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van der Does, H.C.; Duyvesteijn, R.G.E.; Goltstein, P.M.; van Schie, C.C.N.; Manders, E.M.M.; Cornelissen, B.J.C.; Rep, M.

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Expression of effector gene SIX1 of Fusarium oxysporum requires living plant cells

H. Charlotte van der Does a, Roselinde G.E. Duyvesteijn a, Pieter M. Goltstein b, Chris C.N. van Schie a, Erik M.M. Manders c, Ben J.C. Cornelissen a, Martijn Rep a, b, *

a Plant Pathology, Swammerdam Institute for Life Sciences, University of Amsterdam, Kruislaan 318, 1098 SM Amsterdam, The Netherlands
b Center for Neuroscience, Swammerdam Institute for Life Sciences, University of Amsterdam, 1090 GB Amsterdam, The Netherlands
c Plant Pathology, Swammerdam Institute for Life Sciences, University of Amsterdam, Kruislaan 318, 1098 SM Amsterdam, The Netherlands

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A B S T R A C T
Fusarium oxysporum is an asexual, soil inhabiting fungus that comprises many different formae specialae, each pathogenic towards a different host plant. In absence of a suitable host all F. oxysporum isolates appear to have a very similar lifestyle, feeding on plant debris and colonizing the rhizosphere of living plants. Upon infection F. oxysporum switches from a saprophytic to an infectious lifestyle, which probably includes the reprogramming of gene expression. In this work we show that the expression of the known effector gene SIX1 of F. oxysporum f. sp. lycopersici is strongly upregulated during colonization of the host plant. Using GFP (green fluorescent protein) as reporter, we show that induction of SIX1 expression starts immediately upon penetration of the root cortex. Induction requires living plant cells, but is not host specific and does not depend on morphological features of roots, since plant cells in culture can also induce SIX1 expression. Taken together, F. oxysporum seems to be able to distinguish between living and dead plant material, preventing unnecessary switches from a saprophytic to an infectious lifestyle.

Many effector genes that encode small, secreted proteins, like SIX1, are not or weakly expressed in axenic cultures, and are upregulated specifically during infection (Rep, 2005). Some of these genes, like CgDIN3 (Colletotrichum gloeosporioides), AVR9 (Cladosporium fulvum) and MPG1 (Magnaporthe grisea) are also upregulated during conditions of nitrogen starvation (Stephenson et al., 2000; Talbot et al., 1993; Van den Ackerveken et al., 1994). For AVR9 and Mpg1 it was shown that expression (partly) depends on a general nitrogen response factors (NRF1 and NPR1, respectively) (Lau and Hamer, 1996; Perez-Garcia et al., 2001; Soanes et al., 2002). However, expression of other in planta induced genes does not respond to changes in nitrogen availability, for example AVR4, ECP1 and ECP2 (C. fulvum), AvrLm1 (Leptosphaeria maculans), MIG1 and the MIG2 gene cluster (Ustilago maydis) (Basse et al., 2002, 2000; Gout et al., 2006; Van den Ackerveken et al., 1994; Wubben et al., 1994). Even for the genes that are expressed in an environment with limited nitrogen, it is not known which circumstances induce expression in planta, since there are indications that within the host plant, nitrogen is not limiting (Solomon and Oliver, 2001, 2002). In F. oxysporum, the genes expressed during nitrogen starvation partially overlap with the genes expressed during infection of host tissue (Divon et al., 2005), but no upregulation of (putative) effector genes was detected.

To study the saprophytic/pathogenic lifestyle switch in pathogenic isolates of F. oxysporum we investigated the expression of the SIX1 gene from F. oxysporum f. sp. lycopersici (Fol). Members of this forma specialis (f. sp.) can infect tomato plants and cause tomato wilt disease. The SIX1 gene (for Secreted In Xylem 1) is found in all isolates of f. sp. lycopersici but not in any other forma specialis (pathogenic on other host plants such as melon, banana, tulip, etc.) (van der Does et al., 2008). The Six1 protein is an effector protein that is secreted into the xylem sap during colonization of xylem vessels and is required for full virulence of Fol (Rep et al., 2005a). In tomato plants carrying the I-3 resistance gene SIX1 can also trigger a recognition reaction that results in resistance of the plant (Rep et al., 2004).

1. Introduction

Members of the Fusarium oxysporum species complex are asexual, soil inhabiting fungi that are generally known as efficient root colonizers. Even though all isolates of F. oxysporum appear to have a very similar lifestyle, notably feeding on plant debris and colonizing the rhizosphere of living plants, some are capable of entering and infecting living plant tissue, while others are not (Gordon and Martyn, 1997; Olivain and Alabouvette, 1999). This suggests the existence of isolate specific genes and the capacity to switch from a saprophytic to an infectious lifestyle, probably involving the reprogramming of gene expression.

To study the saprophytic/pathogenic lifestyle switch in pathogenic isolates of F. oxysporum we investigated the expression of the SIX1 gene from F. oxysporum f. sp. lycopersici (Fol). Members of this forma specialis (f. sp.) can infect tomato plants and cause tomato wilt disease. The SIX1 gene (for Secreted In Xylem 1) is found in all isolates of f. sp. lycopersici but not in any other forma specialis (pathogenic on other host plants such as melon, banana, tulip, etc.) (van der Does et al., 2008). The Six1 protein is an effector protein that is secreted into the xylem sap during colonization of xylem vessels and is required for full virulence of Fol (Rep et al., 2005a). In tomato plants carrying the I-3 resistance gene SIX1 can also trigger a recognition reaction that results in resistance of the plant (Rep et al., 2004).

* Corresponding author.
E-mail address: mrep@uva.nl (M. Rep).

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early during infection, immediately after penetration of the root cortex. We also demonstrate that induced expression is highly dependent on the close proximity of living plant material.

2. Materials and methods

2.1. Expression studies: RNA isolations and PCR

Mycelium from *F. oxysporum* f. sp. *lycopersici* (Fol) isolate Fol007, described in *Mes et al.* (1999) was used to inoculate minimal growth medium (3% sucrose, 1% KNO₃ and 0.17% yeast nitrogen base without amino acids and ammonia). After 5 days of growth (25 °C, 175 rpm), microconidia were isolated and used to inoculate the test medium (25 ml with 5 × 10⁶ microconidia). Mycelium was harvested after 2 days at 25 °C, shaking at 175 rpm. For RT-PCR experiments, the mycelium was prepared and RNA isolations were performed as described in *Rep et al.* (2005b).

Roots and hypocotyls of tomato (*Solanum lycopersicum*) were sampled at 4, 8, 12 and 16 days after inoculation with Fol007 (tomato cultivar C32) or at 2, 4, 8 and 14 days after inoculation (tomato cultivar GCR 161), both susceptible interactions. At the first time point, material from 40 individual plants was pooled and at the subsequent time points 20 plants were pooled. Total RNA was isolated using TRIzol (Gibco), followed by an additional Lithium Chloride precipitation. The isolated RNA was used to make cDNA using Promega Rnasin (ribonuclease inhibitor) and Gibco Superscript II RNase H⁻ reverse transcriptase, according to the instructions of the manufacturer (Gibco).

PCR reactions to check for the presence of *SIX1* and *FEM1* were performed on 2 μl cDNA in a total volume of 25 μl, using a forward primer on the gene of interest (p12-F1 [CCCCGAATTGAGGTGAAG] for *SIX1* and FemATG [ATGAAGTACACTCCGCTACC] for *FEM1*) and a reverse primer on the polyA tail. Primers were allowed to anneal at 55 °C, elongation was 1 min in 35 cycles. PCR products were separated on 1% agarose gels and visualized with ethidium bromide. Target sequences were amplified by PCR (using Pfu polymerase), introducing XbaI restriction site in the following way: in pGEMT-easy containing the *SIX1* ORF, present in a NcoI–SpeI genomic fragment containing the *SIX1* gene in the pGEMT-easy vector, was first replaced by an XbaI restriction site in the following way: in pGEMT-easy containing the NcoI–SpeI fragment with *SIX1*, the entire *SIX1* open reading frame was deleted and replaced by an XbaI restriction site. This was done by PCR amplification of vector plus *SIX1* flanking sequences using primers P12-ATC-R (aaataactagatgcctcaagtcacctc) and P12-TAA-F (aaataactagatgcctcaagtcacctc) followed by XbaI digestion of the linkers and religation. The *GFP* ORF was amplified by PCR (using Pfu polymerase), introducing XbaI restriction sites on both ends, which allowed cloning of *GFP* directly between the *SIX1* promoter and terminator in the above mentioned construct. Constructs were sequenced to check for the right orientation and rule out PCR mistakes. To facilitate homologous recombination of *GFP* into the *SIX1* locus in Fol, the 3’ end of cassette was extended with the neighboring 1.5 kb Spel–XbaI genomic DNA fragment. The correct orientation of this 1.5 kb extension was checked by restriction analyses. Finally, the *BLE* resistance gene (conferring resistance to zeocin) was introduced between the *SIX1* terminator (the region corresponding to the mRNA trailer) and the 3’ flank for homologous recombination. For this, the *BLE* gene was retrieved from the pAN8.1 vector (Punt and van den Houdel, 1992) as an Agel–XbaI fragment and cloned into the SgrAI–SpeI digested *SIX1* locus–*GFP* construct. HindIII and EcoRI were used to transform the construct to pZIP2000, a binary vector for *Agrobacteria*-mediated transformation (ATMT) of *Fusarium* (Hajdukiewicz et al., 1994). Constructs were transformed to the *SIX1* knockout strain (described in *Rep et al.*, 2004) in which the *SIX1* ORF had been replaced by a hygromycin resistance gene. After ATMT zeocin resistant transformants were checked for loss of hygromycin resistance (indicating homologous recombination at the *SIX1* locus), and of those correct insertion of the cassette was checked by PCR.

To make the construct with RFP under the control of the constitutive *CPS* promoter, the coding sequences of the hygromycin resistance protein (*aph*) and the monomeric Red fluorescent protein (*mRFP*) were fused. For this, the *mRFP* coding sequence was inserted in frame after the *APH*-encoding sequence (*hph*) in the dip method (Mes et al., 1999; Wellman, 1939). Spores were isolated from 5-day-old potato dextrose broth (PDB) cultures (Difco) or 3–5-day-old cultures in minimal medium (1% KNO₃, 3% sucrose and 0.17% Yeast Nitrogen Base without amino acids or ammonia). After washing with water, the spores were diluted to 10⁷ spores/ml. The seedlings were dipped in a spore suspension for about 1 min and subsequently transferred to vermiculite (Agra-vermiculite, Eveleen, Aalsmeer, The Netherlands) and the plants were given extra nutrition (NPK 20:10:20 final concentration 1 g/l, Peters Professional, Heerlen, The Netherlands) three times a week. Seedlings inoculated in this way were used for imaging root slices under the confocal microscope (Fig. 4) and for RNA extraction of infected seedlings.

For the rest of the microscopic analyses (Figs. 3, 5 and 6 and Supplementary Fig. 2), 10-day-old tomato seedlings were taken carefully from the potting soil in which they were sown and the root system was washed in tap water. Clean plantlets were placed in Petri dishes, with the roots spread out on the bottom of the dish and the hypocotyl leaning to the vertical wall, with the leaves outside the Petri dish. The dish was filled with 25 ml water to which Fol spores were added to a final concentration of 10⁵ spores/ml. Holes in the lid allowed the Petri dish to be closed (to minimize evaporation) with the top parts of the plant sticking out.

2.4. Construction of GFP/RFP-expressing strains of Fol

The construct used for GFP-marking of Fol with GFP behind the constitutive *GPD* promoter is described elsewhere (Duyvestein et al., 2005). For construction of the *SIX1*-promoter–*GFP* construct the *SIX1* ORF, present in a Ncol–SpeI genomic fragment containing the *SIX1* gene in the pGEMT-easy vector, was first replaced by an XbaI restriction site in the following way: in pGEMT-easy containing the Ncol–SpeI fragment with *SIX1*, the entire *SIX1* open reading frame was deleted and replaced by an XbaI restriction site. This was done by PCR amplification of vector plus *SIX1* flanking sequences using primers P12-ATC-R (aaataactagatgcctcaagtcacctc) and P12-TAA-F (aaataactagatgcctcaagtcacctc) followed by XbaI digestion of the linkers and religation. The *GFP* ORF was amplified by PCR (using Pfu polymerase), introducing XbaI restriction sites on both ends, which allowed cloning of GFP directly between the *SIX1* promoter and terminator in the above mentioned construct. Constructs were sequenced to check for the right orientation and rule out PCR mistakes. To facilitate homologous recombination of *GFP* into the *SIX1* locus in Fol, the 3’ end of cassette was extended with the neighboring 1.7 kb Spel–XbaI genomic DNA fragment. The correct orientation of this 1.7 kb extension was checked by restriction analyses. Finally, the *BLE* resistance gene (conferring resistance to zeocin) was introduced between the *SIX1* terminator (the region corresponding to the mRNA trailer) and the 3’ flank for homologous recombination. For this, the *BLE* gene was retrieved from the pAN8.1 vector (Punt and van den Houdel, 1992) as an Agel–XbaI fragment and cloned into the SgrAI–SpeI digested *SIX1* locus–*GFP* construct. HindIII and EcoRI were used to transform the construct to pZIP2000, a binary vector for *Agrobacteria*-mediated transformation (ATMT) of *Fusarium* (Hajdukiewicz et al., 1994). Constructs were transformed to the *SIX1* knockout strain (described in *Rep et al.*, 2004) in which the *SIX1* ORF had been replaced by a hygromycin resistance gene. After ATMT zeocin resistant transformants were checked for loss of hygromycin resistance (indicating homologous recombination at the *SIX1* locus), and of those correct insertion of the cassette was checked by PCR.

To make the construct with RFP under the control of the constitutive *CPS* promoter, the coding sequences of the hygromycin resistance protein (*aph*) and the monomeric Red fluorescent protein (*mRFP*) were fused. For this, the *mRFP* coding sequence was inserted in frame after the *APH*-encoding sequence (*hph*) in the
binary plasmid pPK2 (Covert et al., 2001). First, an Apal site was created before the stop codon of the hph gene in pPK2 by PCR amplification of the entire plasmid pPK2 with the primers HPH-End-Apal-R (AAAGGGCCCTTTCTTTGGCCCTGGACGA, Apal site underlined) and HPH-Fwd2-Apal (AAAGGGCCTAGGGATCCACT TAAAGTTAC, Apal site underlined), followed by digestion with Apal, ligation and transformation to Escherichia coli. This resulted in plasmid pPK2–HPH-Apal. Then, the mRFP coding sequence, kindly provided by Roger Tsien (Campbell et al., 2002), was amplified by PCR with primers mRFP-Apal-F (AAAGGGCCATGG CCTCTCAGGGGACGT, Apal site underlined) and mRFP-Apal-R (AAAGGGCCTTTAGGGCGGCGGATGCG, Apal site underlined). The PCR fragment was digested with Apal and ligated into the Apal site of pPK2–HPH-Apal. The resulting plasmid was checked with restriction analyses for the correct orientation, sequenced to check for PCR mistakes and called pPK2–HPH-RFP. Transcription of the hph-RFP fusion in this plasmid is driven by the Aspergillus nidulans gpdA promoter and terminated by the A. nidulans trpC terminator (Roberts et al., 1989).

Agrobacterium-mediated Fusarium transformation of Fol was performed as described in (Takken et al., 2004).

2.5. Preparation of microscope slides

For preparation of slides for confocal microscopy presented in Fig. 4, infected plants were carefully taken out of the vermiculite and washed with water. Plant material was manually sliced into ~0.5 mm thick slices with a scalpel and the pieces were placed in a drop of water on glass slides. The cover glass was used to squash the material.

For two-photon microscopy, root-surface-confocal microscopy and stereo microscopy (Figs. 3, 5 and 6 and Supplementary Fig. 2), infection was performed in a Petri dish. For microscopic inspection with two-photon or confocal microscopy, plants were taken from the Petri dish and part of the root system was cut off for examination. The root was placed on a microscope slide in water. Adjacent to the root two coverslips had been glued to the microscope slide. A third coverslip was used to cover the root, leaning on the two adjacent coverslips, thus making a bridge under which a drop of water on glass slides. A third coverslip was used to cover the root, leaning on the two adjacent coverslips, thus making a bridge under which a drop of water on glass slides. A third coverslip was used to cover the root, leaning on the two adjacent coverslips, thus making a bridge under which a drop of water on glass slides. A third coverslip was used to cover the root, leaning on the two adjacent coverslips, thus making a bridge under which a drop of water on glass slides.

General inspection of GFP expression on roots (Fig. 6 and Supplementary Fig. 2) was done while the plantlets were still in the Petri dish, on the Leica MZ FLIII stereo microscope, magnifying from 10 × 0.8 to 10 times.

2.6. Confocal microscopy

Microscopic analysis was performed with a confocal scanning laser microscope (LSM 510, Zeiss, Germany). Excitation was provided by an Ar-ion laser (488 nm) and a HeNe laser (543 nm). Fluorescence of GFP was detected at 505–550 nm and plant tissue autofluorescence at 650–700 nm. Images were scanned using Zeiss Plan-Neofluar 40×/1.3 oil or Plan-Neofluar 100×/1.3 oil objectives and a pinhole at 1 airy unit. For imaging the surface of tomato roots inoculated with a double-labeled Fol strain (Psix1::GFP and Psix1::RFP) the Zeiss LSM510 confocal microscope was used with the same lasers (488 and 543 nm). Images were scanned in a multi-track, GFP was recorded at 505–550 nm and RFP through a LP560 long pass filter, with a pinhole size of 2.0 airy units. All confocal pictures were analyzed with the Zeiss LSM510 software (v3.0 SP3).

2.7. Two-photon microscopy

Two-photon imaging was done on a Leica TCS SP5 microscope, coupled to a SpectraPhysics Mai Tai, Mode-locked Ti:Sapphire Laser at 850 nm. Standard green and red filters were used for the detection of GFP (green) and plant autofluorescence (red).

2.8. GFP expression in plant cell cultures

Microconidia (10²) from a SIX1-promoter-GFP-GDP-promoter-RFP Fol transformant were used to inoculate 1 ml of a 1-week-old plant cell culture, standard cell culture medium or cell culture filtrate, obtained by filtering medium from a 1-week-old cell culture through a 0.22 μm filter (low protein binding durapore (PVDF), Millipore). Plant cell cultures (Arabidopsis thaliana, tomato and Nicotiana benthamiana) are described in (Testerink et al., 2004) and (Van Leeuwen et al., 2007).

GFP and RFP fluorescence was recorded after 24 h on a wide field fluorescence microscope BX (Olympus, Japan) using Objet Image analysis.

3. Results

3.1. SIX1 is strongly expressed in planta but not or very weakly in axenic cultures

The SIX1 gene encodes a protein that is secreted by F. oxysporum f. sp. lycopersici into the xylem sap during colonization of tomato plants. To investigate whether expression of SIX1 is regulated, RT-PCR reactions on SIX1 were performed with cDNA derived from infected plants and from axenic Fol cultures. In axenic cultures, SIX1 mRNA levels were lower than or comparable to the level of FEM1, a constitutively expressed gene coding for a structural cell wall protein, here used as a reference for the amount of fungal biomass (Schoffelmeier et al., 2001). Fig. 1A shows SIX1 expression in axenic cultures under different medium conditions. Two independent experiments are shown for each condition. Standard media used to grow Fusarium (potato dextrose broth [PDB, rich] and Czapek Dox [CD, minimal]) did not result in high expression levels of SIX1, but on a minimal medium based on 3% sucrose and 1% KNO₃ the SIX1 expression level was comparable to that of FEM1. Media designed to resemble plant and/or xylem sap conditions (Dixon and Pegg, 1972; Iwai et al., 2003; Joosten et al., 1990) did not induce SIX1 expression.

![Image 1. SIX1 expression is much higher in planta compared to expression in axenic cultures. Expression was visualized with RT-PCR on SIX1 and FEM1 (internal control for the amount of Fusarium derived cDNA). (A) cDNA extracted from Fol007 mycelium, grown axenically in the indicated medium for 2 days at 150 rpm, 25 °C. Each growth condition was tested in two separate experiments. Media were used as indicated, PDB: potato dextrose broth, CDB: Czapek Dox broth, all other media also contain 0.17% YNB (yeast nitrogen base without amino acids or ammonia) in addition to the indicated C- and N-source. (B) cDNA extracted from infected tomato seedlings, 11 days after inoculation. The first lane is an RT-PCR under standard conditions, in the subsequent lanes 10-, 100- and 1000-fold dilutions of template were used, respectively.](image-url)
In plants, on the other hand, SIX1 expression greatly exceeded FEM1 transcript levels (Fig. 1B). Using FEM1 expression as an internal standard, SIX1 expression in planta was significantly higher compared to axenic cultures. Based on these experiments, we concluded that the strong expression during infection cannot be attributed to the presence of some well known cell wall components (pectin or polygalacturonase) nor to alternative nitrogen sources. Starvation for carbon or nitrogen also failed to induce SIX1 expression as did the use of xylem sap harvested from tomato plants as growth medium (data not shown).

3.2. During infection SIX1 is expressed early, transiently and mainly in the roots

To determine at which stage of host colonization SIX1 expression is induced, expression in planta was visualized in more detail in an RT-PCR time series of infected plants. Seedlings were harvested at 4, 8, 12 and 16 DPI (days post inoculation) and RNA extractions were done separately on the roots and hypocotyls. SIX1 expression levels were compared to FEM1 expression levels. As can be seen in Fig. 2 the amount of fungal mass, represented by the level of FEM1 transcript, increased in time, in both roots and hypocotyls. SIX1 expression starts very early and is predominant in the roots. It probably starts before day 4 and diminishes later. Expression in the hypocotyl was less strong, started later, and diminished later and only slightly.

To determine the differences in expression of SIX1 between axenic cultures and different stages of host colonization more accurately, quantitative PCR (qPCR) was performed on cDNA from mycelium grown in PDB, CDB or MM (sucrose and KNO3) and on cDNA from infected plants. We also included a 2 DPI time point in this experiment to obtain information on SIX1 expression earlier than 4 days after inoculation. For this experiment, we used Fol EF-1α as a constitutive control, as the primers designed on this gene were more reliable in the qPCR than FEM1 primers. Assuming constitutive EF-1α expression, SIX1 expression in planta at 2, 4, 8 and

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Fig. 2. Onset of SIX1 expression during colonization of tomato roots. SIX1 expression in roots is stronger, earlier and more transient compared to expression in hypocotyls. RT-PCR was performed on SIX1 and FEM1 (a control for the amount of Fol derived cDNA). RNA was extracted from infected tomato seedling roots or hypocotyls, 4, 8, 12 and 16 days after inoculation. Equal amounts of RNA were used to generate cDNA. Of each panel, representing a specific time point after inoculation, the first lane represents an RT-PCR under standard conditions and the subsequent lanes 10-, 100- and 1000-fold dilutions of template DNA.

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Fig. 3. Fol colonizing tomato xylem vessels, expressing Psix1::GFP. GFP fluorescence was visualized using two-photon imaging and is depicted in green. Tomato root autofluorescence is shown in red. The white bars are 25 μm in length. The image consists of 924 optical sections with a total depth of 280 μM. (A) A projection of the optical sections, showing colonization of the tomato xylem tissue in a longitudinal view through the root. (B) An cross-section of the same root calculated from the optical sections. (C) and (D) Two of the optical sections of the stack shown in (A).

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Fig. 4. Various types of hyphae in xylem vessels express Psix1::GFP. Similar hyphal shapes were observed in Pgpd::GFP (constitutive) and Psix1::GFP (inducible) expressing strains. Confocal images show fluorescent Fol (GFP, green) colonizing the tomato xylem system (autofluorescence, red), all longitudinal sections. The white bars are 10 μm in length. (A) A xylem vessel with abnormally shaped Fol hypha expressing Pgpd::GFP. (B) Fol hyphae in a xylem vessel expressing Pgpd::GFP. The hyphae make extensions that fill cavities in the cell wall of the xylem vessel elements (pit chambers). (C) Enlargement of a section of (B). (D) Xylem vessel with abnormally shaped Fol hyphae expressing Psix1::GFP. (E) Fol hyphae expressing Psix1::GFP making extensions.
14 DPI was, respectively, about 100, 200, 700 and 40 times higher than in MM confirming a strong increase of expression during infection (Supplementary Table 1). SIX1 expression in PDB cultures was about 240 times lower than in MM and expression in CDB 2–3 times higher. The latter value is higher than apparent in the experiment shown in Fig. 1A, which might be explained by the different constitutive control that was used (FEM1 versus EF-1α).

3.3. Psix1::GFP is expressed in hyphae colonizing the xylem vessels

Because the Six1 protein was originally discovered in the xylem sap of infected plants, we expected the hyphae growing in xylem vessels to express SIX1. To test this, a strain carrying a SIX1-promoter-GFP fusion construct was made (Psix::GFP). The reporter construct was designed in such a way that it was suitable for homologous recombination at the original SIX1 locus, to avoid artificial expression due to position effects (Supplementary Fig. 1). Fol transformants harboring this construct (i.e. with the SIX1 open reading frame replaced by GFP) are still pathogenic towards seedlings (as expected for a SIX1 knockout strain (Rep et al., 2005a, 2004), data not shown), and were used to inoculate 10-day-old tomato seedlings. GFP fluorescence was imaged between 2 and 5 days after inoculation using two-photon microscopy (Fig. 3).

3.4. In xylem vessels Fol hyphae can have different shapes which all can express Psix1::GFP

To visualize the fungus in the xylem vessels in more detail, we sliced inoculated tomato roots (manually, ~0.5 mm thick) and viewed them with confocal microscopy (Fig. 4). For comparison, a Fol strain expressing GFP behind the constitutive GPD promoter (glucose 6-phosphate dehydrogenase from A. nidulans (Roberts et al., 1989)) was used. Hyphae of this Pgpd::GFP strain in xylem vessels sometimes appeared swollen or abnormally shaped (Fig. 4A), and can form extensions that fill cavities in the xylem vessel cell wall (pit chambers) (Figs. 4B and C, arrow). Psix1::GFP-expressing hyphae were observed in all the above situations: they were found sometimes exhibit similar abnormal shapes, penetrate cells and make extensions to fill pit chambers (Figs. 4D and E, arrows). These results suggest that in the xylem the SIX1 promoter is active in all hyphae, as no obvious differences in GFP-expressing hyphal structures were observed.

![Image](image-url)
3.5. Psix1::GFP expression starts immediately upon penetration of the root

To pinpoint the moment of initial induction of SIX1 expression, we visualized the transition of a non-SIX1-expressing hypha to a SIX1-expressing hypha. To do this, the Psix1::GFP strain was transformed with RFP (encoding red fluorescent protein) behind the constitutive GPD promoter (Pgpd::RFP) so that hyphae that do not express Psix1::GFP could be visualized using RFP fluorescence. Tomato roots were inoculated with this double-labeled Fol and the surface was inspected with confocal microscopy.

Fol was found to form a mycelial mass around the tomato root and the hyphae on the outside of the root did not express Psix1::GFP, only Pgpd::RFP (Fig. 5). Psix1::GFP, on the other hand, appeared to be expressed after (or shortly before) the moment Fol actually enters the root. We observed Psix1::GFP expression at distinct locations along the root (roughly 20 'infections patches' per root system). At these entry points, GFP was present in the hyphae inside one or a few cells of the outer root tissue and in one or two hyphae outside the root connected to hyphae inside (Fig. 5). Apparently, the SIX1 promoter is activated immediately upon penetration of the plant root epidermis. The optical sections of these scans are available as movies in the Supplementary Materials.

3.6. Psix1::GFP is not expressed on dead plant material

Remarkably, Psix1::GFP expression, but not root colonization, was lost when the tomato seedlings were killed before inoculation. Killing of the seedlings was done either by boiling, submersion in 70% ethanol, snap freezing, removal of all non-root tissue (including hypocotyl, cotyledons, leaves and meristem) or BASTA treatment. BASTA treatment needed to be performed 1 day prior to inoculation, the other methods could be applied just before inoculation and still result in loss of SIX1 expression. Also, ground or chopped seedling roots did not induce Psix1::GFP expression when provided in agar plates. Similarly, root exudate could not trigger expression of Psix1::GFP (data not shown). This indicates that the cue that induces SIX1 expression is only present in or around living tomato roots and not in their lifeless components or exudates. When the seedlings were put in the dark 1 day prior to inoculation and during infection, the number of infection patches was somewhat reduced, but still significant (Supplementary Fig. 2). This suggests that the ability to photosynthesize is not the main prerequisite for SIX1 expression.

3.7. On non-host plants Psix1::GFP expression is rare or absent

To see if the cue that induces SIX1 expression is specific for tomato, expression of Psix1::GFP was also tested on non-host plants. On all non-host seedlings that were tested (Arabidopsis thaliana, Zea mays and Nicotiana benthamiana) Fol was able to colonize the root surface (visualized with the Pgpd::GFP strain [constitutive], data not shown). None of these plants developed Fusarium wilt disease, confirming that these are indeed non-host plants for Fol. On N. benthamiana and Z. mays only very occasionally Psix1::GFP expression was observed in single, short hyphae (on N. benthamiana on average once per root system), but not on A. thaliana (Fig. 6). Possibly, the Psix1::GFP expression on N. benthamiana and Z. mays was the result of rare instances of limited entry of root tissue. However, in this experiment we could not determine whether the general absence of expression of Psix1::GFP on non-host plants was caused by the inability of the tissue to induce SIX1 expression or that it was a result of the inability of Fol to enter these (non-host) roots and reach the place where induction normally would occur.

3.8. Plant cell cultures can induce Psix1::GFP expression

To better distinguish between these possibilities we investigated whether cell cultures could be used as a system to monitor the induction of SIX1 expression without the need for actual infection. We found that cell cultures of tomato were indeed able to induce SIX1 expression. When a conidial suspension of Fol was added to tomato MSK8 cell cultures, after 24 h a fraction (an estimated 5–20% of the hyphae) expressed Psix1::GFP (Fig. 7). Tobacco BY2 cell cultures had the same effect (Fig. 7), but an A. thaliana cell culture did not induce expression (data not shown). Freezing or boiling the plant cells before inoculation prevented the induction of expression (data not shown). When observed under the microscope, it seemed that the hyphae expressing Psix1::GFP did not necessarily need to be in physical contact with the plant cells, nor did we observe penetration of the plants cells. However, when only the medium of the MSK8 tomato cell cultures was used (after removal of the MSK8 cells) expression was reduced to almost background levels when compared to the situation where the cells were present (Fig. 7, panels culture filtrate). This shows that the presence of plant cells (either host [MSK8] or non-host [BY2]) is required for Psix1::GFP expression.

4. Discussion

In this work we show that expression of the SIX1 gene is very high at the earliest stages of infection, and very low or absent in fungi growing on the root surface or in artificial medium (axenic cultures). None of the culture conditions or tomato extracts tested...
SIX1 expression is induced in tomato cell cultures, showing that specific structural features or specific root cells are not required for induction of SIX1 expression. A tobacco cell culture (BY2) was capable of inducing SIX1 expression to a similar level as a tomato (MSK8) cell culture, showing that the cue is not host specific. This suggests that the rare Psix1::GFP expression that we observed on non-host plants may be attributed to occasional and limited penetration of the outer root (failed infection attempts), rather than the absence of the proper signals in these plants.

It is not clear what the biological relevance is of the low, but detectable, SIX1 expression observed in CDB and minimal medium with sucrose and KNO3, or how to interpret the observation that only 5–20% of hyphae express SIX1 when growing in tomato cell cultures. While in planta all hyphae penetrating the root seem to strongly express SIX1, in these two circumstances only a fraction of the SIX1-expressing capacity is triggered. Curiously, penetration of plant cells does not seem to occur in cell cultures, whereas penetration of the tissue is a requirement for expression in plants. The slight SIX1 expression in sucrose/KNO3 medium seems to be caused by all hyphae very weakly expressing SIX1, with some having somewhat higher expression (Psix1::GFP expression, data not shown), whereas the expression in cell cultures is very strong in a fraction of the hyphae and absent in the rest of the mycelium. This suggests that the regulation of SIX1 expression might be mediated by different repressing and/or activating pathways, which only work together optimally in planta.

The SIX1 promoter does not contain any known motifs. We did notice that SIX1 and the other known SIX genes (SIX2, SIX3 and SIX4, all encoding small proteins secreted in xylem during infection) share some common characteristics in the promoter (Houterman et al., 2007). In or close to each of the promoters a transposon (miniature impala) is present and each contains a variant of the motif ‘TGCGCATTTW’. The function of these features is still unclear. For other plant induced genes, like MIG1 and LtmM, serial deletions in the promoter region provided information on the different effects of subregions on expression levels (Basse et al., 2000; May et al., 2008). LtmM expression was also shown to vary depending on the type of infected tissue (May et al., 2008).

Host signals for induction of virulence genes that have been identified previously comprise hydrophobic surfaces or ridged surfaces that can influence the formation of infection structures (Beckerman and Ebbole, 1996; Collins et al., 2001; Kolattukudy et al., 1995; Lee and Dean, 1993), as well as relatively stable chemical substances. In some cases topographical and chemical signals act synergistically (Collins et al., 2001; Soanes et al., 2002) and for some genes only a chemical signal is sufficient. Some examples of the latter are cell wall components that induce expression of cell wall degrading enzymes (Huertas-Gonzalez et al., 1999; Ruiz-Roldan et al., 1999; Sexton et al., 2000), phytoalexins that induce the enzymes that can detoxify them (e.g. pisatin demethylase 1) (Staney and VanEtten, 1994), and the amino acids homoserine and asparagine, found in high levels in pea seedling hypocotyls and capable of inducing expression of pelD (Yang et al., 2005).

The apparent inability to induce full SIX1 expression with anything but living material points to a type of host signal that has not been described before. Translated to the natural situation, our findings show that F. oxysporum is highly effective in distinguishing dead (plant) material from living plants. For a fungus like F. oxysporum that can live on dead plant material as well as colonize living plants, this is a trait that could be very useful to prevent unnecessary switches from saprophytic to combat mode.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.fgb.2008.06.002.