability to synthesize GLVs had an effect on Arabidopsis susceptibility to pathogenic bacteria, we compared Landsberg erecta (Ler) and an introgression line between Col-0 and Ler that can synthesize only trace amounts of GLVs, hpl1 (Shoji et al., 2012), for the susceptibility to Pseudomonas syringae pv. tomato DC3000. To ensure infection throughout the entire leaf, we used the syringe infiltration method since it overcomes stomatal defenses and maximizes the number of responding cells (de Torres Zabala et al., 2009), and bacterial populations were determined 72 hpi (hours post-infection). Figure 1 shows that DC3000 populations were lower in the hpl1 line. The difference measured in bacterial population between Ler and hpl1 (~4.6-fold) was statistically significant (t-test, P < 0.05). This indicates that the hpl1 line is less susceptible to DC3000 than Ler.

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CALLOSE QUANTIFICATION

Callose was quantified from digital photographs as the number of white pixels, covering the whole leaf material, using Photoshop CS7 software. Contrast settings of photographs were adjusted to obtain an optimal separation of the callose signal from the background signal. Callose was selected automatically, using the “Color Range” tool. In cases in which the contrast settings resulted in significant loss of callose signal, due to high autofluorescence of vasculature tissue, callose was selected manually, using the “Magic Wand” tool of Photoshop CS7. Relative callose intensities were quantified as the number of fluorescent callose-corresponding pixels relative to the total number of pixels covering plant material (Liu et al., 2013).

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FIGURE 1 | hpl1 influences bacterial growth. Bacterial populations of DC3000 in infected Ler and hpl1 leaves 1 hours post infection (hpi) and 72 hpi. Values are the mean of 27 sets of two leaf disks from 20 plants. Error bars represent standard error. Bars annotated with an asterisk indicate significant differences among 1hpi samples (P < 0.05, according to Student’s t-test analysis). The data presented are from a representative experiment that was repeated four times with similar results.
apf1 influences JA and SA levels during the infection with DC3000

It is well known that the balance between JA and SA is crucial for the interaction that will be established between a pathogen and its host (Spoel and Dong, 2008; Grant and Jones, 2009; Pieterse et al., 2009). We therefore monitored the changes in JA and SA in Ler and the hpl1 plants, prior to the bacterial population measurement, at 2, 24, and 48 hpi. As shown in Figure 2A, the levels of JA were up at 2 hpi in all treatments, most likely because of the mechanical damage caused by the inoculation with the syringe. At 24 hpi, this wound response was reset, as JA levels were very low, comparable to the mock inoculation. The situation changed at 48 hpi when JA levels increased in DC3000-infested leaves, in Ler approximately threefold higher than in hpl1. SA levels (Figure 2B) changed already at 24 hpi, with levels being approximately 1.7-fold higher in apf1 than in Ler, suggesting that SA-related defenses are activated earlier in apf1. In Ler, the SA levels were higher than in hpl1 at 48 hpi suggesting that these defenses are mounted later in Ler.

JA marker genes are less induced in hpl1 than Ler when infected with DC3000

In order to determine whether the differences in hormone levels had an effect on the expression of relevant marker genes in our system, we performed qRT-PCR for genes downstream of JA and SA. We chose VSP2 and LEC for JA (Potter et al., 1993; Penninckx et al., 1998; Thomma et al., 1998; Liu et al., 2005; Pré et al., 2008) and FR-1 for SA (Bowling et al., 1997; Clarke et al., 2001). PBI expression was clearly induced by DC3000 at 48 hpi, however, to similar levels in Ler and hpl1 plants (Figure A1 in Appendix). In contrast, transcript levels of both VSP2 and LEC at 48 hpi (and 24 hpi) were much lower in hpl1 than in Ler (Figures 3A, B). This result is consistent with the observed lower JA levels in hpl1 at 48 hpi (Figure 2A).

Ler (hpl1) and apf1 differ in the number of dead cells and in callose deposition

To investigate further the differences between Ler and hpl1 in mounting plant defense responses, we decided to look at the appearance of dead cells and callose deposition. Dead cells are indicative of programmed cell death (or the hypersensitive response, HR) and enhanced resistance, usually occurring when an pathogenic effector is recognized by the host (Alfano and Collmer, 1996), whereas callose is typically triggered by conserved pathogen-associated molecular patterns (PAMPs), such as flagellin, at the sites of infection during the relatively early stages of pathogen invasion (Brown et al., 1998; Gómez-Gómez et al., 1999; Jones and Dangl, 2006). Dead cells appeared earlier and more abundantly in the more susceptible Ler (Figures 4A–C). Dead cells appeared at day 2 in hpl1, whereas in Ler they were not present at all, even at day 3. Ler started to deposit callose massively at day 1, while much less papillae at this time could be observed in hpl1. Moreover, even at later stages of infection, at days 2 and 3, Ler showed more callose deposition than hpl1.

E-2-hexenal treatment increases susceptibility to DC3000

Since apf1 is unable to produce GLVs, we addressed the question whether application of GLVs would restore its susceptibility to DC3000 comparable to Ler. We chose to use the C6-aldehyde E-2-hexenal, one of the most active GLVs, and treated hpl1 and Ler plants with 3 μM aerial E-2-hexenal or with the carrier methanol (MeOH) for the control treatment. Figure 5A shows that the treatment with the C6-aldehyde turned both hpl1 and Ler more susceptible to DC3000, as bacterial populations increased about five- and ninefold, respectively, in the E-2-hexenal pre-treated

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Hydroperoxide lyase promotes susceptibility to Pseudomonas

FIGURE 3 | JA-dependent gene expression is higher in infected Ler plants. (A) VSP2 transcript levels and (B) LEC transcript levels were measured by qRT-PCR in Ler and hpl1 infected with DC3000 at 24 and 48 hpi and normalized for SAND transcript levels. Bars represent the ratio between the transcript levels in infected and mock samples. Three infected or mock infiltrated leaves were harvested from three different plants and pooled for RNA isolation. Bars represent the mean of three independent experiments. Error bars represent standard error. Bars annotated with asterisk indicate significant differences among samples (P < 0.05, according to t-test analysis).

FIGURE 4 | Dead cells and callose deposition are different in Ler and hpl1. (A) Trypan blue staining showing small clusters of dead cells in hpl1 but not in Ler leaves infected with DC3000. (B) Aniline blue stained leaf tissues observed under UV illumination showing earlier and higher callose deposition in Ler than in hpl1 leaves infected with DC3000. (C) Relative callose intensity. Bars represent the mean of three different experiments. Error bars represent standard error. Bars annotated with an asterisk indicate a significant difference among samples (P < 0.05, according to t-test analysis).

leaves compared to the control pre-treatment (Figure 3B). Additionally, we measured JA and SA levels in Ler and hpl1 plants infected with DC3000 after pre-treatment with E-2-hexenal or MeOH. Although JA and SA levels increased 48 hpi after DC3000 infection, no significant differences in hormone levels were detected between the E-2-hexenal and the control treatment or between Ler and hpl1 (Figure A2 in Appendix).

THE EFFECT OF E-2-HEXENAL ON BACTERIAL GROWTH ACTS VIA ORA59.

Since a functional HPL leads to higher susceptibility and higher JA levels upon DC3000 infection and E-2-hexenal pre-treatment increased susceptibility of Arabidopsis to DC3000 we sought to elucidate part of the signaling pathways involved, by testing if Arabidopsis mutants in the JA-signaling pathway were still more susceptible to DC3000 after treatment with E-2-hexenal. We chose to analyze MYC2 and ORA59 impaired lines since these are the main players in regulating JA-dependent responses and are located in two different branches of the JA-signaling pathway (Lorenzo et al., 2003, 2004; Anderson and Badruzzaufari, 2004; Dombrecht et al., 2007; Oñate-Sánchez et al., 2007; Kazan and Manners, 2008;
FIGURE 5 | 2-hexenal pre-treatment increases susceptibility to DC3000. (A) DC3000 populations in Ler and hpl1 pre-treated with 3 μM E-2-hexenal or methanol were measured 72 hpi. Values are the mean of 16 sets of two leaf disks from 12 plants. Error bars represent standard error. The data presented are from a representative experiment that was repeated four times with similar results. All pre-treatments with E-2-hexenal were significantly different from the control treatment (P < 0.05, according to Student’s t-test analysis). (B) Bars represent the ratio between cfu/cm² with E-2-hexenal pre-treatment and cfu/cm² with methanol pre-treatment (control). Values are the mean of three independent experiments. Error bars represent standard error.

Pré et al., 2008). As shown in Figure 6A, myc2 (jin1-7) plants were more resistant to DC3000 as has been reported (Fernández-Calvo et al., 2011). Moreover, myc2 as well as wild-type plants showed increased susceptibility to DC3000 when pre-treated with E-2-hexenal, seemingly excluding a role for MYC2 in mediating this phenomenon. In contrast, the same assay performed on RNAi-ORA59 plants (Pré et al., 2008) showed that the bacterial populations increased significantly less in the ORA59 silenced plants compared to the corresponding control line after E-2-hexenal treatment (Figure 6B). This indicates an involvement of ORA59 in this response to E-2-hexenal.

THE E-2-HEXENAL EFFECT IS CORONATINE DEPENDENT

Pseudomonas syringae pv. tomato strain DC3000 synthesizes COR (Mitchell, 1982), a phytotoxin that mimics JA-Ile (Thines et al., 2007; Yan et al., 2009), in order to antagonize the SA-dependent defenses (Brooks et al., 2005; Glazebrook, 2005). Therefore, we also determined whether the production of COR was necessary for DC3000 to proliferate more in E-2-hexenal treated plants. For this, Ler and bplf plants were infected with the Pseudomonas syringae mutant strain DC3682 (Ma et al., 1991), that is unable to produce COR, after pre-treatment with E-2-hexenal or methanol. Figure 7 shows that the bacterial populations of the cor mutant were only slightly, but significantly, higher in Ler or bplf plants treated with E-2-hexenal compared to the control plants, but that this increase was much lower than for DC3000 (Figure 1). Thus COR seems to be necessary for DC3000 to benefit from the E-2-hexenal treatment.

DISCUSSION

Green leaf volatiles have received considerable attention for their ability to induce direct and indirect defense responses in plants and can be considered important players in the already complex network regulated during biotic stress. However the mechanisms by which GLVs influence pathogenesis, and the signaling pathways involved in these responses, are not well known. To address this, we used Ler and its Arabidopsis introgression line, bplf, lacking GLV synthesis, and analyzed their response during infection with the bacterial pathogen Pseudomonas syringae pv. tomato (DC3000). DC3000 was chosen because in some plant species such as lima bean and tobacco, infection triggers E-2-hexenal emission (Croft...
et al., 1993; Heslen et al., 2003). We hypothesized that hpl1 plants would be more susceptible to DC3000 since there is evidence that GLVs and E-2-hexenal have antimicrobial properties (Prost et al., 2005), induce defense-related genes or biosynthesis of defense-related secondary metabolites (Bate and Rothstein, 1998; Arimura et al., 2005, 2006; Paschold et al., 2006), and increase very recently shown in rice where the mutant Os

Figure 1

). A similar result was found the opposite result: plants impaired in GLV production

HPL

(Tong et al., 2012).

Figure 7| The effect of E-2-hexenal is partially dependent on

coronatine. Bacterial populations of the col mutant (DC3080) in inoculated Ler and hpl1 leaves at 72 hpi. Plants were pre-treated 24 h with 3 μM E-2-hexenal or methanol. Values are the mean of 24 sets of two-leaf data from 20 plants. Error bars represent standard error. All pre-treatments with E-2-hexenal were significantly different from the control treatment (P < 0.05, according to Student's t-test analysis). The data presented are from a representation experiment that was repeated three times with similar results.

et al., 2005). However, we found the opposite result: plants impaired in GLV production were more resistant to DC3000 (Figure 1). A similar result was very recently shown in rice where the mutant Oshpl3, not able to synthesize GLVs, was more resistant to Xanthomonas oryzae pv. oryzae (Tong et al., 2012).

Subsequently, we investigated some of the mechanisms underpinning this result by analyzing the populations of SA and JA since it is well known that these phytohormones and their antagonism are crucial for the development of pathogenesis in Arabidopsis (Spoel and Dong, 2008; Grant and Jones, 2009; Pieterse et al., 2009). Hormone measurements clearly showed that JA levels were much lower in hpl1 than in Ler (Figure 2A). Conversely, hpl1 showed an earlier induction of SA than Ler (Figure 2B). These data suggest that a non-functional HPL gene influences the JA branch of the oxylipin pathway, leading to lower production of JA when Arabidopsis is challenged with Pseudomonas. Thus, this is not related to substrate competition as previously shown in Arabidopsis where ectopic expression of HPL led to lower JA levels upon wounding (Cheláb et al., 2006). Reduction of HPL expression in rice and N. attenuata also influenced JA levels but differently: Oshpl3 and assppl1 had increased JA levels (Haltmichke et al., 2004; Tong et al., 2012), in N. attenuata probably due to crosstalk between the GLV and JA pathway (Allmann et al., 2010).

Since JA-signaling downstream of COI1 occurs via two different branches, regulated by MYC2 or ORA59, we used markers for both branches to study their activation after DC3000 infection. LEC, a lectin-like gene, was used for the ORA59 pathway since it is induced by methyl-jasmonate and upon ORA59 overexpression (Scherer et al., 2005; Pré et al., 2008), while VSP2 was used for the MYC2 pathway (Abe et al., 2003; Dombrecht et al., 2007). Both VSP2 and LEC transcript levels were much lower in hpl1 than in Ler (Figures 3A, B) concurrent with the lower JA levels. Thus DC3000 activates in Ler, with an active HPL unlike Col-0 (Duan et al., 2005), with which most DC3000 experiments are carried out, both branches of the JA-signaling pathway and antagonistic control of these distinct branches of the JA pathway (Verhage et al., 2011) is apparently minor. Transcript levels of the SA-marker PR-1 were higher upon DC3000 infection, similarly in hpl1 and Ler (Figure A1 in Appendix), probably because the differences in SA levels between the two genotypes were not big enough to cause a difference. Thus it seems that the lower JA levels in hpl1 plants leads to less activation of the JA-signaling pathways and renders them less susceptible to DC3000.

A hallmark of basal plant defenses to pathogen infection is the deposition of callose. PAMP-induced callose deposition has recently been defined with essential roles for the DC3000 type III effector HopM1 and COR suppressing callose deposition, the latter being, interestingly, partly COH1-independent (Geng et al., 2012). Our results showed that in hpl1, although with smaller bacterial populations than in Ler, clearly less callose was deposited (Figures 4B, C). Ethylene (ET) signaling is crucial for callose deposition in response to flagellin (Clay et al., 2009). It is possible that ET signaling is less activated in hpl1, leading to less callose deposition. Support for this comes from our complementation studies with the hpl1 mutant, a response that is largely dependent on ORA59, a TF that integrates JA and ET signaling (Figure 6B). Perhaps related to this is the fact that DC3000 is apparently less effective in preventing cell death in hpl1 than in Ler (Figure 6A), with fewer living cells producing less callose. DC3000 apparently triggers in hpl1 a higher rate of cell death, which is related to higher resistance (Jones and Dong, 2006).

With the aim to overcome the hpl1 phenotype in response to DC3000 infection, we decided to treat these, and Ler, plants with E-2-hexenal. The pre-treatment with 3 μM E-2-hexenal for 24 h prior to DC3000 infection made hpl1 plants considerably more susceptible to DC3000 (Figures 5A, B). The increase in bacterial populations was about ninefold in Ler and fivefold in hpl1 plants. Thus Ler plants remained more susceptible to DC3000 than hpl1 plants, most likely due to the functional HPL. Due to its high reactivity for being a reactive electrophile species (RES), E-2-hexenal, either induced during the HR or exogenously applied, can undergo conjugation to cellular proteins has been reported to occur for several RES, including E-2-hexenal (Davoine et al., 2006; Myung et al., 2007; Dreckershoff et al., 2008; Muller et al., 2008; Yamauchi et al., 2008). Therefore, we cannot exclude the possibility that, through conjugation, E-2-hexenal affects the
function of proteins involved in the plant defense responses to DC3000, making Arabidopsis more susceptible to this pathogen. A similar effect has been reported for syringolin, a toxin with an unsaturated α-carbonyl moiety, that makes it a RES, produced by, e.g., Pseudomonas syringae pv. syringae. This toxin specifically inhibits the proteasome in order to suppress host defenses (Groell et al., 2008; Schmutz et al., 2009).

Analyses of phytohormone levels after treatment of E-2-hexenal and DC3000 infection showed that there were no statistically significant differences in SA and JA levels between control and treatment (Figure A2 in Appendix). So far only in monocots (maize) an increase in JA has been measured after a GL V treatment (Engelberth et al., 2004, Engelberth, 2011). In the JA-signaling pathway COI1 plays a central role and mutants in this gene are blocked in almost all JA responses (Feng et al., 2005; Devoto et al., 2008; Wang et al., 2008). Downstream of COI1, different TFs regulate specific JA-dependent responses, MYC2 and ORA59 are the main players involved. The MYC2-dependent branch is associated with wound response, responses against herbivores and is also regulated by abscisic acid (ABA; Lorenzo et al., 2003). Thus basic helix-loop-helix (bHLH) transcription factor regulates a large number of JA-responsive genes (Dombretch et al., 2007), among which VEGETATIVE STORAGE PROTEIN2 (VSP2; Liu et al., 2003).

In the other branch, ORA59 integrates JA and ET signaling (Priet et al., 2008). Interestingly, in spite of the absence of difference in JA and SA levels, the higher susceptibility of Arabidopsis plants to DC3000 after E-2-hexenal treatment was dependent on ORA59. The DC3000 bacterial populations increased only slightly in or-ora59 plants after E-2-hexenal treatment as compared to control (35S-GUS) plants (Figure 6B), indicating the lowering of JA signaling, and perhaps ET signaling. A role for MYC2 in this process was excluded based on the fact that myc2 mutants still responded to eugenol E-2-hexenal treatment (Figure 6A).

From the bacterial side we investigated whether the production of COR was necessary to benefit from the E-2-hexenal treatment. For this we employed a cor, a COR-deficient strain, to infect plants, after the E-2-hexenal or control treatment. The result showed that there was a small but significant increase in bacterial populations of the cor strain after the E-2-hexenal treatment (Figure 7). Nevertheless this difference was much smaller than for DC3000, suggesting that COR is necessary for DC3000 to fully benefit from GLVs.

Our data show that a functional SPL1 in Arabidopsis promotes susceptibility to DC3000. This effect is partially mediated by ORA59 and by COR in the bacteria.

The question remains how DC3000 precisely exploits HPL or its products, GLVs or the C12 compounds that are also formed in the HPL pathway (Kallenbach et al., 2011), for its benefit. Since it is clear that some herbivores can lower HPL transcript levels (Halitschke et al., 2004; Savchenko et al., 2012), we propose that HPL may be a target for DC3000 to employ in Arabidopsis, albeit to its own advantage.

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REFERENCES


Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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APPENDIX

FIGURE A1 | PR-1 expression is equally induced in Ler and hpl1. PR-1 transcript levels were measured by qRT-PCR in Ler and hpl1 infected with DC3000 48 hpi and normalized for SAND transcript levels. Error bars represent standard error.

FIGURE A2 | E-2-hexenal does not induce changes in JA and SA levels in Ler and hpl1 plants infected with DC3000. (A) JA levels in Ler and hpl1 plants pre-treated with E-2-hexenal or MeOH and subsequently infected with DC3000 (4 hpi). (B) SA levels in Ler and hpl1 plants pre-treated with E-2-hexenal or MeOH and subsequently infected with DC3000 (24 hpi). In both cases the hormone levels in the 10 mM MgSO4 (mock) infiltrated plants are also shown. Nine leaves were harvested, in pools of three from mock-infiltrated or bacteria-infiltrated plants at specified timepoints and used for plant hormone quantification. Bars represent the mean of three independent experiments. Error bars represent standard error. Bars annotated with different letters indicate statistically different hormone levels (P < 0.05, according to ANOVA, followed by a LSD post hoc test).