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Published in: Molecular Plant Pathology

DOI: 10.1111/mpp.12559

Link to publication

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Citation for published version (APA):
Di, X., Gomila, J., & Takken, F. L. W. (2017). Involvement of salicylic acid, ethylene and jasmonic acid signalling pathways in the susceptibility of tomato to Fusarium oxysporum. Molecular Plant Pathology, 18(7), 1024–1035. https://doi.org/10.1111/mpp.12559

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Involvement of salicylic acid, ethylene and jasmonic acid signalling pathways in the susceptibility of tomato to *Fusarium oxysporum*

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SUMMARY

Phytohormones, such as salicylic acid (SA), ethylene (ET) and jasmonic acid (JA), play key roles in plant defence following pathogen attack. The involvement of these hormones in susceptibility following *Fusarium oxysporum* (Fo) infection has mostly been studied in Arabidopsis thaliana. However, Fo causes vascular wilt disease in a broad range of crops, including tomato (*Solanum lycopersicum*). Surprisingly little is known about the involvement of these phytohormones in the susceptibility of tomato towards Fo f. sp. lycopersici (Fol). Here, we investigate their involvement by the analysis of the expression of ET, JA and SA marker genes following Fol infection, and by bioassays of tomato mutants affected in either hormone production or perception. Fol inoculation triggered the expression of SA and ET marker genes, showing the activation of these pathways. NahG tomato, in which SA is degraded, became hypersusceptible to Fol infection and showed stronger disease symptoms than wild-type. In contrast, ACD and Never ripe (Nr) mutants, in which ET biosynthesis and perception, respectively, are impaired, showed decreased disease symptoms and reduced fungal colonization on infection. The susceptibility of the def1 tomato mutant, and a prosystemin over-expressing line, in which JA signalling is compromised or constitutively activated, respectively, was unaltered. Our results show that SA is a negative and ET a positive regulator of Fol susceptibility. The SA and ET signalling pathways appear to act synergistically, as an intact ET pathway is required for the induction of an SA marker gene, and vice versa.

Keywords: ET, *Fusarium oxysporum*, JA, SA, susceptibility, tomato.

INTRODUCTION

The root-infecting fungal pathogen *Fusarium oxysporum* (Fo) causes vascular wilt disease in over 100 different plant species, including banana, cotton, palm, Arabidopsis and tomato (Michielse and Rep, 2009). Fo represents a species complex comprising many individual pathogenic strains, each capable of infecting one or a few host species only. Based on host specificity, strains have been grouped into *formae speciales*. Infection by Fo starts on attachment of fungal hyphae to the plant root surface. Subsequently, fungal hyphae enter the roots through wounds or cracks at the root tip, or at sites of lateral root formation. Ultimately, the fungus reaches the xylem vessels and proliferates, causing disease to ensue (Berrocal-Lobo and Molina, 2008; di Pietro et al., 2003; Rep et al., 2002). In attempting to arrest pathogen spread through the vasculature, the plant blocks its infected vessels and compromises their ability to transport water and nutrients. Vascular browning, stunting, progressive wilting and, eventually, plant death are typical disease symptoms of infected plants (Agrios, 2005; di Pietro et al., 2003).

In general, plant defence responses against pathogens are controlled by complex signalling routes that often involve the classical defence phytohormones salicylic acid (SA), ethylene (ET) and jasmonic acid (JA) (Robert-Seilaniantz et al., 2011). Usually, SA signalling triggers resistance against biotrophic and hemibiotrophic pathogens, whereas a combination of JA and ET signalling activates resistance against necrotrophs (Glazebrook, 2005).

As a result of the extensive availability of genetic and genomic resources, most studies on phytohormone involvement in defence against Fo have been performed in Arabidopsis (Edgar et al., 2006). Arabidopsis is susceptible to *Fo forma specialis* (f. sp.) conglutinans (Focn). Arabidopsis lines that express the salicylate hydroxylase transgene (NahG), or that carry the SA induction-deficient 2 (sid2) mutant, are impaired in SA accumulation. Both lines show increased susceptibility to Fo, indicating the involvement of SA in reducing disease susceptibility (Berrocal-Lobo and Molina, 2004; Diener and Ausubel, 2005).

Pretreatment of Arabidopsis seedlings with either methyl jasmonate (MeJA) or the ET precursor 1-aminocyclopropane-1-carboxylic acid (ACC) leads to enhanced disease symptom development on Fo inoculation, indicating that both ET and JA are involved in disease susceptibility (Trusov et al., 2009). The ET-insensitive Arabidopsis mutants *ethylene insensitive2* (ein2-1) and *ethylene receptor 1* (etr1-1) show a reduction in disease symptoms compared with Col-0 plants when inoculated with Focn...
(Pantelides et al., 2013; Trusov et al., 2009). In contrast, various JA biosynthesis mutants, such as jasmonate resistant 1 (jar1-1) and allene oxide synthase (aos), do not exhibit increased susceptibility to Fo (Thatcher et al., 2009; Trusov et al., 2009). Surprisingly, a point mutation in CORONATINE INSENSITIVE1 (COI1), an essential component of JA perception, strongly reduces disease symptom development following Fo infection (Thatcher et al., 2009; Trusov et al., 2009). In addition, disruption of MYC2, PFT1 and LBD20, transcriptional regulators of JA signalling, also results in an increased resistance to Fo (Anderson et al., 2004; Kidd et al., 2009; Thatcher et al., 2012). Taken together, ET and JA are positive regulators of susceptibility in Arabidopsis.

The role of phytohormones in determining host colonization and disease symptom development is known to vary for different formae specialis of Fo and their respective hosts (Di et al., 2016). To obtain a better insight into these processes, it is therefore crucial to investigate the role of phytohormones in defence responses to Fo in plant species other than Arabidopsis. Tomato (Solanum lycopersicum), a major and important vegetable crop (Panthee and Chen, 2010), is susceptible to Fo f. sp. lycopersici (Fo), resulting in significant yield losses each year (McGovern, 2015). The interaction between tomato and Fo has been well studied (Takken and Rep, 2010). Like other formae specialis of Fo, Fol colonizes the vasculature, and infected plants exhibit vascular browning, leaf epinasty, stunting, progressive wilting and, eventually, death (di Pietro et al., 2003). During colonization, the fungus secretes virulence factors, called effector proteins (Houterman et al., 2007). The deletion of specific effectors, such as Avr2, typically compromises fungal virulence, resulting in strains that are reduced in pathogenicity (Houterman et al., 2007, 2009).

For tomato, a large collection of lines is available which are compromised in hormone perception, metabolism or signalling. In our study, mutants affected in the biosynthesis and signalling pathway of specific defence-related hormones were analysed for their susceptibility to Fol. The lines used in this study include the following: (i) transgenic NahG plants that express the bacterial enzyme salicylate hydroxylase, which converts SA into biologically inactive catechol, resulting in plants deficient in SA accumulation (Brading et al., 2000); (ii) Never ripe (Nh), a dominant ET-insensitive mutant, carrying a single base substitution in the region encoding the N-terminus of ETR3, a homologue of the Arabidopsis ETR1 receptor (Wilkinson et al., 1995); (iii) a transgenic line that expresses ACCD (1-amino-cyclopropane-1-carboxylic acid deaminase), which encodes the ACCd enzyme that catalyses the degradation of ACC; (iv) the JA-deficient mutant defenselless-1 (def1), which has a defect in the jasmonate pathway between 13-hydroperoxy-octadecatetraenoic acid (13-HPOT) and 12-oxophytodienoic acid; this mutant fails to produce JA and does not systemically accumulate proteinase inhibitors (PIs) in response to treatment with systemin or oligosaccharide elicitors (chitosan and polygalacturonide) (Li et al., 2002); and (v) a 35S::prosystemin transgenic line overexpressing prosystemin; prosystemin is a positive regulator of JA signalling, and hence these plants constitutively accumulate high levels of P1 proteins (Howe and Ryan, 1999).

Here, we report our inoculation assays, using both wild-type Fol and a FolΔAvr2 mutant, of the various tomato lines affected in SA, ET or JA signalling. In contrast with JA signalling, both SA and ET play major and opposing roles in disease susceptibility and development. The SA and ET signalling pathways appear to act synergistically, as an intact ET pathway is required for the induction of an SA reporter gene, and vice versa. A model for the role of SA, ET and JA signalling in tomato in the susceptibility to Fol is proposed and compared with that in Arabidopsis.

RESULTS

NahG tomato plants show enhanced disease symptom development on Fol infection

To assess the potential role of SA in the modulation of susceptibility to Fol, 3-week-old wild-type tomato plants (cultivar Money-maker) and transgenic NahG plants impaired in SA accumulation were inoculated with either water (mock) or wild-type Fol, notably a race 2 isolate called Fol007. In addition, to allow the assessment of hypersusceptibility, a Fol007 Avr2 knockout strain (FolΔAvr2) was included. This mutant is compromised in virulence and causes fewer disease symptoms than wild-type Fol on susceptible plants (Houterman et al., 2009). As shown in Fig. 1a, NahG plants inoculated with Fol007 exhibited stronger disease symptoms than did wild-type plants. These symptoms included extensive wilting and a greater stunting 3 weeks after inoculation. Consistent with this, the fresh weight of Fol007-infected NahG tomato plants was significantly lower than that of corresponding wild-type plants (Fig. 1b). Moreover, all vascular bundles of infected NahG plants had turned brown, and plants were either dead or very small and wilted. On a scale from 0–4 (Rep et al., 2005), infected NahG plants scored the maximal disease index (Fig. 1c). As expected, FolΔAvr2-inoculated plants developed weaker disease symptoms (Fig. 1a). Similar to Fol007, FolΔAvr2-infected NahG plants showed a significant reduction in fresh weight and a higher disease index relative to infected wild-type plants (Fig. 1b,c).

To investigate whether the augmented disease symptom development in NahG plants correlated with increased host colonization, a fungal recovery assay was performed. Sections were taken from race 2 inoculated wild-type and NahG plants at different heights of the stem, notably at the position of the cotyledon node, second node and fourth node. Following sterilization, the sections were placed on potato dextrose agar (PDA) plates and incubated for 5 days at 25 °C. As shown in Fig. 1d,e, wild-type Fol colonized the stems more extensively than did the FolΔAvr2 strain. In all cases,
Fig. 1 Impaired salicylic acid (SA) signalling enhances *Fusarium oxysporum* f. sp. *lycopersici* (Fol) disease symptom development in tomato. (a) Three-week-old wild-type Moneymaker and NahG tomato plants inoculated with water (mock), Fol007 or FolΔAvr2 at 21 days post-infection (dpi). Disease development was scored by measuring the fresh plant weight (b) and determining the disease index (range, 0–4) (c) of 20 plants per treatment/genotype combination. Circles and squares indicate Moneymaker and NahG plants, respectively. Plant weight was subjected to a pairwise comparison with a Student’s *t*-test, whereas the disease index was analysed by a non-parametric Mann–Whitney *U*-test (*P* < 0.05; **P** < 0.01; ***P*** < 0.001). The bioassay was repeated three times with similar results. (d) Representative stem sections taken from the cotyledon node (top left), second node (top right) and fourth node (bottom) of individual treated plants (*n* = 6) after incubation for 5 days on potato dextrose agar (PDA) plates. (e) Percentage of infected slices showing fungal outgrowth. Fungal progression in the stem was expressed as the infected percentage of all stem pieces. The experiment was performed twice with similar results. Transcription patterns of phenylalanine ammonia-lyase (*PAL*) (f), isochorismate (*ICS*) (g) and pathogenesis-related 1a (*PR1a*) (h) in Fol007-inoculated wild-type Moneymaker and NahG plants at 0, 3, 7 and 14 dpi. Gene expression levels relative to the internal control *tubulin* genes were quantified by quantitative polymerase chain reaction (qPCR). The data are expressed as the mean ± standard deviation (SD). Three biological replicates for each line per time point were analysed. The different letters show significant difference at *P* < 0.05 as determined by Duncan’s multiple-range test. The experiment was performed twice with similar results.
the wild-type fungus was able to reach the second or even fourth node, whereas, in the Avr2 knockout, only 30% reached the second node and the majority of the fungus was contained at the cotyledon node or below. Notably, the FolΔAvr2 strain was able to more effectively colonize NahG plants, and fungal outgrowth was observed in the fourth node in 70% of the infections (Fig. 1e). The NahG plants were also hypersusceptible to the wild-type fungus, as depicted by the higher percentage of plants in which fungal outgrowth was seen from the fourth node. Together, these data suggest that NahG plants are hypersusceptible to *Fusarium* infection, and that the increased disease symptoms correlate with increased fungal colonization of the transgenic plants.

SA is synthesized through both the isochorismate (ICS) and phenylalanine ammonia-lyase (PAL) pathways (Lee *et al*., 1995; Wildermuth *et al*., 2001). To assess the expression of the PAL and ICS genes during *Fol* infection, a reverse transcription-quantitative polymerase chain reaction (RT-qPCR) analysis was carried out on hypocotyls. Samples were taken at 0, 3, 7 and 14 days post-infection (dpi) of wild-type and NahG plants. PAL and ICS expression levels were measured and normalized to tubulin. We found that, in NahG plants, only at 14 dpi transcript levels of PAL were significantly up-regulated relative to that at 0 dpi (Fig. 1f). In the wild-type Moneymaker plants, no significant induction of PAL was observed at any time point. ICS expression in NahG plants was significantly induced at 7 and 14 dpi relative to that at 0 dpi (Fig. 1g). In the wild-type plants, a significant, but only transient, induction of ICS was observed at 3 dpi. Together, these data indicate the involvement of SA biosynthesis genes in the *Fol*-tomato interaction. Possibly, the high SA turnover in NahG plants elicits a feedback mechanism activating the PAL and ICS SA biosynthesis pathways following *Fol* infection.

Pathogenesis-related 1a (PR1a) expression is often used as a reporter for SA-dependent defence signalling (Kunkel and Brooks, 2002). To assess whether PR1a expression is altered during *Fol* infection, its expression at 0, 3, 7 and 14 dpi was measured. Transcript levels of PR1a were significantly induced in wild-type plants at 7 and 14 dpi, suggesting that SA signalling is activated late during *Fol* infection (Fig. 1h). Compared with wild-type plants, the expression of PR1a in infected NahG plants was less strongly induced. This weaker induction correlates with the loss of SA accumulation in NahG plants, confirming the proposed of the transgenic line. Overall, these data show that impaired SA signalling enhances susceptibility to *Fol* and disease symptom development in tomato.

**ET enhances susceptibility to *Fol* in tomato plants**

Pretreatment of Arabidopsis seedlings with the ET precursor ACC leads to enhanced disease symptom development on *Focn* inoculation, indicating that ET is involved in disease susceptibility (Trussov *et al*., 2009).

To investigate the role of ET in disease symptom development in tomato, transgenic plants impaired in ET biosynthesis were analysed for their susceptibility to *Fol*. In the transgenic ACD line, constitutively expressing a bacterial ACC deaminase gene, ET production is reduced by 90% relative to the wild-type (Klee *et al*., 1991). As the transgene is present in cultivar UC82B, this cultivar was used as wild-type control. Although wild-type UC82B showed severe wilting and stunting following *Fol* infection, most ACD plants showed only mild disease symptoms (Fig. 2a). The weight of infected ACD plants was also significantly higher than that of infected wild-type plants (Fig. 2b). In addition, the disease index in ACD plants was significantly attenuated relative to that in wild-type plants (Fig. 2c). A similar reduction in symptom development was also observed in ACD lines inoculated with FolΔAvr2. To monitor fungal colonization, stem sections were taken and incubated on PDA plates. The fungal recovery assay showed that Fol007 grew-out from most stem sections of both wild-type and ACD plants, whereas much less fungal growth was observed in FolΔAvr2-inoculated ACD plants. A typical example of a plate assay is shown in Fig. 2d and the data from the fungal recovery assay are summarized in Fig. 2e. FolΔAvr2 was found to efficiently colonize wild-type UC82B plants, as fungal outgrowth was often observed up to the fourth node. In contrast, colonization of ACD plants was much reduced: in 80% of cases, the fungus was only observed in stem sections collected at the cotyledon node. These data indicate that the ACD line exerts a reduced susceptibility towards *Fol* infection concomitant with a reduction in symptom development.

It has been reported that the ET receptor gene *ETR* and ET-responsive factors *ERFs* are induced following *Fol* infection (Berrocal-Lobo and Molina, 2008; Pantelides *et al*., 2013). A well-characterized ERF family member in tomato is Pti4, which has been shown to specifically bind to the GCC-box cis-element present in the promoter of PR genes (Wu *et al*., 2002). GCC-box binding by ERFs induces PR gene expression and Pti4 could be a functional tomato homologue of *ERF1* (Wu *et al*., 2002). In Arabidopsis, *ERF1* overexpression enhances resistance to *Fol* (Berrocal-Lobo and Molina, 2004). As shown in Fig. 2f,g, the transcription of *Pti4* and *ETR4* was strongly induced in wild-type plants at 7 and 14 days, respectively, following *Fol* inoculation. Compared with wild-type plants, *Fol*-infected ACD plants showed a weaker increase in expression of the two ET marker genes, which confirms the proposed plant genotypes. In addition, the weaker induction of *ETR4* and *Pti4* expression in the ACD line is a further indication that ET-mediated signalling is activated during *Fol* infection. To further test how ET signalling contributes to increased susceptibility, the involvement of ET perception by the host was investigated. Bioassays were performed with wild-type tomato cultivar Pearson and the ET-insensitive Pearson mutant *Nr*. Following the inoculation of wild-type Pearson with Fol007, the older
Fig. 2 Impaired ethylene (ET) biosynthesis and production in tomato reduces disease susceptibility to *Fusarium oxysporum* f. sp. *lycopersici* (*Fol*). (a) Three-week-old wild-type UC82B and ACD tomato plants inoculated with water (mock), *Fol007* or *FolΔAvr2* at 21 days post-infection (dpi). Disease development was scored by measuring the fresh weight (b) and disease index (range, 0–4) (c) of 20 plants per treatment/genotype combination. Circles and squares indicate UC82B and ACD plants, respectively. Plant weight was subjected to a pairwise comparison using a Student’s *t*-test, whereas the disease index was analysed by a non-parametric Mann–Whitney *U*-test (*P* < 0.05; **P** < 0.01; ***P** < 0.001). The bioassay was repeated three times with similar results. (d) Representative stem sections taken from the cotyledon node (top left), second node (top right) and fourth node (bottom) of individual treated plants (*n* = 6) after incubation for 5 days on potato dextrose agar (PDA) plates. (e) Colonization is expressed as the percentage of infected slices of all stem pieces (*n* = 6). The experiment was performed twice with similar results. (f, g) Transcription patterns of ET-regulated marker genes *Pti4* and *ETR4* in *Fol007*-inoculated UC82B and ACD at 0, 3, 7 and 14 dpi. Gene expression levels relative to the internal control *tubulin* genes were quantified by quantitative polymerase chain reaction (qPCR). The data are expressed as the mean ± standard deviation (SD). Three biological replicates for each line per time point were analysed. The different letters show the significant difference at *P* < 0.05 as determined by Duncan’s multiple-range test. The experiment was performed twice with similar results.
leaves of infected plants became chlorotic and the plants showed mild wilting symptoms (Fig. 3a). On inoculation with Fol\(\Delta\)Avr2, wild-type Pearson plants showed hardly any symptoms (Fig. 3a). Notably, no obvious disease symptoms were observed in \(\text{Nr}\) plants inoculated with either Fol007 or Fol\(\Delta\)Avr2. Although the fresh weight of \(\text{Nr}\) plants was identical to that of Pearson plants after Fol007 infection (Fig. 3b), the \(\text{Nr}\) plants exhibited a significantly lower disease index than Pearson plants; fewer brown vessels were observed in the stems (Fig. 3c). Fungal recovery assays revealed that Fol\(\Delta\)Avr2 either completely failed to colonize \(\text{Nr}\) plants or, in the rare cases it did, it only reached the basal part of the stem that forms the hypocotyl (Fig. 3d,e). Taken together, the data suggest that both the ability to synthesize ET and the ability to perceive the hormone are essential for disease development and the ability of the fungus to colonize the plant.

**Perturbation of JA signalling has no detectable effect on plant susceptibility and disease symptom development**

In Arabidopsis, various JA biosynthesis mutants, such as jasmonate resistant 1 (jar1-1) and allene oxide synthase (aos), do not
exhibit increased susceptibility to Focn (Thatcher et al., 2009; Trusov et al., 2009). To investigate the role of JA biosynthesis in the susceptibility of tomato to Foc, we used the def1 mutant. This line has a defect in its octadecanoid biosynthesis pathway, which provides precursors for JA synthesis, making the plant hypersusceptible to herbivores because of its impaired accumulation of PIs I and II in response to wounding (Lightner et al., 1993). In addition to def1, 35S::prosystemin plants were included in our assays. In these plants, the prosystemin gene is constitutively overexpressed by the 35S cauliflower mosaic virus promoter. Prosystemin is the precursor of systemin, which initiates a signalling pathway that leads to the synthesis of JA from linolenic acid (Ryan, 2000). The constitutive induction of the JA pathway in 35S::prosystemin plants results in the systemic accumulation of high levels of PIs in these plants (McGurl et al., 1994).

To confirm the genotype of def1 and 35S::prosystemin plants, the transcript levels of PI-I were examined in leaves of wild-type Castlemart, def1 and 35S::prosystemin plants in response to wounding. As shown in Fig. S1 (see Supporting Information), wounding of wild-type plants triggered the induction of PI-I expression. In contrast, no PI-I accumulation was observed on wounding of def1 plants, whereas a constitutive expression of PI-I was observed in 35S::prosystemin plants irrespective of treatment. These results confirm the plant genotypes and the involvement of def1 and 35S::prosystemin in JA signalling.

To test whether JA signalling affects the susceptibility to Foc, the JA mutant lines were inoculated with the fungus. As shown in Fig. 4a, Fol007-infected def1 and 35S::prosystemin lines became equally chlorotic as the wild-type Castlemart. Inoculation with the less pathogenic FolΔAvr2 strain did not result in obvious disease
symptoms in any of the lines. No significant differences in fresh weight or disease index were observed between Castlemart and its derivatives following either Fol007 or FolDAvr2 inoculation (Fig. 4b,c).

Fungal recovery assay revealed that, in wild-type Castlemart, Fol007 was present in all probed stem sections, showing that the fungus colonized the stem until the fourth node (Fig. 4d,e). In most of the inoculated def1 and 35S::prosystemin plants, Fol007 had also colonized the entire stem until the fourth node. In contrast with Fol007, FolDAvr2 completely failed to colonize wild-type Castlemart plants, which is consistent with the lack of disease symptoms observed in these plants. However, in the 35S::prosystemin plants and def1 mutants, the FolDAvr2 strain was detected at a limited number of stem sections collected at either the position of the cotyledon node or the second node (Fig. 4e). The latter data suggest that disturbed JA signalling might facilitate fungal colonization.

To assess whether JA signalling is induced following Fol007 inoculation, the expression of PI-I was monitored at 0, 3, 7 and 14 dpi. As shown in Fig. 4f, no significant difference in PI-I expression was observed in Fol-inoculated wild-type plants at any time point. The same low levels of PI-I expression were detected in the def1 mutant, and these levels did not change during infection.

Taken together, these data imply that perturbation of JA signalling has no detectable effect on the susceptibility to Fol.

SA and ET signalling pathways act synergistically in tomato susceptibility to Fol infection

The degradation of SA was found to enhance the susceptibility to Fol, whereas impaired ET signalling reduced the susceptibility. We therefore wanted to test whether these pathways interact following Fol infection. The expression of PR1a was monitored over time (0–14 dpi) in both the ACD ET synthesis mutant and in wild-type UC82B plants on Fol007 infection. As shown in Fig. 5a, expression of the SA marker gene PR1a was strongly induced in wild-type plants, but much less so in ACD lines. This finding indicates that the induction of PR1a following Fol infection requires an intact ET pathway. Subsequently, the expression of Pti4 and ETR4 was assessed in the NahG line and its parental Moneymaker background following Fol007 inoculation. As shown in Fig. 5b,c, expression of both ET marker genes was strongly induced in wild-type plants, but not in NahG plants, following Fol infection. This finding suggests that an intact SA signalling pathway is required for Pti4 and ETR4 induction.

Fig. 5 Time course of transcription patterns of salicylic acid (SA) and ethylene (ET) marker genes on Fusarium oxysporum f. sp. lycopersici (Fol) inoculation. (a) Expression of the SA marker gene pathogenesis-related 1a (PR1a) in wild-type UC82B and the transgenic ACD line at 0, 3, 7 and 14 days post-infection (dpi). (b, c) Transcription patterns of the ET marker genes Pti4 and ETR4 in NahG and the Moneymaker progenitor at 0, 3, 7 and 14 dpi. Gene expression levels relative to the internal control tubulin genes were quantified by quantitative polymerase chain reaction (qPCR). The data are expressed as the mean ± standard deviation (SD). Three biological replicates for each line per time point were analysed. The different letters show the significant difference at P < 0.05 as determined by Duncan’s multiple-range test. The experiment was performed twice with similar results.
DISCUSSION

Here, the role of SA, ET and JA in the modulation of the susceptibility of tomato plants to Fol was investigated. NahG plants that failed to accumulate SA were hypersusceptible to Fol infection and showed severe disease symptoms and extensive fungal colonization of their xylem vessels. Together with the strong induction of the SA marker gene PR1a in wild-type plants, which was not strongly induced in NahG plants, these data show that SA plays a positive role in reducing disease susceptibility. This conclusion is in agreement with chemical studies, in which exogenous application of SA to tomato through root feeding or foliar sprays reduced vascular browning, leaf yellowing and wilting following Fol inoculation (Mandal et al., 2009). The positive role of SA in Fol resistance in tomato is consistent with studies with NahG Arabidopsis, showing an increased susceptibility to Fo (Berrocral-Lobo and Molina, 2004; Diener and Ausubel, 2005; Thatcher et al., 2009; Trusov et al., 2009). Therefore, the role of SA in Fo susceptibility seems to be conserved in both plant species. Interestingly, in several studies, elevated SA has been reported to enhance the susceptibility to necrotrophic pathogens, but to promote resistance to hemibiotrophs (Bari and Jones, 2009; El Oirdi et al., 2011). Our findings, in which SA reduces the susceptibility of tomato plants to Fol, are in line with the hemibiotrophic lifestyle of the latter (Di et al., 2016).

The ACD tomato line, in which ET biosynthesis is compromised, showed a reduced susceptibility to Fol infection. On Fol inoculation, the transgenic line showed fewer disease symptoms and a reduced fungal colonization relative to the wild-type UC82B cultivar (Fig. 2). The ET marker genes ETR4 and Pti4 were highly induced in wild-type plants, but not in the ACD line, indicating that ET signalling is induced in response to Fol infection and is important for disease development. The ET-insensitive Nr mutant was also found to be less susceptible than wild-type Pearson plants to infection with Fol007 (Fig. 3). These data are consistent with studies by Lund et al. (1998) and Francia et al. (2007), which also reported a reduction in Fol disease symptoms in the Nr mutant. The fact that both ET synthesis and perception were found to be important for disease development and fungal colonization suggests that ET signalling is important for full susceptibility to Fol.

The role of ET is multifaceted in Arabidopsis (Di et al., 2016). Similar to Nr in tomato, soil-grown ein2-1 and etr1-1 mutants of Arabidopsis showed a reduction in disease symptoms relative to wild-type Col-0 plants when inoculated with Focn (Pantelides et al., 2013; Trusov et al., 2009). Fo inoculation of Arabidopsis plants carrying the ein2-5 allele revealed a markedly enhanced susceptibility to Fo in plate assays (Berrocral-Lobo and Molina, 2004). These differences might be explained by the different mutations, or by the different inoculation methods. As inoculation of soil-grown plants best mimics the natural infection process, which resembles that of our tomato assays, it seems that, in both plant species, the role of ET is conserved, in that its absence reduces disease symptom development (Pantelides et al., 2013; Trusov et al., 2009).

No significant difference in disease index and fresh weight between the wild-type and JA-deficient def1 line was found after Fol007 or Fol\Avr2 inoculation (Fig. 4). These findings contrast those of Thaler et al. (2004), who showed that the weight of def1, but not wild-type tomato plants, was reduced on inoculation with a race 1 Fol isolate. The reason for the discrepancy might be that a different Fusarium race or different assay conditions were used. On Fol007 infection, 35S::prosystemin plants also did not show a significant difference in disease index or fresh weight relative to wild-type tomato. Thus, under our assay conditions, JA does not appear to play a major role in the development of disease symptoms or disease susceptibility.

In different host–Fo pathosystems, JA can promote either resistance or susceptibility (Di et al., 2016). A point mutation in COI1 in Arabidopsis, an essential component for JA perception, strongly reduces the susceptibility to Fo (Thatcher et al., 2009; Trusov et al., 2009). In contrast, jar1 mutants, which are defective in the synthesis of the bioactive JA–isoleucine (JA-Ile) conjugate, show wild-type-like symptoms or only a slight increase in susceptibility (Thatcher et al., 2009; Trusov et al., 2009). In addition, Cole et al. (2014) have reported that infection by Focn and Fo f. sp. matthioli, which produce JA-Ile and leucine-conjugated JA (JA-Leu), respectively, is suppressed in coi1. In contrast, the coi1 mutation has no effect on infection by Fo f. sp. raphani, which produces no detectable JA-Ile/JA-Leu. Furthermore, the JA-insensitive mutation (jai1) has no effect on the infection of tomato plants by Fol, which produces no detectable jasmonates. Therefore, different formae speciales may adopt different strategies to infect their host and to cause disease symptoms.

The SA, ET and JA signalling pathways are entangled in a complex network in which the different pathways influence each other through positive and negative regulatory interactions (Grant and Jones, 2009). We observed that, relative to wild-type plants, the expression of PR1a was less strongly induced in the ET biosynthesis mutant ACD (Fig. 5). Similarly, following Fol inoculation, ET signalling, as monitored by ETR4 and Pti4 expression, was strongly induced in wild-type plants, but less so in NahG plants. Collectively, these results indicate that, in tomato, SA and ET signalling might act synergistically during Fol infection, as an intact ET pathway is required for the induction of the SA reporter gene, and vice versa. In addition, for Xanthomonas campestris pv. vesicatoria infection of tomato, accumulation of SA was found to require ET synthesis, suggesting that ET positively regulates SA-induced defences (O’Donnell et al., 2003).

Altogether, these data allow us to propose a model for the involvement of SA, ET and JA signalling in tomato in susceptibility...
to Fol (Fig. 6a). SA and ET signalling interact and have opposite roles in disease susceptibility. The infection of tomato plants by Fol activates both the ET and SA pathways. The ET response enhances the susceptibility to Fol infection and disease development, whereas SA responses restrict colonization. No apparent role for JA was shown in the interaction, as disease symptoms in JA mutants were indistinguishable from those of the wild-type plants. A comparison with the reported roles of these phytohormones in Arabidopsis in Fo infection reveals shared and unique effects between Arabidopsis and tomato. As shown in Fig. 6b, SA signalling also negatively regulates susceptibility to Fo, whereas ET signalling likewise positively enhances susceptibility. Notably, JA can be hijacked by the fungus to enhance pathogenicity in Arabidopsis, but apparently does not play an important role in tomato.

Although the Arabidopsis–Fo system serves as a useful model for some plant–Fo interactions, the tomato system can be used to study Fo–plant interactions in which JA does not play a major role. It will be interesting to also investigate other plant–Fo systems to identify whether there may be more species-specific aspects that differ from either model. These insights are relevant to allow the translation of molecular mechanisms obtained in these models into various crops to aim for a reduced susceptibility to wilt disease. The molecular mechanisms underlying susceptibility, however, are currently unknown and their elucidation is a challenge for future studies.

**EXPERIMENTAL PROCEDURES**

Ten different tomato (*Solanum lycopersicum*) genotypes were used in these studies, including the four wild-type cultivars from which these mutants were derived: Moneymaker, UC82B, Pearson and Castlemart. The transgenic NahG line, which is compromised in SA accumulation, is in a Moneymaker background (Brading et al., 2000). The ET-impaired mutant ACD (Klee et al., 1991) and the Nr mutation (Lanahan et al., 1994) are in a UC82B and Pearson background, respectively. The JA-impaired mutant def1 (Howe et al., 1996) and the prosystemin-overexpressing line (35S::prosystemin) are in the Castlemart background (McGurl et al., 1994). Tomato seedlings were grown in a conditioned glasshouse with day–night temperatures of 23 °C–18 °C and a 16-h light/8-h dark regime.

**Fusarium inoculation assay**

Wild-type *Fusarium* strain Fol007 (race 2) and the derived FolΔAvr2 mutant have been described previously (Houterman et al., 2009). *Fol* strains were grown on PDA (Oxoid Ltd., Basingstoke, Hampshire, UK) at 25 °C for 7–10 days. Subsequently, a piece of agar carrying the fungus was transferred to 100 mL minimal medium (100 mM KNO₃, 3% sucrose and 0.17% yeast nitrogen base without amino acids or ammonia). Conidial spores were harvested after 3–5 days of cultivation at 25 °C with shaking. After washing with sterilized water, the spores were diluted to 10⁶ spores/mL. For bioassay, 3-week-old tomato seedlings were uprooted from the soil. The seedlings were placed for 5 min in the Fol spor suspension (10⁵ spores/mL) and subsequently potted. Disease progression was evaluated after 3 weeks. Plant weight and disease index (Rep et al., 2005) were scored for 20 plants/treatment.

**Fungal recovery assay**

Fungal colonization in tomato plants was assessed at 21 dpi. Representative stem sections taken from the cotyledon node, second node and fourth node were collected separately. The stem pieces were surface sterilized in 70% ethanol and rinsed in sterile distilled water, after which the ends of the stems were removed with a sterile scalpel. Stem sections about 5 mm thick were cut and placed on PDA supplemented with 200 mg/L streptomycin and 100 mg/L penicillin at 25 °C, allowing the fungus to grow out of the stem sections. Photographs were taken after 5 days of incubation at 25 °C. Data were expressed as a percentage of slices showing fungal outgrowth.
Wounding assay

Wounding experiments have been described previously (Howe et al., 1996). Briefly, a haemostat was used to inflict damage to the primary leaf of 15-day-old tomato plants. Twenty-four hours later, the wounded leaf and an upper unwounded leaf were dissected andsnap frozen in liquid N2 to use for expression analysis.

Analysis of gene expression by RT-qPCR

RNA isolation and cDNA synthesis were performed as described previously (Gawehs et al., 2014). Briefly, total RNA from tomato stem beneath the cotyledon was extracted using Trizol-Reagent (Invitrogen, Life Technologies, Grand Island, NY, USA) according to the manufacturer’s instructions. The RNA was subsequently purified with an RNaseasy Mini kit (Qiagen, Düesseldorf, Germany) and DNA was removed by on-column treatment with RNase-free DNase (Qiagen). cDNA was synthesized using the M-MuV reverse-transcriptase RNase H minus kit (Fermentas, Thermo Scientific, Pittsburgh, PA, USA). Stem tissue was collected from tomato plants at 0, 3, 7 and 14 dpi. The conditions of the RT-qPCR experiments and the relative quantification of specific mRNA levels were performed according to Lopez-Raez et al. (2010) and using the gene-specific primers described in Table S1 (see Supporting Information). PCRs were performed in an ABI 7500 Real-Time PCR system (Applied Biosystems, http://www.appliedbiosystems.com Foster City, CA, USA) using the Platinum SYBR Green qPCR SuperMix-UDG kit (Invitrogen). The 20-μL PCRs contained 0.25 μM of each primer, 0.1 μL ROX reference dye and 1 μL of cDNA. The cycling programme was set to 5 min at 50°C, 5 min at 95°C, 40 cycles of 1 s at 95°C and 1 min at 60°C, followed by a melting curve analysis. The expression levels of selected genes were normalized to tomato α-tubulin (SolyCo4g072020.2) expression. Relative gene expression was calculated using the 2−ΔΔCT method. Three biological replicates for each of the selected genes were performed.

Statistical analyses

The statistical significance of the results was determined by performing PRISM 5.0 (GraphPad, http://www.graphpad.com). The data on plant weight were subjected to a pairwise comparison with Student’s t-test. For data on the disease index in tomato plants, a Mann–Whitney test was performed for each genotype. Gene expression data were statistically evaluated, and bars annotated with different letters were significantly different according to Duncan’s multiple-range test.

ACKNOWLEDGEMENTS

We thank Jonathan D. G. Jones (Sainsbury Laboratory, Norwich, Norfolk, UK) for providing the transgenic NahG line. ACD and Nr mutants were obtained from M. Mudgett, Stanford University, Stanford, CA, USA (provided by H. Klee, University of Florida, Gainesville, FL, USA). def1 was obtained from M. Mudgett (provided by G. Howe, Michigan State University, East Lansing, MI, USA). We also thank M. Kant (University of Amsterdam, Amsterdam, the Netherlands) for providing JSS:prosystemin. The authors wish to thank Ben Cornelissen for critical reading and comments on the manuscript. X.D. was financially supported by the China Scholarship Council program grant number 201206180034 and by the ZonMw Program ‘Enabling Technologies Hotels’ file number 435000001. F.L.W.T. received funding from the European Union’s Horizon 2020 research and innovation program under the Marie Sklodowska-Curie grant agreement No. 676480 (Bestpass), and from the NWO-Earth and Life Sciences funded VICI project No. 865.14.003.

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**SUPPORTING INFORMATION**

Additional Supporting Information may be found in the online version of this article at the publisher’s website.

Fig. S1 The expression of *proteinase inhibitor I (PI-I)* was examined by reverse transcription-polymerase chain reaction (RT-PCR) in unwounded (u) and wounded (w) leaves of Castle-mart, *defl* and *35S::prosystemin*. Two biological replicates for each line were analysed.

Table S1 Primer sequences used in the gene expression analysis.