PthA4\textsuperscript{AT}, a 7.5-repeats transcription activator-like (TAL) effector from \textit{Xanthomonas citri} ssp. \textit{citri}, triggers citrus canker resistance

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SUMMARY

Transcription activator-like effectors (TALEs) are important effectors of \textit{Xanthomonas} spp. that manipulate the transcriptome of the host plant, conferring susceptibility or resistance to bacterial infection. \textit{Xanthomonas citri} ssp. \textit{citri} variant A\textsuperscript{1} (\textit{X. citri} A\textsuperscript{1}) triggers a host-specific hypersensitive response (HR) that suppresses citrus canker development. However, the bacterial effector that elicits this process is unknown. In this study, we show that a 7.5-repeat TALE is responsible for triggering the HR. PthA4\textsuperscript{AT} was identified within the \textit{pthA} repertoire of \textit{X. citri} A\textsuperscript{1} followed by assay of the effects on different hosts. The mode of action of PthA4\textsuperscript{AT} was characterized using protein-binding microarrays and testing the effects of deletion of the nuclear localization signals and activation domain on plant responses. PthA4\textsuperscript{AT} is able to bind DNA and activate transcription in an effector binding element-dependent manner. Moreover, HR requires PthA4\textsuperscript{AT} nuclear localization, suggesting the activation of executor resistance (R) genes in host and non-host plants. This is the first case where a TALE of unusually short length performs a biological function by means of its repeat domain, indicating that the action of these effectors to reprogramme the host transcriptome following nuclear localization is not limited to `classical' TALEs.

Keywords: citrus, hypersensitive response (HR), \textit{Nicotiana benthamiana}, transcription activator-like (TAL) effectors, \textit{Xanthomonas citri}.

INTRODUCTION

Understanding how plants perceive and hamper the attack by potential pathogens has been a fundamental question for plant biologists in recent decades. We now know that bacterial infection normally fails because plants carry genes whose products detect conserved pathogen-associated molecular patterns (PAMPs) and trigger a complex defence response (PAMP-triggered immunity, PTI) that restricts pathogen growth (Macho and Zipfel, 2014). Evolution has provided many bacteria with the ability to suppress this basal plant immune system and hence facilitate infection through the action of a battery of proteins called effectors (Macho, 2016). These effectors are expressed during the course of the infection and are translocated into the host mesophyll cells by means of the type III secretion system (T3SS) where they interact with specific plant components. As a countermeasure, some plants have evolved the ability to detect specific bacterial effectors, restricting effector-mediated bacterial infection by triggering a second layer of defence responses called effector-triggered immunity (ETI) (Toruño \textit{et al.}, 2016). The ability of the pathogen to avoid plant recognition relies then on effector evolution, in a never-ending struggle between both organisms (Carella \textit{et al.}, 2018).

Transcription activator-like effectors (TALEs), belonging to the \textit{Xanthomonas} AvrBs3/PthA family of T3SS effectors, function in any medium, provided the original work is properly cited.
as eukaryotic transcription factors in plant cells, playing a central role in promoting bacterial disease by the induction of host susceptibility (S) genes. Contrary to the mode of action of other families of bacterial effectors that exert their function in the cytoplasm, TALEs are translocated into the plant cell nucleus and bind to the promoter regions of plant target genes whose transcription facilitates bacterial colonization and spread (Boch and Bonas, 2010; Bogdanove et al., 2010). The specificity of action of different TALEs is determined by the structure of these proteins. They contain T3SS translocation signals in the N-terminal region, a central DNA-binding domain and a C-terminal region with nuclear localization signals (NLS) followed by an acidic activation domain (AD). TALEs vary mostly in their central region, which consists of a number of tandemly arranged repeats of 33–34 amino acids with hypervariable di-amino acids at positions 12 and 13, termed the repeat-variable diresidue (RVD). Each repeat interacts with a nucleotide in the DNA, and these two residues determine the specificity of each repeat for a particular nucleotide. Thus, the RVD sequence of each TALE defines the effector-binding element (EBE) in the promoter region of the target genes (Boch et al., 2009; Moscou and Bogdanove, 2009). Over the course of evolution, some plants have evaded the activation of susceptibility genes by modification of their promoters (Bogdanove et al., 2010; Hutin et al., 2015), or co-opted the TALE mechanism of gene activation for resistance, by means of gene traps (executor resistance (R) genes) that contain EBEs in their promoter regions, and whose activation by the corresponding TALE triggers a host resistance response (Römer et al., 2007; Zhang et al., 2015).

*Xanthomonas citri* ssp. *citrinum* (*X. citri*) is the causal agent of citrus canker, a serious economic disease that provokes losses worldwide. Infected fruits have decreased commercial quality, compromising their acceptance by most markets (Canteros et al., 2017; Ference et al., 2018). Outbreaks occur sporadically and copper-based products and eradication of infected trees are the strategies employed to control the disease so far (Behlau et al., 2010; Favaro et al., 2017). Canker lesions are characterized by raised spongy eruptions caused by bacterial-induced cell hypertrophy and hyperplasia in leaves and fruits (Graham et al., 2004). The pathogenic reference strain *X. citri* 306 contains four TALE genes (*pthA1, pthA2, pthA3* and *pthA4* harbouring 16.5, 15.5, 15.5 and 17.5 repeats, respectively) located on plasmids pXAC33 (pthA1/pthA2) and pXAC64 (pthA3/pthA4) (da Silva et al., 2002). TALE PthA4 promotes the expression of citrus lateral organ boundaries gene (*CsLOB1*), a transcription factor involved in hypertrophy and hyperplasia of the cells (Duan et al., 1999; Hu et al., 2014; Pereira et al., 2014). Moreover, TALE PthA1 and PthA3 also contribute to canker symptoms in a host-dependent manner (Yukari Abe and Benedetti, 2015).

Several reports suggest specific recognition of effectors by host gene products that render plants resistant to *X. citri*, i.e. interactions in which the effector acts as an avirulence factor (Chen et al., 2012; Deng et al., 2010; Khalaf et al., 2011; Lee et al., 2009). Recently, we have isolated a *X. citri* strain (*X. citri* A1) that triggers a host-specific defence response in *Citrus limon* that is associated with the interference of biofilm development and arrest of bacterial growth (Chiesa et al., 2013; Roeschlin et al., 2017). The occurrence of an oxidative burst, the accumulation of salicylic acid and phenolic compounds, and the hypersensitive response (HR) together suggest that it is an ETI response. However, the avirulence effector that elicits these processes is unknown.

In this study, we demonstrate that the causal agent of the triggering of the defence response to *X. citri* A1 strain is a short TALE containing 7.5 repeats. In nature, the number of TALEs in a single bacterial strain is highly variable and the RVDs range from 1.5 to 33.5 (Boch and Bonas, 2010; Cox et al., 2017; Denancé et al., 2018). However, the optimal length for specificity ranges between 15.5 and 19.5 repeats (Rinaldi et al., 2017). The screening of *X. citri* diversity in different citrus-growing regions has identified TALEs ranging from 6.5 to 29 repeats, which likely contain different RVDs. It is suggested that the diversification is driven by recombination, facilitated by the repetitive structure of the central region, leading to variants differing in the number of repeats (Al-Saadi et al., 2007; Gochez et al., 2018; Lee et al., 2008; Shiotani et al., 2007; Ye et al., 2013). It has been demonstrated that TALEs shorter than 6.5 repeats are non-functional in terms of gene activation; these just could be by-products of recombination events (Boch et al., 2009). It is not known, however, if TALEs of intermediate length are functional for gene activation.

Here we show that this 7.5-repeat TALE of the *X. citri* A1 strain is necessary and sufficient to induce HR in *C. limon* and *C. sinensis*. The protein is able to bind DNA *in vitro* and to activate transcription in an EBE-dependent manner. The HR is triggered only if the TALE protein reaches the plant cell nucleus, and the resistance requires transcriptional activation, suggesting a classical TALE mode of action via activation of executor gene(s).

**RESULTS**

A new repertoire of *pthA* genes is present in the *X. citri* A1 strain

Previous reports have shown a great variability in the size of the *pthA* genes from different *X. citri* strains (Al-Saadi et al., 2007; Gochez et al., 2018; Lee et al., 2008; Ye et al., 2013). Given the mode of action of these TALE proteins, it is expected that this variability will contribute to explain differences in pathogenicity among the strains. To define the *pthA* ‘repertoire’ of the *X. citri* A1 strain, Southern blot assays using a *pthA* probe over EcoRI- and BamHI-digested DNA of the two *X. citri* plasmids were performed. EcoRI digestion of *X. citri* A1 showed the presence of four bands, similar to the reference strain *X. citri* 306, indicating the
presence of four pthA genes. However, after BamHI digestion a new pattern of three discrete 3.8-, 3.2- and 2.4-kb bands was observed in X. citri AT that differed to the one previously reported for X. citri 306 (3.4-kb for pthA4, 3.3-kb for pthA1 and 3.2-kb for pthA2/pthA3 genes; da Silva et al., 2002) (Fig. 1a). To further investigate the functionality of the pthA genes of X. citri AT, the BamHI bands, revealing the number of repetitions, were cloned and sequenced. The 3.2-kb band was in fact a double-band containing the central region of two different pthA genes of the same size that were identical to the pthA2 and pthA3 genes of X. citri 306. However, the two other pthA genes differed in the number of central repeats in the coded proteins compared with those of X. citri 306. The 3.8-kb band corresponds to a pthA gene encoding a TALE containing 21.5 repeats. The smallest 2.4-kb BamHI band contains a pthA gene encoding a TALE with 7.5 repeat domains. Sequence analysis revealed that the 21.5-repeat protein is identical to other members of the PthA1 group, differing only in three RVDs in positions 13–15 (Figs 1b and S1). The new 7.5-repeat protein is identical to PthA4 from X. citri 306 in the N- and C-terminal regions, but has an internal deletion of 10 central repeats (Figs 1b and S2). We named these proteins PthA1AT and PthA4AT, respectively.

**PthA4AT is necessary and sufficient for the host-specific induction of hypersensitive response in citrus**

Although many genes from X. citri 306 contribute to pathogenicity, the pthA4 17.5-repeat TALE gene is a major effector,
promoting canker disease symptoms (Duan et al., 1999; Da Silva et al., 2002; Yukari Abe and Benedetti 2015). To determine if the immune response triggered by \( X. \ citri \) \( A^T \) is still induced in the presence of a full-length \( pthA4 \) gene, a pBBR plasmid expressing \( PthA4 \) from \( X. \ citri \) 306 was transferred to \( X. \ citri \) \( A^T \) and the expression was evaluated by western blot (Fig. S3). The \( pthA4 \)-expressing \( X. \ citri \) \( A^T \) was still able to triggered HR in \( C. \ limon \) (Fig. S4), indicating that an active \( PthA4 \) does not suppress HR.

To evaluate whether any of the two new \( pthA \) genes found in \( X. \ citri \) \( A^T \) play any role in this HR, the gene for each TALE was cloned in a pBBR plasmid and expressed in \( X. \ citri \) 306 (Fig. S3). No difference in symptoms was observed in \( C. \ limon \) after infection with the natural pathogenic \( X. \ citri \) 306 or the \( pthA4^\Delta \)-expressing \( X. \ citri \) 306. However, \( pthA4^\Delta \)-expressing \( X. \ citri \) 306 was unable to cause canker symptoms and induced an HR on \( C. \ limon \) (Fig. 2a). Similar results were obtained when these two \( pthA \) genes were expressed in the Argentinian pathogenic T strain, which is related to \( X. \ citri \) 306 (Fig. S5). To confirm these results, each of three \( X. \ citri \) 306 mutant strains (\( \Delta pthA1 \), \( \Delta pthA4 \) or \( \Delta pthA1,4 \)) were transformed with either \( pthA4^\Delta \) or \( pthA4^\Delta \)-expressing plasmids (Fig. S3). The \( X. \ citri \) 306 mutant strains expressing \( pthA4^\Delta \) exhibited the same symptoms in \( C. \ limon \) as the wild-type 306 strain (Fig. 2b). By contrast, the presence of \( PthA4^\Delta \) either in \( \Delta pthA4 \) or \( \Delta pthA1,4 \) caused an HR similar to that caused by \( X. \ citri \) \( A^T \) (Fig. 2c). These results suggest that the presence of \( PthA4^\Delta \) is necessary for the HR observed in \( C. \ limon \). In further experiments, the \( pthA4^\Delta \) gene was cloned under the control of the CaMV 35S promoter and transiently expressed in planta. Agroinfiltration assays showed that transient expression of \( PthA4^\Delta \) triggered an HR (Fig. 2d), suggesting that the presence of this protein is necessary and sufficient for the induction of this response in \( C. \ limon \).

**Nuclear localization of \( PthA4^\Delta \) is needed to trigger host defense response in \( C. \ limon \)**

The results presented above suggest that \( PthA4^\Delta \) recognition by the host plant is the initial step triggering the HR observed in \( C. \ limon \). In order to assess if nuclear localization of \( PthA4^\Delta \) is necessary for recognition, two \( PthA4^\Delta \)-modified proteins were designed: one with an 87-amino acid deletion in the C-terminal region, eliminating the three conserved nuclear localization signals (\( \Delta NLS^{AT} \)), and a second one with point mutations in the same three NLS (mutNLS\(^{AT} \)) (Fig. S6). The constructs were introduced into \( \Delta pthA4 \) (Fig. S3) and assayed in \( C. \ limon \) following pressure infiltration into the leaves or swab inoculation of the leaf surface. As observed in Fig. 3, none of the two mutant versions of the protein impaired in nuclear localization was able to trigger an HR. Similar results were obtained when \( X. \ citri \) 306 was transfected with these constructs (Fig. S7). Moreover, when the NLS of the SV40 (Kalderon et al., 1994; Szurek et al., 2001) was fused to the impaired \( \Delta NLS^{AT} \) protein (Fig. S6), the HR was restored (Fig. 3). Taken together, these results indicate that \( PthA4^\Delta \) must be localized in the plant cell nucleus to trigger the defense response.

**\( PthA4^\Delta \) is able to bind DNA following the TALE code and to activate transcription in an EBE-dependent manner**

To elucidate whether the 7.5-repeat \( PthA4^\Delta \) TALE was able to bind to DNA in vitro, and to determine the specificity of binding, a PBM11 protein-binding microarray was employed (Godoy et al., 2011) that contains all possible double-stranded 11-mers (approximately 4.2 million sequences) in approximately 180,000 oligonucleotides of 35 bp. Probing PBM11 with \( PthA4^\Delta \) for determination of DNA-binding specificity yielded an E-score of 0.48 to the TATTACCTT sequence, with similar affinity to variants of this motif containing one mismatch (Table S6). Considering that it is generally assumed that motifs with E-score > 0.45 reflect high binding specificity (Berger and Bulyk, 2009; Weirauch et al., 2013, 2014), we obtained the consensus recognition sequence for \( PthA4^\Delta \) from DNA motifs with E-scores > 0.45 (Fig. 4a). This motif matches quite well with the expected binding domain for \( PthA4^\Delta \) according to its TALE code (Boch et al., 2009).

\( X. \ citri \) \( A^T \) generates HR in \( C. \ sinensis \) similarly to generation in \( C. \ limon \) and \( X. \ citri \) 306 \( \Delta pthA4 \), and \( \Delta pthA1,4 \)-expressing \( PthA4^\Delta \) also behaves similarly in \( C. \ sinensis \) and \( C. \ limon \), indicating that the same mechanisms of defense are triggered in both species (Fig. S8). Since the \( C. \ sinensis \) genome sequence is available (Wu et al., 2014; Xu et al., 2013) we used \( C. \ sinensis \) for molecular analysis of predicted targets (Grau et al., 2013). TALgetter consensus-predicted sequences for \( PthA4^\Delta \) using \( C. \ sinensis \) promoterome are shown in Fig. 4a.

Although both consensus sequences described above are very similar, it is interesting to note that the second repeat of \( PthA4^\Delta \) (\( N^* \)) binds preferably to T in the protein binding microarray (PBM) assay, whereas this position is predicted C/T by TALgetter. Moreover, the third repeat (NG), predicted T by TALgetter, binds equally to C and T in the PBM assay. In order to quantify the subtle differences in both consensus sequences in our PBM assay, we extracted signal intensities for the probes containing the sequence determined in PBM (TATYRCCCT) and the predicted by TALgetter (TAYTMCCCTT). This analysis revealed a significantly higher binding of \( PthA4^\Delta \) to the sequence determined in PBM (TATYRCCCT). Nevertheless, both groups of sequences performed much better binding than the average array probes (Fig. 4b). The second repeat (\( N^* \)) is shared between \( PthA4 \) and \( PthA4^\Delta \). Interestingly, the two known targets of \( PthA4 \) (\( LOB1 \) and \( SWEET \); Hu et al., 2014) contain a T in this position, reinforcing the use of this high-throughput methodology for experimental determination of DNA motifs recognized by TALEs.
To estimate the ability of PthA4AT to activate transcription in planta, five putative target promoters of C. sinensis genes containing an EBE in their proximal region (400 bp upstream + 200 bp downstream of the transcription start site) were fused to the uidA (β-glucuronidase [GUS]) reporter gene and transiently co-expressed with the 35S promoter-driven pthA4AT via Agrobacterium into N. benthamiana leaves. According to the different behaviour of X. citri ΔpthA1 and ΔpthA4 in C. sinensis and C. clementina (Chiesa et al., 2013), the five
genes were selected to fulfill the criteria of being predicted targets of PthA4AT by TALgetter (P value < 10\(^{-5}\)) in C. sinensis but not in C. clementine and the consensus sequences obtained for PMB assay (Fig. 5a). As shown in Fig. 5b, transient expression assays indicate that PthA4AT was able to activate GUS expression when this reporter was under the control of the Cs4-promoter, indicating that the 7.5-repeat TALE is able to bind DNA and activate transcription in planta. The other four promoters were not able to activate GUS PthA4AT-dependent transcription, indicating that not all predicted binding sites are functional in planta. Next, to clarify if the PthA4AT-dependent transcription of GUS under the Cs4 promoter was dependent on the EBE, we mutated this box in the C. sinensis promoter. As shown in Fig. 5c, the construct with the mutated EBE lost the ability to activate transcription of the uidA gene when co-delivered with the 35S promoter-driven pthA4AT, indicating that the PthA4AT-mediating transcription observed for the Cs4 promoter is EBE-dependent.

HR development is mediated by PthA4AT-dependent transcriptional activation

The PthA4AT protein presents an activation domain (AD) in its C-terminal region, identical to the one in AvrBs3 protein from Xanthomonas campestris pv. vesicatoria (Szurék et al., 2001). To
ascertain the relevance of transcriptional activation on the PthA4AT-mediated defence response, a PthA4AT deletion construct without the 27 amino acids marked in Szurek et al. (2001) as AD was generated (ΔADAT). The expression of ΔADAT was unable to prevent canker development by X. citri wild-type strains (Figs 6a and S9), suggesting that this activation domain is necessary for triggering an HR. Interestingly, the expression of ΔADAT in ΔpthA4-X. citri 306 strain showed a delay in the manifestation of HR after C. limon leaves inoculation, as assessed by conductivity assays. As shown in Fig. 6b, a significant reduction in electrolyte leakage was observed at 48 h after inoculation with ΔADAT-expressing ΔpthA4 as compared with inoculation with ΔpthA4 strain expressing the full-length pthA4AT gene. As for the control, no cell death was observed after ΔpthA4 inoculation. To establish whether the action of PthA4 as a virulence factor is similarly dependent on the activation domain, a deletion derivative of the X. citri 306 pthA4 lacking the 27 amino acids of the activation domain (ΔAD) was generated and transformed into ΔpthA4 mutant of X. citri 306. Interestingly, canker development was delayed after infection with ΔpthA4-expressing ΔAD as compared with that containing the full-length pthA4 gene, as shown in Fig. 6c. Taken together, these results suggest that the deletion of AD in both pthA4 and pthA4AT genes reduces, but does not completely abolish, gene activation, suggesting that HR development is mediated by PthA4AT-dependent transcriptional activation, as a canonical TAL effector, presumably of an unknown executor R gene.

**PthA4AT triggers hypersensitive response on non-host Nicotiana benthamiana**

To study the effect of the expression of PthA4AT on the activation of HR in non-host plants, the TAL effector was analysed via Agrobacterium-mediated transient expression in leaves of Arabidopsis thaliana, Solanum tuberosum and N. benthamiana, and plant reactions were scored over a 5-day period. As shown in Fig. 7a, PhA4AT was able to trigger a macroscopic cell death only on N. benthamiana leaves, suggesting that PthA4AT induces an HR in this non-host plant. To determine if this response required the C-terminal domains of the protein, transient expression of PthA4AT derivatives (∆NLS AT, mutNLS AT, ∆NLS AT-SV40, ∆ADAT) was assessed. Similar to citrus, ∆NLSAT and mutNLSAT constructs did not develop a visible HR and ∆NLSAT-SV40 partially restored the cell death response (Fig. 7b). This suggests that, as with citrus, PthA4AT action in N. benthamiana requires localization to the nuclei. Moreover, the full HR manifestation required the presence of a functional AD (Fig. 7b), suggesting that in this non-host plant PthA4AT is acting as a canonical TAL effector.

**DISCUSSION**

Surveys of the size of TALEs in nature indicate that the great majority of them contain a mean of 18.5 RVDs, indicating that this length has been selected by evolution to achieve high target specificity (Boch and Bonas, 2010; Rinaldi et al., 2017). The presence of very short TALEs in some bacterial strains has been documented, as exemplified by the 1.5-repeat AvrXa3 of Xanthomonas oryzae pv. oryzae (Xoo) (Wu et al., 2006), but they are likely non-functional for transcriptional activation (Boch et al., 2009). These short TALEs are probably by-products of the complex sequence rearrangement that shapes the TALomes of the different strains (Denancé et al., 2018). For TALEs containing 6.5 to 9.5 RVDs, transcriptional activation is still possible, although it is much weaker than for longer RVDs (Boch et al., 2009). This raises the question of whether these
intermediate-length TALEs are biologically functional or not, given that their shorter length will translate into an increased number of potential targets, which in addition will presumably not be highly expressed (Richter et al., 2016). Tn5-based mutagenesis in Xoo generated a mutant with an insertion in a gene encoding a TALE with 8.5 RVDs; the mutation conferred increased avirulence to rice cultivars carrying the Xa3 R gene (Li et al., 2004). However, the effect was maintained in a second mutant expressing a 124 amino acid open reading frame containing only the NLS and the C-terminal activation domains. These results suggested that the effect was not dependent on the RVD, but rather on the recognition of the C-terminal part of the protein by Xa3, in a similar way to Bs4 and Xo1 R proteins in pepper and rice, respectively (Schornack et al., 2004; Triplett et al., 2016). In the current study, the evidence suggests that the avirulence of PthA4AT on C. limon and C. sinensis is dependent upon the protein entering the nucleus activating transcription of an executor R gene. As was demonstrated, nuclear localization and transcriptional activation are necessary for triggering a proper HR (Figs 3 and 6). To our knowledge, this is the first case where a ‘short’ 7.5-repeat TALE exerts a biological function via the RVD and transcriptional activation, i.e. in the manner of a classical TALE.

The C-terminal region of all members of the PthA/AvrBs3 family contains an acidic amino acid domain, a property typical of eukaryotic acidic transcription AD. This motif is required for avirulence activity of the AvrXa10 protein in rice (Zhu et al., 1998, 1999) and of the AvrBs3 protein in pepper (Szurek et al., 2001). When the same 27 amino acids critical for avirulence of AvrBs3 were removed from PthA4AT (to give the ΔADAT derivative), its ability to restrict canker development was lost, indicating the importance of this activation domain for PthA4AT avirulence (Fig. 6b). However, when ΔADAT is expressed into the ΔpthA4 mutant strain, an HR is still developed, although it is retarded, suggesting that the deletion in the activation domain did not completely abolish gene activation. Interestingly, similar results were obtained in the non-host N. benthamiana (Fig. 7b). Although activation domains are characterized by the
presence of acidic amino acids, acidity is not the sole characteristic of an activating region and the net negative charge does not strictly correlate with the efficiency (Gill et al., 1990). Powerful artificially generated transcriptional activation domain completely devoid of acidic residues has been generated (Lu et al., 2000). It is thought that the role of these domains is merely to stick to the transcriptional machinery and thereby to recruit it to DNA (Ptashne and Gann, 1997; Yuan et al., 2016). There are data from other TALEs with nearly identical C-terminal regions that support our results. In AvrBs3, the deletion of the 27 amino acids AD does not avoid transcriptional activation in yeast (Szurek et al., 2001) and similar results were observed for the AvrXa10 protein of Xoo (Zhu et al., 1998). Moreover, only 50% reduction in transcriptional activity was observed when the 28 amino acids immediately upstream of the NLS and AD domain of X. campestris pv. armoraciae Hax3 protein were truncated (Zhang et al., 2011). In these three truncated-AD TALEs, and in ∆AD pthAs as well (Fig. 6), this stretch still contains 21% of acidic amino acids that could make the protein stick to the transcriptional machinery.

The C-terminal portion of PthA also encodes three NLS that are critical for localization to the host cell nucleus (Yang and Gabriel, 1995). It was demonstrated that PthA4 TALE targeted to the nucleus by interaction with different host nuclear factors (Domingues et al., 2010; Soprano et al., 2013; de Souza et al., 2012). Using a dominant-negative strategy, Yang et al. (2011) generated transgenic C. sinensis resistant to canker by overexpressing the NLS of PthA4, this NLS playing an importin-binding interference role. It could be argued that the mechanism by which PthA4AT exerts its role in pathogenic X. citri strains is similar, and that ∆NLSAT and mutNLSAT derivatives lost their ability to generate the HR only because they cannot interfere anymore...
with the host importins. However, this is unlikely, as expression of PthA1AT (with identical NLS region) on X. citri strains does not influence canker development after infection of C. limon, and PthA1AT expression on the ΔpthA1,4 or ΔpthA1 mutants did not cause HR (Fig. 2). All this evidence suggests that canker protection caused by PthA4AT goes via a different mechanism, presumably via the activation of an R executor gene. Until now, only five of those genes have been identified (Zhang et al., 2015). They trigger host responses associated with HR, similarly to classical R genes like receptor-like-kinases (RLK) and nucleotide binding site-leucine-rich repeat (NBS-LRR) genes, but if the resistance pathways triggered by the TALE-mediated executor R genes intersect with those of the other R genes remain unknown. Agrobacterium-mediated delivery of a 35S promoter-driven executor Bs3 coding-region did not cause a visible HR in citrus (Shantharaj et al., 2017). The functionality of the other known executor R proteins in citrus is unknown. We could not find homologous to the known executor R genes on the TALgetter predicted PthA4AT target genes list (Table S3). This would suggest a different mechanism for PthA4AT-induced HR activation in citrus.

X. citri A can still develop canker lesions without the presence of the pthA4 virulence gene in C. clementina and X. aurantifolia (Chiesa et al., 2013). This indicates that the absence of canker in X. citri A-infected C. limon is not solely an effect of the absence of the pthA4 gene. In support of this contention, reintroduction of the pthA4 virulence gene into X. citri A does not restore canker development in C. limon. Finally, the host specificity observed for X. citri A weakens the hypothesis that PthA4AT could be acting indiscriminately over many gene targets, generating a cytotoxic effect by the serendipitous activation of some or many of them, leading to metabolic perturbation as suggested by Reyon et al. (2012). This is unlikely, as predictions by TALgetter indicate that the number of potential targets for such a short TALE is huge not only in C. sinensis, where the HR is observed, but also in the susceptible C. clementine; many of the targets are coincident (Tables S3 and S4). As expected, we could determine that not all the potential targets will be activated by PthA4AT (Hummel et al., 2012; Pereira et al., 2014). In fact, we could obtain transcriptional activation in only one out of the five promoters tested (Fig. 5b). This confirms that PthA4AT-dependent transcriptional activation is possible, but suggests a gene (or genes)-specific activation preference that requires a more thorough approach to decipher. The generation of artificial PthA4AT derivatives, using combinatorial cloning (Geißler et al., 2011) coupled with pathogenicity tests on C. limon and non-host N. benthamiana, could help to define PthA4AT specificity and thereafter to narrow down the number of targets in the search for those triggering the defence response. Transcriptome profiling using X. citri strains containing the different derivatives of PthA4AT generated in this study will support the criterion for the identification of the R genes (Boch et al., 2014; Strauss et al., 2012). Given the short length of PthA4AT, a specific pattern of activation across multiple targets, as proposed for the 18-repeat Tal2a gene that elicits HR in rice (Hummel et al., 2017), is plausible.

Any selective advantage was found for X. citri A in any of the hosts assayed (Chiesa et al., 2013). The existence of the pthA4AT gene is perhaps just an accident, a by-product of a recombination event in the course of effector evolution. Interestingly, Ye and colleagues (2013) showed that two further strains of X. citri (029-2 and 049) with attenuated virulence and reduced bacterial growth in planta were characterized by the absence of the 3.4-kb band characteristic of the pthA44 gene, and by the appearance of a smaller band of around 2.4 kb, in a similar way to X. citri A (Fig. 1). It would be interesting to isolate and sequence those genes, and test if they also can confer avirulence on citrus hosts. Recently, Pacbio sequencing of X. citri strains also revealed a 6.5-repeat pthA1 variant in the LM180 strain, obtained from infected grapefruit samples (Göchez et al., 2018), but the biological relevance of this TALE gene is unknown. The discovery of a TALE conferring canker resistant in C. limon and C. sinensis paves the way to identify citrus R genes involved in this important aspect of citriculture.

**EXPERIMENTAL PROCEDURES**

**Bacterial strains growth conditions, plant material and inoculation assays**

The strains and plasmids used in this study are listed in Tables S1 and S2, respectively. X. citri strains were cultured at 28 °C with shaking in peptone yeast and malt extract (PYM) medium (Cadmus et al., 1976). Escherichia coli strains DH5α and BL21 and Agrobacterium tumefaciens GV3101 were grown in Luria-Bertani (LB) medium at 37 °C and 28 °C, respectively. Recombinants plasmids were introduced into the X. citri and Agrobacterium strains by electroporation (Roesschlin et al., 2017). When required, the antibiotics ampicillin (100 µg/mL), kanamycin (50 µg/mL), rifampicin (50 µg/mL) or spectinomycin (100 µg/mL) were added to the growth media.

‘Eureka’ lemon (C. limon (L.) Burm. f.) grafted onto Troyer citrange, ‘Valencia Late’ sweet orange (C. sinensis (L.) Osbeck) grafted onto citrange Carrizo, Arabidopsis thaliana ecotype Col-0, Solanum tuberosum ‘Spunta’ and N. benthamiana plants were grown under controlled conditions in a growth chamber with a temperature of 25–27 °C and photoperiod of 16 h light/8 h dark. For pathogenicity assays on Citrus spp., new shoots were selected according to Roesschlin et al. (2017). Bacterial suspensions of 10^7 or 10^8 colony-forming units (cfu) per milliliter were prepared in 10 mM MgCl2 and inoculated by infiltration or cotton swab onto 20-day-old leaves of the new shoots, respectively. The plants were maintained for 15 days in a growth chamber. Symptoms progression was phenotypically monitored using an
The repeat region of pthA genes was cloned as a BamHI fragment. Cloning and sequencing of TALE genes were conducted as described by Chiesa et al. (2019). For Agrobacterium-mediated transient expression, strains preparation and induction were conducted as described by Enrique et al. (2011).

Southern hybridization analysis

Plasmid DNA from X. citri strains was isolated according to the manufacturer’s instructions (QIAGEN Plasmid Midi Kit; QIAGEN, Mainz, Germany). DNA (10 µg) was digested with EcoRI or BamHI overnight at 37 °C and subjected to electrophoresis on 0.8% agarose gel. DNAs were transferred to Hybond N+ nylon membrane (Amersham International, UK) using standard protocols (Sambrook et al., 1989). The blots were hybridized with a non-radioactive labelled DNA probe (pthA), generated by a polymerase chain reaction (PCR) product, using the primer pairs Jpth1/Jpth2 (Cubero and Graham, 2002). Probe labelling and signal detection were performed according to the manufacturer’s instructions (AlkPhos DIRECT kit, GE Healthcare UK Limited Amersham, Little Chalfont, Buckinghamshire, UK).

Cloning and sequencing of TALE genes

The repeat region of pthA genes was cloned as a BamHI fragment into pUC18 vector (ThermoFisher Scientific, Waltham, MA, USA), screened by PCR with Jpth1/Jpth2 primers and Sanger sequenced (DNA Sequencing Facility, University of Maine, USA). To obtain the 5’ and 3’ terminal regions of PthAs, plasmids from X. citri A1 were sequenced using Roche (454) pyrosequencing technology. Reads were assembled with Newbler v. 2.6 software (Roche 454 Life Sciences, Branford, CT, USA). The final sequence of the two circular plasmids was identical to the reference plasmids (pXAC64 and pXAC33) from X. citri strain 306 (da Silva et al., 2002). PthAs sequences were deposited at GenBank under the accession numbers MK425208, MK425209, MK425210 and MK425211.

To obtain full-length pthA genes, BamHI-fragments were subcloned into pUC57-RR linearized BamHI vector (Data S1) and then cloned into pUC18 vector (ThermoFisher Scientific, Waltham, MA, USA), yielding maltose binding protein (MBP) N-terminal fusions. MBP–pthA4 constructs were transformed into E. coli BL-21 strains and selected with the corresponding antibiotic. Cultures with an optical density at 600 nm of 0.8 were incubated at 37 °C for 15 min with 2 mM betaine monohydrate (Sigma-Aldrich) and then induced for 2 h with 0.5 mM isopropyl β-D-thiogalactopyranoside (Sigma-Aldrich). Expression of MBP-pthA4 was analysed by Coomassie blue staining of standard SDS-PAGE and recombinant protein extracts were obtained from 25 ml of induced cultures. The PBM was performed as described previously (Godoy et al., 2011). Normalization of probe intensities and calculation of E-scores and Z-scores of all the possible 8-mers were carried out with the PBM Analysis Suite. To obtain a single representative motif, we followed the method ‘PWM_align_E’, in which the 9-mer motifs with E-score > 0.45 were aligned and each sequence in the alignment is first weighted by the E-score of the corresponding sequence. Then, the positions present in at least half of the sequences in the alignment were considered, and the resulting alignment is converted to a position frequency matrix with Enologos (http://www.benoslab.pitt.edu/cgi-bin/enologos/enologos.cgi).

TAyletter predictions in Citrus spp. and GUS assay

PthAA7 binding elements were searched in C. sinensis and C. clementina promoterome (400 bp upstream + 200 bp downstream of the transcription start site) by using TAyletter software and considering both strands (http://galaxy2.informatik.uni-halle.de:8976/; Grau et al., 2013; Streubel et al., 2017). The candidate promoters are listed in Tables S3 and S4. Selected promoter regions were amplified from the corresponding genomic DNA using designed primers (Table S5). The promoter fragments were digested with the corresponding restriction enzyme (BamHI or XbaI with Ncol) and fused with uidA (GUS) gene in pCAMBIA1303 expression vector. Positive clones were analysed by PCR amplification and DNA sequencing, and transformed into A. tumefaciens GV3101. EBE-mutated Cs4 promoter was generated by overlapping PCR using primers incorporating mutations in the EBE site (Table S5).
For GUS expression in *N. benthamiana* leaves, two *Agrobacterium* suspensions were mixed in a ratio of 1:1. Forty-eight hours post-infiltration, leaf disks were stained on GUS staining buffer (50 mM NaPO$_4$ (pH 7.0), 0.1% Triton X-100, 10 mM EDTA, 1 mM K$_2$Fe(CN)$_6$, 1 mM K$_4$Fe(CN)$_6$, 0.5 mg/mL X-gluc) and incubated at 37 °C for 3 h. Then, the disks were cleared in ethanol and photographed.

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**ACCESSION NUMBERS**

MK425208, MK425209, MK425210 and MK425211.

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**SUPPORTING INFORMATION**

Additional supporting information may be found in the online version of this article at the publisher’s web site:

**Fig. S1** Alignment of PthA1 from *X. citri* A and *X. citri* 306.

**Fig. S2** Alignment of PthA4 from *X. citri* A and *X. citri* 306.

**Fig. S3** Western-blot analysis of PthA expression on *X. citri* strains.

**Fig. S4** Macrosopic symptoms developed by *X. citri* A and *X. citri* 306 PthA4 mutant expressing pthA4.

**Fig. S5** Phenotypic response of PthA1A and PthA4A expressed in Argentinian *X. citri* T strain in *Citrus limon* leaves.

**Fig. S6** Mutations in the PthA4AT C-terminal region.

**Fig. S7** Phenotypic response of *X. citri* 306 strain expressing mutant version in nuclear localization of PthA4AT.

**Fig. S8** PthA4AT triggers host defense response in *Citrus sinensis* leaves.

**Fig. S9** Phenotypic response on *C. limon* leaves inoculated with *X. citri* T transformed with ∆AD AT.

**Table S1.** Bacterial strains.

**Table S2.** Plasmids used in this study.

**Table S3.** TALgetter results of candidate promoters to PthA4AT on *C. clementina*.

**Table S4.** TALgetter results of candidate promoters to PthA4AT on *C. sinensis*.

**Table S5.** List of oligonucleotide primers used in this study.

**Table S6.** List of motifs variants obtained with PBM11 protein-binding microarrays for PthA4AT.

**Data S1.** Design sequences for synthesis and cloning of the full-length of pthAs and mutant construction.